SNARK14: A PROGRAMMING SYSTEM FOR THE RECONSTRUCTION OF 2D IMAGES FROM 1D PROJECTIONS

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Chapter 1

INTRODUCTION

“Just the place for a Snark!” the Bellman cried,
As he landed his crew with care;
Supporting each man on the top of the tide
By a finger entwined in his hair.

“Just the place for a Snark! I have said it twice:
That alone should encourage the crew.
Just the place for a Snark! I have said it thrice:
What I tell you three times is true.”

Fit the First - The Landing
The Hunting of the Snark (an agony in eight fits)
by Lewis Carroll

In the area of image reconstruction, researchers often desire to compare two or more reconstruction techniques and assess their relative merits. SNARK14 provides a uniform framework in which the algorithms are implemented and their performance is evaluated. SNARK14 has been designed to treat both parallel and divergent projection geometries and can create test data for use by reconstruction algorithms. A number of frequently-used reconstruction algorithms are incorporated.

SNARK14 has been designed to be usable in many application areas and to be transportable to a wide variety of computers, in places at the expense of efficiency. (For example, SNARK14, as it is now distributed in a VirtualBox version -see, Subsection 1.2.1- will most likely run slightly slower than if it were installed specifically for a host system, but it will return the same outputs irrespective of the host computer, be it a pc, or a mac, or whatever.) While SNARK14 can be used to reconstruct repeatedly from data collected by a particular device, it is likely that one can design a more efficient special purpose program just for that device.

This manual of SNARK14 is written for the practitioner in the field of reconstruction. The novice will find it necessary to get acquainted first with one of the many tutorial works in the field, such as [29] or [48].

1.1 Statement of purpose and history

The reconstruction problem has arisen in a large number of scientific fields (including electron microscopy, radiology, radio astronomy and holography) and many different methods (algorithms) have been suggested
for its solution. The reader is referred to [29] for a survey of such algorithms and to [26, 44] for discussions on some of the application areas.

SNARK14 is a programming system designed to help researchers interested in developing and evaluating reconstruction algorithms. It is a descendant of earlier releases of SNARK, the first one of which was written by Richard Gordon in 1970.

SNARK77 [42] and SNARK89 [37] followed the original SNARK and were specifically designed to help with the problem of reconstructing cross-sections of the x-ray absorption coefficient distribution inside the body from x-ray projections. SNARK93 [10] extended this capability to include positron emission tomography, PET (where the problem is that of reconstructing cross-sections of isotope concentrations inside the body from γ-ray projections). A related programming system, specifically designed for emission studies, is RECLBL produced by Huesman et al. [45]. More recent relevant software packages are briefly surveyed in [48, Section 1.2].

The SNARK93 programming system was implemented in FORTRAN77. It was designed to

1. be capable of dealing with many modes of data collection (different geometrical arrangements of x-ray source and detectors, different x-ray spectra, etc.);
2. contain many of the published reconstruction algorithms;
3. be capable of generating mathematically described phantoms that realistically represent various cross-sections of the human body, together with mathematically simulated projection data of these cross-sections reflecting the characteristics (including noise) of various possible tomography devices;
4. contain subroutines to carry out work which appears to be common to many reconstruction algorithms, so as to ease the incorporation of additional (user-defined) algorithms;
5. be capable of a variety of display modes;
6. contain routines for the statistical evaluation of reconstruction algorithms;
7. provide a methodology for testing for statistically significant differences between reconstruction algorithms.

The successor of SNARK93 was SNARK05. The following were the major advances that were incorporated into the SNARK05 package:

1. SNARK05 was implemented in C++;
2. the file structures for holding projection data, phantoms and reconstructions had been redesigned to match the capabilities of the typical computer environment at the beginning of the third millennium (specifically, XML headers are used in data files);
3. all iterative algorithms were capable of handling image representations that use “blobs” [54, 56], as well as those that use “pixels”;
4. the efficient data access ordering proposed in [38] was a standard feature of SNARK05;
5. all artificial restrictions on sizes were removed - the only remaining restrictions were those imposed by the hardware, compiler and operating system.

SNARK09 is an updated version of SNARK05. The following are the major advances that are incorporated into the SNARK09 package:

1. capability of generating mathematically described phantoms that include inhomogeneity;
2. capability of applying beam hardening correction to polychromatic x-ray projection data;
3. inclusion of the imagewise-region-of-interest figure of merit (FOM) [59];
4. handles up to 10 user-implemented algorithms, at most five using blobs;
5. the user can implement up to five user-defined FOMs.

SNARK14 is an updated version of SNARK09 and includes the following major updates:

1. inclusion of the superiorization methodology described in [21], see Section 5.10;
2. new stopping criteria: MLEM-STOP, Kullback-Leibler distance, residual, weighted squared distance, see Section 5.9;
3. new FOMs for SNARK EXPERIMENTER: Kullback-Leibler distance and weighted squared distance, see Subsections 8.2.6.5 and 8.2.6.6;
4. addition of the SART algorithm, see Section 7.7.

In addition to changes to the ability of the software package (as enumerated above), a major change has been made to its transportability. While SNARK09 was designed to run as a Linux/Unix program, the complete SNARK14 can be downloaded as an independent package onto any computer system that has a VirtualBox capability. This makes SNARK14 essentially universally available. The next section is devoted to describing how SNARK14 can be installed on just about any current computer system.

1.2 Installation of SNARK14

1.2.1 Downloading instructions

Instructions for acquiring SNARK14 can be found at

http://turing.iimas.unam.mx/SNARK14M/

This distribution includes the complete source code for SNARK14.

We are distributing a VirtualBox version of SNARK14. To download the VirtualBox platform package that is appropriate for your operating system, go to

https://www.virtualbox.org/wiki/Downloads

To use SNARK14, you need to download and save the file CentOSwithsnark.zip. You can initiate this process by visiting

http://turing.iimas.unam.mx/SNARK14M/CentOSwithsnark.zip (Location 1 - North America)
http://snark.cappatec.com/CentOSwithsnark.zip (Location 2 - Europe)

After you downloaded the zip file, you need to unzip it. (Note that some unzipping tools may not be compatible with the provided zip file; in case of problems, a different tool should be used for the extraction.) After this you should have in the directory in which you unzipped CentOSwithsnark.zip access to two additional files: CentOS.vmdk and CentOS.vbox.

Clicking on CentOS.vbox should result in generating a Virtual Machine named CentOS+SNARK14.

You should now initiate this (for example, by clicking on its name in the Oracle VM VirtualBox Manager). After this you may receive some warning/error message that should be ignored (for example, by clicking on OK whenever that option is available). The same instruction is valid regarding warning/error messages that occur as a result of doing steps that are recommended below in this section.

This should result in a window (we refer to it below as the virtual machine) with a header such as:

CentOS+SNARK14(Running)-Oracle VM VirtualBox.
The window was configured to occupy a large region of the screen; however, you may wish to adjust the size of the display panel in the virtual machine by clicking on System, Preferences, Display and selecting a new Resolution.

You should now be able to run SNARK14 (by opening a terminal in the virtual machine and typing snark14 in that terminal) and also its Graphical User Interface utilities (snark14Input and snark14Display); for more details on these, see Sections 1.4.1 and 1.4.2.

1.2.2 Validation of downloaded software

If SNARK14 is correctly installed, then there should be a snark14Examples folder in the Desktop directory. To check that SNARK14 is installed properly, you need to open a terminal in the virtual machine and type the following:

```
cd ~/Desktop/snark14Examples
./run_all
./regression
```

For a proper installation, SNARK14 should report "No differences found" for each of the examples b1 to b11.

1.2.3 Sharing files between the host system and the virtual machine

A directory in the virtual machine can be shared with the host operating system. The method for setting up such a shared directory is as follows.

1. Select “Shared Folders” under the menu Devices of the virtual machine.
2. A window called CentOS+SNARK14 - Settings should pop up with the header Shared Folders.
3. There is an option of “Add Shared Folder” (on some systems this is indicated by a green plus sign) in the above window. Clicking on the icon for that results in the opening of a new window with the header “Add Share.”
4. Now you have to specify the Folder Path and the Folder Name. The Folder Path is that to the to-be-shared directory on the host computer and the Folder Name refers to the name to be assigned to the shared folder in the virtual machine.
5. Also, there are options present for Read-only, Auto-mount, and Make Permanent. We suggest that you enable the options for Auto-Mount and Make Permanent, so that this process need not be repeated every time the VirtualBox is started.
6. Restart the system by rebooting the Virtual Machine. You can do this by executing the `reboot` command in a terminal.
7. Now, to check whether or not the shared directory is created, open the “Computer” directory present on desktop of virtual machine and open “media.” The shared folder must be present in this directory with the name as: sf_name, where name is that of the shared folder specified above in virtual machine.
8. A link of this shared directory can be created on the desktop of virtual machine. This can be done by using a terminal. Open a terminal, and type the following command:

```
ln -s /media/sf_name ~/Desktop/Name
```

Here, Name is the name of the folder that will be created on the desktop of virtual machine that is linked with the shared folder present in media.
1.3 Running SNARK14

If SNARK14 was downloaded according to the instructions provided in Section 1.2.1, a SNARK14 run can be initiated by opening a terminal in the virtual machine, going to a desired directory and typing the following at the command prompt:

```
snark14 input.in >output.out
```

As a result of this, SNARK14 will read the INPUT from the file input.in in the current directory and will save the OUTPUT in the file output.out in the current directory.

If input.in is missing, then SNARK14 will expect the INPUT to be entered as the standard input, which typically means entering the file INPUT in the terminal line-by-line. Each command will be executed line-by-line after it has been completely entered. As soon as the command END is entered, the SNARK14 run will be terminated.

If output.out is missing, then SNARK14 will use the standard output for OUTPUT, which typically means that the output will appear in the terminal.

All other files that will be created during a typical SNARK14 run (such as file11, prjfil, recfil, punch and eval) are saved in the current directory. If a file with the same name already exists in that directory, then it will be overwritten. It is therefore important to note that, if these files are to be saved, either rename them and/or move them into another directory prior to the next SNARK14 run.

1.4 Interactive interfaces

To ease the use of SNARK14, interactive interfaces have been designed for making and running a SNARK14 INPUT file and for observing the results of a SNARK14 run as images and/or as graphs. We now provide pointers to these.

1.4.1 Graphical interface for creating and running a SNARK14 INPUT

This interactive graphical interface, called snark14Input, can be used to produce and/or run an INPUT file for a SNARK14 run. It can be initiated by opening a terminal in the virtual machine, going to a desired directory and typing in the command prompt:

```
snark14Input
```

Alternatively, snark14Input can be initiated by clicking on its icon on the Desktop of the virtual machine.

1.4.2 Graphical interface for displaying the results of a SNARK14 run

This interactive graphical interface, called snark14Display, allows the user to display the results of a SNARK14 run. It can be initiated by opening a terminal in the virtual machine, going to a desired directory and typing in the command prompt:

```
snark14Display
```

snark14Display has two primary functions. One is to read images from prjfil and recfil files and display them as gray-level intensity maps, and plot their row/column profiles. The other is to plot results stored in an eval file.

Alternatively, snark14Display can be initiated by clicking on its icon on the Desktop of the virtual machine.

1.5 Outline

This manual has eight chapters, whose topics are as follows:

1. this introduction;
2. a discussion of the physical meaning of the concepts used in SNARK14;
3. an introduction to the information flow and the files used by SNARK14;
4. a description of the notational and format conventions;

5. a description of the SNARK14 language;

6. a description of the method of implementing user-defined algorithms and the support routines available;

7. a description of the use of the SNARK14 built-in reconstruction algorithms;

8. a description of SNARK experimenter, a facility for testing for statistically significant differences between reconstruction algorithms.

In addition, there are four appendices: the first provides detailed examples of the use of SNARK14, the second provides information on how a user may enter the projection data to be used by the reconstruction algorithms, the third describes the structure of two essential files produced by SNARK14 (one stores the projection data and the other stores a phantom and/or reconstructions), and the fourth describes the location of the source code in the distribution and the usage of utility scripts that are part of the SNARK14 package.

1.6 Acknowledgments

In addition to the authors of this manual, a major contributor to SNARK09 was Joanna Klukowska [48] and a major contributor to the transition from SNARK09 to SNARK14 was Bernhard Prommegger.

SNARK09 was an adaptation from and improvement upon SNARK05 that was a product of the Discrete Imaging and Graphics Group in the Department of Computer Science, The Graduate Center of the City University of New York, written by Bruno Carvalho, Wei Chen, Joel Dubowy, Gabor T. Herman, Mirosław Kalinowski, Hstau Y. Liao, Lajos Rodek, László Ruskó, Stuart W. Rowland and Eilat Vardi-Gonen. In producing SNARK05, we had the help and advice of our colleagues in the Ph.D. Program in Computer Science at the Graduate Center, CUNY, especially Edgar Garduño, Xingjian Li, Roberto Marabini, Deniz Sarioz, and Gary Weng.

SNARK05 was an adaptation from SNARK93 that was a product of the Medical Image Processing Group in the Department of Radiology, University of Pennsylvania, written by Jolyon A. Browne, Gabor T. Herman, and Dewey Odhner. Its production was helped by many coworkers, including Lyle Berkowitz, Alvaro De Pierro, Paul Edholm, Robert M. Lewitt, David Roberts and Jingsheng Zheng.

The previously released SNARK77 (written by Gabor T. Herman and Stuart W. Rowland) and SNARK89 (written by Gabor T. Herman, Robert M. Lewitt, Dewey Odhner, and Stuart W. Rowland) were also products of the Medical Image Processing Group, originally in the Department of Computer Science at the State University of New York at Buffalo and then in the Department of Radiology, University of Pennsylvania. Contributors to their development include Martin Altschuler, Ehud Artzy, Yair Censor, Tao Chang, Paul Eggermont, Gideon Frieder, James Hinds, Julieann Kostyo, Yuan-hern Kuo, A.V. Lakshminarayanan, Arnold Lent, Hsun-kao Liu, Shirley Long, Hsi-ping Lung, Peter Lutz, Roger Peretti, Seshagiri Sadananda, James Turner, Mann-may Yau, and Daniel Yeung.

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There are many packages available for reconstruction from projections, some of them are briefly surveyed in Section 1.2 of [48]. Here we single out for mention jSNARK [1] that incorporates a large subset of the capabilities of SNARK14 for reconstructing 2D objects from their 1D projections, but it also extends those capabilities to reconstructing 3D objects from their 2D projections. It is written in Java allowing for greater platform flexibility and for user-defined routines written as plugins.
Chapter 2

THE SNARK14 FRAMEWORK

This chapter is written to acquaint the user with the physical meaning of the concepts used in SNARK14.

2.1 Units and constants in SNARK14

SNARK14 deals with physically measurable quantities, such as the distance between the x-ray source and detector or the linear attenuation (per unit length) at a point inside an object. The actual values assigned to these quantities are dependent on the assumed unit of length. While the unit of length does not have to be specified for SNARK14 (in fact, there is no facility for its specification) consistency must be maintained throughout a single SNARK14 run.

In particular, we shall assume a fixed two-dimensional coordinate system. The point \( (x, y) \) in this system represents the physical location whose abscissa is \( x \) and ordinate is \( y \), as measured in the assumed unit of length.

There are two particular constants, called ZERO and INFIN, which are defined by SNARK14 and whose meanings need to be clearly understood (especially since their names are potentially misleading). ZERO is a very small positive floating point number (\( 10^{-20} \) to be exact) and INFIN is a very large positive floating point number (\( 10^{20} \) to be exact). These values are referred to below (e.g., SNARK14 requires that some input items must have a value greater than ZERO, rather than just be positive). Also, they are available to those users who wish to create their own routines; they can, in particular, be used for checking for underflow and overflow conditions. Other constants that are available to the user of SNARK14 to a high accuracy by referring to them by their names are PI (\( \pi \)), TWOP (\( 2\pi \)), PISQ (\( \pi^2 \)), PID2 (\( \pi/2 \)), SQRT3 (\( \sqrt{3} \)) and ISQRT3 (\( 1/\sqrt{3} \)). The actual naming of these constants in user-written code is explained in Subsection 6.3.2.

2.2 Pictures and digitization

SNARK14 deals with “pictures” defined over the 2D plane of points \( (x, y) \) in some assumed fixed coordinate system. To be exact, a picture has two components:

1. the picture region, which is a square whose center is at the origin of the coordinate system and whose sides are parallel to its axes;

2. a function of two variables whose value is zero outside the picture region.

Sometimes, when this is not confusing, we shall call the function as the “picture.” However, identical functions may give rise to different pictures if the picture regions are different.

We shall often refer to the value \( f(x, y) \) of the picture \( f \) at the point \( (x, y) \) as the density of \( f \) at \( (x, y) \). Within SNARK14, \( f(x, y) \) is often specified by a grid \( G \) (which is a finite set \( \{(g_1, h_1), \ldots, (g_J, h_J)\} \) of points in the plane), a basic basis function \( b \) (which is just a function of two variables), and a coefficient \( c_j \) associated with each grid point \( (g_j, h_j) \) as follows. For \( 1 \leq j \leq J \), each of the functions

\[ b_j(x, y) = b(x - g_j, y - h_j) \]  

(2.1)
is called a basis function and $f$ is defined by

$$f(x, y) = \sum_{j=1}^{J} c_j b_j(x, y); \quad (2.2)$$

i.e., as an expansion into the basis functions $b_j$ with coefficients $c_j$. SNARK14 allows the use of two different kinds of basis functions: pixels and blobs, each with its own type of grid.

The exact definition of a pixel basis function depends on a variable called PIXSIZ that is specified by the input to SNARK14. (How PIXSIZ, and many other variables, are specified by the input is explained in Section 5.3.) The basic pixel basis function is then defined to have the value 1 at points strictly inside the square that is centered at the origin and that has edges of length PIXSIZ parallel to the coordinate axes, and to have the value 0 at points strictly outside this square. (While this does not make any difference in any possible application of SNARK14, for completeness we can define the basic pixel basis function to have the value 0.5 on the edges and the value 0.25 at the corners of the square.) The associated grid $G$ is defined, by an additional input-specified variable called NELEM (which is restricted to be an odd positive integer), to be the set

$$\{(m \times \text{PIXSIZ}, n \times \text{PIXSIZ}) \mid m \text{ and } n \text{ integers, } \max\{|m|, |n|\} \leq \text{NELEM}/2\}, \quad (2.3)$$

where $|\cdot|$ denotes the absolute value. This approach subdivides the picture region into $\text{NELEM}^2$ equal squares. Each of these smaller squares is called a pixel (short for picture element). In the interior of a pixel, the density of the function, as defined by (2.2), is uniform. An arbitrary picture can be approximated by such an expansion by simply assigning to each $c_j$ the average density of the picture in the corresponding pixel; such an approximation is referred to as the $\text{NELEM}^2$ digitization of the picture. In SNARK14, the picture region (which is sometimes referred to as the reconstruction region) is determined by the program (based on the input-specified variables PIXSIZ and NELEM) as the square whose corners have coordinates $(c, c)$, $(-c, c)$, $(-c, -c)$, $(c, -c)$, where

$$c = \frac{\text{PIXSIZ} \times \text{NELEM}}{2}. \quad (2.4)$$

A blob basis function also depends on some input-specified variables. A basic blob basis function is a generalization of a well-known class of window functions in digital signal processing called Kaiser-Bessel [54]; it is circularly symmetric, has nonzero values only in a circular disk around the origin, and smoothly decreases from a positive value at the origin to zero at the edge of the disk. The exact definition depends on three input-specified variables (SUPPORT and DELTA that have to be greater than ZERO, and SHAPE that has to be nonnegative) as follows:

$$b(x, y) = \begin{cases} C \times I_2(\text{SHAPE} \times \sqrt{1 - r^2}) \times (1 - r^2), & \text{if } 0 \leq r \leq 1, \\ 0, & \text{otherwise,} \end{cases} \quad (2.5)$$

where $I_i$ denotes the so-called modified Bessel function of the first kind of order $i$, $r = \sqrt{x^2 + y^2}$ and

$$C = \frac{\sqrt{3} \times \text{DELTA}^2 \times \text{SHAPE}}{4 \times \pi \times \text{SUPPORT} \times I_2(\text{SHAPE})}.$$ 

The grid $G$ that determines the blob basis functions using (2.1) is hexagonal [28]; it is defined as the set of all those points in the set

$$\left\{ (m/2 \times \text{DELTA}, \sqrt{3}n/2 \times \text{DELTA}) \mid m \text{ and } n \text{ integers and } m + n \text{ even} \right\} \quad (2.6)$$

that are also inside the reconstruction region specified by (2.4).

It is not unusual that one desires to reconstruct only part of a picture. This can be achieved in SNARK14 by specifying a reconstruction region which is smaller than the region of the picture from which data have been collected. Some reconstruction methods can handle such a situation, others will give erroneous results. It is the user’s responsibility to choose the correct reconstruction algorithm.
2.3 Rays and ray sums

There are two kinds of rays in SNARK14:

1. a LINE ray, which is a straight line, and
2. a STRIP ray, which is a region of the plane between a pair of parallel straight lines.

Given a picture and a ray, the real ray sum is the integral of the picture along the ray. (This may be a line integral or a strip integral.) In this terminology, the reconstruction problem that is treated by SNARK14 may roughly be stated as follows: given approximations (based on physical measurements) of the real ray sums of a picture for a number of rays, estimate the NELEM\textsuperscript{2} digitization of the picture.

SNARK14 also deals with pseudo ray sums; these are defined only for expansions of the form (2.2). In the LINE case, the pseudo ray sum is the real ray sum of the picture defined by the function $f$ of (2.2) and a picture region large enough to contain all points at which the value of $f$ is not zero. (Since $G$ is finite, it is always possible to find such a picture region.) In the STRIP case, the pseudo ray sum is defined as

$$\left(\sum_{j \in S} c_j \right) \times \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} b(x, y) dx dy,$$

where $S$ contains exactly those $j$ ($1 \leq j \leq J$) for which $(g_j, h_j)$ is in the strip. Note that the integral in the above equation depends only on the basic basis function; it is PIXSIZ\textsuperscript{2} in the pixel case.

2.4 Geometry of data collection

SNARK14 is not capable of handling an arbitrary arrangement of rays, but it can handle a number of arrangements of rays that are typical of what one might come across in practice.

First of all, the set of all rays along which data are collected is divided into a number of subsets, called projections, each one of which contains the same number of rays. (PRJNUM denotes the number of projections and USRAYS denotes the number of rays along which data have been collected in any one projection. In SNARK14, USRAYS must be an odd number.) There are two basically different modes of data collection: DIVERGENT and PARALLEL.

In DIVERGENT geometry (Figure 2.1), a projection consists of a set of LINE rays that go through a common point (the source position). In all the projections, the source is at a fixed distance (RADIUS) from the origin. The angle between the line from origin to source and the $x$-axis (marked THETA in Figure 2.1) is called the projection angle. The rays in one projection connect the source to points (detectors) which lie either on an arc of a circle whose center is at the source or on a straight line. In either case, one of the detectors (marked $C$ in Figure 2.1) lies on the line connecting the source to the origin, at a distance STOD from the source. The other detectors are spaced symmetrically at equal intervals on the two sides of $C$, either on the ARC whose center is the source or on the TANGENT line to this ARC at $C$. The spacing between detectors (the length of the ARC or that of the TANGENT line between two neighboring detectors) is denoted by PINC (specified, as usual, by the input to SNARK14).

In PARALLEL geometry (Figure 2.2), a projection consists of a set of parallel LINE or STRIP rays. The angle these rays make with the $x$-axis (denoted by THETA in Figure 2.2) is called the projection angle. If we consider the LINE case, one of the rays goes through the origin and if the STRIP case is considered, the origin is equidistant to the two lines bounding one of the strips. The other rays are spaced symmetrically at equal intervals on the two sides of this ray. In the STRIP case, the rays are abutting. Let $d$ denote the distance between the rays in the LINE case or the width of the rays in the STRIP case; it is determined as follows. The input specifies the variable PINC and also whether the ray spacing is to be UNIFORM or VARIABLE. In the UNIFORM case, $d = PINC$, for all projections. In the VARIABLE case it depends on the projection angle THETA: $d = PINC \times \max\{|\sin\text{THETA}|, |\cos\text{THETA}|\}$. (A consequence of this definition is that the distance between two consecutive intercepts with either the $x$- or the $y$-axis will be PINC.)
2.5 Number of rays in a projection

As has been discussed in the last section, in SNARK14 the variable USRAYS denotes the number of rays along which data have been collected in any one projection. Since the value of USRAYS and the values of NELEM and PIXSIZ (see Section 2.2) are independently defined, it is possible that many of the rays along which data have been collected miss the reconstruction region, or that only a small part of the reconstruction region is covered by the rays along which data have been collected. We introduce the variable SNRAYS to denote the minimum number of rays needed to cover the reconstruction region in all projections. SNRAYS is calculated by SNARK14 based on the input-supplied values of NELEM, PIXSIZ, PINC, etc., according to the following method.

Let $D$ be the distance along the detector strip between the center point of the detector strip (marked $C$ in Figures 2.1 and 2.2) and the points on the detector strip where the tangents from the source to the smallest circle that contains the reconstruction region meet the detector strip (marked $A$ in Figures 2.1 and 2.2). Let $e$ be PINC, except in the PARALLEL VARIABLE case in which $e = \text{PINC}/\sqrt{2}$. Let $\lceil x \rceil$ denote the smallest integer that is not smaller than the real number $x$. Then $\text{SNRAYS} = 2 \times \lceil \frac{D}{e} \rceil + 1$.

Just like USRAYS, SNRAYS is an odd integer. Either of these two variables may have a value greater than the other: we use the variable NRAYS to denote their maximum.

In SNARK14 reconstructions the rays are referred to by a double index (NP, NR) where $0 \leq \text{NP} < \text{PRJNUM}$ and $0 \leq \text{NR} < \text{NRAYS}$. The value of NP is the projection number, it is determined by the order
in which the projection angles have been specified. (There is no restriction on the projection angles having
to be specified in increasing, decreasing or any other order.) The value of NR is the ray number. The rays
are assumed to be numbered clockwise on the detector strip relative to the origin (see Figures 2.1 and 2.2).
The ray numbered \((\text{NRAYS}−1)/2\) goes through the origin.

If USRAYS < SNRAYS = NRAYS, then SNARK14 assumes that the value of the real ray sum for a ray
along which data have not been collected is zero. In order to give the user the ability to access only the
central USRAYS or SNRAYS, SNARK14 evaluates four further variables: FUSRAY, LUSRAY, FSNRAY
and LSNRAY, defined as follows:

\[
FUSRAY = \frac{\text{NRAYS} − \text{USRAYS}}{2}, \tag{2.8}
\]

\[
LUSRAY = \frac{\text{NRAYS} + \text{USRAYS}}{2} − 1, \tag{2.9}
\]

\[
FSNRAY = \frac{\text{NRAYS} − \text{SNRAYS}}{2}, \tag{2.10}
\]

\[
LSNRAY = \frac{\text{NRAYS} + \text{SNRAYS}}{2} − 1. \tag{2.11}
\]
2.6 SNARK14 input/output

The following summarizes the input requirements of SNARK14 that we have discussed and some additional input and output possibilities. An exhaustive description is given in the following chapters.

Typical inputs to SNARK14:

- Geometry information
  - Number of elements in a row or column of the pixel grid (NELEM)
  - Pixel size (PIXSIZ)
  - Detector spacing (PINC)
  - PARALLEL or DIVERGENT geometry
    - If PARALLEL, then the input also specifies STRIP or LINE integrals, number of projections (PRJNUM), and UNIFORM or VARIABLE detector spacing
    - If DIVERGENT, then the input also specifies TANGENT or ARC, source-to-origin distance (RADIUS) and source-to-detector distance (STOD)
  - Environment for data collection: e.g., noise (quantum, scatter, etc.)
  - Number of projections (PRJNUM)
  - List of projection angles

- Test picture (optional)
  - This is either taken from a previous SNARK14 run or is specified by a description in terms of geometrical figures

- Projection data
  - Gathered experimentally or generated by SNARK14 (from a test picture)

Typical outputs from SNARK14:

- Comparison of reconstructions with the test picture with respect to average density, relative error, variance, standard deviation, and residual
- A file containing decimal values of the test picture, if present, and selected reconstructions
- A comparison of the exact values of a test picture and a reconstruction for every row of the object in selected columns
- The CPU time used for each command and each iteration of an algorithm

The following chapters describe in detail the required structure of the input/output commands, their associated interpretation and expected results. The reader is also referred to Appendix A, where examples of input files and the corresponding outputs are presented.
Chapter 3

SNARK14 INFORMATION FLOW AND FILES

A SNARK14 run consists of up to three phases:

1. data generation phase;
2. initialization and reconstruction phase;
3. analysis phase.

Each of these phases requires some input files and produces some output files. Some of the output files are used as the input files of a later (or even the same) phase. Provided that the appropriate input files are available, a single SNARK14 run may consist of just one of the three phases, or either of two consecutive phases, or all three phases.

We now proceed with a description of each of the three phases together with the input files required and output files produced by the respective phases. The reader should consult Figure 3.1 for an overview. The following file descriptions are rather brief. With the exception of the INPUT file, all files are written (and subsequently accessed) by SNARK14, and the user need to be concerned only with their formats if involved in the process of extending the capabilities of SNARK14 by additional code.

Warning: The SNARK14 manual refers to files named INPUT and OUTPUT. (These names, as many other names in the manual, are for descriptive purposes only. Within the code these files are referred to by names that are more appropriate for the C++ programming language in which the SNARK14 program is written.) The three files referred to in Figure 3.1 and elsewhere in the manual as Data Generation Input file, Initialization and Reconstruction Input file, and Analysis Input file are in fact not three separate files, but rather three consecutive parts of the single file INPUT. Similarly, the Data Generation Output file, the Initialization and Reconstruction Output file, and the Analysis Output file are three consecutive sections of the single file OUTPUT. Distinctions between the different sections of the INPUT and OUTPUT files are made to simplify the description of what is read from INPUT and what is written to OUTPUT during the three phases of a SNARK14 run. INPUT is the standard input, OUTPUT is the standard output. They are usually redirected to disk files when the SNARK14 program is executed.

The last section of this chapter points out the availability (outside SNARK14) of some interactive applications that have been designed to ease the creation of the SNARK14 INPUT file and to observe the results of a SNARK14 run as images and/or as graphs.

3.1 Data generation phase

During this phase, SNARK14 generates a test picture (a phantom) and/or projection data of it. The projection data consist of real ray sums of the phantom, possibly contaminated by the different types of noise that one may come across in a device used for collecting data for reconstruction.
CHAPTER 3. SNARK14 INFORMATION FLOW AND FILES

Figure 3.1: Information flow within SNARK14. Optional paths are marked by ||.

The Data Generation Input file is the section of the file INPUT that contains the commands that cause the generation of the test picture and the projection data. The SNARK14 commands permitted to appear in this section are TRACE, MODE, CREATE, and END (see Chapter 5).

file11 is a text file that contains the description of the phantom and/or its projection data. This description contains information on how the phantom and/or data have been specified, as well as the actual density values assigned to the pixels in the phantom and/or to the ray sums in the projection data. See Appendix B for instructions on how to create a file11 containing user supplied data.

The Data Generation Output file is the section of the file OUTPUT that echoes the data generation input file and reports on the work carried out by the data generation phase.

3.2 Initialization and reconstruction phase

The Initialization and Reconstruction Input file is the section of the file INPUT that contains the commands specifying where the initialization information is coming from and what reconstructions are to be carried out. The SNARK14 commands that are permitted to appear in this section are TRACE, MODE, PICTURE,
CHAPTER 3. SNARK14 INFORMATION FLOW AND FILES

PROJECTION, SELECT, BASIS, STOP, EXECUTE, and END (see Chapter 5). The Initialization and Reconstruction Output file is the section of the file OUTPUT that echoes the initialization and reconstruction input file and reports on the work carried out by the initialization and reconstruction phase.

This phase can be broken up into two subphases: the initialization subphase and the reconstruction subphase. The latter cannot be performed without the former having been performed in the same run.

3.2.1 Initialization subphase

During this subphase the nature of the grid for the reconstruction region (NELEM and PIXSIZ) as well as the assumed geometry of data collection are determined. If there is a test picture, it will be read from file11 and put on recfil (see below). If the projection data set is not available on the file prjfil (see below), it is transferred onto this file.

*prjfil* is a file that contains a description of the geometry of data collection and, for every projection, the projection angle and the estimates of the ray sums in that projection from rays FUSRAY to LUSRAY (see Section 2.5). The structure of prjfil is discussed in Appendix C.

*recfil* is a file that contains a description of the phantom and/or the reconstructions performed during the reconstruction subphase. The structure of recfil is discussed in Appendix C.

3.2.2 Reconstruction subphase

During this subphase, the reconstruction algorithms specified by the initialization and reconstruction input file are carried out and the results are put on recfil.

If additional files are required for any user-written subroutine, they should be explicitly defined and opened by that subroutine (and closed when the work of the subroutine is done).

3.3 Analysis phase

During this phase various displays of the phantom and/or the reconstructions are generated based on the information in recfil. Statistical analysis of the results as well as comparisons of the reconstructions to the phantom may also be carried out.

The Analysis Input file is the section of the file INPUT that contains the commands specifying the displays, analysis, and comparisons to be generated. The SNARK14 commands permitted to appear in this section are TRACE, MODE, EVALUATE, DISPLAY, PUNCH, LINES, SKUNK, and END (see Chapter 5).

*punch* is a text file that contains descriptions of specified reconstructions in the format in which a phantom is described in file11. These may be used as a file11 in a later run.

*eval* is a text file that contains the evaluation of reconstructed images with respect to the phantom. This file can be read by a plotting program outside SNARK14 (see Subsection 1.4.2).

The Analysis Output file is the section of the file OUTPUT that echoes the analysis input file and reports on work carried out by the analysis phase, including details of the specified comparisons, analyzes, and displays.
Chapter 4

NOTATIONAL AND FORMAT CONVENTIONS

In this chapter we discuss the notational and format conventions for the file INPUT (that contains some, maybe all, of the data generation input file, initialization and reconstruction input file, and the analysis input file). The file INPUT is a sequence of lines. These are read one-by-one and, typically, they result in some action by SNARK14 before the next line is read. The INPUT file is logically divided into SNARK14 commands, each command occupying one or more lines in the input file.

4.1 Comment lines in the input file

Any line that begins with an * (an asterisk) in column 1 will be treated as a comment. It will be echoed in the OUTPUT, but it will otherwise be ignored by SNARK14. The only purpose of the comment lines is to make the files INPUT and OUTPUT more informative to humans who read them. Comments may appear almost anywhere in the SNARK14 INPUT file. The exception is where the input calls for a “name-of-...” command line (see 5.3.3 for an example), a line starting with an asterisk is treated as the name, not as a comment.

4.2 Commands and their levels

The part of the file INPUT that determines what gets computed during a SNARK14 run consists of the SNARK14 commands; each one of which occupies one or more (consecutive) lines in the input file.

A command starts with a command line in which the first continuous sequence of four letters identifies the type of command that is to be carried out. The exact details of what is to be done are specified by putting additional information on the same command line and, usually, on the lines immediately following it. Chapter 5 describes, for each of the fifteen commands, the precise contents and format in which the information has to be provided.

There are fifteen commands in SNARK14, which are classified into six levels as follows:

1. General (may appear in any one of the three input files mentioned above): TRACE, MODE.
2. Data generation command: CREATE.
3. Initialization commands: PICTURE, PROJECTION.
4. Reconstruction commands: SELECT, BASIS, SUPERIORIZE, STOP, EXECUTE.
5. Analysis commands: EVALUATE, DISPLAY, PUNCH, LINES, SKUNK.
6. Termination command: END.
There are some rules that must be observed regarding the order in which commands may appear in the INPUT file of a single SNARK14 run. Violation of these rules will result in termination of the run. To explain these rules we make use of the variable $CL$ (the current level of the run) in addition to the variable $L$ (the level of a command). The following are the rules:

- At the beginning of a run, $CL = 1$.
- Level 1 commands can occur (repeatedly) anywhere in the command sequence.
- If the level $L$ of a command is greater than 1, then it must be the case that $CL \leq L$ and, after the execution of the command we will have $CL = L$.
- The CREATE, PICTURE, and PROJECTION commands may appear only once.
- An EXECUTE command must be preceded by a PROJECTION command and a PROJECTION command must be preceded by a PICTURE command.
- If the level of the first command in the sequence is 3, 4, or 5, then the file specified below must be present in the current directory:
  - for 3, file11 is required if either PICTURE TEST (see Section 5.4) or PROJECTION REAL (see Section 5.5) is specified,
  - for 4, prjfil must be present,
  - for 5, recfil must be present and prjfil is required if residuals are computed.
- An END command must occur in the sequence.

With the exception of CREATE, PICTURE, and PROJECTION, all SNARK14 commands may occur repeatedly in the INPUT file of a SNARK14 run. The first occurrence of END will cause the termination of the run and further lines on the INPUT file will not be read. The SNARK14 run will also be terminated if any rule regarding the contents of INPUT that is specified above or in the following chapters is violated.

### 4.3 Notations used in syntax

In describing the contents of the command lines which make up the commands we shall assume the following conventions.

**SNARK14 commands** will be identified by a greater than (>) symbol at the left margin followed by about one inch of white space.

**Key words.** If a capital word appears in the syntax, the first four letters of this word, or the whole word if its length is less than four, must appear together (without any blanks between them) at the corresponding position in the command. For words of length greater than four, the first four letters may optionally be followed by other symbols; all symbols up to the first blank following these letters will be ignored by SNARK14. In other words, in place of a long key word, the programmer may use any contiguous sequence of non-blank characters, provided only that the first four characters of this sequence coincide with the first four letters of the keyword. The keyword may be written on the INPUT file in either upper case or lower case or a mixture of both.

**Lower-case words.** Lower case words represent generic terms, values of which must be supplied by the user in the corresponding position in the command.

**Braces.** When words or phrases written underneath each other are enclosed in braces { }, a choice of one of the enclosed words or phrases must be made.

**Brackets.** When a word or phrase is enclosed in brackets [ ], the word or phrase is an optional feature of the instruction. Users may include the feature by coding according to the syntax enclosed in the brackets or they may omit the feature completely. When one of a number of optional features is permitted at a particular position, these are written underneath each other and are enclosed in brackets.
4.4 Control command line format

Some of the command lines in the INPUT file will be identified as control command lines. These are command lines which contain information in a free format, subject to some restrictions which we now describe.

Control command lines contain a sequence of three types of modifiers: word, integer and floating point. A modifier must be followed by a blank, unless it is the last modifier on the line. Additional blanks preceding or following the modifier are ignored.

A **word modifier** is any contiguous sequence of non-blank characters. Examples: CREATE, ART2, SMOOTH. In a word modifier all characters after the first four are ignored by SNARK14.

When SNARK14 is looking for a word modifier in a control command line, it ignores all characters and blanks until it comes across the first four characters of the sought-after word modifier or the whole of the word modifier followed by a blank or the end of the line. If it finds a word that is not one of the possible expected word modifiers, it skips that word and tries again. If a required word modifier is not found in the line, then the SNARK14 run is terminated.

In this manual, all word modifiers are written in upper case. Processing of the INPUT file, however, is case insensitive. Word modifiers may be in either upper or lower case or a mixture of them.

An **integer modifier** is a contiguous nonempty sequence of digits (0-9) of length between one and nine, possibly preceded by a minus sign (−). Examples −123456789, 003.

A **floating point modifier** is a string satisfying the regular expression:

```
[\-'] {digit+ [\. digit*] , \. digit+} [ {\E, \e} \aten', \aten'} digit [digit] ]
```

where digit is one of the characters 0..9, 'x' is the literal character x, an asterisk (*) is zero or more repetitions of the preceding item, a plus (+) is one or more repetitions of the preceding item, brackets ([]) indicate optional items, braces ({{}) indicate required items, and a comma (,) separates choices. In words, a floating point modifier is either any contiguous nonempty sequence of digits, possibly preceded by a minus sign, and possibly followed by a decimal point (.) followed by another sequence of digits, or it is a decimal point, possibly preceded by a minus sign followed by one or more digits. These may further be followed by the letter E or e, possibly a plus (+) or a minus (-) sign and one or two digits. Examples: 4, 0, 35.6E4, -25., 35e-64, .7071, 12345678912.12345678912.

When SNARK14 is looking for a number modifier in a control command line, it ignores all alphabetic characters (a to z and A to Z) as well as the equal sign (=) preceding the number modifier. This can be used to make the input file more readable, as will be illustrated later (e.g., in Section 5.2). If a required number modifier is not found in the line, then the SNARK14 run is terminated.

Every command in SNARK14 starts with a control command line, the first modifier of which is the word modifier indicating the command type.

4.5 Iteration-flag-line format

Some of the command lines in the INPUT file will be identified as an

```
> iteration-flag-line
```

Such a command line contains a string of digits 0 to 9 (a blank is assumed to be 0) in its first 51 columns. A command contains at most one iteration-flag-line. When describing the effect of the contents of the iteration-flag-line on the execution of the command, the following notation is used.

\[ fl(0) \] is the digit in the first column of the iteration-flag-line.

For any positive integer \( q \), \( fl(q) \) is the digit in column \( t + 1 \) of the iteration-flag-line, where \( 1 \leq t \leq 50 \) and \( q \equiv t \pmod{50} \). For example, \( fl(357) \) is the digit in column 8 of the iteration-flag-line.

An important use of the iteration-flag-line occurs in conjunction with the EVALUATE command (Section 5.11), it controls what gets written on the eval file (see Section 3.3) about the images that are produced after \( q \) iterations; for details, see Section 5.11.
4.6 Names used in the manual vs. names used in the code

This manual has been written with the desire (not always achieved) to be readable. For this reason, names are given to things in the manual that are not identical to the names for the same things in the code. (The names in the code reflect the structure of the program as it is written in C++; such names tend to be long and “funny looking” to ordinary mortals.) In the manual, variables are given names that usually consist of capital letters. (Many examples of this have appeared already: ZERO, PIXSIZ, NELEM, etc.) For those users who wish to write their own subroutines to be used in conjunction with SNARK14, precise instructions are given below at the appropriate places as to the names of the corresponding variables in the code.
Chapter 5

SNARK14 COMMANDS

In this chapter we describe the fifteen SNARK14 commands in detail.

5.1 TRACE

> TRACE [trace-level]

Because SNARK14 was primarily designed as a test-bed for algorithm development, for debugging purposes it is essential to have a built-in method of examining key parameter values during program execution. The TRACE command provides such a method. Because it is a general command, TRACE may appear anywhere in the SNARK14 INPUT file. Effective placement of this command should eliminate useless trace information.

The TRACE keyword is followed (optionally) by an integer that specifies the desired trace level. If an integer is not specified, the level is set to 0. The trace levels are defined by the following. (For a detailed description of the terms used below, the reader is referred to Chapter 6). If the trace-level is not positive, then the TRACE is off. Other trace-levels are interpreted as follow:

1. Provided so that the user can insert trace statements in a user specified algorithm and turn these debugging aids on and off. These statements should have the form
   if (trace > 0) output . . .

2. Not used.

3. Not used.

4. Not used.

5. Prints projections (NP) and rays (NR) selected by PICK (6.4.1).

6. Prints the real ray sum (or pseudo ray sum) as well as NP and NR for the NP-th projection and NR-th ray used by the function PRDTA (6.3.6.2) (or PSEUDO (6.4.4) or BPSEUDO (6.3.4.5)).

7. Prints the number of basis functions intersected (NUMB), the sum of the squares of the integrals of the intersected basis functions over the ray (SNORM), NP, and NR, for the NP-th projection and NR-th ray used in RAY (6.4.3), WRAY (6.4.2), BRAY (6.3.4.4), or BWRAY (6.3.4.3).

8. Prints the equation of the current ray consisting of a point on the ray (AX,AY), and the direction of the ray (MX,MY) as produced by POSIT (6.4.7).

9. Not used.
10. Prints the indices of the basis functions intersected by the NPth projection and NR-th ray as produced by RAY, WRAY, BRAY, or BWRAY. Additionally, for WRAY and BWRAY, the integrals of the intersected basis functions over the ray will be printed in the same order as their indices are listed (see Sections 6.3.4.3, 6.3.4.4, 6.4.2, and 6.4.3).

TRACE is an inclusive command, i.e., the integer specified produces the trace described above, as well as all traces for integers less than the specified integer. For example, TRACE 4 produces also a trace of algorithm execution (TRACE 1).

5.2 MODE

MODE enables the user to set two logical flags named LOFL and UPFL, and to give values to two floating point variables named LOWER and UPPER. If there is no modifier following MODE, the values of LOFL and UPFL are set to FALSE, and the values of LOWER and UPPER remain unchanged (SNARK14 initializes LOFL and UPFL to have the value FALSE, and LOWER and UPPER to have the values 0.0 and 1.0 respectively). If the modifier LOWER follows MODE, LOFL is set to TRUE and the variable LOWER is set to lower-value. (Note that, since alphabetic characters and the equal sign between the modifiers LOWER and lower-value are ignored by SNARK14, the commands

```
MODE LOWER = -1.0
```

```
MODE LOWER CONSTRAINT IS SET AT -1.0
```

are both legitimate and have the same effect.) If the modifier UPPER follows MODE, UPFL is set to TRUE and the variable UPPER is set to upper-value. If only one of the two modifiers LOWER and UPPER follow MODE, the logical flag associated with the other one is set to FALSE. **Warning:** If both LOFL and UPFL are set to TRUE, then lower-value must not be greater than upper-value.

This instruction has two purposes. Primarily, the values of LOFL, UPFL, LOWER and UPPER are available to all algorithms and may be used by them. (They may be especially useful in reconstruction algorithms, see Chapters 6 and 7.) Secondly, they tell SNARK14 how to interpret the reconstruction when performing an evaluation or display of a reconstruction. If both LOFL and UPFL are FALSE, then the picture values stored on recfil (see Section 3.2) are used unchanged; if LOFL is TRUE, all densities less than LOWER are considered to be equal to LOWER; if UPFL is TRUE, all densities greater than UPPER are considered to be equal to UPPER. While performing the evaluation or display of a reconstruction (which at such time would be residing on recfil) the stored values in the phantom and the reconstruction are not changed, but they are interpreted according to the rules described above for the purpose of evaluation or display.

**Example.** If on a particular scale the picture values associated with air, brain, and skull are about 0.0, 1.0, and 2.0 respectively, then we can evaluate how well the brain is reconstructed by setting LOWER to 0.5 and UPPER to 1.5 and LOFL and UPFL set to TRUE. This will cause the regions of the picture that are associated with air and skull to have values 0.5 and 1.5, respectively, in both the original and the reconstruction (unless the reconstruction is grossly inaccurate). Thus the error statistics reported on by SNARK14 will be influenced only by the accuracy of reconstruction of the brain matter.

When a reconstruction is being performed in BLOB mode (see Sections 2.2 and 5.7), the values of LOWER and UPPER are applied to the blob coefficients. Because blobs overlap, when such a reconstruction is converted to pixels the pixel values may exceed these bounds.

5.3 CREATE

```
> CREATE
```

This command enables the user to create test phantoms and their projection data. The data so generated are then written on file11 in the format required for use by the PICTURE and PROJECTION commands
(see Sections 5.4 and 5.5). See Appendix B for instructions on how to create a file containing user supplied data.

Under the CREATE command the user can make use of any of the following features:

1. The objects giving rise to absorption of incident rays (phantom) are approximated by superimposing a number of elemental objects, which may be one of the following: ellipse (circle), rectangle (square), isosceles triangle, sector or segment of a circle.

2. Data corresponding to a monochromatic or a discrete polychromatic input energy spectrum (of up to 7 different energy levels) may be approximated.

3. Projection data for either divergent or parallel ray geometries may be created.

4. Accuracy in calculating the phantom densities and projection data may be improved by sampling finer than finally desired and taking an average.

5. An aperture function may be specified, which would weight the above average so as to simulate an uneven dispersion of intensities of a detected ray across the face of a detector when the detectors are not assumed to be points but of finite spatial extent.

6. In order to simulate non-ideal situations like noise due to photon counting statistics (quantum noise) and scattering from neighboring rays, the user may specify photon distribution and scattering characteristics. In addition, mathematically convenient additive and multiplicative noise may be introduced in the projection data.

7. A background absorption at each energy level may be specified.

Since this is by far the most complex SNARK14 command, both in the length and complexity of its follow up input sequence and in what it has to accomplish, its description is broken up into subsections.

5.3.1 Creation of the phantom

A phantom is created when PHANTOM AVERAGE is specified as part of the CREATE command and the user provides all the necessary information (see Section 5.3.3). The phantom is based on a test picture region that is a square with center at the origin and is divided into equal non-overlapping smaller squares (pixels). This region is defined by the number of pixels to a side (NELEM) and the length of a side of the pixel (PIXSIZ). NELEM must be an odd integer. The origin is assumed to lie at the center of the central pixel.

The phantom is put together by superimposing a number of elemental objects, placed at desired positions, at desired orientations, and of desired size and (absorption) density. The density of the elemental objects may be negative. The density (picture value) at any point is then defined as the sum of the densities associated with all the elemental objects within which the point lies.

To obtain a measure of the average density within a pixel, the user specifies the variable NAVE1, which has the effect that the density within a pixel is determined by averaging the value of the density at NAVE1×NAVE1 uniformly spaced points within the pixel. NAVE1 must be odd.

The user specifies the absorption $d_{j,i}$ at each energy level $i$ and for each elemental object $j$. From this information we obtain, for each pixel and for each energy level $i$, an average density defined by

$$\frac{1}{(\text{NAVE1})^2} \sum_{k=1}^{\text{NAVE1}} \sum_{j=1}^{\text{NOBJ}} \delta_{k,j} d_{j,i},$$

(5.1)

(where NOBJ is the number of elemental objects in the phantom and $\delta_{k,j}$ is 1 if the $k$th point of the pixel is inside the $j$th elemental object and is 0 otherwise) and an inhomogeneity that is obtained by multiplying the average density with a random sample from a zero mean Gaussian distribution with standard deviation sd (see Section 5.3.3, Set 3). What we call the phantom in SNARK14 is obtained by summing, at each pixel, the average density and the inhomogeneity for that pixel at the first energy level.
The type and location of an elemental object is described by the six variables TYPE, CX, CY, U, V, and ANG. TYPE can assume the values ELIPSE (note misspelling), RECTANGLE, TRIANGLE, SEGMENT, and SECTOR. For each one of these cases, the explanation of the rest of the variables is given by Figure 5.1. The boundary of an elemental object is considered to be part of the object.

5.3.2 Creation of raysums

Raysums (projection data) are created for a number of rays and a number of projections when RAYSUMS AVERAGE is specified as part of the CREATE command and the user provides all the necessary geometry and measurement information (see Section 5.3.3). Projection data calculated by CREATE are approximations to the real ray sums in the divergent ray geometry (Figure 2.1) or the parallel ray geometry (Figure 2.2). A real ray sum is defined as the integral of the density along a ray. As we have seen in the last section, SNARK14 allows multiple densities associated with each point (one for each energy level), which makes the definition of real ray sums inapplicable in the polychromatic case.

The mathematically simplest way of defining the real raysums in the presence of inhomogeneities is to think of each pixel as an additional square-shaped elemental objects whose density at energy level \(i\) is the inhomogeneity (as defined in the last subsection) at that pixel and energy level. Then, for each energy level \(i\), the real ray sum \(R_i\) for a LINE ray (the STRIP case will be discussed below) is the sum

\[
R_i = \sum_{j=1}^{\text{NOBJ}+(\text{NELEM})^2} l_j d_{j,i},
\]

where \(l_j\) is the length of intersection of the ray with the \(j\)th elemental object (\(l_j\) may be 0), and \(d_{j,i}\) is the density of the \(j\)th elemental object at energy level \(i\).

Projection data that are experimentally collected can only approximate this sum. CREATE contains a number of features that enable it to generate data that approximate the idealized projection data in the same way as projection data obtained from x-rays would. This is explained in the following paragraphs. The explanation assumes a minimal amount of knowledge of how x-rays interact with matter. Such knowledge can be obtained, for instance, from [24, 29].

Figure 5.1: Elemental objects
The approximation to the ray sum produced by CREATE is a function of \( p \), where

\[
p = -\ln \frac{A}{C},
\]

where \( C \) is the calibration measurement (proportional to the number of photons counted by the detector before the insertion of the object to be reconstructed), \( A \) is the actual measurement (proportional to the number of photons counted by the detector with the object of interest in place), and \( \ln \) denotes the natural logarithm. In the following paragraphs we discuss how the number of photons reaching the detector is estimated in increasingly complicated situations.

It is important that the user has a clear understanding of the intended interpretation of the density value \( d_{j,i} \) assigned to the elemental object \( j \) at energy level \( i \). SNARK14 allows two different interpretations: \( d_{j,i} \) is an absolute attenuation coefficient or \( d_{j,i} \) is an attenuation coefficient relative to some standard (background) material, such as water. In the latter case, it is assumed that calibration is done with the background material between the source and the detector, and during the actual measurement the background material is (partially) replaced by the object to be reconstructed. It is also assumed that, for each energy level \( i \), the attenuation by the background material is constant, \( B_i \), for all rays. A special case of this is obtained by assuming that the background material is vacuum and all \( B_i \)s are zero. This special case is the same as using absolute attenuation coefficients.

The calibration measurement \( C \) is estimated in a way that depends on the arrangement of the x-ray source and detector(s). In certain scanners, the value of \( C \) is constant for all rays of one projection, but varies from projection to projection. In other scanners, the value of \( C \) is constant for all projections for a particular ray (say, the fifth ray), but varies from ray to ray. Yet in other cases, \( C \) may be different for each ray in each projection. We use the variable QUANIN to indicate which of these three cases applies. The value of QUANIN is 1 in the first case, 2 in the second, and 3 in the third. (The value of QUANIN is determined by the CREATE follow up command lines.) QUANIN may also assume the value 0. This indicates that data are to be generated without any noise due to photon statistics (quantum noise), in which case \( C \) need not be calculated at all, as we shall see below.

In order to take care of the variability in the strength of the x-ray source a reference x-ray beam is used. Thus \( C \) itself is calculated as a ratio

\[
C = \frac{C_0}{C_r},
\]

where \( C_0 \) is the number of photons counted by the detector under consideration and \( C_r \) is the number of photons counted during the same period by a reference detector during the calibration measurement.

The expected values of \( C_0 \) and \( C_r \) are the same number; \( C_0 \) and \( C_r \) differ from each other only because of the statistical nature of the counting process, which results in the so-called quantum noise. Hence, if QUANIN = 0, we may assume that \( C = 1 \).

Since we assume that, for each energy level \( i \), the attenuation by the background material is a constant, \( B_i \), for all rays, we get that (see [24]), if \( \lambda \) is the expected number of photons that would be detected by the detector when the ray went through vacuum, then the expected number of photons that are detected when the ray goes through the background material is

\[
\lambda \sum_{i=1}^{\text{ENERGY}} p_i e^{-B_i},
\]

where \( \text{ENERGY} \) is the number of energy levels and \( p_i \) is the portion of the energy spectrum at level \( i \) \((\sum_{i=1}^{\text{ENERGY}} p_i = 1)\).

In case the follow up command lines of CREATE indicate that quantum noise is to be introduced in the projection data (QUANIN > 0), \( C \) is calculated as the ratio of two instances from the normal distribution whose mean is given by Equation (5.5) and whose standard deviation is the square root of its mean. The \( \lambda \) in this case is defined by the product QUANMNxQUANCM, where the values of QUANMN and QUANCM are supplied by the follow up command lines of CREATE.

The actual measurement is also estimated as a ratio

\[
A = \frac{A_0}{A_r},
\]
Figure 5.2: Substrip interpretation for DIVERGENT-TANGENT geometry. (It is assumed that the source is a mathematical point, even though in practice it would have some extent.)

where \( A_0 \) is the number of photons counted by the detector under consideration and \( A_r \) is the number of photons counted by the reference detector during the actual measurement.

If quantum noise is to be introduced in the projection data, the value of \( A_r \) is an instance from the normal distribution whose mean is given by Equation (5.5) and whose standard deviation is the square root of its mean. The \( \lambda \) in this case is defined to be QUANMN. (Thus QUANCM is the ratio of the number of photons used for the calibration measurements to the number of photons used in the actual measurements.)

The calculation of \( A_0 \) is more complex, since the total attenuation along different lines from the source to the detector can no longer be assumed to be the same. For the purpose of estimating \( A_0 \), we assume that photons are collected from within a strip that, in the DIVERGENT-TANGENT and in the PARALLEL geometries, meets the line of detectors in a line segment of width PINC (or \( \text{PINC} \times \max(|\sin \theta|, |\cos \theta|) \) in the parallel case if VARIABLE detector spacing is specified) centered around the mathematical position of the detector (see Figure 5.2). In the DIVERGENT-ARC geometry the definition is similar, but now the strip is on an arc (see Figure 2.1).

To simulate what happens in practice, the user specifies a variable NAVE2 and an array NAPER(1), ... , NAPER(NAVE2). NAVE2, a positive integer, determines the number of smaller strips into which the projection strip is divided for the purpose of calculating \( A_0 \) (see Figure 5.2). The number of photons that is assumed to enter the \( n \)th substrip is

\[
r_n = \frac{\text{NAPER}(n)}{\sum_{k=1}^{\text{NAVE2}} \text{NAPER}(k)}
\]

(5.7)
times the total number of photons entering the strip. Thus, NAPER defines an aperture function.

Let \( R_{i,n} \) be the real sum for the \( i \)th energy level for the central ray of the \( n \)th substrip (defined by Equation (5.2)). Then the expected number of photons that is detected by the detector is estimated by

\[
\text{QUANMN} \sum_{n=1}^{\text{NAVE2}} \sum_{i=1}^{\text{ENERGY}} r_n e^{-(R_{i,n} + B_i)}.
\]

(5.8)

If quantum noise is to be introduced in the projection data, the actual value of \( A_0 \) is an instance of a random variable. Let \( Q \) be the value given by Equation (5.8). If \( Q \) is less than 100.0, then \( A_0 \) is an instance of a Poisson distribution whose mean is \( Q \). Otherwise, \( A_0 \) is an instance of a normal distribution whose mean is \( Q \) and whose standard deviation is the square root of \( Q \). If quantum noise is not to be introduced...
in the projection data, $A_0$ is given by Equation (5.8), $A_r$ is given by Equation (5.5) with $\lambda = QUANMN$, and so the value of QUANMN is irrelevant in estimating $A$ by Equation (5.6).

**Warning:** The way quantum noise is dealt in SNARK14 is based on the assumptions that the means are reasonably large. If the means are small it may be incorrect [29].

Whether or not quantum noise is to be introduced in the projection data, the value of $A_0$ may be further modified before substitution into Equation (5.6). The purpose of this modification is to simulate the change in $A_0$ due to photons scattered from nearby rays and cross-talk between neighboring detectors. The model used to simulate these effects is such that it would not change the expected values of $C_0$ and we assume that such effects do not enter into the working of the reference detectors. Hence, when scatter noise is specified by the CREATE follow up sequence, only $A_0$ is modified from the value given to it above.

In order to explain the scatter model precisely, let $A_i$ and $\overline{A}_i$ denote the value of $A_0$ for the $i$th detector ($FUSRAY \leq i \leq LUSRAY$) before and after scatter has been introduced.

$$A_i = \left( \sum_{j=FUSRAY}^{LUSRAY} v_{i-j} \overline{A}_j \right) / V_i$$ (5.9)

where $v_k$ and $V_i$ are calculated as follows. The user provides in the CREATE follow up command lines two variables: SCTNPK (scattering peak) and SCTNWD (scattering width). For all integers $k$, let

$$v_k = \begin{cases} 
0, & \text{if } |k \times PINC| > SCTNWD, \\
SCTNPK(1 - |k \times PINC| / SCTNWD), & \text{if } k \neq 0 \text{ and } |k \times PINC| \leq SCTNWD, \\
1 + SCTNPK, & \text{if } k = 0,
\end{cases}$$ (5.10)

and let

$$V_i = \sum_{j=FUSRAY}^{LUSRAY} v_{i-j}.$$ (5.11)

In the PARALLEL VARIABLE case, every occurrence of PINC in these formulas must be replaced by $PINC \times \max (|\sin \theta|, |\cos \theta|)$ where $\theta$ is the projection angle. (Thus, scattering is modeled by convolution with a triangle shaped function, such that the total number of photons detected by all the detectors remain constant, except for edge effects.) Strictly speaking, scattering should increase the total number of photons detected, but the ratio of increase would be the same during the calibration measurement, and the two increases cancel out.

To summarize, real ray sum in the LINE case is estimated by Equation (5.3), where $C$ and $A$ are given by Equations (5.4) and (5.6), respectively. This estimation may incorporate the effects of calibration with a background material, polychromaticity, wide detector with a nonuniform detecting efficiency across its face, quantum noise and scatter. In addition, the user may specify additive and multiplicative noise to further degrade the projection data. If the follow up command lines so indicate, CREATE will first multiply $p$ by an instance from a normal distribution and then add to the resulting value an instance from another normal distribution. The means and standard deviations of these distributions are provided by the user in the CREATE follow up command lines. It is this finally altered value of $p$ that is stored by CREATE on file11.

In the PARALLEL geometry situation, we allow for STRIP integrals by multiplying the value obtained as described above by PINC, if UNIFORM detector spacing is specified, or by $PINC \times \max (|\sin \theta|, |\cos \theta|)$ if VARIABLE detector spacing is specified ($\theta$ is the projection angle, denoted as THETA in Figure 2.2).

### 5.3.2.1 Simulating PET with SNARK14

In positron emission tomography (PET) we are interested in the uptake of positron-emitting isotopes by various parts of the human body. When a positron is emitted it annihilates with a nearby electron and produces two $\gamma$-ray photons of identical energy traveling in approximately opposite directions. The two photons are detected in near coincidence by a pair of opposite detectors. The annihilation, and thus the positron emission, is known to take place somewhere along the line joining the detector pair. We count such coincidences for a number of detector pairs around the body. From these measured counts our aim is to estimate the concentration of the positron emitter at various points in the body cross-section.
Figure 5.3 shows a simplified PET geometry consisting of a ring of 8 detectors. For simplicity, we assume that each detector is coupled with 3 opposite detectors to detect (near) coincidence arrivals of photons. Thus the lines sampled by each detector form a divergent pattern as shown in Figure 5.3. By analogy with x-ray CT, we refer to the collections of such (divergent) lines as a view and the lines themselves as rays in the view [50]. Thus in Figure 5.3 we have 8 views with 3 rays per view and 12 rays in total \((8 \times 3)\) in all the views.

To simulate measurements by a PET system, SNARK14 utilizes many of the existing routines previously written to simulate x-ray CT measurements. In generating the PET data, SNARK14 attempts to simulate the general characteristics of data that would be collected by a PET scanner, rather than attempt to simulate a particular PET device. To see how SNARK14 uses its x-ray CT organization to simulate data collection for the simplified PET geometry in Figure 5.3, consider Figure 5.4 that shows a schematic of a SNARK14 DIVERGENT x-ray CT geometry with the detectors located on an arc (Section 2.4). The raysums (defined by Equation (5.2) in Section 5.3.2) are measured along lines joining the source and three opposite detectors located on an arc of a circle whose center is at the source. Figure 5.4 illustrates the situation when the source is at location \(D_2\) and the detectors are on the arc \(D_7, D_6, D_5\). The locations \(D_1 - D_8\) in Figure 5.4 correspond to the detector positions in Figure 5.3. It is clear from Figure 5.4 that the detector locations (except for the central detector) are not the same as those in the PET geometry of Figure 5.3. In Figure 5.4 a full scan is made by measuring the raysums as the source rotates through locations \(D_1-D_8\). The PET data simulation is completed by generating, for each raysum, a Poisson random variable whose mean is given by the value of the raysum. Thus, it is easy to see that while the CT geometry of Figure 5.4 does not precisely simulate the PET geometry of Figure 5.3, the measurements obtained by the CT system possess similar characteristics of the data that would be collected by the PET system. Note that as a consequence of using its x-ray CT organization to simulate the PET system of Figure 5.3, SNARK14 generates a total of 24 raysums (instead of the 12 measurements that would be obtained in Figure 5.3), since two separate measurements (raysums) are obtained for each pair of PET detectors.

In SNARK14, PET data are simulated by using a value of 4 for the variable QUANIN. In this case, the values of QUANMN and QUANCM are ignored, except for the sign of QUANMN. If QUANMN \(\geq 0.0\) then each raysum is fed to a Poisson random number generator. If QUANMN \(< 0.0\), then the raysum is not fed to the Poisson random number generator (i.e. the data are noise-free). The “noise” in the data is adjusted by scaling the phantom values to achieve the desired total number of photon counts. This scaling is achieved by means of the LAST command line of the OBJECTS command (Section 5.3.3, Set 3), and the
total count is equal to the value of the parameter TOTDEN written to the file OUTPUT generated after a
SNARK14 PET run. The procedure for achieving a total count of, say, \( T_2 \) is the following. Let \( T_1 \) be the
total count with unit scaling (i.e.
\[ \text{scale}=1 \text{ in the LAST command line of Section 5.3.3, Set 3}. \]
Then \[ \text{scale} = \frac{T_2}{T_1} \]
will produce the count \( T_2 \). (An example of a SNARK14 run that simulates PET data collection is given in
Appendix A, Section A.7).

Note: When simulating PET data collection SNARK14 ignores attenuation effects.

5.3.3 Description of the CREATE input sequence

The CREATE command line is followed by a certain input in a specific form and order in the Data Generation Input file. This input sets out all the information necessary for the generation of phantom and/or projection data. The input has been separated into eight sets of logically divided segments for convenience in presentation, implementation, and use. It has been designed to enable the user to identify each input quantity easily (and as such may appear redundant in places). This is done by making generous use of descriptive words. The following provides a description of each set of records (command lines); the entire command is the totality of these command lines taken in order.

Certain restrictions are imposed on input quantities so that they are computationally meaningful or physically acceptable. These are also indicated. Errors are trapped during input and error messages are issued. Errors stop the input processing and the program aborts. Examples of input sequences are given in Appendix A.

SET 1: IDENTIFYING HEADER

1.1 FORMAT: string of up to 80 characters

\[ \text{name-of-the-pattern} \]

This name is used for identification of the phantom and projection data. A command line beginning with
an asterisk is not treated as a comment here. It is the name of the pattern.

SET 2: ENERGY SPECTRUM
2.1 FORMAT: control command line format (see Section 4.4)

\[> \text{SPECTRUM} \left\{ \begin{array}{l}
\text{MONOCHROMATIC energy} \\
\text{POLYCHROMATIC energy}
\end{array} \right. \]

Both energy and nergy are integer modifiers.

The value of energy is used for echo checking purposes only. For example, the value 70 may be assigned to energy to indicate that we intend to simulate a monochromatic x-ray beam at 70 keV. The output produced on file11 by CREATE will carry this information in its headers for both the phantom (see Section 5.4) and the projection data (see Section 5.5), but it will not be influenced in any other way by the value given to energy.

The value of nergy is the number of energy levels and is assigned to the variable NERGY. Restriction: 1 \( \leq \text{nergy} \leq 7 \).

2.2 FORMAT: control command line format

\[> \text{energy}(1) \text{ percent}(1) \ldots \text{energy}(\text{NERGY}) \text{ percent}(\text{NERGY}) \]

\(\text{energy}(i), \text{percent}(i) (1 \leq i \leq \text{NERGY})\) are integer modifiers.

Restriction: This command line is absent in the MONOCHROMATIC case. The value of energy\((i)\) \(1 \leq i \leq \text{NERGY}\) is used for the \(i\)th energy level in the polychromatic case exactly the same way as energy is used in the monochromatic case (see command line 2.1 above).

Restriction: The values of percent\((1)\), \ldots, percent \((\text{NERGY})\) must be nonnegative integers and add up to 100. The portion \(p_i\) of the energy spectrum at level \(i\) (used in Section 5.3.2) is defined by \(p_i = \text{percent}(i)/100\).

SET 3: ELEMENTAL OBJECTS

3.1 FORMAT: control command line format

\[> \text{OBJECTS} \]

3.(2n) \(1 \leq n \leq \text{NOBJ}\) FORMAT: control command line format

\[
> \left\{ \begin{array}{l}
\text{ELIPSE} \\
\text{RECTANGLE} \\
\text{TRIANGLE} \\
\text{SEGMENT} \\
\text{SECTOR}
\end{array} \right. \quad c_x \; c_y \; u \; v \; \text{ang} \; \text{den}(1)
\]

\(c_x, c_y, u, v, \text{ang}, \text{and den}(1)\) are all floating point modifiers.

This command line describes an elemental object. The values of \(c_x, c_y, u, v, \text{and ang}\) are assigned to the variables CX, CY, U, V, and ANG, which (together with the shape name) define the elemental object as described in Section 5.3.1, especially in Figure 5.1. The value of \(\text{den}(1)\) is the density of this elemental object at energy level 1, in the polychromatic case, or at the only energy level in the monochromatic case. Restriction: \(u > \text{ZERO}\) and \(v > \text{ZERO}\).

This command line appears NOBJ (number of elementary objects) times. In the polychromatic case, if \(\text{NERGY} > 1\), it is always followed by:

3.(2n+1) \(1 \leq n \leq \text{NOBJ}\) FORMAT: control command line format

\[> \text{DENSITY den}(2) \ldots \text{den}(\text{NERGY}) \]

\(\text{den}(2) \ldots \text{den}(\text{NERGY})\) are floating point modifiers.

Restriction: This command line is absent in the monochromatic case or if \(\text{NERGY} = 1\). The value of \(\text{den}(i)\) \(2 \leq i \leq \text{NERGY}\) is the density of the elemental object defined by the previous command line at the \(i\)th energy level.
3. (2 NOBJ + 2) FORMAT: control command line format

> LAST scale [seed sd]

scale is a floating point modifier, seed is an integer modifier and sd is a floating point modifier. If seed and sd are not specified, their values are assumed to be 0.

This command line indicates the end of the part of the input stream describing the elemental objects. Note that NOBJ is not explicitly read in, but is defined by the number of command lines between command line OBJECTS and the command line LAST. All previously defined densities are changed by multiplication by the value of scale. It is not necessary that there be any objects between the OBJECTS and LAST control lines; i.e. NOBJ can be 0.

Restrictions: scale > ZERO and sd ≥ 0.

If seed and sd are specified, then to each pixel density \( d \) (see Equation (5.1)) is altered by adding a random sample from a zero-mean normal distribution with standard deviation \( sd \times d \), where seed controls the random number generator for producing the instances from the normal distribution (see Section 5.3.1) as follows:

- If seed < 0, the current time (using the Linux system call "time") is used as the seed of the random number generator.
- If seed = 0, a default sequence of random numbers is produced.
- If seed > 0, a sequence of random numbers is produced that is dependent on the value of seed.

SET 4: PHANTOM GENERATION

4.1 FORMAT: control command line format

> PHANTOM [AVERAGE nave1]

Restriction: The value of the integer modifier nave1 must be positive and odd. In case AVERAGE is specified, a test phantom is generated and put on file11. The value of nave1 is assigned to the variable NAVE1, whose purpose is described in Section 5.3.1.

In case AVERAGE is not specified, a test phantom is not generated. With our conventions the user may in this case use the command line

PHANTOM IS NOT GENERATED

4.2 FORMAT: control command line format

> nelem pixel-size

Restrictions: This command line is absent if AVERAGE is not specified on the previous command line. nelem > 0 and odd, pixel-size > ZERO. The value of nelem is assigned to the variable NELEM and the value of pixel-size is assigned to PIXSIZ, the purpose of which is explained in Section 2.2.

SET 5: RAYSUM GENERATION

5.1 FORMAT: control command line format

> RAYSUM [AVERAGE nave2]

Restriction: The value of the integer modifier nave2 must be positive, odd and not greater than 13.

In case AVERAGE is specified, projection data are generated and put on file11 (following the test phantom data if such have been generated due to command line 4.1). The value of nave2 is assigned to the variable NAVE2 whose purpose is described in Section 5.3.2.

In case AVERAGE is not specified, projection data are not generated.

Restriction: If AVERAGE is not specified there must be no further follow up command lines in the CREATE command.

5.2 FORMAT: control command line format
CHAPTER 5. SNARK14 COMMANDS

> naper(1) ... naper(NAVE2)

Restriction: The value of each of the integer modifiers naper must be nonnegative and their sum must be positive.

The value of naper(i) is assigned to the variable NAPER(i) (for 1 ≤ i ≤ NAPER) whose purpose is described in Section 5.3.2.

SET 6: PROJECTION GEOMETRY SPECIFICATION

6.1 FORMAT: control command line format

> GEOMETRY

This command line introduces the projection geometry.

6.2 FORMAT: control command line format

> PARALLEL \{ UNIFORM \} \{ VARIABLE \} \{ STRIP \} \{ LINE \}

> DIVERGENT \{ ARC \} \{ TANGENT \} \{ source-to-origin \} \{ source-to-detector \}

> LINOGRAM

The first word on this command line determines whether rays in a single projection are parallel (as in Figure 2.2) or divergent (as in Figure 2.1).

In the PARALLEL case the spacing between the detectors may be the same in all projections (UNIFORM) or it may vary from projection to projection (VARIABLE). The actual size of detector spacing is determined by information read on the next command line. The ray sum in the STRIP case is the ray sum in the LINE case multiplied by the detector spacing (see Section 5.3.2).

In the DIVERGENT case, the detector strip may be a circular ARC with its center at the source or a TANGENT to this arc (see Figure 2.1). The value of the floating point modifier source-to-origin is the RADIUS of the circle on which the source is located, the value of the floating point modifier source-to-detector is the distance (STOD) of the source to the detector strip (see Figure 2.1). Restrictions: source-to-origin > ZERO and source-to-detector > ZERO.

If LINOGRAM is specified, PHANTOM AVERAGE nave1 and its follow-up line (see create command Set 4 on the preceding page) are required and therefore a phantom will be generated on file11.

In the LINOGRAM case, the following relationship between the object size, the number of projections and the number of rays per projection holds. Let 2N + 1 be the number of pixels along a side of the digitized picture of the object. Then there are a total of 2(4N + 3) projections with 4N + 3 rays per projection. Moreover, the 2(4N + 3) projections are generated over two sets of angles as follows:

\[ \theta \in \left\{ \arctan \left( \frac{2i}{4N + 3} \right) + \frac{\pi}{2} | \ - (2N + 1) \leq i \leq (2N + 1) \right\} \cup \left\{ \arctan \left( \frac{2i}{4N + 3} \right) + \pi | \ - (2N + 1) \leq i \leq (2N + 1) \right\} \]

Thus for the first set of angles we have \( \frac{\pi}{4} < \theta < \frac{3\pi}{4} \) and for the second set of angles we have \( \frac{3\pi}{4} < \theta < \frac{5\pi}{4} \). Further, LINOGRAM implies PARALLEL VARIABLE ray geometry.

Warning: Due to the assumptions in the routines ray in Section 6.4.3 and wray in Section 6.4.2, reconstructions from STRIP data may produce poor reconstructions unless VARIABLE is also specified and PINC is an integer multiple of PIXSIZ.

6.3 FORMAT: control command line format

> RAYS \{ USER user-rays \} \{ PROGRAM nelem pixel-size \} detector-spacing
If USER is specified, the real ray sum is estimated in each projection for as many rays as is the value of the integer modifier user-rays. The value of user-rays is assigned to the variable USRAYS. Restrictions: The value of user-rays must be a positive odd integer. The central one of these rays goes through the origin, the others are symmetrically distributed around the central one (see Section 2.4). In the DIVERGENT ARC case \((user-rays - 1) \times \text{detector-spacing} < \text{STOD} \times \pi\).

If PROGRAM is specified, the number of rays is calculated based on the values of nelem, pixel-size and detector-spacing. The value of USRAYS is calculated by the formula given for SNRAYS in Section 2.5, with the values of NELEM, PIXSIZ and PINC determined by nelem, pixel-size and detector-spacing. The values of nelem and pixel-size on command line 6.3 are given for the sole purpose of calculating SNRAYS; they do not have to be the same as the values of the corresponding modifiers on command line 4.2. Restriction: nelem > 0 and odd, and pixel-size > ZERO. Also \(\text{nelem} \times \text{pixel-size} / \sqrt{2} < \text{RADIUS}\).

The value of detector-spacing is the distance (PINC) between the centers of the detectors in all but the PARALLEL VARIABLE case. In this special case the distance between the centers of the detectors in a projection is the value of detector-spacing multiplied by the maximum of \(|\sin(\text{THETA})|\) and \(|\cos(\text{THETA})|\), where the angle THETA is defined as in Figure 2.2.

This line is absent in the LINOGRAM case.

Restriction: detector-spacing > ZERO.

6.4 FORMAT: control command line format

\[
> \text{ANGLES prjnum [ EQUAL SPACING ]}
\]

The value of the integer modifier prjnum is the number of projections for which projection data are to be calculated. It is assigned to the variable PRJNUM.

This line is absent in the LINOGRAM case.

Restriction: prjnum > 0 and if EQUAL SPACING is specified then prjnum > 1.

6.5 FORMAT: control command line format

\[
> \{ \text{angle}(0) \text{angle}(\text{PRJNUM}-1) \\
> \{ \text{angle}(0) \text{angle}(1) \ldots \text{angle}(\text{PRJNUM}-1) \}
\]

angle(0), angle(1), \ldots, angle(\text{PRJNUM}-1) are floating point modifiers.

The value of angle(i) is used as the value in degrees of the angle \(\text{THETA}\) for the \(i\)th projection, \(0 \leq i < \text{PRJNUM}\) (see Figures 2.1 and 2.2). In case EQUAL SPACING is specified on the previous command line, the first option indicated above is used and angle is calculated by

\[
\text{angle}(i) = \text{angle}(0) + \frac{\text{angle}(\text{PRJNUM}-1) - \text{angle}(0)}{\text{PRJNUM} - 1} i.
\]

If EQUAL SPACING is not specified, the values of angle(0), angle(1), \ldots, angle(\text{PRJNUM}-1) are read in this order from command line 6.5 and lines following 6.5 until PRJNUM floating point values are read.

The list of angles is missing in the LINOGRAM case.

SET 7: MEASUREMENT STATISTICS

7.1 FORMAT: control command line format

\[
> \text{MEASUREMENT \{ PERFECT \}}
\]

If the option PERFECT is specified, then in the calculation of raysums it is assumed that measurements are unaffected by quantum noise, scatter, additive, or multiplicative noise (see Section 5.3.2). In this case command lines 7.2 and 7.3 are to be omitted. If the option NOISY is specified, at least one of the four sources of noise mentioned above is assumed to be present. The various sources of noise are described on (possibly multiple appearances of) command line 7.2. If neither PERFECT or NOISY is specified, PERFECT is assumed.
7.2 FORMAT: control command line format

\[
\begin{align*}
\text{QUANTUM} & \quad \text{quanmn} \quad \text{quancm} \quad \text{CALIBRATION} \quad \text{quanin} \\
\text{SCATTER} & \quad \text{sctnpk} \quad \text{sctnwd} \\
\text{ADDITIVE} & \quad \text{addnmn} \quad \text{addnsd} \\
\text{MULTIPLICATIVE} & \quad \text{multnmn} \quad \text{multnsd}
\end{align*}
\]

Restriction: Command line 7.2 is omitted if PERFECT is specified on command line 7.1.

The first key-word of this command line indicates what type of noise is described by the command line. Multiple versions of this command line may appear in the input sequence at this point, one for each possible type of noise. If there is no command line 7.2 for a particular type of noise, then that type of noise will not be used in the calculation of the ray sums.

The values of the floating-point modifiers quanmn, quancm, sctnpk and sctnwd are assigned to the variables QUANMN, QUANCM, SCTNPK, and SCTNWD, whose purpose has been explained in Section 5.3.2. The value of the integer modifier quanin is assigned to the variable QUANIN, which controls the nature of the assumed calibration methods (for x-ray CT data simulation); as discussed in Section 5.3.2.1, when simulating PET data QUANIN should be set to 4. Restrictions: quanmn > ZERO, quancm > ZERO (these restrictions on quanmn and quancm do not apply when PET is simulated; see Section 5.3.2.1 for details), sctnpk > ZERO and sctnwd \( \geq \) PINC, \( 1 \leq \) quanin \( \leq 4 \).

The values of the floating point modifiers addnmn and addnsd are the mean, ADDNMN, and standard deviation, ADDNSD, of the normal distribution an instance from which is used as additive noise (see Section 5.3.2), and the values of the floating point modifiers multnmn and multnsd are the mean, ULTNMN, and standard deviation, ULTNSD, of the normal distribution an instance from which is used as multiplicative noise. Restriction: \( |\text{multnmn}| > \) ZERO. In mathematical notation, in the presence of these types of noise SNARK14 provides an estimate \( P_{\text{new}} \) of the ray sum based on the estimate \( P_{\text{old}} \) of the ray sum without additive or multiplicative noise by the formula

\[
P_{\text{new}} = P_{\text{old}} \times \text{gauss}(\text{ULTNMN}, \text{ULTNSD}) + \text{gauss}(\text{ADDNMN}, \text{ADDNSD}),
\]

see Section 6.4.18 for definition of \text{gauss}.

In case there is more than one command line 7.2 with a particular type of noise in the input sequence, only the last of these command lines is effective. If there is no command line 7.2 for a particular type of noise, default values are assigned to the variables mentioned above. These default values are all zeros. For SCATTER, ADDITIVE, and MULTIPLICATIVE noise there are logical variables, (SCTNFL, ADDNFL, and ULTNFL, respectively) the value of each of which is set to TRUE if and only if a command line 7.2 for that particular noise is present. The presence of QUANTUM noise is indicated by the value of QUANIN > 0.

7.3 FORMAT: control command line format

\[ > \quad \text{SEED} \quad [ \text{seed} ] \]

Restriction: This command line appears in the input sequence only when it is preceded by a command line of the form 7.2 with one of the key-words QUANTUM, ADDITIVE or MULTIPLICATIVE. It controls the random number generator that is used for producing instances from normal distributions for the various types of noise.

The value of the integer modifier seed controls the random number sequence as follows. If no seed value is specified, 0 is assumed.

If seed < 0, the current time (using the Linux system call “time”) is used as the seed to the random number generator.

If seed = 0, a default sequence of random numbers is produced.

If seed > 0, a sequence of random numbers is produced that is dependent on the value of seed.

7.4 FORMAT: control command line format

\[ > \quad \text{BACKGROUND} \quad \text{backgr}(1) \ldots \text{backgr}(\text{ENERGY}) \]
The value of the floating-point modifier backgr(i) is the value of $B_i$, the assumed attenuation by the background material at energy level $i$ (see Section 5.3.2).

**SET 8: RUN COMMAND**

8.1 FORMAT: control command line format

> RUN

5.4 PICTURE

> PICTURE { RECONSTRUCTION nelem pixel-size }

This command specifies the values of the variables NELEM and PIXSIZ for the picture to be reconstructed (see Section 2.2).

If RECONSTRUCTION is specified, these values are provided by the integer modifier nelem and floating-point modifier pixel-size respectively. **Restrictions:** nelem > 0 and odd, and pixel-size > ZERO.

If TEST is specified then it is assumed that file11 is present and it contains the following command lines:

I. Command lines that are in the order and format of Sets 1, 2, 3, and 4 of the CREATE follow up sequence. Apart from specifying NELEM and PIXSIZ, these command lines have the purpose of keeping a complete record of how the test-phantom has been created.

II. These are followed by the values given to the pixels in the test-phantom. The order of pixels is row-by-row (top row first) and, within rows, left-to-right. Each new row starts on a new command line.

This instruction results in the beginning of the creation of recfil, a binary file that is used during the analysis phase (see Section 3.3). NELEM and PIXSIZ are stored on this file, as well as the name-of-the-pattern (from command line 1.1 of the CREATE follow up sequence) and the pixel values of the phantom, if TEST is specified. The name of the pattern appears in an identifying header of any phantom-dependent output produced during the analysis phase.

5.5 PROJECTION

> PROJECTION { OLD [BEAM HARDENING CORRECTION] }

The purpose of this command is to create the binary file prjfil (see Section 3.2.1), which contains information on the projection data both for the reconstruction subphase and the analysis phase. In addition, the PROJECTION command causes the determination of the values of all variables (other than NELEM and PIXSIZ) that are needed by the reconstruction subphase (e.g., PINC, PRJNUM, NRAYS, etc.). Of particular importance is the assignment to the variable AVEDEN, the estimated value based on the projection data, of the average density of the picture to be reconstructed. The exact method by which AVEDEN is calculated is explained in Section 6.3.3. **Restriction:** A PROJECTION command must be preceded by a PICTURE command in the Initialization and Reconstruction Input file.

If OLD is specified, it is assumed that prjfil is already present. In this case, values of the variables that are needed in the reconstruction subphase are read in from prjfil, but these values are not echo-checked on the Initialization and Reconstruction Output file. For this reason the use of this option is recommended only if the creation of prjfil by the appropriate alternative option (REAL or PSEUDO) would be time consuming.

If REAL is specified, it is assumed that file11 is present and is positioned at the beginning of the following sequence of command lines:

I. Command lines that are of the order and format of Sets 1, 2, 3, 5, 6, and 7 of the CREATE follow up sequence. If command line 6.2 specifies LINOGRAM, then the projection angles are computed to a high degree of accuracy. The projection angles in the projection data (see below) are expected to match these computed angles. **Restrictions:** On command line 6.3 only the USER option may be used. In the DIVERGENT case detector-spacing $\times$ user-rays $< \pi \times$ source-to-detector and $\sqrt{2} \times$ source-to-origin $\geq$ nelem $\times$
pixel-size. (The values of nelem and pixel-size are determined by the PICTURE command that precedes the
PROJECTION command.)

II. These are followed by command lines containing the projection data. These are arranged projection-
by-projection. For each projection, the first command line contains the projection angle THETA of Figures
2.1 and 2.2 in radians and the same angle in degrees (restriction: these must match with the angles as
specified in degrees by command line 6.5), and the following command lines contain the USRAYS ray sums,
where the value of USRAYS is determined by the integer modifier user-rays on command line 6.3. See
Appendix B for instructions on how to create a file11 containing user supplied data.

If REAL is specified, the geometry of data collection described on file11 is also the geometry of data
collection described on prjfil.

If BEAM HARDENING CORRECTION is specified, the projection data stored on file11 are corrected
for beam hardening that occurs when a polychromatic x-ray source is used. The corrected projections are
estimates of monochromatic projections at the first energy level. This option is ignored if called in a run
that uses monochromatic projections. The option requires the follow-up sequence described below.

> niters ndegree
The integer modifier niters is the number of iterative steps in the correction. The integer modifier ndegree
is the degree of the polynomial used to approximate monochromatic projection values based on the
polychromatic projection data. The coefficients of this polynomial are provided on the next line of the
input:

> a(0) ... a(ndegree)
The floating-point modifiers a(0) ... a(ndegree) are the ndegree+1 coefficients of the polynomial.

If the value of niters is 0, the rest of the followup sequence is not read and can be omitted.

> nergy
The integer modifier nergy must have the same value as NERGY, i.e., the number of energy levels as
specified in Set 2 of the CREATE followup sequence (it is here just as means of verification).

The beam hardening correction uses iterative data refinement in order to improve on the rough correction
provided by the above polynomial [25]. The attenuation values at energy levels 2 to energy(nergy) are
approximated based on the piecewise linear function provided by the user on the following lines of the input:

> npoints
The integer modifier npoints is the number of points used in the piecewise linear approximation of the pixel
values at energy levels 2 ... nergy based on the value at the first energy level.

> x(2)(1)  y(2)(1)
> ...
> x(2)(npoints)  y(2)(npoints)
> ...
> x(nergy)(1)  y(nergy)(1)
> ...
> x(nergy)(npoints)  y(nergy)(npoints)
The interpretation of these sequence of floating point modifiers is the following.
It is assumed that if the density is 0 at the first energy level, then it is also 0 at all other energy levels. Further, for $2 \leq i \leq \text{nergy}$ and $1 \leq j \leq \text{npoints}$, it is assumed that if the density is $x(i)(j)$ at the first energy level, then it is $y(i)(j)$ at the $i$th energy level.

Restrictions: If BEAM HARDENING CORRECTION is specified, the projection angles need to be specified in increasing order, i.e. $\text{angle}(i) < \text{angle}(i+1)$ on control command line 6.5.

If PSEUDO is specified, the PROJECTION command line must be followed by command lines that are of the order and format of Sets 1, 6, and 7 of the CREATE follow up sequence. Restriction: PSEUDO can only be specified if the PICTURE command specified TEST. In this case, prjfil will contain the pseudo ray sums of the NELEM $\times$ NELEM digitized picture that is the test phantom (see Sections 2.2 and 2.3) for all rays of the geometry specified in Set 6 of the CREATE follow up sequence. These ray sums will be contaminated by noise according to the specifications of Set 7 of the CREATE follow up sequence. It will be assumed that the number of energy levels (NERGY) is 1.

Warning: In all cases, the ray sums stored on prjfil will be corrected for bias. Thus, if REAL is specified, then the ray sum on file11 is first reduced by ADDNNMN and then is divided by ULTNNMN prior to being stored on prjfil. If the user needs the value of a ray sum, the function \texttt{prdta} (see Section 6.3.6.2) returns the unbiased value on prjfil. The values of ULTNNMN and ADDNNMN are available to the user, so that the original biased value may be recalculated.

The prjfil will contain an 80 character long name-of-the-projection. If OLD is specified, this is of course the already existing name-of-the-projection on the file. If REAL is specified, the name-of-the-projection is what is read in from command line 1.1 of the CREATE follow up sequence on file11. If PSEUDO is specified, the name-of-the-projection is provided by the line immediately following the PROJECTION command line.

In any output produced during the analysis phase reporting on reconstructions based on prjfil the name-of-the-projection appears in an identifying header.

Warning: The file punch records only the first 30 characters of the name-of-the-projection (see Section 5.13).

### 5.6 SELECT

As will be discussed in Section 6.4.1, a function is available to the user for selecting the next ray to be considered in a reconstruction by SNARK14. This function is called \texttt{PICK(NP,NR)} and it returns a projection number $NP$ ($0 \leq NP < \text{PRJNUM}$) and a ray number $NR$ (if USER is specified FUSRAY $\leq NR < \text{LUSRAY}$, and if SNARK is specified FSNRAY $\leq NR < \text{LSNRAY}$, see Section 2.5).

The word modifiers type1 and type2 may have values RAYSEQ, PROJSEQ, and RANDOM. Restriction: $n1 > 0$ and $n2 > 0$.

When all four modifiers type1, n1, type2, n2 are present, then the command is interpreted to mean that repeatedly $n1$ actions of type1 are followed by $n2$ actions of type2. If $n2$ is absent, SNARK14 behaves as if $n2$ were infinity (i.e., $n1$ actions of type 1 are followed by as many actions of type2 as there are calls of \texttt{PICK(NP, NR)}). If only type1 is present, SNARK14 behaves as if $n1$ were infinity. Restriction: If both type1 and type2 are present, then exactly one of them must be RANDOM.

In RANDOM mode, \texttt{PICK(NP,NR)} returns a randomly selected ray in a randomly selected projection. In order to understand how the other two modes operate, we need to specify a fairly complicated ordering mechanism. Let $A$ and $B$ be integers in the ranges $[AF, AL]$ and $[BF, BL]$, respectively, and let $AI$ and $BI$ be positive integers. The following C++-like code describes a way of writing all pairs $\{(A,B) | AF \leq A \leq AL, BF \leq B \leq BL\}$ in a particular order without any repeats:

```c++
for (int i = AF; i < min(AF+AI, AL+1); ++i) {
    for (int j = BF; j < min(BF+BI, BL+1), ++j) {
        for (int b = j; b < BL+1; b += BI) {
            for (int a = i; a < AL+1; a += AI) {
                printf("%d %d\n", a, b);
            }
        }
    }
}
```
For example, if $AI = 1$ and $BI = 1$, the sequence will be $(AF,BF), (AF+1,BF), \ldots, (AL,BF), (AF,BF+1), \ldots, (AL,BF+1), \ldots, (AL,BL)$. If $AF = 5$, $AL = 7$, $AI = 2$, $BF = 3$, $BL = 7$, $BI = 3$, the sequence will be $(5,3), (7,3), (5,6), (7,6), (5,4), (7,4), (5,7), (7,7), (5,5), (7,5), (6,3), (6,6), (6,4), (6,7), (6,5)$.

We use the notation $\text{SEQ}(AF,AL,AI,BF,BL,BI)$ to denote the infinite sequence of pairs $(A,B)$ produced by repetition of the sequence described above.

If type1 is RAYSEQ or PROJSEQ or type2 is RAYSEQ or PROJSEQ, the SELECT command line must be followed by a command line in control command line format whose content is

```
> STEP mod1 mod2
```
specified). In order to achieve efficiency, it is important that the \( P \) be decomposable into many (preferably small) prime factors.

If this command is omitted, the default behavior of PICK is as if

\[
\text{SELECT USER EFFICIENT}
\]

had been executed.

### 5.7 BASIS

\[
> \text{BASIS} \begin{cases} \text{PIXEL} \\ \text{BLOB} \text{[support shape delta]} \end{cases}
\]

The BASIS command controls the basis functions for the algebraic algorithms. They may either be PIXELs or BLOBs (see Section 2.2). The command has no effect on transform methods of reconstruction, but it changes the behavior of the series expansion methods [29]. If BLOB is selected, it may optionally be followed by three floating point parameters that control the shape of the blob. If they are omitted, they are set to the following default values:

\[
\begin{align*}
\text{DELTA} &= 2 \times \text{pixel-size}/\sqrt{3}, \\
\text{SHAPE} &= 11.2828631556, \text{ and} \\
\text{SUPPORT} &= 1.7865601396 \times \text{delta}.
\end{align*}
\]

If this command is omitted, \text{BASIS PIXEL} is assumed.

### 5.8 EXECUTE

“To seek it with thimbles, to seek it with care;

To pursue it with forks and hope;

To threaten its life with a railway share;

To charm it with smiles and soap!

“For the Snark’s a peculiar creature, that won’t

Be caught in a common place way.

Do all that you know, and try all that you don’t:

Not a chance must be wasted today!”

Fit the Fourth - The Hunting

The Hunting of the Snark (an agony in eight fits)

by Lewis Carroll

\[
> \text{EXECUTE} \begin{bmatrix} \text{ZERO} \\ \text{AVERAGE} \\ \text{CONTINUE} \\ \text{PHANTOM} \end{bmatrix} \text{alname} \begin{bmatrix} \text{CONTOUR} \\ \text{SMOOTH} \end{bmatrix}
\]

\textit{Restriction:} This command must be preceded by a PICTURE and a PROJECTION command in the Initialization and Reconstruction Input file.

The EXECUTE command line must always be followed by a command line containing
Only the first 80 characters of this command line are significant. Characters in excess of 80 are discarded. The name-of-the-execution appears on all outputs produced during the analysis phase that report on reconstructions produced by this EXECUTE command line. A command line beginning with an asterisk is not treated as a comment here. It is the name of the execution.

Warning: The file punch records only the first 30 characters of the name-of-the-execution (see Section 5.13).

The EXECUTE command produces reconstructions from the projection data on prjfil and stores them on the recfil. If an iterative algorithm is used, the reconstruction after each iteration (together with the iteration number) is stored on recfil. The total number of iterations caused by the EXECUTE command is determined by the most recently executed STOP command (see Sections 5.9 and 6.1). When BASIS BLOB is in effect, blob reconstructions are converted from blobs to pixels before storing them on recfil.

The options ZERO, AVERAGE, CONTINUE, and PHANTOM determine how the reconstruction region is initialized. (If these are absent, ZERO is assumed.) If ZERO is specified, then the elements of the array that is used to store the reconstructed picture are set to 0.0 at the very beginning of the reconstruction process. If AVERAGE is specified, then the elements of the array that is used to store the reconstructed pictures are set to AVEDEN at the beginning of the reconstruction process. (See Section 6.3.3 for definition of AVEDEN.) If CONTINUE is specified, then the content of the reconstruction region (i.e., the reconstructed picture due to the last EXECUTE command) is used unaltered at the beginning of the reconstruction algorithm. This enables us, for example, to use the result of an algorithm as the starting point (0’th iterate) of a different algorithm. If CONTINUE is specified by the first EXECUTE command in the initialization and reconstruction input file, it is treated as if ZERO had been specified. If the previous algorithm produced a pixel reconstruction and the current algorithm is a blob based algorithm, the reconstruction is converted from pixels to blobs before the algorithm is invoked. Similarly, if the previous reconstruction was a blob reconstruction and the current algorithm is a pixel algorithm, the reconstruction is converted from blobs to pixels before the algorithm is invoked. If the previous algorithm produced a blob reconstruction and the current algorithm is also a blob algorithm, then the blob parameters must be the same for both executions. If the blob parameters have changed, the algorithm is not executed. If PHANTOM is specified the reconstruction region is initialized to the phantom that was read in (see Section 5.4).

The word modifier algname may assume the following values: BACKPROJECTION, CONVOLUTION, RFL, FOURIER, DCONV, ART, MART, QUADRATIC, SIRT, EMAP, LINO, ALP1, ALP2, ALP3, ALP4, ALP5, ALB1, ALB2, ALB3, ALB4, and ALB5. (The algorithms ART, MART, QUADRATIC, SIRT, ALB1, ALB2, ALB3, ALB4, and ALB5 produce either pixel or blob images depending on the BASIS -see Section 5.7- that is in effect. The other algorithms always produce pixel images.) All but ALP1, ALP2, ALP3, ALP4, ALP5, ALB1, ALB2, ALB3, ALB4, and ALB5 refer to built-in SNARK14 algorithms that can be called to do a reconstruction. They are described in detail in Chapter 7. If any of ALP1, ALP2, ALP3, ALP4, ALP5, ALB1, ALB2, ALB3, ALB4, and ALB5 is specified, the reconstruction algorithm is defined by the user in a C++ class, whose name is alp1, alp2, alp3, alp4, alp5, alb1, alb2, alb3, alb4 or alb5, respectively (see Section 6.1). This class must be compiled and bound with the rest of SNARK14 prior to execution. The default implementations of these user defined routines are do-nothing reconstruction algorithms. That is, they leave the reconstruction region unchanged.

If either CONTOUR or SMOOTH is specified, the name-of-the-execution command line is followed by a command line in control command line format

```plaintext
> threshold weight-1 weight-2 weight-3
```

and an

```plaintext
> iteration-flag-line
```

(see Section 4.5) Restriction: These two command lines are absent if neither CONTOUR nor SMOOTH is specified on the EXECUTE control command line.

The effect of CONTOUR and SMOOTH is that some of the reconstructions are modified prior to being stored on recfil. If BASIS BLOB is in effect, the modifications are performed after the blob image is converted to a pixel image. These modifications have the following forms.
If CONTOUR is specified, and weight-3 ≤ ZERO, all reconstructed densities that are less than or equal to threshold are set to weight-1, and all reconstructed densities that are greater than threshold are set to weight-2. If weight-3 > ZERO, essentially the same process is carried out except that the user-defined value of threshold is replaced by another value defined as follows. While executing the PROJECTION command, the average density of the picture to be reconstructed is estimated based on the projection data and is stored in a variable called AVEDEN (see Section 6.3.3 for a precise definition of AVEDEN). If weight-3 > ZERO, threshold is chosen so that the average density of the contoured picture is as near to AVEDEN as is possible for the given weight-1 and weight-2, unless AVEDEN < weight-1 or AVEDEN > weight-2 or if the reconstruction (prior to contouring) has the same value in all pixels or blobs. (If any of these conditions exist, the reconstruction is not changed and a warning message to that effect is printed.)

If SMOOTH is specified, let $V_1 \ldots V_9$ denote the reconstructed densities in a pixel and its neighbors before smoothing, as indicated by the diagram below.

```
  V_6  V_2  V_7
  V_3  V_1  V_4
  V_8  V_5  V_9
```

The value of the center pixel that is stored on recfil will be

$$\frac{W_1 \times V_1 + W_2 \times \sum_{i=2}^{5} f_i V_i + W_3 \times \sum_{i=6}^{9} f_i V_i}{W_1 + W_2 \times \sum_{i=2}^{5} f_i + W_3 \times \sum_{i=6}^{9} f_i},$$

where

$$f_i = \begin{cases} 
1, & \text{if } |V_i - V_1| \leq \text{threshold}, \\
0, & \text{if } |V_i - V_1| > \text{threshold},
\end{cases}$$

and $W_i$ denotes the value of weight-$i$ from the command line, for $1 \leq i \leq 3$. If the pixel labeled by 1 is on an edge, and therefore doesn’t have a neighbor labeled by $i$, then $f_i$ is assumed to be 0.

If the fraction defined above has a value greater than INFIN (an overflow condition, see Section 2.1), SNARK14 stores INFIN for the corresponding pixel and gives a warning message on the Initialization and Reconstruction Output file.

The iteration-flag-line determines which of the reconstructions produced by EXECUTE are altered in this fashion prior to being stored on recfil. If $fl(q) > 0$, then the operation (of contouring or smoothing) will be performed on the reconstruction after $q$ iterations (unless the number of iterations is exactly $q$) if $q > 0$ and on the final reconstruction of the EXECUTE command if $fl(0) > 0$. (For definition of “reconstruction after $q$ iterations”, see Section 5.9.) The following sequence can be used to save both the original and smoothed reconstructions from the convolution algorithm on recfil:

```
STOP ITERATION 2
EXECUTE CONVOLUTION SMOOTH
Both original and smoothed convolution reconstructions
0.5 4.0 2.0 1.0
1
... rest of convolution parameters
```

These command lines may have to be followed with other command lines, containing input required by the algorithm to be executed. The formats and contents of these command lines for the internal SNARK14 algorithms are described in Chapter 7.
5.9 STOP

The purpose of this command is to control the number of iterations used by an algorithm. It terminates an iterative algorithm when the specified stopping criterion is satisfied. This is achieved as follows (see Section 6.1 for additional details).

The EXECUTE command (Section 5.8) causes SNARK14 to execute the instructions of a reconstruction algorithm. Some algorithms are iterative, i.e., the same set of instructions need to be executed repeatedly, so as to improve the result. One complete execution of a set of such instructions is called an iteration.

SNARK14 updates a NELEM×NELEM array in each iteration. The elements of this array are perceived as estimates of the pixel densities of the picture to be reconstructed. For this reason, the digitized picture whose values are based on the values in this array after q iterations is called the reconstruction after q iterations. In the blob case, the NELEM×NELEM array is the result of converting the blob reconstruction to a pixel reconstruction using blob2pix (see Section 6.3.4.1).

A single EXECUTE command causes as many iterations of an iterative algorithm to be carried out as is specified by the most recently executed STOP command. If there are no STOP commands executed prior to the EXECUTE command, the behavior of the EXECUTE is the same as if

\[
\text{STOP ITERATION} = 1
\]

had been executed.

If ITERATION is specified, an EXECUTE command results in iter iterations. \textit{Restriction}: iter > 0.

If TERMINATION is specified, then at the end of each iteration the Run method of an instance of the \texttt{termtest} class, specified by the word modifier VARIANCE, MLST, KLDS, RESI, TRM1, or TRM2, is invoked. This method tests whether certain conditions are satisfied and SNARK14 decides whether to carry out another iteration based on the outcome of these tests.

If VARIANCE is specified, the iterative process is terminated as follows. Let \( \rho^q_i \) be the density assigned to the \( i \)th pixel of the reconstruction after \( q \) iterations and before any SMOOTHING or CONTOURING that may have been specified (see Section 5.8). Let \( \text{AREA} = \text{NELEM}^2 \) be the number of pixels in the reconstruction. Let \( \overline{\rho}^q \) be the average density of the reconstruction after \( q \) iterations. We define

\[
v^q = \frac{1}{\text{AREA}} \sum_{i=0}^{\text{AREA}-1} (\rho^q_i - \overline{\rho}^q)^2.
\]

(5.15)

The iterative process stops after the \( q \)th iteration if \( q > 1 \) and \( |v^q - v^{q-1}| < \epsilon \times v^{q-1} \). \textit{Restriction}: \( \epsilon > 0 \).

If MLST is specified, the execution of the algorithm is stopped as soon as the indicator function \( D(x) \), which is advocated to be used for MLEM-STOP in [5], reaches a value which is less than or equal to 1. It is defined as:

\[
D(x) = \frac{\sum_{i=1}^{I} \left( b_i - \sum_{j=1}^{J} a_{ij} x_j \right)^2}{\sum_{i=1}^{I} \sum_{j=1}^{J} (a_{ij} x_j)},
\]

(5.16)

where \( x \) denotes the reconstructed image, \( I \) denotes the number of lines of response (LOR), \( J \) denotes the number of pixels for which the activity needs to be determined by the reconstruction process, \( b_i \) is defined as the count of events in the \( i \)th LOR, and \( a_{ij} \) is defined as length of intersection of the \( i \)th LOR with the \( j \)th pixel, which is equivalent to the probability of counting an event generated in the \( j \)th pixel for the \( i \)th LOR.
LOR. MLST supports the output of the current value of \( D(x) \) by setting the RPRT flag and will report to the command line as well as to the file RPRT.mlst. \([n]\) indicates the \( n \)th iteration of the iterative algorithm; specifying the value of \( n \) will cause STOP to report only on the first, last and every \( n \)-th iteration.

If KLDS is specified, the iterative process is terminated if the value of the Kullback-Leibler distance (KLDS) of the reconstructed image is less than or equal to the specified value of epsilon. The Kullback-Leibler distance is a proximity value and it is defined as:

\[
KL(x) = \sum_{i=1}^{I} \left( b_i \ln \frac{b_i}{\sum_{j=1}^{J} a_{ij} x_j} + \sum_{j=1}^{J} a_{ij} x_j - b_i \right),
\]

where \( x \) denotes the reconstructed image, \( I \) denotes the number of lines of response (LOR) and \( J \) denotes the number of pixels for which the activity needs to be determined by the reconstruction process, \( b_i \) is defined as the count of events in the \( i \)th LOR and \( a_{ij} \) is defined as the probability of counting an event generated in the \( j \)th pixel for the \( i \)th LOR. KLDS supports the output of the current value of \( Pr(x) \) by setting the RPRT flag and will report to the command line as well as to the file RPRT.klds. Specifying the value of \( n \) will cause STOP to report only on the first, last and every \( n \)-th iteration.

If RESI is specified, the reconstruction process is stopped once the residual reaches a value less than or equal to the specified epsilon. Calculation of the residual is performed similarly to its calculation for the eval file; see (5.31). RESI supports the output of its current value by setting the RPRT flag and will report to the command line as well as to the file RPRT.resi. Specifying the value of \( n \) will cause STOP to report only on the first, last and every \( n \)-th iteration.

If WSQD is specified, the reconstruction is terminated if the value of the weighted squared distance of the reconstructed image is less than or equal to the specified value of epsilon. The weighted squared distance is a proximity value [46] and it is defined as:

\[
WS(x) = \sum_{i=1}^{I} \left( \frac{b_i - \sum_{j=1}^{J} a_{ij} x_j}{\sum_{j=1}^{J} a_{ij}} \right)^2,
\]

where the meaning of the various variables is the same as for the KLDS proximity value above. WSQD supports the output of its current value by setting the RPRT flag and will report to the command line as well as to the file RPRT.wsqd. Specifying the value of \( n \) will cause STOP to report only on the first, last and every \( n \)-th iteration.

If TRM1 or TRM2 are specified, the termination test is defined by the user in a C++ class whose name is trm1_class or trm2_class, respectively (see Section 6.1). This class must be compiled and bound with the rest of SNARK14 prior to execution. The Init method of this class is invoked during the STOP command processing so that it may read its run time parameters, if any, using the methods of the InputFile_class (see Section 6.3.8).

### 5.10 SUPERIORIZE

\[
> \text{SUPERIORIZE N a b \{ TVAR SMOO SCR3 SCR4 SCR5 \} [POSI] [ATL1 ATL2] [RPRT [u]]}
\]

SUPERIORIZE is an implementation of the Superiorization Methodology [21]. If this command is inserted into the INPUT file, then any EXECUTE command calling an iterative algorithm that follows it in the INPUT file will be automatically superiorized according to a specified secondary optimization criterion, whose name is one of TVAR, SMOO, SCR3, SCR4 or SCR5. (The first two of these are built into SNARK14, the other three are user defined; see Section: 5.10.1.) We explain the roles of the various modifiers in the
SUPERIORIZE control command line using a pseudocode specification (Algorithm 5.1), in which the name of the secondary criterion is denoted by $\phi$. (Warning: This command can be applied only with PIXEL basis functions.)

Suppose that the iterative algorithm that is to be superiorized is specified by the algorithmic operator $P$, such that if the AREA-dimensional vector $x$ specifies the contents of the array that is used to store the reconstructed picture at the beginning of an iterative step, then $Px$ specifies the contents of the same array at the end of the iterative step. The array in question is referred to by the name $\text{recon}$ in Sections 6.1 and 6.2. The pseudocode below defines how the superiorized version of the iterative algorithm behaves; the next few lines explain some of the terminology in the pseudocode.

The stopping criterion is provided by the command STOP of Section 5.9.

The notation $\text{random}(k, \ell)$ denotes a randomly selected integer not smaller than $\ell$ and not larger than $k$. The code to generate this integer makes use of the function Rand; see Section 6.4.17.

We use $x^{(k)}$ to denote the AREA-dimensional column vector whose $j$th component, $x^{(k)}_j$ is $\text{recon}[j-1]$ after the $k$th step. In particular, $x^{(0)}$ represents the contents of the $\text{recon}$ array at the beginning of the reconstruction process, as determined by the ZERO, AVERAGE, or CONTINUE option of the EXECUTE command (see Section 5.8).

The choice of a “nonascending vector for $\phi$ at $x^{(k,n)}$” is discussed in Section 5.10.2.

The set $\Delta$ is the set of all AREA-dimensional vectors unless POSI is specified, in which case an AREA-dimensional vector is in $\Delta$ only if all its components are nonnegative. (Warning: Specifying POSI may result in an endless loop if combined with a reconstruction algorithm that allows negative values in the reconstruction, such as ART without MODE LOWER 0.)

Algorithm 5.1 Superiorized Version of an Iterative Algorithm

1. set $k = 0$
2. set $\ell = 0$
3. while stopping criterion is not satisfied
4. if ATL1 has been specified set $\ell = k$
5. if ATL2 has been specified set $\ell = \text{random}(k, \ell)$
6. set $n = 0$
7. set $x^{(k,n)} = x^{(k)}$
8. while $n < N$
9. set $v^{(k,n)}$ to be a nonascending vector for $\phi$ at $x^{(k,n)}$
10. set $\text{loop}=true$
11. while $\text{loop}$
12. $\beta = b \times a^\ell$
13. set $\ell = \ell + 1$
14. set $z = x^{(k,n)} + \beta v^{(k,n)}$
15. if $z \in \Delta$ and $\phi(z) \leq \phi(x^{(k)})$ then
16. set $n = n + 1$
17. set $x^{(k,n)} = z$
18. set $\text{loop} = false$
19. \textbf{set} \( x^{(k+1)} = P x^{(k,N)} \)
20. \textbf{set} \( k = k + 1 \)
21. \textbf{return} \( x^{(k)} \)

SUPERIORIZE supports the output of the current values of \( \ell \) and \( \phi \) by setting the RPRT flag and will report to the command line as well as to the file RPRTSuperiorization. Specifying the value of \( n \) will cause SUPERIORIZE to report only on the first, last and every \( n \)-th iteration.

5.10.1 Secondary optimization criteria

The secondary optimization criterion \( \phi \) indicates how well a vector \( x \in \Delta \) satisfies a desired condition. A vector \( x_1 \in \Delta \) is considered superior to the vector \( x_2 \in \Delta \) if \( \phi(x_1) < \phi(x_2) \). Currently, there are two built-in secondary optimization criteria in SNARK14: TVAR and SMOO.

TVAR calculates the total variation (TV) of a reconstruction \( x \) and is defined as:

\[
TV(x) = \sum_{c \in C} \sqrt{(x_c - x_{\rho(c)})^2 + (x_c - x_{\xi(c)})^2},
\]

(5.19)

where \( C \) is the set of all indices of pixels that are not in the rightmost column or the bottom row of the pixel array. For any pixel with index \( c \) in \( C \), \( \rho(c) \) and \( \xi(c) \) are the indices of the pixels to its right and below it.

SMOO calculates a measure of smoothness. It is an implementation of the penalty function \( \psi \) recommended in [53] and is defined as:

\[
\psi(x) = \sum_{r \in M} \left( x_r - \frac{1}{8} \sum_{l \in M_r} x_l \right)^2,
\]

(5.20)

where \( x \) is a reconstructed image, \( M \) is the set of indices \( r \) such that the \( r \)-th pixel is not on the border of the image region and \( M_r \), for \( r \in M \), is the set of indices associated with the eight pixels neighboring the \( r \)-th pixel.

If SCR3, SCR4 or SCR5 are specified, the secondary criterion must be defined by the user in a C++ class whose name is \texttt{scr3\_class}, \texttt{scr4\_class} or \texttt{scr5\_class}, respectively (see Section 6.1). This class must be compiled and bound with the rest of SNARK14 prior to execution. The \texttt{Init} method of this class is invoked during the SUPERIORIZE command processing so that it may read its run time parameters, if any, using the methods of the \texttt{InputFile\_class} (see Section 6.3.8).

5.10.2 Nonascending vectors

For the Superiorization Methodology to work as presented in [21], it is necessary to obtain a nonascending vector for the secondary optimization criterion \( \phi \) at the point \( x^{(k,n)} \), see line 9 of Algorithm 5.1. We define \( d \) to be of a nonascending vector for \( \phi \) at a point \( x \) if the following condition is satisfied:

\[
\text{there is a } \delta > 0 \text{ such that for all } \lambda \in [0, \delta], \quad (x + \lambda d) \in \Delta \text{ and } \phi(x + \lambda d) \leq \phi(x).
\]

(5.21)

The set \( \Delta \) is defined just above Algorithm 5.1.

One way to obtain a nonascending AREA-dimensional vector \( d \) is specified by Theorem 2 of [21], as follows. Consider any AREA-dimensional vector \( g \) that satisfies the property: For \( 1 \leq j \leq J \), if the \( j \)-th component \( g_j \) of \( g \) is not zero, then the partial derivative \( \frac{\partial \phi}{\partial x_j} (x) \) of \( \phi \) at \( x \) exists and its value is \( g_j \). Define \( d \) to be the zero vector if \( \| g \| = 0 \) and to be \( -g / \| g \| \) otherwise. Then \( d \) is a nonascending vector for \( \phi \) at \( x \). There exist other methods to obtain nonascending vectors, but the one just described is a powerful one; for example, it is guaranteed to work if \( \phi \) is a convex function.

Currently, there are only two built-in procedures in SNARK14 to compute nonascending vectors. They compute a nonascending vector for the cases when \( \phi(x) \) is the \( TV \) of (5.19) or the \( \psi(x) \) of (5.20), respectively, and they are invoked appropriately when the keywords TVAR and SMOO are used. (For example,
when the keyword TVAR is used, then SNARK14 will employ a procedure to compute a nonascending vector for the secondary optimization criterion $TV(x)$.

If SCR3, SCR4 or SCR5 are specified, the procedure to compute the nonascending vector for the corresponding secondary criteria must be defined by the user in a C++ class whose name is `nav3_class`, `nav4_class` or `nav5_class`, respectively (see the previous subsection and Section 6.1). This class must be compiled and bound with the rest of SNARK14 prior to execution (see Appendix D3).

### 5.11 EVALUATE

“My poor client’s fate now depends on your votes.”

Here the speaker sat down in his place,
And directed the Judge to refer to his notes
   And briefly to sum up the case.

But the Judge said he had never summed up before;
So the Snark undertook it instead,
And summed it so well that it came to far more
   Than the witness ever had said!

Fit the Sixth - The Barrister’s Dream
The Hunting of the Snark (An agony in eight fits)
by Lewis Carroll

> EVALUATE

This command causes the evaluation of some quantitative measures of the overall difference between a test picture and reconstructions. (Restriction: The test picture must be present on recfil.) For the purpose of comparison only, the pixel values in both the test picture and the reconstruction are interpreted according to the current values of LOFL, UPFL, LOWER and UPPER (see Section 5.2). The measures of difference are reported in a file called eval, see Section 3.3.

The EVALUATE command line must always be followed by a command line containing

> name-of-the-evaluation

This name of the evaluation as it appears in the first line of the eval file.

The name-of-the-evaluation command line is followed by a region selection command line:

> 

The effect on evaluation with the setting of a density window is very different from that of the flags: LOFL, and UPFL, and density thresholds: LOWER and UPPER as described in Section 5.2. The latter has the effect of clipping both the phantom and reconstruction densities to the specified density range, the pixels with clipped density values are then used in the evaluation process. (See also the remarks on the computation of residual given at the end of this section.)

If SELECTIVE is chosen, it has to be followed by specifications of the regions. Each region is defined by a region specification line:
> shape cx cy u v ang [lowden highden]

The input of region specifications is terminated by the line

> LAST

In each region specification line, the keyword “shape” describes the type of object used to define the region. This keyword can either be ELIPSE or RECTANGLE. The next five parameters have the same meanings as in object definitions for the phantom (see command Set 3 on page 35) that specify the center coordinates, the sizes of the principal axes and the orientation of the object. If the specified region is not entirely within the picture region, it is clipped at the boundaries and a warning message is issued. The last two parameters lowden and highden are optional for setting the density window within each region. The usage is the same as with the WHOLEPIC command line described above. If more than one region is specified, the measures are computed separately for each region.

The EVALUATE command input is completed with an

> iteration-flag-line
(see Section 4.5). The first digit controls which measures will be reported on the eval file for the last iteration. The other digits on the iteration-flag-line can be set either to 0 or to the same as the first digit. The eval file does not report the measures for an iteration if \( f_l(q) = 0 \).

We now define the measures provided by EVALUATE. We use \( \rho_{i,j}^q \) to denote the density assigned to the pixel in the \( i \)th row and \( j \)th column of the reconstruction after \( q \) iterations (see Section 5.9 for definition of terminology) if \( q \geq 1 \), and the density in the corresponding pixel in the phantom if \( q = 0 \). Let \( S \) denote the set of pairs \( (i,j) \) where the pixel in the \( i \)th row and \( j \)th column is in the region of interest, i.e., it is within the shape and lowden \( \leq \rho_{i,j}^0 \leq \text{highden} \).

\[
\alpha = \sum_{(i,j) \in S} 1.
\]

(5.22)

\[
\bar{\rho}^q = \frac{1}{\alpha} \sum_{(i,j) \in S} \rho_{i,j}^q.
\]

(5.23)

\[
u^q = \frac{1}{\alpha} \sum_{(i,j) \in S} (\rho_{i,j}^q - \bar{\rho}^q)^2.
\]

(5.24)

\[
\sigma^q = \sqrt{\nu^q}.
\]

(5.25)

\[
\delta^q = \begin{cases} 
\frac{1}{\alpha} \sqrt{\frac{1}{\alpha} \sum_{(i,j) \in S} (\rho_{i,j}^q - \rho_{i,j}^0)^2}, & \text{if } \sigma^0 > \text{ZERO}, \\
\frac{1}{\alpha} \sum_{(i,j) \in S} (\rho_{i,j}^q - \rho_{i,j}^0)^2, & \text{if } \sigma^0 \leq \text{ZERO}.
\end{cases}
\]

(5.26)

\[
m = \sum_{(i,j) \in S} |\rho_{i,j}^0|.
\]

(5.27)

\[
R^q = \begin{cases} 
\frac{1}{m} \left( \sum_{(i,j) \in S} |\rho_{i,j}^q - \rho_{i,j}^0| \right) / m, & \text{if } m > \text{ZERO}, \\
\frac{1}{m} \left( \sum_{(i,j) \in S} |\rho_{i,j}^q - \rho_{i,j}^0| \right), & \text{if } m \leq \text{ZERO}.
\end{cases}
\]

(5.28)

The following measures are defined only if all pixels in the full picture are included in the evaluation, and will not be computed if a “region of interest” is specified either through density windowing or region selection (or both).

For the definition of the next set of measures, we need to introduce some preliminary concepts. For any \( n \times n \) digitized picture \( p \), we use \( p(k) \) to denote the \( \lfloor \frac{n}{2^k} \rfloor \times \lfloor \frac{n}{2^k} \rfloor \) (where \( \lfloor x \rfloor \) is the greatest integer \( \leq x \)) digitized picture obtained from \( p \) by averaging the grayness of \( 2^k \times 2^k \) pixels of \( p \) into one pixel of \( p(k) \). If \( 2^k \) does not divide \( n \), the right-most columns and the bottom rows of \( p \) are discarded in the calculation of \( p(k) \). For any two \( n \times n \) digitized pictures \( p \) and \( p' \), we define

\[
E(p,p') = \max_{0 \leq i < n, 0 \leq j < n} |p_{i,j} - p'_{i,j}|.
\]

(5.29)
where \( p_{i,j} \) and \( p'_{i,j} \) denote the values assigned to the pixel in the \( i \)th row and \( j \)th column of \( p \) and \( p' \), respectively. Using these concepts we define, for any integer \( k \), such that \( 1 \leq 2^k \leq \text{NELEM} \),

\[
E(2^k)^q = E(\rho^q(k), \rho^0(k)).
\]

(5.30)

Let \( R_{p,r} \) denote the estimate of the real ray sum, as stored on prjfil, of the \( r \)th ray of the \( p \)th projection. Let \( R_{0,p,r}^q \) and \( R_{0,p,r}^0 \) denote the pseudo ray sum of the \( r \)th ray of the \( p \)th projection of the reconstructed picture and test phantom, respectively, except if LINE is specified on the EVALUATE control command line and data generation was in STRIP mode. In this latter case, \( R_{0,p,r}^q \) (respectively, \( R_{0,p,r}^0 \)) denotes PINC times the real ray sum of the reconstructed picture (respectively, test phantom) along the central line of the \( r \)th ray in the \( p \)th projection.

\[
r^q = \sqrt{\sum_{p=0}^{\text{PRJNUM}-1} \sum_{r=FUSRAY}^{\text{LUSRAY}} (R_{0,p,r}^q - R_{p,r})^2}.
\]

(5.31)

If \text{RESOLUTION} is specified, SNARK14 puts the values of \( \alpha \) (\( \text{AREA} \), see (5.22)), \( \rho^0 \) (\( \text{TEST AVERAGE} \), see (5.23)), \( v^0 \) (\( \text{TEST VARIANCE} \), see (5.24)), \( \sigma^0 \) (\( \text{TEST STD DEV} \), see (5.25)) are put on the eval file. If \( \text{fl}(0) = 2 \) (see Section 4.5), \( r^0 \) (\( \text{TEST RESIDUAL} \), see (5.31)) is also put on the eval file. If \( \text{fl}(0) = 3 \) (see Section 4.5), \( K\Sigma(\rho^q) \) (\( \text{TEST KULLBACK-LEIBLER DISTANCE} \), see (5.17)) and \( W\Sigma(\rho^q) \) (\( \text{TEST WEIGHTED SQUARE DISTANCE} \), see (5.18)) are also put on the eval file. \( \text{Note:} \) The Kullback-Leibler distance is derived based on the assumption that the \( b_i \) in (5.17) are all nonnegative. If this condition is violated, then the value put on the eval file will be “nan.” Unless \( \text{fl}(0) = 0 \), corresponding values are reported also for each reconstruction after \( q \) iterations for which \( \text{fl}(q) = \text{fl}(0) \). If \text{POINT} is specified, SNARK14 reports on the values of \( E(2^k)^q \) (\( \text{POINTWISE DISTANCE} \), see (5.30)), for \( 1 \leq 2^k \leq \text{NELEM} \), for each reconstruction after \( q \) iterations for which \( \text{fl}(q) \geq 1 \).

In both cases, the reconstructions after the final iteration of an \text{EXECUTE} command are always reported (in the same fashion) provided that \( \text{fl}(0) \geq 1 \).

If \text{BOTH} is specified, SNARK14 puts both the reports specified by \text{RESOLUTION} as well as \text{POINT} on the eval file. This also happens if none of \text{RESOLUTION}, \text{POINT}, or \text{BOTH} is specified.

\textbf{Remarks:} There are two remarks concerning the use of the \text{SELECTIVE} command. The first is that the “residual” \( r^q \) (even if requested) cannot and will not be computed as the projection data for individual regions are not available from the projection data file prjfil; nor will \( E(2^k)^q \) be computed. The second remark concerns the warning message about the specified region not residing entirely within the picture. As explained below, such a warning message could be a false alarm in the case of an elliptical object oriented at an angle to the coordinate axes.

To minimize the search area within the picture for pixels that are within the region, a bounding rectangle that encloses the region is estimated as follows. The smallest bounding rectangle with the same orientation as the elliptical region is first formed (see Figure 5.5). A second bounding rectangle, whose sides are parallel to the picture, that just encloses the first rectangle is then formed. All pixels that are within the given object must therefore fall inside this rectangular boundary and only pixels within this boundary need the rigorous “within region test”. If the estimated rectangular boundary is not entirely inside the picture, it is clipped at the picture boundary and a warning message is issued. As illustrated in the figure, because of the estimation, this could happen even if the original elliptical object is entirely within the picture. In general, one can use the reported area (number of pixels within the region) as an index or conduct a simple experiment to verify whether the specified object is entirely within the picture or not.

\section{5.12 DISPLAY}

This command causes some of the digitized pictures on recfil to be listed on the \textit{Analysis Output file}. The density values of the pixels are interpreted according to the current values of LOFL, UPFL, LOWER and \texttt{UPPER} (see Section 5.2) and, if \texttt{SCALE} is specified, then these are multiplied by the value of the floating point modifier scale prior to printing. \textit{Restriction:} scale \( > \) \texttt{ZERO}.
If PHANTOM is specified, the test phantom is listed, if there is such a phantom on recfil.
The DISPLAY control command line is followed by an

```plaintext
> iteration-flag-line
```
(see Section 4.5). SNARK14 puts on the Analysis Output file a listing of each reconstruction after $q$ iterations
(unless the number of iterations is exactly $q$, see Section 5.9 for definition) for which $f_l(q) \geq 1$ and puts listings
of all final reconstructions of EXECUTE command if $f_l(0) \geq 1$.

## 5.13 PUNCH

```plaintext
> PUNCH [PHANTOM]
```

This command causes some of the digitized pictures on recfil to be copied onto the file punch (see Section 3.3). This file is of the same format as the initial part of file11 that is read by PICTURE TEST (see Section 5.4). This command name is an anachronism. The command was originally used to output reconstructions on 80 column Hollerith punched cards. It is now used to output the reconstructions in ASCII in a limited width format.

The PUNCH control command line is followed by an

```plaintext
> iteration-flag-line
```
(see Section 4.5).

The precise content of the punch file for each picture is determined as follows (consult Sections 5.4 and 5.3 if needed):

- The name-of-the-pattern is that on the recfil if the test phantom is being put on the punch file. If a reconstruction is being put on the punch file, the 80 columns of the name-of-the-pattern on the punch file are put together as:
### CHAPTER 5. SNARK14 COMMANDS

#### 5.14 LINES

> **LINES [SCALE scale][COLUMNS column1 [column2 [column3 [column4]]]]**

This command results in a comparison of the exact densities of all the pixels in selected columns of the test phantom and reconstructions. **Restriction:** Test phantom must be present on recfil. The density values of the pixels are first interpreted according to the current values of LOFL, UPFL, LOWER, and UPPER (see Section 5.2) and are then multiplied by the floating point modifier scale prior to the comparisons being made. **Restriction:** scale > ZERO. If SCALE is not specified, scale = 1.

The columns for which the comparisons are to be carried out are specified by the integer modifiers column1, column2, column3, and column4. (**Warning:** If the value of any of these modifiers is outside the range [0, NELEM), then that modifier is ignored.)

The LINES command is followed by an

> **iteration-flag-line**

(see Section 4.5). Comparisons with the test phantom are made for reconstructions after $q$ iterations (unless the number of iterations is exactly $q$, see Section 5.9 for definition) whenever $f_l(q) \geq 1$, and comparisons with the test phantom are made for all final reconstructions of the EXECUTE command if $f_l(0) \geq 1$.

The values of the pixels in the specified columns in the test phantom and the reconstruction, as well as their differences, are reported on the Analysis Output file.
5.15 SKUNK

> SKUNK PHANTOM DIFFERENCE MINIMUM min MAXIMUM max AMPLITUDE INTENSITY

This command causes some of the digitized pictures on recfil to be written to the current directory in PGM format. The densities in the pixels are interpreted according to the current values of LOFL, UPFL, LOWER and UPPER (see Section 5.2). This command name is an anachronism. It was originally used to create pseudo half-tone images on a line printer by means of overprinting. It is now used to create images in the PGM format. The phantom PGM image is named with the first 40 characters of the phantom name with leading and trailing spaces removed as given in the CREATE or PICTURE command. Reconstructions are named as PROJ_REC_ALG_ITER_TYPE_INTAMP.pgm where PROJ is the first 12 characters of the projection data as given in the CREATE or PROJECTION command, REC is the first 12 characters of the name of the reconstruction as given in the EXECUTE command, ALG is the 4 character algorithm name, ITER is the 4 digit iteration number, TYPE is either “r” or “d” for reconstruction or difference, respectively, and INTAMP is either “i” or “a” for intensity or amplitude, respectively. In both cases, embedded spaces in the name are replaced with the underscore character.

If PHANTOM is specified, the test phantom is written, if there is such a phantom on the recfil. If PHANTOM is not specified, only the reconstructions are written.

If DIFFERENCE is specified, reconstructions are reported on by creating the picture whose value in a pixel is the absolute value of the difference between the values in the corresponding pixel of the test phantom and the reconstruction.

If DIFFERENCE is not specified, the reconstructions themselves are written by the method described below.

Restriction: If DIFFERENCE is specified, recfil must contain a test phantom.

The SKUNK control command line is followed by an

> iteration-flag-line

(see Section 4.5). Reconstructions after q iterations (unless the number of iterations is exactly q, see Section 5.9 for definition) are reported on if fl(q) ≥ 1, and final reconstructions of EXECUTE commands are reported on if fl(0) ≥ 1.

Thus, a SKUNK command results in half-tone displays of a sequence of pictures. We now describe the display method.

Let LO be the value of the floating point modifier min if MINIMUM is specified, or the smallest pixel density in the first picture to be displayed otherwise.

Let HI be the value of the floating point modifier max if MAXIMUM is specified, or the largest pixel density in the first picture to be displayed otherwise.

Restriction: HI - LO > ZERO.

We define the function d by

\[ d(x) = \min \left( 1, \max \left( 0, \frac{x - LO}{HI - LO} \right) \right). \]

For each picture to be displayed we form a new picture by replacing a pixel density x by \( d(x) \) if AMPLITUDE is specified, or by \( \sqrt{d(x)} \) if INTENSITY is specified. (If neither is specified, AMPLITUDE is assumed.)

5.16 END

> END

This command causes the SNARK14 run to terminate. If the file INPUT does not have this command at the end of it, improper termination of SNARK14 will take place (see Section 4.4).
Chapter 6

IMPLEMENTING USER-DEFINED ALGORITHMS

He had bought a large map representing the sea,
   Without the least vestige of land;
And the crew were much pleased when they found it to be
   A map they all could understand.

“What’s the good of Mercator’s North Poles and Equators,
   Tropics, Zones, and Meridian Lines?”
So the Bellman would cry: and the crew would reply
   “They are merely conventional signs!

“Other maps are such shapes, with their islands and capes!
   But we’ve got our brave Captain to thank”
(So the crew would protest) “that he’s bought us the best-
   A perfect and absolute blank!”

Fit the Second - The Bellman’s Speech
The Hunting of the Snark (an agony in eight fits)
by Lewis Carroll

6.1 Introduction

SNARK14 provides the option for users to define their own reconstruction algorithms (ALP1-ALP5 and ALB1-ALB5, see Section 5.8), termination tests (TRM1 and TRM2, see Section 5.9) and Superiorization-related functions (SCR3-SCR5, NAV3-NAV5, see Section 5.10). In this introduction we describe how SNARK14 makes use of these algorithms. Suppose that SNARK14 encounters an EXECUTE command (Section 5.8) on the INPUT file. This will cause a subroutine (named \texttt{exalg}) to be called, which controls the execution of the reconstruction algorithm. We now describe those actions of \texttt{exalg} that are relevant to the user-defined algorithms. Some of these actions are influenced by the last STOP command (Section 5.9) on the INPUT file prior to the EXECUTE command. We shall refer to this as the active STOP command. If there is no STOP command prior to the EXECUTE command under consideration,
STOP ITERATION = 1

is assumed.

exalg has a list of the algorithms that can perform blob reconstructions. ALB1-ALB5 are in the list and ALP1-ALP5 are not. If BASIS BLOB is in effect and an algorithm that is in the list is invoked, a blob reconstruction is performed. In all other cases a pixel reconstruction is performed.

All SNARK14 algorithms are descendants of the C++ class alg_class:

```cpp
class alg_class
{
  private:
  public:
    virtual INTEGER Init();
    virtual BOOLEAN Run(REAL* recon, INTEGER* list, REAL* weight, INTEGER iter);
    virtual INTEGER Reset();
};
```

Default (do nothing) implementations of these methods are provided by alg_class.

All SNARK14 termination tests are descendants of the C++ class termtest_class:

```cpp
class termtest_class
{
  public:
    virtual void Init();
    virtual BOOLEAN Run(REAL* recon, INTEGER* list, REAL* weight, INTEGER iter);
};
```

Default (do nothing) implementations of these methods are provided by termtest_class. The Init method is invoked by the STOP command (see Section 5.9) for the purpose of collecting user-defined parameters for the termination test and the Run method is invoked during algorithm execution as described below.

Executing a reconstruction algorithm involves the following steps:

Step (i). If this is the first EXECUTE command in the INPUT file, or if CONTINUE is not specified on the EXECUTE control command line, an array of size GeoPar.area (see Section 6.3.3), which is used to hold the reconstruction, is initialized (see Section 5.8). (Otherwise, this array will contain the final reconstruction of the last EXECUTE command). If this is the first blob reconstruction (see Section 5.7), a second array of size Blob.area (see Section 6.3.4) is initialized. If both the previous and current algorithms use blobs and CONTINUE is not specified, the Blob.recon array is deleted and reallocated. Also, an integer variable that counts the number of iterations is initialized to 1.

If CONTINUE is specified and the last algorithm returned a blob reconstruction and the current algorithm is performing a pixel reconstruction, the blob reconstruction is converted to a pixel reconstruction. Conversely, if the last algorithm returned a pixel reconstruction and the current algorithm is performing a blob reconstruction, the pixel reconstruction is converted to a blob reconstruction. If the last algorithm returned a blob reconstruction and the current algorithm is performing a blob reconstruction, the blob parameters must be the same for both executions.

Step (ii). exalg invokes the Init method of the instance of the algorithm class associated with the algorithm name on the EXECUTE command. The Init method can be used to parse any parameters needed by the algorithm, allocate any resources that may be needed by the algorithm and must persist from one iteration to the next. The most common resources are dynamic memory and files used to store temporary data. It is also a good place to initialize the dynamic memory if the values do not change from iteration to iteration. The Init method is expected to return 0 on success and a non-zero value if the initialization failed.

Step (iii). exalg calls the Run method of the instance of the algorithm class. exalg passes to Run the array of values of the basis functions in the reconstruction (the name of this array is recon) and the iteration number (the name of this variable is iter). recon is either the pixel reconstruction array or the blob reconstruction array, depending on whether or not a blob reconstruction is being performed. In addition,
exalg passes two arrays, list and weight, which are large enough to hold the longest sequences that can be returned by wray, ray, bray or bray (whichever is appropriate for the current situation, see Section 6.4). The exalg subroutine can invoke extra commands when the SUPERIORIZE command is appropriately used in the input file, see 5.10, and the way the extra calls take place is explained below.

Step (iv). exalg checks whether any of the following is the case: (a) Run returned the value TRUE (this is used to indicate that the algorithm is not applicable to the specified situation and so the values in recon are not the values of a reconstruction), (b) the active STOP command has ITERATION specified and the iteration number is the same as the value of the integer modifier iter on the active STOP command, (c) the active STOP command has TERMINATION specified, and when the Run method of the class whose name is the value of test-name on the active STOP command is called, the value TRUE is returned (this function is provided with the array of pixel or blob values in the reconstruction and the iteration number).

If any of the three conditions (a), (b), or (c) is satisfied, exalg calls the Reset method and returns control to the main program of SNARK14, which moves on to the next command on the INPUT file. If none of the three conditions (a), (b), or (c) is satisfied, the iteration number is increased by 1 and Step (iii) is repeated. The Reset method is where the resources allocated by the Init method are released. The Reset method is expected to return 0 for success and a non-zero value for failure.

After the initialization in Step (i), the only changes to the array of basis function values in the reconstructions are done in Step (iii) by Run. If the iteration number is q when Run is called, Run returns via recon the reconstruction after q iterations (see Section 5.8).

Information is passed to the user-defined algorithms both via the parameters in the formal parameter list and via classes accessed through global variables. Typically such an algorithm begins with some subset of the following statements. (Classes that are not used in the algorithm can of course be omitted.)

```c
#include "anglist.h"
#include "blkdta.h"
#include "blob.h"
#include "consts.h"
#include "geom.h"
#include "inputfile.h"
#include "modefl.h"
#include "noise.h"
#include "objects.h"
#include "projfile.h"
#include "spctrm.h"
#include "uiod.h"
```

The execution of an iterative reconstruction algorithm using PIXEL basis functions may be affected by the command SUPERIORIZE. If such a command appears in the INPUT prior to an EXECUTE command that calls for an the iterative algorithm, then that iterative algorithm is superiorized as explained in Section 5.10. The SUPERIORIZE command invokes a secondary optimization criterion, which may be one of the built-in choices (TVAR or SMOO) or may be user defined (SCR3, SCR4, or SCR5). The user-defined secondary optimization criteria are descendants of the C++ class sec_cri_class:

```c
class sec_cri_class
{
    private:
        public:
        virtual void Init();
        virtual REAL Run(REAL* image);
};
```

Default (do nothing and return the value 0.0) implementations of the user-defined secondary criteria are provided by sec_cri_class when using SCR3, SCR4, and SCR5.

The method Init of any descendant of the sec_cri_class is also executed in Step (ii) and the implementation of this method can be used in a similar fashion as the Init method of class alg_class.

When the SUPERIORIZE command is used, the execution of the Run command of the class alg_class is preceded by a superiorization loop, see lines 8 - 18 of Algorithm 5.1. The Run method of the instance of
the class sec_cri_class is invoked several times, at least \( N + 1 \) times, by \texttt{exalg} during this superiorization loop, see Section 5.10, in the following manner: a) just before starting the superiorization loop, the \texttt{exalg} subroutine invokes the 
\texttt{Run} method and passes the array of values of the pixel basis functions in the reconstruction and b) in the \( n \)th iteration of the superiorization loop \texttt{exalg} calls the 
\texttt{Run} method and passes the array of values of the pixel basis functions in the perturbed reconstruction; in both cases the array passed to the \texttt{Run} method is \texttt{image}. It is important to emphasize that any implementation of the sec_cri_class should provide a \texttt{Run} method that returns an appropriate and useful REAL value.

The superiorization process requires both a secondary optimization criterion function and a procedure to obtain nonascending vectors for it; see Section 5.10. When invoking the \texttt{SUPERIORIZE} command together with a built-in (TVAR or SMOO) secondary optimization criterion, the procedure to obtain a nonascending vector is already defined. When invoking the \texttt{SUPERIORIZE} command together with a user-defined (SCR3, SCR4, or SCR5) secondary optimization criterion, the procedure to obtain a nonascending vector must be defined by the user as well. The user should use the implementations in NAV3, NAV4 and NAV5 corresponding to the secondary optimization criteria SCR3, SCR4 and SCR5, respectively. In SNARK14, all the procedures to obtain the appropriate nonascending vector are descendant of the C++ class \texttt{nav_class}:

```cpp
class nav_class
{
    private:
        virtual void Init();
        virtual void Run(REAL* xkn, REAL* vkn);
};
```

Default (return a nonascending vector whose elements are all zero) implementations of these methods are provided by \texttt{nav_class} when using NAV3, NAV4, and NAV5.

The method \texttt{Init} of any descendant of the \texttt{nav_class} is also executed in \textit{Step (ii)} and the implementation of this method can be used in a similar fashion as the \texttt{Init} method of class \texttt{alg_class}.

The \texttt{Run} method of the instance of the class \texttt{nav_class} is invoked \( N \) times by line 9 of Algorithm 5.1. In the \( n \)th iteration of the superiorization loop \texttt{exalg} calls the \texttt{Run} method and passes the array of values of the pixel basis functions in the superiorized reconstruction (the name of this array is \texttt{xkn}). Before returning control to the \texttt{exalg} subroutine, the \texttt{Run} method must return an array representing the nonascending vector for the user-defined secondary optimization criterion (the name of this array if \texttt{vkn}).

### 6.2 Formal parameter lists of the user-defined algorithms

The formal parameter list for the \texttt{Run} method for a reconstruction algorithm class or a termination test class is:

\[(\text{REAL* recon, INTEGER* list, REAL* weight, INTEGER iter})\]

where the types \texttt{REAL} and \texttt{INTEGER} are defined in Section 6.3.1.

We now explain the nature and purpose of these parameters. \texttt{recon} is a real array. The size of \texttt{recon} is either \texttt{GeoPar.area} or \texttt{Blob.area} depending on whether this is a pixel reconstruction or not. \texttt{recon[0]} is the first element of this array. Each time the user algorithm executes, the reconstructed picture must be stored in the \texttt{recon} array. It is the user’s responsibility to map the reconstructed picture into the linearized \texttt{recon} array according to the following numbering scheme.

For a pixel reconstruction, if \( \rho_{i,j} \) is the density of a pixel in the \( i \)th row and \( j \)th column of the reconstructed picture, then \( \rho_{i,j} \) will map into the \texttt{recon} array element \texttt{recon[i×NELEM+j]}. The coordinates of the center of the pixel are \(((j - c) \times \text{PIXISIZ}, (c - i) \times \text{PIXISIZ})\), where \( c \) is defined in Equation (2.4) on page 14.

For a blob reconstruction, the coordinates of the centers of a blob are given in Equation (2.6) on page 14. Let \( M_2 = \lfloor \text{NELEM} \times \text{PIXISIZ}/\text{DELTA} \rfloor, H_2 = \lfloor \text{NELEM} \times \text{PIXISIZ}/(\sqrt{3} \times \text{DELTA}) \rfloor, M = 2 \times \lfloor M_2 \rfloor + 1, \) and \( H = 2 \times H_2 + 1. \) Then the dimension of the \texttt{recon} array is \( M \times H \) and the \((m,n)\) blob of Equation (2.6) is the \(((m + H_2) \times M + m + M_2)\)th element of the \texttt{recon} array. Note that the restriction that \( m + n \) is even results in \texttt{recon} being twice as big as it needs to be. Those elements corresponding to \( m + n \) odd are unused.
At the end of each execution of the user-defined Run method the recon array is automatically written to recfil by SNARK14, unless the Run method returns the value TRUE (see Section 6.1). list is an integer array (whose size is computed internally by SNARK14) used in wray, ray, pseudo, bray, bray, and bpseudo (see Section 6.4) to store the indices of the basis functions intersected by a specified ray. weight is a real array (whose size is equal to the size of the list array) used in wray, ray, pseudo, bray, bray and bpseudo (see Section 6.4) to store the integrals of the ray across the intersected basis functions in the order given in the list array. The values stored in list and weight are not used by exalg (see Section 6.1), they are purely internal to the user-defined algorithm. They are in the formal parameter list to remove the burden from the user of having to allocate space in the Init method for list and weight when wray, ray, pseudo, bray, bray, or bpseudo is used by this algorithm. iter is an integer variable whose value is the iteration number (see Section 6.1).

Warning: The values of recon should not be altered by a user-defined termination test. Alteration of these values by the termination test may produce results quite different from what the user intended.

6.3 C++ classes in user-defined algorithms

We now explain the contents of each of the C++ classes that may be used in a user-defined algorithm to pass information from the rest of the program to the algorithm. Each of these classes is a singleton [16], although they do not follow the singleton pattern. (A singleton is a class that has at most one instance.) Access to the single instance of each class is provided through a global variable. Warning: The variables in these classes should not be altered in any way by the user-defined algorithm. Alterations of these variables by the algorithm may produce results quite different from what the user intended. Creating new instances of the classes is not recommended as they will have been properly initialized (inheritance the initialization of the variables from the first instance of the class), which again may produce results quite different from what the user intended.

The C++ code listed for each class is not exactly what is contained in the actual header file for the class. Attributes and methods that are for internal SNARK14 use have been deleted. The order may also be changed for a clearer description.

6.3.1 blkdta.h

```c
#define REAL double
#define INTEGER int
#define BOOLEAN bool
#define CHAR char
#define TRUE true
#define FALSE false
#define CHAR2INT(CHAR1, CHAR2, CHAR3, CHAR4) 
  ( (((INTEGER)(CHAR1))<24) | (((INTEGER)(CHAR2))<16) | 
    (((INTEGER)(CHAR3))<8) | (((INTEGER)(CHAR4))) )
#define SQR(NUM1) ((NUM1)*(NUM1))
#define CA(ARRAY, ELEMENT, INDEX) ARRAY[(ELEMENT) + 2 * (INDEX)]
#define MIN0(ARG1, ARG2) (((ARG1) > (ARG2)) ? (ARG2) : (ARG1))
#define MAX0(ARG1, ARG2) (((ARG1) < (ARG2)) ? (ARG2) : (ARG1))
#define round(X) (floor((X) + 0.5))
extern INTEGER trace;
```

blkdta.h defines a number of macros that are used throughout the SNARK14 program. The macros REAL, INTEGER, BOOLEAN, CHAR, TRUE, and FALSE are clear from their names. CHAR2INT packs a sequence of four characters in an integer to simplify comparisons with the four character keywords used in SNARK14. SQR computes the square of its argument. CA is used to access the real or complex components (ELEMENT) of a complex ARRAY. MINO and MAXO return the minimum and maximum of the two arguments, respectively.

round returns the nearest integer to its argument. The reference to the global trace variable is defined here.
It contains the value contained on the last TRACE command (see Section 5.1). A typical user algorithm or termination test trace statement follows the pattern:

```
#include "uiod.h"

if (trace > 0) fprintf(output, "format", args...);
```

where the file output is defined in uiod.h, format is replaced by the appropriate C++ format string and args... by the arguments needed by the format string. The convention in SNARK14 is to put the newline character (\n) at the beginning of the format string.

### 6.3.2 consts.h

```c
extern class Consts_class
{
    public:
    static const REAL zero;
    static const REAL infin;
    static const REAL pi;
    static const REAL twopi;
    static const REAL pisq;
    static const REAL pid2;
    static const REAL sqrt3;
    static const REAL isqrt3;
} Consts;
```

`zero` and `infin` are the smallest and largest positive real numbers that can be used (see Section 2.1). In other sections of this manual, they have been referred to with the names ZERO and INFIN. The other constants `pi`, `twopi`, `pisq`, `pid2`, `sqrt3`, and `isqrt3` are floating point approximations to the mathematical constants $\pi$, $2 \times \pi$, $\pi^2$, $\pi/2$, $\sqrt{3}$, and $1/\sqrt{3}$, respectively; in Section 2.1 we used upper-case letters for naming these.

### 6.3.3 geom.h

```c
extern class Geometry_class
{
    public:
    INTEGER nelem;
    INTEGER area;
    INTEGER midpix;
    REAL pixsiz;
    INTEGER prjnum;
    REAL pinc;
    INTEGER usrays;
    INTEGER snrays;
    INTEGER nrays;
    INTEGER midray;
    INTEGER fsnray;
    INTEGER lsnray;
    INTEGER fusray;
    INTEGER lusray;
    BOOLEAN div;
    BOOLEAN tang;
    BOOLEAN arc;
    REAL radius;
    REAL stod;
```
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BOOLEAN par;
BOOLEAN uni;
BOOLEAN vri;
BOOLEAN strip;
BOOLEAN line;
INTEGER nave2;
INTEGER naper[13];
REAL aveden;
INTEGER numray(INTEGER melen, REAL zisxip);
}

GeoPar;

This class describes the image and projection geometries.

nelem is the number of elements in the reconstruction grid (see Section 2.2). In other sections of this
manual, this has been referred to as NELEM. The value of nelem is determined by the PICTURE command
(see Section 5.4). area is nelem*nelem and midpix is (nelem-1)/2.

pixsiz is the length of the side of a pixel (see Section 2.2). In other sections of this manual, it is referred
to as PIXSIZ. The value of pixsiz is determined by the PICTURE command (see Section 5.4). prjnum is
the number of projections and pinc is (except in the VARIABLE case) the spacing between the detectors
(see Section 2.4). In other sections of this manual, they are referred to as PRJNUM and PINC. The values
of prjnum and pinc are determined by the PROJECTION command (see Section 5.5).

usrays is the number of rays along which data have been collected (see Section 2.5). usrays is determined
by the PROJECTION command (see Section 5.5). snrays is the number of rays needed to cover the
reconstruction region. This is calculated by SNARK14 based on the values of nelem, pixsiz and on the
data collection geometry (see Section 2.5). nrays is the number of rays in a projection. It is the maximum of
usrays and snrays. midray is (nrays-1)/2. In the numbering of the rays in the projection from 0 to nrays-1,
fsnray and lsnray are respectively the numbers of the first and last ray needed to cover the reconstruction
region, and fusray, and lusray are respectively the numbers of the first and last ray along which data have
been collected. The values of these variables are determined by SNARK14 according to formulas given in
Section 2.5. In other sections of the manual, usrays, snrays, nrays, fsnray, lsnray, fusray, and lusray
have been referred to with the names USRAYS, SNRAYS, NRAYS, FSNRAY, LSNRAY, FUSRAY, and
LUSRAY, respectively.

div is a logical variable whose value is TRUE if, and only if, the geometry of data collection is DIVERGENT (see Section 2.4). If div is TRUE, the values of the variables tang, arc, radius, and stod have the following interpretation. tang or arc is TRUE if, and only if, the detectors are spaced along a TANGENT line or an ARC of a circle, respectively. radius is the radius of the circle on which the source is positioned and stod is the source-to-detector distance (see Section 2.4). The values of these variables are determined by
the PROJECTION command (see Section 5.5). If div is FALSE, tang, arc, radius and stod are assigned default values (FALSE and 0). par is a logical variable whose value is TRUE if, and only if, the geometry of data collection is PARALLEL. If par is TRUE, the values of the logical variables uni, vri, strip, and
line are TRUE if, and only if, the ray spacing is UNIFORM, the ray spacing is VARIABLE, the rays are
STRIPS and the rays are LINES, respectively (see Sections 2.3 and 2.4). The values of these variables are
determined by the PROJECTION command (see Section 5.5). If par is FALSE, uni, vri, strip, and
line are assigned the default value FALSE. The variable nave2 and array naper[13] (only the first nave2 elements are defined) describe the aperture function of the detector (see Section 5.3.3, S 5). Their physical interpretation is explained in Section 5.3.2. Their values are determined by the PROJECTION command
(see Section 5.5).

aveden is an estimate, based on the projection data, of the average density of the picture to be recon-
structed. This estimation is done under the control of the PROJECTION command (see Section 5.5). Let
SUMRAY denote the sum of the ray sums (divided by the width of the strips in the STRIP case) that are
stored on prjfil. Let SUMLENGTH denote the sum of the lengths of intersections of the reconstruction region
with the rays (central lines of the rays in the STRIP case) that contribute to SUMRAY. Then aveden =
SUMRAY/SUMLENGTH. In other sections of this manual, the variables radius, stod, nave2, naper, and
aveden have been referred to as RADIUS, STOD, NAVE2, NAPER, and AVEDEN respectively. (Warning:
aveden is only an estimate of the average density in the picture. It may be a very bad estimate if it is based
on too few projections, or if the region of the picture from which projection data have been collected is larger than the reconstruction region (see Section 2.2)).

6.3.3.1 numray

INTEGER numray(INTEGER melen, REAL zisxip);

numray returns the number of rays necessary to span a square shaped picture region whose center is the origin, and whose sides, which are parallel to the axes of the coordinate system, are of length \(melen \times zisxip\). The precise rules for calculating this number of rays are given in Section 2.5. (In that discussion \(melen\) is NELEM, \(zisxip\) is PIXSIZ and the number of rays is SNRAYS). Restriction: \(melen > 0\) and \(zisxip > 0\).

6.3.4 blob.h

extern class Blob_class
{
  public:
    BOOLEAN pix_basis; //true if pixel basis, false if blob basis
    REAL support; // support of a blob
    REAL shape; // shape of a blob
    REAL delta; // resolution of the (hexagonal) grid
    INTEGER M; // number of underlying square grid points in the horizontal direction
    INTEGER H; // number of underlying square grid points in the vertical direction
    INTEGER area; // M*H
    REAL *recon; // array of the blob coefficients

  void blob2pix(REAL *blob_array, REAL *pict);
  void pix2blob(REAL* pict, REAL* blob_array);

  void bwray(
    INTEGER np,
    INTEGER nr,
    INTEGER* list,
    REAL* weight,
    INTEGER* numb,
    REAL* snorm
  );

  void bray(
    INTEGER np,
    INTEGER nr,
    INTEGER* list,
    REAL* weight,
    INTEGER* numb,
    REAL* snorm
  );

  REAL bpseudo(
    REAL* pict,
    INTEGER np,
    INTEGER nr,
    INTEGER* list,
    REAL* weight,
    INTEGER* numb,
    REAL* snorm,
    BOOLEAN line,
    BOOLEAN constr
  );
void bsmooth(
    REAL* a,
    INTEGER H,
    INTEGER M,
    REAL thresh,
    REAL w1,
    REAL w2
);

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This class describes the blobs that may be used in a reconstruction. The class is only usable when pix_basis is FALSE.

support, shape, and delta are described in Section 2.2. In other sections of this manual, they are referred to as SUPPORT, SHAPE, and DELTA. The blob reconstruction region, recon, has H rows and M columns. The size of the blob recon array, area, is H×M. The following C++ code illustrates how to access the elements of the blob recon array:

    INTEGER lhf = (INTEGER)(-Blob.H / 2));
    INTEGER lhl = (INTEGER)((Blob.H - 1) / 2);
    INTEGER lmf = (INTEGER)(-Blob.M / 2);
    INTEGER lml = (INTEGER)((Blob.M - 1) / 2);
    for (INTEGER h = lhf; h <= lhl; ++h) {
        for (INTEGER m = lmf; m <= lml; ++m) {
            if ((m + h) % 2 == 0) {
                // m and h must have the same parity!!
                ind = (h + Blob.H2) * Blob.M + (m + Blob.M2);
                // do blob processing here
                // ind is the index of the blob in Blob.recon
            }
        }
    }

Note: The variable h in the code above processes the blobs from bottom to top; that is in the same direction as the y-axis. This is the opposite of how the pixel array is stored.

The functions bwray, bray, and bpseudo that are specified below are blob equivalents of the pixel functions wray, ray, and pseudo, respectively (see Sections 6.4.2, 6.4.3, and 6.4.4 below).

6.3.4.1 blob2pix

    void blob2pix(REAL *blob_array, REAL *pict);

blob2pix is used to convert a blob image to a pixel image. It is assumed that the blob image, blob_array, is created with the blob parameters in the Blob class and that the pict array can hold at least NELEM × NELEM pixels.

6.3.4.2 pix2blob

    void pix2blob(REAL* pict, REAL* blob_array);

pix2blob is used to convert a pixel image to a blob image. It is assumed that the pixel image, pict, contains NELEM × NELEM pixels and that the blob array can hold at least Blob.area blobs.

6.3.4.3 bwray

    void bwray(
        INTEGER np,
6.3.4.4 \texttt{bray}

\begin{verbatim}
    void bray(
        INTEGER np,
        INTEGER nr,
        INTEGER* list,
        REAL* weight,
        INTEGER* numb,
        REAL* snorm
    );
\end{verbatim}

\texttt{bray} is the blob equivalent of \texttt{ray} (see Section 6.4.3). For the \textit{np}th projection and \textit{nr}th ray, this routine calculates the trace of a STRIP ray through the picture region. \textit{Restriction:} 0 \leq \textit{np} < \text{PRJNUM} and 0 \leq \textit{nr} < \text{NRAYS}. \textit{Warning:} In case of STRIP rays, the subroutine will return values that are appropriate for LINE rays located at the centers of the actual STRIP rays.

\texttt{bray} returns the following information:

- \texttt{numb} For rays that intersect the picture region, this is the number of blobs that are intersected by the ray. For rays that do not intersect the picture region, the value of \texttt{numb} is set to 0.
- \texttt{list[0]}, \ldots, \texttt{list[numb-1]} The indices of the pixels whose centers are in the strip. I.e., if \texttt{j = list[i]}, then \texttt{Blob.recon[j]} is the present density in the \textit{i}th blob whose center is in the ray (see Section 6.2).
- \texttt{weight[0]}, \ldots, \texttt{weight[numb-1]} Are all assigned the value of the integral of a blob.
- \texttt{snorm} Is assigned the value of integral of a blob squared times \texttt{numb}.

\texttt{numb} For rays that intersect the picture region, this is the number of blobs that are intersected by the ray. For rays that do not intersect the picture region, the value of \texttt{numb} is set to 0.

\texttt{list[0]}, \ldots, \texttt{list[numb-1]} The indices of the blobs intersected by the ray. I.e., if \texttt{j = list[i]}, then \texttt{Blob.recon[j]} is the present density in the \textit{i}th blob intersected by the ray (see Section 6.2).

\texttt{weight[0]}, \ldots, \texttt{weight[numb-1]} The LINE integrals of the ray through the blobs in the order given in \texttt{list}.

\texttt{snorm} The sum of the squares of the above weights.
6.3.4.5 bpseudo

```c
REAL bpseudo(
    REAL* pict,
    INTEGER np,
    INTEGER nr,
    INTEGER* list,
    REAL* weight,
    INTEGER* numb,
    REAL* snorm,
    BOOLEAN line,
    BOOLEAN constr
);
```

bpseudo is the blob equivalent of pseudo (see Section 6.4.4). Please refer to that section for the meaning of the arguments.

6.3.4.6 bsmooth

```c
void bsmooth(
    REAL* a,
    INTEGER H,
    INTEGER M,
    REAL thresh,
    REAL w1,
    REAL w2
);
```

bsmooth is the blob equivalent of smooth (see Section 6.4.10). The blob array is assumed to contain $H \times M$ blobs. thresh acts as described in Section 5.8. The main difference between bsmooth and smooth is that each blob only has six neighbors. The weight $w_1$ is applied to the central blob and the weight $w_2$ is applied to its six neighbors.

6.3.5 projfile.h

```c
extern class SnarkPrjFile : private DIGFileSnarkProj
{
    public:
        INTEGER ReadProj(INTEGER np, REAL* data, unsigned INTEGER nsize);
    } ProjFile;
```

This class provides access to the projection data file, prjfil.

6.3.5.1 ReadProj

```c
INTEGER ReadProj(INTEGER np, REAL* data, unsigned INTEGER nsize);
```

Roughly speaking, ReadProj copies from prjfil (see Sections 3.2 and 5.5) the ray sums for the $np$th projection into the array data. Warning: The size of data must be at least nsize.

More precisely, the first nsize values of data are changed. Let prjfil(np, J) denote the Jth ray sum stored on prjfil for the npth projection. (Due to our numbering convention of rays, this is in fact the ray sum for the (fusray + J)th ray in the npth projection; see Section 2.5.) We distinguish between two cases.

Case 1. nsize < usrays (see Section 2.5). In this case we define

$$iskip = \lfloor (usrays - nsize)/2 \rfloor$$
and, for $0 \leq i < \text{nsize}$,

$$\text{data}[i] = \text{prjfil}(\text{np}, \text{iskip} + i).$$

Case 2. $\text{nsize} \geq \text{usrays}$. In this case we define

$$\text{iskip} = \lfloor (\text{usize} - \text{usrays})/2 \rfloor$$

and, for $0 \leq i < \text{nsize}$,

$$\text{data}[i] = \begin{cases} 
\text{prjfil}(\text{np}, i - \text{iskip}), & \text{if } \text{iskip} \leq i < \text{iskip} + \text{usrays}, \\
0, & \text{otherwise.}
\end{cases}$$

6.3.6 anglst.h

```cpp
extern class anglst_class
{
    public:
    void getang(INTEGER np, REAL* theta, REAL* sinth, REAL* costh);
    REAL prdta(INTEGER np, INTEGER nr);
} Anglst;
```

This class provides access to the projection angle data (getang) and individual ray measurements (prdta).

6.3.6.1 getang

```cpp
void getang(INTEGER np, REAL* theta, REAL* sinth, REAL* costh);
```

getang returns the values of theta in radians for the npth projection and the values of the sine and cosine of theta (see Figures 2.1 and 2.2), sinth = sin(theta) and costh = cos(theta). In other sections of the manual, theta is referred to as THETA.

6.3.6.2 prdta

```cpp
REAL prdta(INTEGER np, INTEGER nr);
```

prdta returns as its value the ray sum for the nrth ray of the npth projection, as it is stored on prjfil (see Sections 3.2.1 and 5.5). The numbering of the rays in a projection is from 0 to NRAYS-1, as is explained in Section 2.5. prjfil only contains ray sums for fusray $\leq nr \leq lusray$. If $0 \leq nr < fusray$ or $lusray < nr < nrays$ the function prdta(np, nr) returns the value 0. Restrictions: $0 \leq np < \text{PRJNUM}$ and $0 \leq nr < \text{NRAYS}$.

6.3.7 infile.h

```cpp
#include "inputfile.h"
extern class InFile_class: public InputFile_class
{
    public:
} InFile;
```

This class is used for processing the SNARK14 INPUT file. The methods of interest to the algorithm developer are contained in the super class, `InputFile_class` (see Section 6.3.8).
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6.3.8 inputfile.h

class InputFile_class
{
    public:
        INTEGER getwrd(BOOLEAN NewLine, BOOLEAN* eol, const INTEGER *expect, int nexpect);
        REAL getnum(BOOLEAN NewLine, BOOLEAN* eol);
        INTEGER getint(BOOLEAN NewLine, BOOLEAN* eol);
        void getnxt(BOOLEAN flag);
};

This class maintains a buffer that contains the current command line being parsed and a pointer to the next character in that line to be processed. The getwrd, getnum, and getint methods return the next word modifier, real number, and next integer, respectively. getnxt causes the next command line to be read into the buffer.

6.3.8.1 getnxt

    void getnxt(BOOLEAN flag);

This subroutine reads the next command line (up to 80 characters) from the INPUT file into the buffer and initializes the “scan pointer” to the beginning of the buffer. If the command line is longer than 80 characters, the excess characters are discarded. If the value of the logical variable flag is FALSE, then the output file will carry an echo of the characters read. If the flag is TRUE, then the OUTPUT file will not echo the characters read by this subroutine.

6.3.8.2 getwrd

    INTEGER getwrd(BOOLEAN NewLine, BOOLEAN* eol, const INTEGER *expect, int nexpect);

This function returns the first four characters of a word modifier (see Section 4.4) packed in integer. If NewLine is TRUE, a new command line is read using getnxt before continuing. The current line buffer is searched from the present position of the scan pointer until either a word modifier in the expect array is found or the end of the buffer is reached. In the former case, getwrd returns the first four characters of the word modifier packed into an integer, sets eol to FALSE, and places the scan pointer at the end of the word modifier. In the latter case, getwrd returns blanks (a string of four spaces packed into an integer), sets eol to TRUE, and places the scan pointer at the end of the buffer. getwrd will skip over words that are not in the expect array.

6.3.8.3 getnum

    REAL getnum(BOOLEAN NewLine, BOOLEAN* eol);

This function returns the value of a floating point modifier (see Section 4.4). Restriction: The floating point modifier must be in the precise format described in Section 4.4.

If NewLine is TRUE, a new command line is read using getnxt before continuing. The current line buffer is searched from the present position of the scan pointer until either a floating point modifier is found or the end of the buffer is reached. In the former case, getnum returns the value of the floating point modifier, sets eol to FALSE, and places the scan pointer at the end of the floating point modifier. In the latter case, getnum returns 0.0, sets eol to TRUE, and places the scan pointer at the end of the buffer.
6.3.8.4 getint

    INTEGER getint(BOOLEAN NewLine, BOOLEAN* eol);

This function returns the value of an integer modifier (see Section 4.4). Restriction: The number of digits of the integer modifier must be no more than 9.

If NewLine is TRUE, a new command line is read using gettxt before continuing. The current line buffer is searched from the present position of the scan pointer until either an integer modifier is found or the end of the buffer is reached. In the former case, getint returns the value of the integer modifier, sets eol to FALSE, and places the scan pointer at the end of the integer modifier. In the latter case, getint returns 0, sets eol to TRUE, and places the scan pointer at the end of buffer.

6.3.9 noise.h

    extern class Noise_class
    {
        public:
            INTEGER quanin;
            REAL quanmn;
            REAL quancm;
            BOOLEAN sctnfl;
            REAL sctnpk;
            REAL sctnwd;
            BOOLEAN ultnfl;
            REAL ultnmn;
            REAL ultnsd;
            BOOLEAN addnfl;
            REAL addnmn;
            REAL addnsd;
    } NoisePar;

These attributes describe the nature of noise that exists in the projection data. In other sections of this manual quanin, quanmn, quancm, sctnpk, sctnwd, ultnmn, ultnsd, addnmn, and addnsd are referred to as QUANIN, QUANMN, QUANCM, SCTNPK, SCTNWD, ULTNMN, ULTNSD, ADDNMN, and ADDNSD, respectively. Their meanings are given in Section 5.3.2 and in Section 5.3.3 as part of the description of command line 7.2. The values of the variables are determined by the PROJECTION command (see Section 5.5). Warning: The values of ultnmn and addnmn refer to the original projection data; the data stored on prjfil are corrected for bias (see Section 5.5).

6.3.10 spctrm.h

    extern class spctrm_class
    {
        public:
            INTEGER nergy;
            INTEGER energy[7];
            REAL engwt[7];
            REAL backgr[7];
    } Spctrm;

These attributes describe the energy distribution in the x-ray beam that was used to collect the data and the nature of the background material that was used for the calibration measurements. This is explained in detail in Section 5.3.2. The values of the variables are determined by the PROJECTION command (see Section 5.5) as follows.
ergy is 1 if MONOCHROMATIC is specified on command line 2.1 (see Section 5.3.3) and nergy is the value of nergy if POLYCHROMATIC is specified on command line 2.1. In other sections of this manual, it is referred to as NERGY. In the MONOCHROMATIC case, energy[0] has the value of energy on command line 2.1 and energy[i] = 0 for 0 < i < 7. In the POLYCHROMATIC case, energy[i] has the value of energy(i+1) on command line 2.2 for 0 ≤ i < nergy and 0 for nergy ≤ i < 7.

In the MONOCHROMATIC case, engwt[0] = 1 and engwt[i] = 0 for 0 < i < 7. In the POLYCHROMATIC case, engwt[i] is percent(i+1)/100 from command line 2.2 for 0 ≤ i < nergy, and 0 for nergy ≤ i < 7.

6.3.11 modefl.h

```cpp
extern class modefl_class
{
   public:
      BOOLEAN lofl;
      REAL lower;
      BOOLEAN upfl;
      REAL upper;
   } Modefl;
```

The values of these attributes are assigned by the most recent MODE command. See Section 5.2 for details. In other sections of this manual, lofl, lower, upfl, and upper are referred to as LOFL, LOWER, UPFL, and UPPER, respectively.

6.4 Service routines available to the user

In addition to the methods contained in the various classes described above, there are a number of basic operations that are not associated with any class. These operations are coded in separate subroutines, which are then called by the reconstruction algorithm when needed. Since these subroutines are also likely to make the writing of user-defined algorithms easier, their names, their formal parameter lists and their actions are explained below. These subroutines are also referred to in the explanation of the built-in reconstruction algorithms in Chapter 7.

6.4.1 pick

```cpp
#include "pick.h"

void pick(INTEGER* np, INTEGER* nr);
```

This subroutine assigns to np a projection number and to nr a ray number. The actual values to be returned are selected according to the method determined by the most recently executed SELECT command (see Section 5.6). If no SELECT command has been executed, np and nr are selected in the same way as if the most recently executed SELECT command was

SELECT USER EFFICIENT

**Warning:** Using pick in a termination test is not advisable, since this would alter the sequence of pairs (np, nr) that is returned to the reconstruction algorithm after the first iteration (see Section 6.1).

6.4.2 wray

```cpp
#include "wray.h"

void wray(
    INTEGER np, INTEGER nr,
```
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For the \( np \)th projection and \( nr \)th ray, this routine calculates the trace of a LINE ray through the picture region and the pixels intersected. **Restriction:** \( 0 \leq np < \text{PRJNUM} \) and \( 0 \leq nr < \text{NRAYS} \). **Warning:** In case of STRIP rays, the subroutine will return values that are appropriate for LINE rays located at the centers of the actual STRIP rays.

\texttt{wray} returns the following information:

- \texttt{numb} Number of pixels intersected. When \texttt{numb} = 0, the ray in question does not intersect the picture region.
- \texttt{list[0], \ldots, list[numb-1]} The indices of the pixels intersected by the ray. I.e., if \( j = \text{list}[i] \), then \( \text{recon}[j] \) is the present density in the \( i \)th pixel intersected by the ray (see Section 6.2).
- \texttt{weight[0], \ldots, weight[numb-1]} The lengths of the ray segments within the pixels in the order given in \texttt{list}.
- \texttt{snorm} The sum of the squares of the above lengths.

See Section 6.3.4.3 for the blob equivalent of this subroutine.

### 6.4.3 ray

```c
#include "ray.h"

void ray (
    INTEGER np, INTEGER nr,
    INTEGER* list, REAL* weight,
    INTEGER* numb, REAL* snorm
);
```

For the \( np \)th projection and \( nr \)th ray, this routine calculates the trace of a STRIP ray through the picture region. **Restriction:** \( 0 \leq np < \text{PRJNUM} \) and \( 0 \leq nr < \text{NRAYS} \). **Warnings:** In case of PARALLEL LINE rays, the subroutine will return the values that are appropriate for PARALLEL STRIP rays whose central lines are the actual LINE rays (see Section 2.3). If \texttt{ray} is called in the case of DIVERGENT rays, the SNARK14 run will be terminated.

\texttt{ray} returns the following information:

- \texttt{numb} Number of pixels whose centers are in the ray. When \texttt{numb} = 0, the ray in question does not contain the center of any pixel.
- \texttt{list[0], \ldots, list[numb-1]} The indices of the pixels whose centers are in the ray. I.e., if \( j = \text{list}[i] \), then \( \text{recon}[j] \) is the present density in the \( i \)th pixel whose center is in the ray (see Section 6.2).
- \texttt{weight[0], \ldots, weight[numb-1]} Are all assigned the value \( \text{pixsiz} \times \text{pixsiz} \).
- \texttt{snorm} is assigned the value \( \text{pixsiz} \times \text{pixsiz} \times \text{pixsiz} \times \text{pixsiz} \times \text{numb} \).

See Section 6.3.4.4 for the blob equivalent of this subroutine.

### 6.4.4 pseudo

```c
#include "pseudo.h"

REAL
pseudo(
    REAL* pict, INTEGER np, INTEGER nr,
```
Roughly speaking, this function returns the pseudo ray sum of a picture, whose pixel densities are stored in \texttt{pict}, for the \( nr \)th ray of the \( np \)th projection. The exact operation depends on the values of the logical variables \texttt{line} and \texttt{constr} and is best explained by listing the whole of the rest of the subroutine.

```c
#include <cstdio>
#include "blkdta.h"
#include "modefl.h"
#include "uiod.h"
#include "ray.h"
#include "wray.h"
#include "pseudo.h"

REAL pseudo(
    REAL* pict,
    INTEGER np,
    INTEGER nr,
    INTEGER* list,
    REAL* weight,
    INTEGER* numb,
    REAL* snorm,
    BOOLEAN line,
    BOOLEAN constr
) {
    INTEGER nb, k;
    REAL pictk;
    REAL sum = 0.0;
    if (!line) {
        ray(np, nr, list, weight, numb, snorm);
    } else {
        wray(np, nr, list, weight, numb, snorm);
    }
    if (*numb != 0) {
        for (nb = 0; nb < *numb; nb++) {
            k = list[nb];
            pictk = pict[k];
            if (constr) {
                if (Modefl.lofl) pictk = MAX0(pictk, Modefl.lower);
                if (Modefl.upfl) pictk = MIN0(pictk, Modefl.upper);
            }
            sum += pictk * weight[nb];
        }
    }
    if (trace > 5) {
        fprintf(output,
            "\n            pseudo np = %5i nr = %5i pseudo = %9.4f\n",
            np, nr, sum, line);
    }
    return sum;
}
```
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Note: By calling the function `pseudo`, the variables `list`, `weight`, `numb`, and `snorm` will have their values determined by `wray` or `ray` (see Sections 6.4.2 and 6.4.3).

See Section 6.3.4.5 for the blob equivalent of this subroutine.

6.4.5 qintp

#include "qintp.h"

REAL qintp(REAL pos, REAL* table, INTEGER n, INTEGER interp);

This is a one-dimensional interpolation routine. Suppose the array table is such that `table[i]` is the value of a function at the integer point `i`, for `0 ≤ i < n`. qintp returns the estimated value of the function at the point `pos`, based on the values in the array table and the interpolation method specified by the integer `interp`.

Warning: When using this function, the value of `pos` must lie within certain limits, which will be specified below for each of the interpolation methods separately. Calling the function with a value of `pos` outside the specified range will result in unpredictable consequences. It is also essential that the size of the array table is at least `n`.

In what follows we use `E` to denote the largest integer not greater than `pos` and `F` to denote the largest integer not greater than `pos+0.5` (`F` is the integer nearest to `pos`). The restrictions on `pos` are expressed in terms of `E` or `F`.

There are eight interpolation methods available in qintp. (Restriction: -1 ≤ `interp` ≤ 6.)

1. Modified cubic spline interpolation proposed in [60]. Restriction: 1 ≤ `E` ≤ n-2. If `interp` = -1, qintp returns the value at `pos` of a cubic polynomial whose values at `E` and `E+1` are `table[E]` and `table[E+1]`, respectively, and whose slopes at `E` and `E+1` are \((table[E+1]-table[E-1])/2\) and \((table[E+2]-table[E])/2\), respectively.

2. Band limiting (sinc) interpolation. Restriction: 0 ≤ `F` ≤ n-1. If `interp` = 0, qintp returns a value defined as follows.

   \[
   \text{qintp} = \begin{cases} 
   \text{table}[F], & \text{if } |F - \text{pos}| < \text{ZERO}, \\
   \left(\sum_{k=1}^{n} (-1)^{k+1} \frac{\text{table}[k]}{\text{pos} - k}\right) \frac{\sin(\pi \times \text{pos})}{\pi}, & \text{otherwise}. 
   \end{cases}
   \]

3. Nearest neighbor interpolation. Restriction: 0 ≤ `F` ≤ n-1. If `interp` = 1, qintp returns `table[F]`.

4. Linear interpolation. Restriction: 0 ≤ `E` ≤ n-1. If `interp` = 2, qintp returns \((E+1-\text{pos}) \times \text{table}[E] + (\text{pos}-E) \times \text{table}[E+1]\).

5. Three point Lagrange interpolation. Restriction: 1 ≤ `F` ≤ n-2. If `interp` = 3, qintp returns the value at `pos` of a quadratic polynomial whose values at `F-1`, `F`, and `F+1` are `table[F-1]`, `table[F]`, and `table[F+1]`, respectively.


7. Five point Lagrange interpolation. Restriction: 2 ≤ `F` ≤ n-3. If `interp` = 5, qintp returns the value at `pos` of a quartic polynomial whose value at `i` is `table[i]` for `F - 2 ≤ i ≤ F + 2`.

8. Six point Lagrange interpolation. Restriction: 2 ≤ `E` ≤ n-4. If `interp` = 6, qintp returns the value at `pos` of a quintic polynomial whose value at `i` is `table[i]` for `E - 2 ≤ i ≤ E + 3`. 

6.4.6 bckprj

#include "bckprj.h"

void bckprj(
    REAL* a, INTEGER n, REAL* g, INTEGER m,
    REAL sth, REAL cth, REAL spac, INTEGER interp
    );

Roughly speaking the purpose of this routine is to back-project ("smear") a function of one variable (determined by the array \( g \)) in the direction determined by the unit vector \( (cth, sth) \) onto a picture region, and to add the values of the digitized version of the "smear" picture to array \( a \).

More precisely, \( a \) is an array, such that \( a[i*n+j] \) represents the density of the \( j \)th pixel of the \( i \)th row of an \( n \times n \) digitized picture in which the length of a side of a pixel is \( spac \). (Warning: The size of the array must be at least \( n\times n \).) This is the same indexing as is used for \texttt{recon} (see Section 6.2). \( n \) must be a positive integer, but it need not be odd. It is assumed that the origin of the coordinate system is at the center of the \( \lfloor(n-1)/2\rfloor \)th pixel of the \( \lfloor(n-1)/2\rfloor \)th row, where \( \lfloor x \rfloor \) denotes the largest integer not greater than \( x \).

Consider a line \( L \) through the origin that makes an angle \( \theta \) with the \( y \)-axis (see Figure 6.1), where \( 0 \leq \theta \leq 2\pi \), \( cth = \cos \theta \) and \( sth = \sin \theta \). We measure the position along this line as indicated in Figure 6.1. In particular, the position of the origin is \( \lfloor(m-1)/2\rfloor \). Then it is easy to calculate that the orthogonal projection of the center of the \( (i,j) \)th pixel onto the line that has position \( \text{pos} = |(m-1)/2|-\lfloor j-(n-1)/2 \rfloor \times sth+\lfloor i-(n-1)/2 \rfloor \times cth \times spac \).

\( p \) is an array whose first \( m \) values represent the values of a function \( p \) defined on the line \( L \). (Warning: The dimension of the array \( p \) must be at least \( m \).) The value of \( p(x) \) at a non-integer \( x \) is to be defined by interpolation, as will be explained below.

Now we are in position to explain the precise effect of bckprj. The \( (i*n+j) \)th entry of the array \( a \) has added to it the value of
$qintp(pos, p, m, interp)$ (see Section 6.4.5), where $pos$ is defined by the formula given above. Restrictions: $-1 \leq interp \leq 6$ and the value of $m$ has to be large enough so that $pos$ will lie between the limits specified in Section 6.4.5.

Note: In actual applications of this subroutine the value of $spac$ will be the ratio of pixel size to detector spacing (see, e.g., Section 7.1).

6.4.7 posit

```
#include "posit.h"

void posit(INTEGER np, INTEGER nr, REAL* ax, REAL* ay, REAL* mx, REAL* my);
```

This subroutine returns, for the $nr$th ray of the $np$th projection, the coordinate $(ax, ay)$ of a point on the ray (in the STRIP case a point on the central line of the ray) and the cosine $mx$ and the sine $my$ of the angle that the ray makes with the x-axis. Restrictions: $0 \leq np < PRJNUM$ and $0 \leq nr < NRAYS$.

6.4.8 raylen

```
#include "raylen.h"
#include "objects.h"

REAL raylen(
    SNARK_Object_type type,
    REAL ax, REAL ay, REAL mx, REAL my,
    REAL cx, REAL cy, REAL u, REAL v, REAL px, REAL py
);
```

This function returns the length of the part of a straight line (ray) that lies inside an elemental object. The straight line is determined by the coordinates $(ax, ay)$ of a point on it, and by the cosine $mx$ and the sine $my$ of the angle that the line makes with the x-axis. The type of elemental object (see Section 5.3.1) is determined by the enumerated variable type. Restriction: The value of type must be one of $SOT_{elip}$, $SOT_{rect}$, $SOT_{tria}$, $SOT_{segm}$, $SOT_{sect}$, which are defined in objects.h (see Figure 5.1). The values of $cx$, $cy$, $u$, and $v$ are interpreted according to Figure 5.1. The values of $px$ and $py$ are the cosine and the sine, respectively, of the angle denoted by ANG in Figure 5.1.

6.4.9 contur

```
#include "contur.h"

void contur(REAL* a, INTEGER m, INTEGER n, REAL thresh, REAL w1, REAL w2, REAL w3);
```

This subroutine changes the first $m \times n$ elements of the array $a$, by setting the value to $w1$ or $w2$. If $w3 \leq ZERO$, the value is set depending on whether the original value was $\leq$ or $>$ $thresh$, respectively. If $w3 > ZERO$, the threshold is chosen such that the average density of the resulting image is as close to $AVEDEN$ as possible. (See Section 5.8.) Warning: The size of $a$ must be at least $m \times n$.

6.4.10 smooth

```
#include "smooth.h"

void smooth(REAL* a, INTEGER m, INTEGER n, REAL thresh, REAL w1, REAL w2, REAL w3);
```

This subroutine carries out the nine point selective smoothing procedure, which is described in detail in Section 5.8. For $0 \leq i < m$ and $0 \leq j < n$, the $(i \times n + j)$th element of the array $a$ is interpreted as the value of the $(i, j)$th pixel of an $m \times n$ digitized picture. (We have only defined $N \times N$ digitized pictures in Section
2.2, but the generalized definition is obvious.) Warning: The size of $a$ must be at least $m \times n$. The smoothing of this picture is done in the manner specified in Section 5.8, with the values of $\text{thresh}$, $w1$, $w2$, and $w3$ assigned to the threshold, weight1, weight2, and weight3, respectively.

See Section 6.3.4.6 for the blob equivalent of this subroutine.

### 6.4.11 snfft

```c
#include "snfft.h"

void snfft(REAL* x, INTEGER* n, INTEGER invdir);
```

This subroutine performs complex Fourier transforms on a complex three-dimensional array $f[k, l, m]$. The integer array $n$ is of size 3; $n[i]$ denotes the size of the 3-dimensional array $f[k, l, m]$ in the $i$th dimension. (A one-dimensional array can be treated by this subroutine by setting $n[1] = n[2] = 1$.)

As input, the array $x$ contains $f[k, l, m]$ in a vector fashion. For $0 \leq k < n[0]$, $0 \leq l < n[1]$, and $0 \leq m < n[2]$, the real part of $f[k, l, m]$ is assigned to the $(2 \times (k \times n[1] \times n[2] + l \times n[2] + m))$th location of $x$, the imaginary part of $f[k, l, m]$ to the immediately following location. Warning: The size of $x$ must be at least $2 \times n[0] \times n[1] \times n[2]$. As output, $x$ contains (using the same indexing conventions), the complex discrete Fourier Transform $Ff$ of $f$ if $\text{invdir} = 1$ or the complex inverse discrete Fourier transform $F^{-1}f$ of $f$, if $\text{invdir} = -1$. (These transforms are defined below.) Restriction: the value of $\text{invdir}$ must be 1 or -1.

$$
|Ff|(k, l, m) = \sum_{p=0}^{n[0]-1} \sum_{q=0}^{n[1]-1} \sum_{r=0}^{n[2]-1} f(p, q, r)e^{-2\pi i(pk/n[0]+ql/n[1]+rm/n[2])}
$$

$$
|F^{-1}f|(k, l, m) = \frac{1}{n[0] \times n[1] \times n[2]} \times \sum_{p=0}^{n[0]-1} \sum_{q=0}^{n[1]-1} \sum_{r=0}^{n[2]-1} f(p, q, r)e^{2\pi i(pk/n[0]+ql/n[1]+rm/n[2])}
$$

This subroutine is based on [62].

### 6.4.12 rtfort

```c
#include "rtfort.h"

void rtfort(REAL* x, INTEGER* n, INTEGER invdir);
```

This subroutine performs discrete Fourier transforms on real one or two-dimensional arrays. It also has the capability of performing the inverse discrete Fourier transform of complex arrays to real arrays. It is based on the property that (in one dimension) $|Fg|(X) = |Fg|(-X)^*$, where $z^*$ denotes the conjugate of the complex number $z$, so that we need only compute half of the Fourier Transform of the original data. Therefore, even though the Fourier Transform is complex valued, it requires essentially no more space than the real array (see [7] Section 10-10). Note: Due to the complexity of using this routine, it is recommended that snfft (Section 6.4.11) be used instead.

$x$ is a pointer to a real array. In the forward direction, each element of $x$ is a real value representing the function to be transformed. As the output of routines, each pair of REALs of $x$, $x[2i]$ and $x[2i+1]$, is a complex value representing the Fourier Transform of the function. In the reverse direction, the roles are reversed.

$n$ is a pointer to an integer array of 2 elements that is related to the size of $x$. If $x$ is a one dimensional array, then $n[0] = 1$, otherwise, $n[0]$ is the number of rows in the two dimensional array. $n[1]$ is one-half the number of real elements of $x$ in the one dimensional case and one-half the number of columns of $x$ in the two dimensional case. It may be necessary to pad the array with extra elements so that this value is an
CHAPTER 6. IMPLEMENTING USER-DEFINED ALGORITHMS

integer. Warning: The size of the array x must be at least \(2 \times n[0] \times (n[1] + 1)\) to accommodate the extra elements in the Fourier transform.

\textbf{invdir} is 1 if the discrete Fourier transform is desired and -1 if the inverse discrete Fourier transform is desired.

If \(g(k, l)\) is a real array then, for \(0 \leq k < n[0]\) and \(0 \leq l < 2 \times n[1]\), \(g(k, l)\) is stored in location \((2 \times k \times n[1] + l)\) of x. The subroutine \texttt{rtfort} has the property that the C++ statement

\[
\texttt{rtfort(x, n, 1)};
\]

will place in the array x the (complex) discrete Fourier transform of \(g\). For \(0 \leq k < n[0]\) and \(0 \leq l \leq n[1]\), the real part of \([Fg](k, l)\) is assigned to the \((2 \times (k \times (n[1] + 1)) + l)\)th location in x, and the imaginary part to the immediately following location. Since \(g\) is real, \([Fg](k, l) = ([Fg](n[0] - k, 2n[1] - l))^*\).

Hence, the value of \([Fg](k, l)\) for \(0 \leq k < n[0]\), \(n[1] < l < 2 \times n[1]\) are also easily obtained from the contents of the array x.

The subroutine \texttt{rtfort} also has the property that if

\[
\texttt{rtfort(x, n, -1)};
\]

is applied to the array x that contains in the just described manner the half of the complex discrete Fourier transform \([Fg]\) of \(g\), then the resulting content of the \((2 \times k \times n[1] + l)\)th element of the array x will be the real number \(g(k, l)\), for \(0 \leq k < n[0]\) and \(0 \leq l < 2 \times n[1]\).

This subroutine is based on [61].

6.4.13 qfilt

\#include "qfilt.h"

REAL qfilt(REAL R, REAL cutoff, INTEGER filter);

This function returns the value of a “filter function” \(F\) of one variable at the point \(R\). There are four types of filters in SNARK14. Filters of the same type are distinguished from each other by the value of the parameter \(cutoff\). The type of the filter is determined by the value of the variable \(filter\). (Restriction: \(0 \leq filter \leq 3\).)

We define

\[
\Pi(x) = \begin{cases} 
1, & \text{if } x \leq \frac{1}{2}, \\
0, & \text{if } x > \frac{1}{2}, 
\end{cases}
\]

\[
sinc(x) = \begin{cases} 
\frac{\sin \pi x}{\pi x}, & \text{if } x \neq 0, \\
1, & \text{if } x = 0.
\end{cases}
\]

We use \(C\) to abbreviate the value of \(cutoff\).

(i) \textbf{Band limiting filter} (used if \(FILTER = 0\)):

\[
F(R) = \Pi \left(\frac{R}{2C}\right) \times |R|.
\]

(ii) \textbf{Sinc filter} (used if \(FILTER = 1\)):

\[
F(R) = \text{sinc} \left(\frac{R}{2C}\right) \times \Pi \left(\frac{R}{2C}\right) \times |R|.
\]

(iii) \textbf{Cosine filter} (used if \(FILTER = 2\)):

\[
F(R) = \cos \left(\frac{\pi R}{2C}\right) \times \Pi \left(\frac{R}{2C}\right) \times |R|.
\]

(iv) \textbf{Hamming filter} (used if \(FILTER = 3\)):

\[
F(R) = (C + (1 - C) \cos(\pi R)) \times \Pi \left(\frac{R}{2}\right) \times |R|.
\]
6.4.14 qinit

```c
#include "qinit.h"

void qinit (REAL* table, INTEGER isize, INTEGER filter, REAL cutoff);
```

This subroutine puts in the first isize positions of the array table a discrete “convolving function”. The actual function depends on the “filter” that is indicated by the value of filter and cutoff. **Restriction:** 0 ≤ filter ≤ 3 (see Section 6.4.13 for the meaning of filter). **Warning:** the size of table must be at least isize.

For any permissible value of filter and cutoff let the filter function $F(R)$ be defined as in Section 6.4.13. Then for $0 \leq m < isize$, table\[m\] is assigned half the value of the $m$th Fourier coefficient of the function $F(R)$ defined over the interval [-1,1]. In other words, for $0 \leq m < isize$,

$$
table[m] = \frac{1}{4} \int_{-1}^{1} F(R)e^{\pi imR} dR.
$$

These entries in table are real, since $F$ is symmetric.

The reasoning behind this definition of the “convolving function” has been given in [64]. Various convolving functions proposed in the literature can be produced by adjusting the values of filter and cutoff. These include the convolving functions proposed in [6, 12, 63, 66].

6.4.15 sinc

```c
#include "sinc.h"

REAL sinc(REAL x);
```

This function returns the value 1 if |x| < ZERO and it returns the value $\sin(\pi x)/\pi x$ otherwise.

6.4.16 cin

```c
#include "cin.h"

REAL cin(REAL x);
```

This function returns the estimated value of $\int_{0}^{x} (1 - \cos u)/udu$. The estimation is done using rational approximation as described by [20, 69].

6.4.17 Rand

```c
#include "DIGRand.h"

void Srand(unsigned int pSeed);
REAL Rand();
```

This function is used for generating random numbers uniformly distributed in the range [0.0, 1.0). Srand() is used to set the seed to the random number generator. Rand() return the next random number in the sequence.

**Warning:** The sequence produced by Rand() is installation dependent.

6.4.18 Gauss

```c
#include "DIGRand/DIGGauss.h"

double Gauss(double mean, double std);
```
This function returns a sample from a normal distribution with mean mean and standard deviation std. The method used for calculating the sample is the polar method based on the uniform distribution generated by Rand (see Section 6.4.17). This method is an implementation of one proposed by Knuth [49].

6.4.19 Poisson

```
#include "DIGRand/DIGPoisson.h"

int Poisson(double pALambda);
```

This subroutine returns a sample from a Poisson distribution with mean pALambda. This algorithm is described in [65].

6.4.20 second

```
#include "second.h"

void second(REAL* ctime);
```

This subroutine assigns to the variable ctime the CPU time used by the SNARK14 program measured in seconds. It is used to report on the execution times in the SNARK14 output. The accuracy of ctime is system dependent.
Chapter 7

BUILT-IN RECONSTRUCTION ALGORITHMS

This chapter documents the algorithms existing within SNARK14 and provides the user with a description of the follow-up command lines a particular algorithm requires after the EXECUTE control command line (see Section 5.8). The descriptions of the algorithms provided here are by necessity rather sketchy; the user is referred to the cited literature for derivation of the formulas and for discussion of the properties of the algorithms. Our description will depend heavily on the material introduced in Chapter 6.

The sections of this chapter are entitled by the value of the word modifier algname on the EXECUTE control command line that determines the reconstruction algorithm that will be executed. These names are BACKPROJECTION, CONVOLUTION, RFL, FOURIER, DCONV, ART, MART, QUADRATIC, SIRT, EMAP, and LINO. In each case we describe the necessary follow-up command lines in the EXECUTE command and explain the purpose of the modifiers occurring on these command lines. These command lines are all in control command line format and they immediately follow the last line of the EXECUTE sequence (see Section 5.8).

References that are given to the literature for description of the various methods are not necessarily to sources that originated the method in question. They have been chosen for their informative value rather than for their originality.

7.1 BACKPROJECTION

This is a general implementation of the backprojection or summation reconstruction methods (see [29] Chapter 7). It incorporates two fairly different approaches. Both of them first produce a NELEM×NELEM “preliminary picture” in a fashion that we now describe.

If CONTINUOUS is specified, then, roughly speaking, the preliminary picture has a value assigned to a pixel that is the sum of the ray sums for the rays that go through the center of the pixel. (One and only one ray in each projection is assumed to go through the center of a pixel.)

A precise description of how the preliminary picture is obtained in the CONTINUOUS case is best given by C++ like code that makes use of some subroutines described in Section 6.4.

```c
Anglst.getang(GeoPar.prjnum -1, &theta, &sinth, &costh);
theta0 = theta - thmod;
for (np = 0; np < GeoPar.prjnum; np++) {
    ProjFile.ReadProj(np, g, nsize);
    Anglst.getang(np, &theta1, &sinth, &costh);
    np2 = np + 1;
    if (np == (GeoPar.prjnum - 1)) np2 = 0;
```
Anglst.getang(np2, &theta2, &sinth2, &costh2);
if (np == (GeoPar.prjnum - 1)) theta2 += thmod;
w = (theta2 - theta0) / thfac;

rinc = GeoPar.pinc;
if (GeoPar.div) rinc *= GeoPar.radius / GeoPar.stod;
if (GeoPar.vri) rinc *= (REAL) MAX0(fabs(sinth), fabs(costh));
if (GeoPar.strip) w /= rinc;
theta0 = theta1;
for (nr = 0; nr < nsize; nr++) {
    g[nr] *= w;
}
bckprj(recon, GeoPar.nelem, g, nsize, sinth, costh, GeoPar.pixsiz/rinc, interp);

The variables that are not in one of the C++ classes (see Section 6.3) and appear in the code above have
their values defined as follows. (All these variables are assigned their correct values by SNARK14.)

nsize, the size of the array g, is an integer large enough so that the restriction on the size of m in bckprj
(see Section 6.4.6) is satisfied.

w(np) depends on the geometry of data collection. Let the variable RANGE have the value \( \pi \) in the
PARALLEL case and the value \( 2\pi \) in the DIVERGENT case. Let \( \theta(np) \) denote the projection angle in radians
of the \( np \)th projection for \( 0 \leq np < PRJNUM \), and let \( \theta(-1) \) be \( \theta(PRJNUM)-RANGE \) and \( \theta(PRJNUM) \) be
\( \theta(0) + RANGE \). (Restriction: For \( 0 \leq np \leq PRJNUM \), \( \theta(np-1) < \theta(np) \).) Let WIDTH(np) denote the actual
distance between rays in the PARALLEL LINE case and the actual width of the strips in the PARALLEL
STRIP case. Then,

\[
w(np) = \begin{cases} 
\frac{\theta(np+1)-\theta(np-1)}{2}, & \text{in the PARALLEL LINE case,} \\
\frac{\theta(np+1)-\theta(np-1)}{2} \times \text{WIDTH}(np), & \text{in the PARALLEL STRIP case,} \\
\frac{\theta(np+1)-\theta(np-1)}{4}, & \text{in the DIVERGENT case.}
\end{cases}
\]

SPAC = \begin{cases} 
\frac{\text{PIXSIZ}}{\text{WIDTH}(np)}, & \text{in the PARALLEL case,} \\
\frac{\text{PIXSIZ} \times \text{STOD}}{\text{PINC} \times \text{RADIUS}}, & \text{in the DIVERGENT case.}
\end{cases}

The value assigned to interp is the value of the integer modifier interp. Restriction: \(-1 \leq \text{interp} \leq 6\)
(see Section 6.4.5).

Warning: In the CONTINUOUS case the rays of DIVERGENT geometry are treated as if they were
PARALLEL with UNIFORM ray spacing PINC\times RADIUS/STOD. A large divergence angle will result in
unacceptable reconstructions.

If DISCRETE is specified, then roughly speaking the value of a pixel in the preliminary picture is the
sum of contributions from every ray that intersects the pixel. The size of the contribution is proportional to
the ray sum of the ray and also depends on the size of the intersection with the pixel.

A precise description of how the preliminary picture is obtained in the DISCRETE case is best given by
C++ like code that makes use of some of the subroutines in Section 6.4.

for (np = 0; np < GeoPar.prjnum; np++) {
    ProjFile.ReadProj(np, g, GeoPar.nrays);
    for (nr = GeoPar.fsnray; nr <= GeoPar.lsnray; nr++) {
        if (GeoPar.strip) ray(np, nr, list, weight, &numb, &snorm);
        if (GeoPar.line) wray(np, nr, list, weight, &numb, &snorm);
        if (numb != 0) {
            amt = g[nr];
            if (dist) {
                if (zeros) {
                    snorm = 0.0;
                for (nb = 0; nb < numb; nb++) {

\[ \text{var} = \text{expr} \]
The variables that are not in C++ classes (see Section 6.3) and appear in the code above have their values defined as follows. (All these variables are assigned their correct values by SNARK14.)

zeros is a logical variable whose value is TRUE if the option ZEROS is specified on the follow-up line for this algorithm. If zeros is TRUE then prior to the code described above the algorithm loops through all the rays (from FUSRAY to LUSRAY) in all the projections and flags all the pixels that are intersected by rays whose ray sum is 0.

dist is a logical variable whose value is TRUE if the option DISTRIBUTED is specified on the follow-up line for this algorithm.

The preliminary picture produced by either the CONTINUOUS or DISCRETE method described above is further altered according to the following rules. The values given to the pixels in the preliminary picture are altered either by addition of (if ADDITIVE is specified) or by multiplication by (if MULTIPLICATIVE is specified) a constant (the same constant for all pixels) so that the average density of the resulting picture is AVEDEN (see Section 6.3.3). If neither MULTIPLICATIVE nor ADDITIVE is specified, the preliminary picture is not normalized and is the final reconstructed picture produced by the algorithm.

If the iteration number iter > 1, this algorithm returns control to exalg without changing the contents of the recon array. Multiple iterations may nevertheless be used for smoothing or contouring the reconstruction (see Sections 5.8 and 6.1).

### 7.2 CONVOLUTION

\[
\begin{cases}
\text{BANDLIMITING} \\
\text{SINC} \\
\text{COSINE} \\
\text{HAMMING}
\end{cases}
\]

This is a general implementation of the filtered backprojection, also known as the convolution, method for parallel beams (see, e.g., [29] Chapter 8, or [64]). Roughly speaking, the projection data are first “convolved” by a function based on a “filter”, and then the convolved projection data are backprojected to form the reconstruction.

More precisely, the convolving function is defined by the filter (BANDLIMITING, SINC, COSINE, or HAMMING) and the floating point modifier cutoff. The convolving function is put into the array table by the C++ statement

\[
\text{qinit(table, nsize, filter, c);}
\]

(see Section 6.4.14), where nsize is an integer large enough for the “backprojection” to be discussed below to be a valid operation, filter is 0, 1, 2, or 3 if the filter is BANDLIMITING, SINC, COSINE, or HAMMING,
respectively, and
\[
c = \begin{cases} 
\text{cutoff,} & \text{if zero} < \text{cutoff} \leq 1, \\
\min \left( \frac{2 \times \text{PRJNUM} \times \text{PINC}}{\pi \times \text{NELEM} \times \text{PIXSIZE}}, 1 \right), & \text{if cutoff} < 0, \\
1, & \text{otherwise.}
\end{cases}
\]

The reconstruction proceeds in exactly the same way as was used to obtain the preliminary picture in the CONTINUOUS case of the BACKPROJECTION method (Section 7.1), with one important exception. Immediately after the statement
\[
\text{ProjFile.ReadProj}(np, \text{data}, \text{nsize});
\]
additional code is inserted, as a result of which the array \text{data} is altered. The new value of \text{data}[i], for \(0 \leq i < \text{nsize}\), can be expressed in terms of the old values of the array \text{data} and the \text{table} generated by \text{qinit} above by the convolution formula
\[
\frac{1}{\text{WIDTH}(np)} \sum_{j=0}^{\text{nsize}-1} \text{data}[i] \times \text{table}[|i - j|].
\]
Here \text{WIDTH}(np) denotes (for the \(np\)th projection) the actual distance between the lines in the PARALLEL LINE case, the actual width of the strips in the PARALLEL STRIP case, and \(\text{PINC} \times \text{RADIUS} / \text{STOD}\) in the DIVERGENT case. The result of the continuous backprojection of the convolved data is (without any normalization) the final reconstructed picture produced by the convolution algorithm.

\textit{Restriction:} For \(0 \leq np \leq \text{PRJNUM}, \theta(np-1) < \theta(np)\). (see Section 7.1 for definition of \(\theta(np)\)).

\textit{Warning:} The rays of DIVERGENT geometry are treated as if they were PARALLEL with UNIFORM ray spacing \(\text{PINC} \times \text{RADIUS} / \text{STOD}\). If divergence of rays is so great that this results in unacceptable error, then the use of the DCONV reconstruction algorithm (Section 7.5) is recommended.

If the iteration number \(\text{iter} > 1\), this algorithm returns control to \text{exalg} without changing the contents of the \text{recon} array. Multiple iterations may nevertheless be used for smoothing or contouring the reconstruction (see Sections 5.8 and 6.1).

### 7.3 RFL

\[
> \begin{cases} 
\text{BANDLIMITING} \\
\text{SINC} \\
\text{COSINE} \\
\text{HAMMING}
\end{cases} \text{ cutoff interp [ size ]}
\]

This algorithm, whose name abbreviates \textit{rho filtered layergram} (see, e.g., [64] or [68]), (i) takes the output of the CONTINUOUS BACKPROJECTION, (ii) performs a two-dimensional Fourier transform, (iii) multiplies the values of the Fourier transform at all points by a filter function \(F(\rho, \phi)\), where \(\rho\) denotes the distance of the point from the origin, and then (iv) it performs an inverse two-dimensional Fourier transform to get the reconstructed picture.

(i) An array, which we call \text{lrecon} is set up to hold the densities associated with the pixels of a size\(\times\)size digitized picture. The same indexing is to be used as for \text{recon}, see Section 6.2. (Restriction: size > \text{NELEM} and even.) If size is not specified, its value is taken to be \text{NELEM} + 1. It is assumed that the origin of the coordinate system is at the center of the \((\text{size}/2)\)th pixel of the \((\text{size}/2)\)th row (cf., Section 6.4.6).

A picture is produced in the \text{lrecon} array by exactly the same method by which BACKPROJECTION produces a picture in the \text{recon} array if

\text{CONTINUOUS interp ADDITIVE}

is specified (see Section 7.1). \textit{Restrictions:} \(-1 \leq \text{interp} \leq 6\) (see Section 6.4.5). For \(0 \leq np \leq \text{PRJNUM}, \theta(np) < \theta(np + 1)\) (see Section 7.1 for definition of \(\theta(np)\)).

(ii) We transform the contents of \text{lrecon} by
rtfort(lrecon, n, 1);

(see Section 6.4.12), with \( n[1] = \text{size} \), and \( n[2] = \text{size}/2 \). After this transformation \( \text{lrecon}[i] \), for \( 1 \leq i \leq \text{size} \times \text{size} \), represents the value at some point, whose polar coordinates we denote by \((\rho, \phi_i)\), of the real or imaginary part of the Fourier transform of the picture obtained by backprojection.

(iii) At this point, the subroutine alters \( \text{lrecon}[i] \) by multiplying it by \( F(\rho, \phi_i) \). (Definition of the function \( F \) will be given below).

(iv) The resulting array in \( \text{lrecon} \) is inverse Fourier transformed using

\[
\text{rtfort(\text{lrecon}, n, -1);}
\]

(see Section 6.4.12), producing a picture in the array \( \text{lrecon} \), the central part of which is transferred to \( \text{recon} \) as the reconstructed picture. Finally, the \( \text{recon} \) array is normalized by addition of a constant so that its average density is \( \text{AVEDEN} \). (see Section 6.3.3).

The function \( F \) is defined as follows, based on the filter (BANDLIMITING, SINC, COSINE, or HAMMING) and floating point modifier cutoff.

\[
C = \begin{cases} 
\text{cutoff,} & \text{if ZERO < cutoff \leq 1,} \\
\min \left( \frac{2 \times \text{PRJNUM} \times \text{PINC}}{\pi \times \text{NELEM} \times \text{PIXSIZE}}, 1 \right), & \text{if cutoff < 0,} \\
1, & \text{otherwise.}
\end{cases}
\]

and

\[
A(\phi) = \begin{cases} 
2 \times \text{PINC}, & \text{in the PARALLEL UNIFORM case,} \\
2 \times \text{PINC} \times \max(|\sin \phi|, |\cos \phi|), & \text{in the PARALLEL VARIABLE case,} \\
\frac{2 \times \text{PINC} \times \text{RADIUS}}{\text{STOD}}, & \text{in the DIVERGENT case.}
\end{cases}
\]

Then,

\[ F(\rho, \phi) = \frac{\text{qfilt}(A(\phi) \times \rho, C, \text{filter})}{A(\phi)} \]

where \( \text{qfilt} \) is the function defined in Section 6.4.13 and the value of filter is 1, 2, 3 or 4 if the filter is BANDLIMITING, SINC, COSINE, or HAMMING, respectively. Restrictions stated on the value of \( C \) in Section 6.4.13 apply.

Warning: The rays of DIVERGENT geometry are treated as if they were PARALLEL with UNIFORM ray spacing \( \text{PINC} \times \text{RADIUS}/\text{STOD} \). A large divergence angle will result in unacceptable reconstructions.

If the iteration number \( \text{iter} > 1 \), this algorithm returns control to \text{exalg} without changing the contents of the \( \text{recon} \) array. Multiple iterations may nevertheless be used for smoothing or contouring the reconstruction (see Sections 5.8 and 6.1).

### 7.4 FOURIER

This is a general implementation of the Fourier method (see, e.g., [19, 29, 55, 57]). Roughly speaking, the projection data are first transformed using the one dimensional Fourier transform. This provides us with the values of the two dimensional Fourier transform of the picture on radial lines. From these values the Fourier transform of the picture is estimated at the centers of the pixels of a grid, and the discrete inverse two-dimensional Fourier transform is used to get the reconstructed picture.

More precisely, the method has four stages: (i) Fourier transforming the data; (ii) filtering the Fourier transform; (iii) interpolating the Fourier transform to a square grid; and (iv) taking the inverse Fourier transform. We now explain what happens in each one of these stages.

(i) The variable \( \text{nsize} \) is assigned the value \( \text{NRAYS} + 1 \) if the integer modifier \( \text{size1} < \text{USRAYS} \) or is not specified. If \( \text{size1} \geq \text{USRAYS} \), \( \text{nsize} \) is either \( \text{size1} \) or \( \text{size1} + 1 \), whichever is even.

For \( 0 \leq \text{np} < \text{PRJNUM} \), the discrete Fourier transform of the reordered raysums is taken, according to the following C++-like code:
ProjFile.ReadProj(np, data, nsize);
for (int i = 0; i < (nsize/2)+1; ++i) {
  x[i] = data[(nsize/2)+i-1] / w(np);
}
for (int i = (nsize/2)+1; i < nsize; ++i) {
  x[i] = data[i-(nsize/2)-1] / w(np);
}
rtfort(x, n, 1);

Here \(w(np)\) is the width of the strips in the \(n\)th projection in the PARALLEL STRIP case and is 1 in the PARALLEL LINE or the DIVERGENT case.

At the end of this stage we have that for \(0 \leq k < \text{nsize}/2\) the complex number \(x[2k]+ix[2k+1]\) is \((i \text{ is } \sqrt{-1})\) an estimate of the value of

\[
\frac{1}{\text{WIDTH}(np)} |\mathcal{F}f| \left(\frac{k}{n \times \text{WIDTH}(np)}, \theta(np)\right),
\]

where \(\theta(np)\) is the projection angle of the \(np\)th projection; \(\text{WIDTH}(np)\) is the actual distance between rays in the PARALLEL LINE case, the actual width of the strips in the PARALLEL STRIP case, \(\text{PINC} \times \text{RADIUS} / \text{STOD}\) in the DIVERGENT case; and \(|\mathcal{F}f| (\rho, \phi)\) denotes the Fourier transform of the picture to be reconstructed at the point with polar coordinates.

Restrictions: For \(0 \leq np \leq \text{PRJNUM}\), \(\theta(np) - 1 < \theta(np) \leq \theta(np) + 1 + \alpha\) where \(\alpha = \pi/4\) in the PARALLEL VARIABLE case and is \(\pi/2\) otherwise (see Section 7.1 for definition of \(\theta(-1)\) and \(\theta(\text{PRJNUM})\)).

(ii) Let \((\rho, \phi)\) be any point for which \(|\mathcal{F}f| (\rho, \phi)\) has been computed during the previous stage. Filtering the Fourier transform consists of multiplying \(|\mathcal{F}f| (\rho, \phi)\) by \(F(\rho, \phi)/\rho\), where the function is defined exactly the same way it was defined towards the end of Section 7.3. (Restrictions that occurred in the definition of \(F\) apply.)

(iii) As a result of the calculations performed in the previous stages we may assume that we know the values of the Fourier transform of the picture, \(\mathcal{F}f\), at points with polar coordinates of the form \((k \Delta \rho, \phi)\), where \(\phi = \theta(np)\) for some projection \(np\), \(0 \leq np < \text{PRJNUM}\). For \(-(\text{nsize}/2) \leq k \leq (\text{nsize}/2)\), the values of \(\mathcal{F}f\) are calculated based on the results produced by stage (ii). For \(|k| > (\text{nsize}/2)\) the value of \(|\mathcal{F}f|(k \Delta \rho, \phi)\) is assumed to be 0. During stage (iii) we estimate, using interpolation, the values of the Fourier transform of \(f\) at points whose Cartesian coordinates are of the form \((m \Delta l, n \Delta l)\), where \(\Delta l = 1/(\text{M} \times \text{PIXISIZ})\), \(-(\text{M}/2)+1 \leq m \leq \text{M}/2\), \(0 \leq n \leq \text{M}/2\), where \(M\) is assigned the value \(\text{NELEM}+1\) if the integer modifier \(\text{size2} < \text{NELEM}\) or is not specified, and is either \(\text{size2} + 1\) (whichever is even) if \(\text{size2} \geq \text{NELEM}\).

In the PARALLEL UNIFORM case or in the DIVERGENT case \(\Delta \rho\) is the same for all projections. Hence, for any fixed \(k\), the points \((k \Delta \rho, \phi)\) lie on a circle, as indicated in Figure 7.1. On the other hand, in the PARALLEL VARIABLE case the corresponding points lie on a square, as indicated in Figure 7.2. We use these figures to explain the method of interpolation used to estimate the Fourier transform of \(f\). We shall use the notation \(\mathcal{F}(Q)\) to denote our estimate of the Fourier transform of \(f\) at the point \(Q\).

Let \(O\) denote the origin. We estimate \(\mathcal{F}(O)\) to be zero.

Let \(P\) be the point for which we wish to find \(\mathcal{F}(P)\). We assume that \(P\) is not the origin. Let \(h_1\) and \(h_2\) be the two half-lines (starting at the origin) nearest to \(P\) on either side such that values of \(F\) are known along \(h_1\) and \(h_2\). We assume that \(h_2\) is in the counter clockwise direction from \(h_1\). Let the points \(E\) (respectively \(F\)) be defined as the intersection of \(h_1\) (respectively \(h_2\)) with the circle whose center is at the origin through \(P\) as in Figure 7.1 or with the straight line parallel to the side of the squares through \(P\) as in Figure 7.2. Let \(A\) and \(B\) be the points on \(h_1\) nearest to \(E\) on either side at which \(\mathcal{F}\) is defined, with \(A\) nearer to the origin. Let \(C\) and \(D\) be the points on \(h_2\) nearest to \(F\) on either side at which \(\mathcal{F}\) is defined, with \(C\) nearest to the origin.

interp determines the interpolation method to be used. (Restriction: \(1 \leq \text{interp} \leq 4\).)

If the value of interp is 1, \(\mathcal{F}(P)\) is estimated to be \(\mathcal{F}(Q)\) where \(Q\) is the point nearest to \(P\) among \(A\), \(B\), \(C\), and \(D\). If two or more of these points are at an equal distance from \(P\), the order of preference in choosing \(Q\) is \(A\), \(B\), \(C\), \(D\).

If the value of interp is 2, \(\mathcal{F}(P)\) is estimated to be \(\mathcal{F}(Q)\) where \(Q\) is chosen as follows. We divide the area surrounded by the lines \(AB\) and \(CD\) and the arcs (or lines) \(AC\) and \(BD\) into four parts, labelled I, II,
Figure 7.1: Points at which the Fourier transform of a picture can be estimated using the discrete Fourier transform of the projection data in the PARALLEL UNIFORM and DIVERGENT cases.

III and IV, using the arc (line or lines) that connect the half-way points on $AB$ and $CD$ and the half-way points on $AC$ and $BD$ (see Figures 7.1 and 7.2). If $P$ is in I, $Q$ is chosen as $A$. If $P$ is in II, but not in I, $Q$ is chosen as $B$. If $P$ is in III, but not in I or II, $Q$ is chosen as $C$. If $P$ is in IV, but not in I, II, or III, $Q$ is chosen as $D$.

If the value of interp is 3, $F(P)$ is estimated as follows. Let, for any two points $Q_1$ and $Q_2$, $Q_1Q_2$ denote the distance between $Q_1$ and $Q_2$. We estimate $F(E)$ to be $(BE \times F(A) + AE \times F(B))/(BE + AE)$ and $F(F)$ to be $(DF \times F(C) + FC \times F(D))/(DF + FC)$. Let $PE$ (respectively $PF$) be the distance along the arc (respectively line or lines) connecting $P$ and $E$ (respectively $F$) in Figure 7.1 (respectively in Figure 7.2). The is estimated to be $(PE \times F(F) + PF \times F(E))/(PE + PF)$.

If the value of interp is 4, $F(P)$ is estimated as

$$a \times F(A) + b \times F(B) + c \times F(C) + d \times F(D)$$

$$a + b + c + d$$

where and $a = PF \times PC \times PD$, $b = PA \times PC \times PD$, $c = PA \times PB \times PD$, and $d = PA \times PB \times PC$.

(iv) As a result of the last two stages we now have estimates of the (filtered) Fourier transform of the picture at points whose Cartesian coordinates are $(m\Delta l, n\Delta l)$, where $-(M/2)+1 \leq m \leq M/2$ and $0 \leq n \leq M/2$. Using rtfort we produce from these estimates an $M \times M$ real array, the central $N_{ELEM} \times N_{ELEM}$ part of which is transferred to recon as the reconstructed picture. (The origin is assumed to be at the $(M/2, M/2)$ location of the large array). Finally, the recon array is normalized by addition of a constant so that its average density is $AVEDEN$ (see Section 6.3.3).

Warning: The rays of DIVERGENT geometry are treated as if they were PARALLEL with UNIFORM ray spacing $PINC \times RADIUS / STOD$. A large divergence angle will result in unacceptable reconstructions.

If the iteration number $\text{iter} > 1$, this algorithm returns control to exalg without changing the contents of the recon array. Multiple iterations may nevertheless be used for smoothing or contouring the reconstruction (see Sections 5.8 and 6.1).
CHAPTER 7. BUILT-IN RECONSTRUCTION ALGORITHMS

7.5 DCONV

This is a general implementation of the filtered backprojection, also known as convolution, method for divergent beam projection data (see [11, 29, 32, 39]). (Restriction: This subroutine can only be used for DIVERGENT geometry.) Roughly speaking, the projection data are first convolved with functions based on a “filter”, and then the convolved data are weighted and back-projected to form the reconstruction.

More precisely, the reconstruction is calculated projection by projection. Not all the projections on prjfil are necessarily used. The integer modifier missp determines which projections are used: only the first in every missp projections. (Restriction: 1 \leq missp < PRJNUM.) The procedure for processing data for each projection can be divided into 3 steps, namely, data smoothing, convolution, and back-projection.

Immediately after reading the projection data, \texttt{data}[i], for 0 \leq i < NRAYS, each data item is smoothed with its two neighboring items using the parameter specified by the floating point modifier weight. The smoothed data \( G(i) \), for 0 \leq i < NRAYS, are calculated as follows. (Restriction: 0.0 < weight \leq 1.0.)

\[
G(i) = \text{weight} \times \text{data}[i] + \frac{1 - \text{weight}}{2} \times (\text{data}[i - 1] + \text{data}[i + 1]).
\]

Here we define both \texttt{data}[-1] and \texttt{data}[NRAYS] to be zero.

The next two steps are best explained separately for the ARC and TANGENT geometries (see Section 2.4). We deal with ARC case first.

In the second step the smoothed data are convolved with two convolving functions \( Q1 \) and \( Q2 \) (which will be discussed later). The discrete convolution process can be expressed by the following equation.

\[
\text{MODI}(k) = \sum_{i=-N}^{N} [Q1(|i|) \times G(k - i) \times \cos(k - i)\alpha] + \sum_{i=-N}^{N} [Q2(|i|) \times G(k - i) \times \cos k\alpha].
\]
In the equation above, MODI is the convolved data for 0 ≤ k < NRAYS, α is PINC / STOD and N is the convolution range specified by the integer modifier range by

\[ N = \begin{cases} 
\text{range,} & \text{if } 0 \leq \text{range} < \text{NRAYS}, \\
\text{NRAYS-1,} & \text{otherwise.}
\end{cases} \]

The values of G(i) for i < 0 or i ≥ NRAYS are assumed to be zero. (Restriction: NRAYS > 1.)

The last step of reconstruction is a weighted backprojection process. The contribution of the np-th projection to the reconstructed density of the pixel whose center is at \((x, y)\) is calculated according to the formula

\[ B_{np}(x, y) = \left[ \frac{\theta(np+\text{missp}) - \theta(np-\text{missp})}{8\pi^2} \right] \times \text{RADIUS} \times V \times qintp(P, \text{MODI}, \text{NRAYS}, \text{INTERP}), \]

where the variables that are not in C++ classes (see Section 6.3) have their values defined as follows. (All these variables are assigned their correct values by SNARK14.)

\(\theta(np)\) denotes the projection angle in radians of the np-th projection for 0 ≤ np < PRJNUM. For np ≥ PRJNUM, \(\theta(np)\) is \(\theta(0)+2\pi\). For np < 0, \(\theta(np) = \theta(\text{last-missp})-2\pi\), where last denotes the largest integer not greater than PRJNUM/missp. (Restriction: For \(-1 \leq np \leq \text{PRJNUM}, \theta(np) < \theta(np+1).\))

\(\text{INTERP}\) is assigned the value of the integer modifier interp. (Restriction: \(-1 \leq \text{interp} \leq 6\).)

\(\text{qintp}\) is the function defined in Section 6.4.5. (Restriction: NRAYS must be large enough so that the restrictions stated in Section 6.4.5 are satisfied.)

The definition of \(V \) and \(P\) depend on the integer modifier method.

\[ V = \begin{cases} 
\frac{1}{((x \sin \theta(np) - y \cos \theta(np))^2 + (\text{RADIUS} - x \cos \theta(np) - y \sin \theta(np))^2)}, & \text{if } \text{method} = 0, \\
\frac{1}{\text{RADIUS}} \times 2 \times \frac{\text{RADIUS}^2}{\text{RADIUS}^2 - y^2}, & \text{if } \text{method} \neq 0,
\end{cases} \]

\[ P = \begin{cases} 
\frac{1}{\alpha} \tan^{-1} \left( \frac{-x \sin \theta(np) + y \cos \theta(np)}{\text{RADIUS} - x \cos \theta(np) - y \sin \theta(np)} \right), & \text{if } \text{method} \geq 0, \\
\frac{1}{\alpha} \tan^{-1} \left( \frac{y \cos \theta(np) - \text{RADIUS} \times \sin \theta(np) - y}{\text{RADIUS} \times \sin \theta(np) - y} \right), & \text{if } \text{method} < 0,
\end{cases} \]

with \(\alpha = \text{PINC} / \text{STOD}\). (Note: method = 0 provides the most accurate but most expensive reconstruction, method < 0 provides the least accurate but least expensive reconstruction, with method > 0 in between; see [39].)

The next line in the INPUT file must be

\[
\begin{array}{c}
\text{BANDLIMITING} \\
\text{HAMMING} \\
\text{COSINE} \\
\text{PARABOLIC} \\
\text{EXPONENTIAL} \\
\text{SINC} \\
\text{SHEPP-LOGAN} \\
\text{LINE}
\end{array}
\]

The filter is used to specify the convolving functions Q1 and Q2 used in the algorithm.

When a filter other than BANDLIMITING is specified, additional information about the filter has to be supplied by the user. Except for the LINE filter, this information takes the form

\[
> \text{cutoff} [\alpha]
\]

Restriction: This line is absent if BANDLIMITING is specified and has a different form if LINE is specified.

The values of Q1(m) and Q2(m) for 0 < m ≤ N are determined according to the following equations.

\[ Q1(m) = \frac{-m\alpha Q(m\alpha)}{\sin^2(m\alpha)}, \]
\[ Q2(m) = \frac{Q(m\alpha) + m\alpha Q'(m\alpha)}{\sin(m\alpha)}, \]
where
\[ Q(u) = 2\pi \int_0^C f(\xi) \sin 2\pi \xi u d\xi, \]
and \(Q1(0)\) and \(Q2(0)\) are defined by their “limit values”; see [39].

The parameter \(C\) is specified by the floating point modifier cutoff. \((\text{Restriction: } 0 < C \leq 1.)\) When BANDLIMITING or LINE is specified \(C\) is automatically set to be 1. With the exception of LINE filter, the “filter” function \(f(\xi)\) is determined by the word modifier filter as shown below.

<table>
<thead>
<tr>
<th>filter</th>
<th>(f(\xi))</th>
</tr>
</thead>
<tbody>
<tr>
<td>BANDLIMITING</td>
<td>1</td>
</tr>
<tr>
<td>HAMMING</td>
<td>(\alpha + (1 - \alpha) \cos(2\pi \xi/A))</td>
</tr>
<tr>
<td>COSINE</td>
<td>(\cos(\pi \xi/A))</td>
</tr>
<tr>
<td>PARABOLIC</td>
<td>((1 - (2\pi/A)^2)</td>
</tr>
<tr>
<td>EXPONENTIAL</td>
<td>((e - e^{2\xi/A})/(e - 1))</td>
</tr>
<tr>
<td>SINC</td>
<td>(\text{sinc}(2\pi \xi/A))</td>
</tr>
<tr>
<td>SHEPPE-LOGAN</td>
<td>(\text{sinc}(\xi/A))</td>
</tr>
</tbody>
</table>

where \(A = C \times \text{STOD}/\text{PINC}, \) \(\text{sinc}(X) = \sin(\pi x)/(\pi x)\) and the alpha in Hamming filter is specified by the floating point modifier \(\alpha.\) \((\text{Restriction: } 0 \leq \alpha \leq 1.)\) If alpha is not specified, \(\alpha = 1\) is assumed.

In case LINE is specified, users design their own filter function by supplying the following information.

> \[ x_1 \ y_1 \ x_2 \ y_2 \ x_3 \ y_3 \ ... \ x_l \ y_l \ \text{[}] \]

\(\text{Restriction: This line is present only if LINE is specified. Note: The information may occupy more than one line. The program will keep reading pairs of floating point modifiers } (x_i, y_i) \text{ until it comes across a } y_i \text{ whose value is 0.0. Restrictions: } 0 \leq x_1 \leq x_2 \leq \ldots \leq x_l \leq 1, 1 \geq y_1 \geq y_2 \geq \ldots \geq y_l = 0.\)

This sequence of pairs of numbers defines the filter function in the range \([0, 1/2]\) if \(B\) is specified. If \(B\) is not specified, \(B = 0\) is assumed.

The TANGENT geometry is handled somewhat differently. Unless the filter specified is BANDLIMITING, ray sums are estimated, using linear interpolation, for rays that form a DIVERTED ARC data set with angular spacing \(\alpha = \tan^{-1}(\frac{\text{NRAYS}-1/2}{\text{STOD}}) \times \frac{\text{PINC}}{\text{STOD}}\). The algorithm operates on this data set according to the rules described above.

If BANDLIMITING is specified, the convolution step takes the form

\[ M(k) = \sum_{i=-N}^{N} \frac{Q1(|i|) \times G(k-i)}{\sqrt{1+(k-i)^2 \times a^2}}, \]

where \(a = \text{PINC}/\text{STOD}\) and all terms have the same meaning as in the ARC case, except for \(Q1,\) which is defined by

\[ Q1(m) = \begin{cases} \frac{x^2}{2\pi^2}, & \text{if } m = 0, \\ \frac{-2}{m^2 \pi^2}, & \text{if } m \text{ is an odd integer,} \\ 0, & \text{otherwise.} \end{cases} \]

The back-projection step is analogous to the back-projection step in the ARC case except for the definition of \(P,\) which is

\[ P = \begin{cases} \frac{\text{PINC}}{\text{STOD}} \times \frac{-x \sin \theta(\text{STOD}) + y \cos \theta(\text{STOD})}{\text{RADIUS}} \times \frac{-x \sin \theta(\text{PINC}) + y \cos \theta(\text{PINC})}{\text{RADIUS}} \times \frac{\text{RADIUS} \times \text{sin} \theta(\text{STOD}) - y}{\text{RADIUS} \times \text{sin} \theta(\text{PINC}) - y}, & \text{if method } \geq 0, \\ \frac{\text{PINC}}{\text{STOD}} \times \frac{x \cos \theta(\text{PINC}) + y \sin \theta(\text{PINC})}{\text{RADIUS} - x \cos \theta(\text{STOD}) - y \sin \theta(\text{STOD})}, & \text{if method } < 0. \end{cases} \]

If the iteration number \(\text{iter} > 1,\) this algorithm returns control to \texttt{exalg} without changing the contents of the \texttt{recon} array. Multiple iterations may nevertheless be used for smoothing or contouring the reconstruction (see Sections 5.8 and 6.1).
7.6 ART

This is a general implementation of the additive Algebraic Reconstruction Techniques (ART). It incorporates the features and options described in [22, 23, 27, 31, 35, 36, 38]. In our description we shall follow, as closely as possible, the notation of [33], which provides a survey of ART-type methods.

The method is an iterative procedure that, starting from an initial estimate of the picture to be reconstructed, updates the estimate through a sequence of steps. A single step is influenced by exactly one ray for which we have an estimate of the ray sum. Only those basis function (pixel or blob) densities are updated that contribute to the associated pseudo ray sum. The updating is done by the addition of a correction term (related to the contribution of the basis function to the pseudo ray sum) to the density in each such basis function, so that after the correction the pseudo ray sum for the ray in question will be nearer to the estimated ray sum.

More precisely, let \( n \) be the number of basis functions (either \( \text{NELEM}^2 \) in the pixel case or \( \text{Blob.area} \) in the blob case) and \( m \) abbreviate \( \text{PRJNUM} \times \text{NRAYS} \). (In introducing our notation we assume familiarity with Sections 6.2 and 6.3.) We use \( x^{(k)} \) to denote the \( n \)-dimensional column vector whose \( j \)th component, \( x_j^{(k)} \), is \( \text{recon}[j+1] \) after the \( k \)th step. In particular, \( x^{(0)} \) represents the contents of the \( \text{recon} \) array at the beginning of the reconstruction process, as determined by the ZERO, AVERAGE, or CONTINUE option of the EXECUTE command (see Section 5.8). We use \( p \) to denote the \( m \)-dimensional column vector, whose \( i \)th component, \( p_i \), is the value returned by \( \text{Anglst.prdta}(np, nr) \) when \( i = np \times \text{NRAYS} + nr + 1 \) with \( 0 \leq np < \text{PRJNUM} \) and \( 0 \leq nr < \text{NRAYS} \) (see Section 6.3.6.2).

For \( 1 \leq i \leq m \), we also define an \( n \)-dimensional column vector \( m_i \), as follows. Let \( np \) and \( nr \) be defined as in the last paragraph. Let the integer \( \text{numb} \) and the arrays \( \text{list} \) and \( \text{weight} \) be defined by one of:

\[
\begin{align*}
\text{wray}(np, nr, \text{list}, \text{weight}, \&\text{numb}, \&\text{snorm}); & \quad \text{in the pixel LINE case} \\
\text{ray}(np, nr, \text{list}, \text{weight}, \&\text{numb}, \&\text{snorm}); & \quad \text{in the pixel STRIP case} \\
\text{Blob.bray}(np, nr, \text{list}, \text{weight}, \&\text{numb}, \&\text{snorm}); & \quad \text{in the blob LINE case} \\
\text{Blob.bray}(np, nr, \text{list}, \text{weight}, \&\text{numb}, \&\text{snorm}); & \quad \text{in the blob STRIP case}
\end{align*}
\]

(see Sections 6.4.2, 6.4.3, 6.3.4.3, and 6.3.4.4). Recall that the blob STRIP case does not result in useful reconstructions (see Section 6.3.4.4). The \( j \)th component of \( m_i \), \( m_{i,j} \), is defined by

\[
m_{i,j} = \begin{cases} 
\text{weight}[k], & \text{if list}[k] = j - 1 \text{ for some } k, 0 \leq k < \text{numb}, \\
0, & \text{otherwise.}
\end{cases}
\]

Some versions of the ART algorithm also make use of a set of auxiliary variables, one variable for each ray. We let \( u^{(k)} \) denote the \( m \)-dimensional column vector whose \( i \)th component, \( u_i^{(k)} \), is the auxiliary variable associated with the \( nr \)th ray in the \( np \)th projection (\( i = np \times \text{NRAYS} + nr + 1 \) after the \( k \)th step). \( u^{(0)} \) is defined to be the vector whose components are all 0. We use \( e_i \) to denote the \( m \)-dimensional column vector whose only nonzero component is a 1 in the \( i \)th row.

At the beginning of the \((k+1)\)st step of an ART algorithm \( x^{(k)} \) and \( u^{(k)} \) are stored in memory. A ray is selected by

\[
pick(\&np, \&nr);
\]

(see Section 6.4.1), and \( i \) is defined by \( np \times \text{NRAYS} + nr + 1 \). Then \( x^{(k+1)} \) and \( u^{(k+1)} \) are defined by

\[
\begin{align*}
\hat{x}^{(k+1)} &= x^{(k)} + r^{(k)} c^{(k)} m_i, \\
x^{(k+1)} &= \Psi(x^{(k)}, \hat{x}^{(k+1)}), \\
u^{(k+1)} &= u^{(k)} + r^{(k)} d^{(k)} e_i.
\end{align*}
\]

The function \( \Psi \), which produces the \( j \)th component of \( x^{(k+1)} \) from the \( j \)th components of \( x^{(k)} \) and \( \hat{x}^{(k+1)} \), will be defined below. The basic difference between the different ART algorithms is the way \( c^{(k)} \), \( d^{(k)} \), and \( r^{(k)} \) are chosen. We first describe this, starting with \( r^{(k)} \).
The value of $r^{(k)}$ is determined by what follows the optional word RELAXATION. (If this word is missing, RELAXATION CONSTANT 1.0 is assumed). If CONSTANT is specified, then the value of $r^{(k)}$ is equal to the value of the floating point modifier $r$, for all $k$. If VARIABLE is specified, then the user must replace the default subroutine

```c
REAL art_class::rset(
    REAL* recon,
    INTEGER iter,
    INTEGER np,
    INTEGER nr,
    INTEGER iflag,
    REAL raysum,
    INTEGER* list,
    REAL* weight,
    BOOLEAN *flag
);
```

with one that returns the value of $r^{(k)}$. Here `recon`, `list`, `weight`, and `iter` are the formal parameters of the reconstruction algorithm (see Section 6.2); `np` and `nr` have been returned by `pick`; the value of the integer variable `iflag` is 1 the first time `rset` is called and it can be changed only by `rset`; `raysum` is the value of $p_i$; and `flag` is a logical variable whose value is set to TRUE if, and only if, the value of `rset` cannot be calculated for some reason.

The definitions of $c^{(k)}$ and $d^{(k)}$ depend on whether ART3, ART4, or BAYESIAN is specified. They also depend on what follows the optional words NORM and TOLERANCE. We first explain the effect of these words.

The integer modifier following NORM is used to give a definition to the notation $||m||^l$ that we shall use below. (If the word NORM is missing NORM 2 is assumed.)

```
||m||^l = \sum_{j=1}^{n}(m_{i,j})^l
```

*Restriction:* $l$ must be a positive integer.

What follows the optional word TOLERANCE determines the value of the number $\epsilon$ that will be used in the formulas for $c^{(k)}$ below. *Restriction:* $\epsilon \geq 0.0$ (If the word TOLERANCE is missing TOLERANCE FIXED 0.0 is assumed.) If FIXED is specified, $\epsilon$ is assigned the value of the floating point modifier $t$. If VARIABLE is specified, then the user must replace the default subroutine

```c
REAL art_class::tset(
    REAL* recon,
    INTEGER iter,
    INTEGER np,
    INTEGER nr,
    INTEGER iflag,
    REAL raysum,
    INTEGER* list,
    REAL* weight,
    BOOLEAN *flag
);
```

with one that returns the value of $\epsilon$. The parameters have the same meaning as for `rset` defined above. If NOISE is specified, the value of $\epsilon$ is defined to be $t \times \sqrt{\nu}$, where $t$ is the floating point modifier following NOISE and

$v = D \times C \times e^{(p_i/E)} \times E^2 + B \times p_i + A,$
where
\[ A = \begin{cases} (\text{ADDNSD})^2, & \text{if ADDNFL is TRUE,} \\ 0, & \text{otherwise,} \end{cases} \]
\[ B = \begin{cases} (\text{ULTNSD})^2, & \text{if ULTNFL is TRUE,} \\ 0, & \text{otherwise,} \end{cases} \]
\[ C = \begin{cases} \frac{\text{QUANMIN} \times \sum_{k=1}^{N\text{ENERGY}} \frac{1}{\text{ENGWT}(k) \times e^{-\text{BACKGR}(k)}}}{}, & \text{if QUANIN}>0, \\ 0, & \text{otherwise,} \end{cases} \]
\[ D = \begin{cases} 2.0 \times C + C, & \text{if QUANIN}>0, \\ 0, & \text{otherwise,} \end{cases} \]
\[ E = \begin{cases} \text{PINC}, & \text{in the UNIFORM STRIP case,} \\ \text{PINC} \times \max(|\sin \theta_{np}|, |\cos \theta_{np}|), & \text{in the VARIABLE STRIP case,} \\ 1, & \text{in the LINE case.} \end{cases} \]

This \( \nu \) is an estimate based on the ray sum of the variance of the noise in the ray sum.

The values of \( c(k) \) and \( d(k) \) depend also on the value of a variable DIFF, which is the difference between the ray sum (as it appears on prjfil) and the pseudo ray sum of a constrained version of the picture in recon (represented by \( x(k) \)). The method of constraining is determined by the contents of the next line in the INPUT file.

We define, for \( 1 \leq j \leq n \),
\[ p_i = \sum_{j=1}^{n} m_{i,j} x_j^{(k)}. \]

We are now in position to define \( c(k) \) and \( d(k) \).

Whenever \( ||m_i|| \leq \text{ZERO} \), \( c(k) = d(k) = 0 \). Otherwise \( c(k) \) and \( d(k) \) depend on whether ART3, ART4, or BAYESIAN is specified.

If ART3 is specified,
\[ c(k) = \begin{cases} 0, & \text{if } |\text{DIFF}| \leq \epsilon, \\ \frac{2 \times (\text{DIFF} - \epsilon)}{||m_i||^T}, & \text{if } \epsilon < \text{DIFF} < 2 \epsilon, \\ \frac{2 \times (\text{DIFF} + \epsilon)}{||m_i||^T}, & \text{if } \epsilon < -\text{DIFF} < 2 \epsilon, \\ \text{DIFF}, & \text{if } 2 \epsilon \leq |\text{DIFF}|, \end{cases} \]
\[ d(k) = 0. \]

If ART4 is specified,
\[ c(k) = \text{mid} \left\{ u_i^{(k)} \frac{\text{DIFF} + \epsilon}{||m_i||^T}, \frac{\text{DIFF} - \epsilon}{||m_i||^T} \right\}, \]
\[ d(k) = -c(k), \]

where \( \text{mid}\{a, b, c\} \) denotes the median of the three numbers \( a, b, \) and \( c \).

If BAYESIAN is specified,
\[ c(k) = (\text{snr})^2 \frac{\text{DIFF} - u_i^{(k)}}{1 + (\text{snr})^2 ||m_i||^T}, \]
\[ d^{(k)} = c^{(k)}/(\text{snr})^2. \]

(Restriction: \((\text{snr})^2 > \text{ZERO}\).)

To complete the specification of a single step of the ART method we need to describe how, for \(1 \leq j \leq n\), \(x_j^{(k+1)}\) is obtained from \(\hat{x}_j^{(k+1)}\) and \(x_j^{(k)}\).

If ART2 is specified
\[ x_j^{(k+1)} = \hat{x}_j^{(k+1)}. \]

If BOUND is specified \[ x_j^{(k+1)} = \begin{cases} \hat{x}_j^{(k+1)} + (\text{cr})^{(k)} (\text{LOWER} - \hat{x}_j^{(k+1)}), & \text{if LOFL is TRUE and } \hat{x}_j^{(k+1)} < \text{LOWER}, \\ \hat{x}_j^{(k+1)} + (\text{cr})^{(k)} (\text{UPPER} - \hat{x}_j^{(k+1)}), & \text{if UPFL is TRUE and } \hat{x}_j^{(k+1)} > \text{UPPER}, \\ \hat{x}_j^{(k+1)}, & \text{otherwise}, \end{cases} \]

where \((\text{cr})^{(k)}\) is defined as follows. If CONRELAX is not specified \(\text{cr}^{(k)} = 1\). If CONRELAX is specified, \((\text{cr})^{(k)}\) is obtained by the method we described for \(r^{(k)}\) above, except that in the VARIABLE case the user must replace the default subroutine

\[
\text{REAL art_class::crset(}
\text{REAL* recon,}
\text{INTEGER iter,}
\text{INTEGER np,}
\text{INTEGER nr,}
\text{INTEGER iflag,}
\text{REAL raysum,}
\text{INTEGER* list,}
\text{REAL* weight,}
\text{BOOLEAN* flag)};
\]

with one that returns the value of \((\text{cr})^{(k)}\). The parameters are as described for the function \textbf{rset} above.

If BART is specified, the definition of \(x_j^{(k+1)}\) makes use of some auxiliary concepts. Let \(\text{HALFWAY} = (\text{UPPER} + \text{LOWER})/2\). (Restriction: If BART is specified, both LOFL and UPFL must be TRUE.) Let \(\text{ABOVE} = \text{HALFWAY} + (\text{UPPER} - \text{LOWER})/1000\) and \(\text{BELOW} = \text{HALFWAY} - (\text{UPPER} - \text{LOWER})/1000\). In addition, we define two sequences of numbers \(\lambda^{(k)}\) and \(\mu^{(k)}\), based on the integer modifier \(\text{kount}\). (Restriction: \(\text{kount}\) is a positive integer.) If \(\text{kount}\) is not specified, its value is \(\text{PRJNUM} \times \text{SNRAYS}\) if SELECT SNARK is specified or \(\text{PRJNUM} \times \text{USRAYS}\) if SELECT USER is specified (see Section 5.6).

\[ \lambda^{(0)} = \text{LOWER}, \]
\[ \lambda^{(k+1)} = \lambda^{(k)} + \frac{\text{HALFWAY} - \text{LOWER}}{\text{kount} \times 2^{\text{iter}}}, \]
\[ \mu^{(0)} = \text{UPPER}, \]
\[ \mu^{(k+1)} = \mu^{(k)} - \frac{\text{UPPER} - \text{HALFWAY}}{\text{kount} \times 2^{\text{iter}}}. \]

If BART is specified
\[ \hat{x}_j^{(k+1)} = \begin{cases} \hat{x}_j^{(k+1)} + (\text{cr})^{(k)} (\text{LOWER} - \hat{x}_j^{(k+1)}), & \text{if } \hat{x}_j^{(k+1)} < \lambda^{(k)}, \\ \hat{x}_j^{(k+1)} + (\text{cr})^{(k)} (\text{UPPER} - \hat{x}_j^{(k+1)}), & \text{if } \hat{x}_j^{(k+1)} > \mu^{(k)}, \\ \hat{x}_j^{(k+1)}, & \text{otherwise}, \end{cases} \]
where \((cr)^{(k)}\) is defined just as in the case when BOUND is specified.

\[
x_j^{(k+1)} = \begin{cases} 
\text{BELOW,} & \text{if } x_j^{(k)} \leq \lambda^{(k)} \text{ and } x_j^{(k+1)} \geq \text{HALFWAY,} \\
\text{ABOVE,} & \text{if } x_j^{(k)} \geq \mu^{(k)} \text{ and } x_j^{(k+1)} \leq \text{HALFWAY,} \\
x_j^{(k+1)}, & \text{otherwise.}
\end{cases}
\]

This completes the description of a single step of an ART algorithm. One SNARK14 iteration of the algorithm (see Section 6.1) consists of \(k\) steps. (Restriction: \(k > 0\).) The contents of the \(\text{recon}\) array at the end of the iteration with iteration number \(\text{iter}\) are described by \(x_j^{(k)}\) with \(k = \text{iter} \times k\), unless \(\text{NOMLZ} \) is specified. If \(\text{NOMLZ} \) is specified, then prior to returning control to \(\text{exalg}\) the ART subroutine adds to each entry of \(\text{recon}\) the value \((\text{AVEDEN} - \frac{1}{n} \sum_{j=1}^{n} x_j^{(k)}) \). If another iteration is called, the initial value of \(x_j^{(k)}\) for the new iteration will be the content of \(\text{recon}[j-1]\) at the end of the last iteration.

### 7.7 SART

> SART [RELAXATION CONSTANT \(r\)]

SART is an implementation of the additive Simultaneous Algebraic Reconstruction Technique algorithm according to [2, 46, 47]. (The intended aim of SART is to minimize the weighted squared distance \(WS\) as defined in (5.18).) The SART algorithm is based on the ART algorithm of the previous section and so we use the notation from that section to specify the iterative step of SART from \(x_j^{(k)}\) to \(x_j^{(k+1)}\): For \(1 \leq j \leq n\),

\[
x_j^{(k+1)} = x_j^{(k)} + r \frac{1}{m} \sum_{i=1}^{m} \sum_{j'=1}^{n} \left\{ \frac{p_i - \sum_{j'=1}^{n} m_{i,j'} x_j^{(k)}}{a_{i,j}} \right\}. 
\]

The value of \(r\) is determined by what follows the option RELAXATION CONSTANT. If this option is not chosen, then \(r\) is given the default value 1. (Restriction: \(0 < r \leq 2\). If this restriction is violated, then \(r\) is given the default value 1.

### 7.8 MART

> METHOD \(\{\text{GBH, LENT, LAK1, LAK2}\}\) kount relax data-zero [NORMAL] [ENTROPY]

This is a general implementation of the multiplicative Algebraic Reconstruction Techniques (MART. It incorporates features and options described in [18, 19, 52], as well as two versions intended to reduce computer time invented by A.V. Lakshminarayanan (unpublished). In our description we shall follow, as closely as possible, the notation of [33], which provides a survey of ART-type methods.

The method is an iterative procedure that, starting from an initial estimate of the picture to be reconstructed, updates the estimate through a sequence of steps. A single step is influenced by exactly one ray for which we have an estimate of the ray sum. Only those basis function densities that contribute to the associated pseudo ray sum are updated. The updating is done by multiplying by a correction term (related to the contribution of the basis function to the pseudo ray sum) the density in each such basis function, so that after the correction the pseudo ray sum for the ray in question will be nearer to the estimated ray sum.

For the more precise description we adapt the definitions given in Section 7.6 for \(n, m, x_j^{(k)}, p, m_i,\) and \(m_{i,j}\).

There are four versions of MART. All MART methods assume that ray sums are nonnegative. (Restriction: AVEDEN > ZERO.) This is insured by the use of the floating point modifier data-zero. (Warning:
If data-zero < 0, the program will operate as if data-zero were specified to be 0.0.) The algorithms use an m-dimensional column vector q, whose ith component, q_i, is defined by

\[ q_i = \begin{cases} 
0, & \text{if } p_i \leq \text{data-zero}, \\
p_i, & \text{if } p_i > \text{data-zero}.
\end{cases} \]

The first difference between the methods is the way the initial estimate is defined. (Warning: This overrides how recon is initialized according to the EXECUTE control command line.)

In Method GBH, \( x_j^{(0)} = \text{AVEDEN} \), for \(1 \leq j \leq n\).

Let J be the set of all js such that \(1 \leq j \leq n\), and there exists an i satisfying \(1 \leq i \leq m\), \(q_i = 0\), and \(m_{i,j} > 0\). (In other words, \(j \in J\) if the jth basis function is intersected by a ray whose modified ray sum is 0.) If every j between 1 and n is in \(J\), all elements of the recon array are set to 0, a warning message is printed, and control is passed back to exalg (see Section 6.1). Otherwise, suppose that there are \(u\) values of \(j\) between 1 and \(n\) that are not in \(J\). In Methods LENT, LAK1, and LAK2, we define, for \(1 \leq j \leq n\),

\[ x_j^{(0)} = \begin{cases} 
0, & \text{if } j \in J, \\
\frac{u}{n} \times \text{AVEDEN}, & \text{if } j \notin J.
\end{cases} \]

At the beginning of the \((k+1)\)st step of a MART algorithm, \(x^{(k)}\) is stored in memory. A ray is selected by

\[ \text{pick}(\&np, \&nr); \]
(see Section 6.4.1), and \(i\) is defined by

\[ i = np \times \text{NRAYS} + nr + 1. \]

We also define \(s_i\) to be \(\sum_{j=1}^{n} m_{i,j} x_j^{(k)}\). (Note that it will always be the case that \(s_i \geq 0\).)

If \(q_i = 0\),

\[ x_j^{(k+1)} = \begin{cases} 
0, & \text{if } m_{i,j} > 0, \\
x_j^{(k)}, & \text{otherwise}.
\end{cases} \]

If \(q_i > 0\) and \(s_i = 0\), \(x^{(k+1)} = x^{(k)}\).

If \(q_i > 0\) and \(s_i > 0\), then the four methods behave differently.

In Methods GBH and LENT,

\[ x_j^{(k+1)} = x_j^{(k)} \left( \frac{q_i}{s_i} \right)^{(rm_{i,j})/A_i}, \]

where \(r\) is the value of the floating point modifier relax if relax > 0, and \(r = 1\) if relax ≤ 0; and \(A_i = 1\) in Method GBH and \(A_i = \max_{1 \leq j \leq n}(m_{i,j})\) in Method LENT.

For Methods LAK1 and LAK2, we define, for \(1 \leq j \leq n\),

\[ \alpha_j = \frac{rm_{i,j}}{A}, \]

where \(r\) is the value of the floating point modifier relax if relax > 0, and \(r = 1\) if relax ≤ 0; and \(A = \max_{1 \leq j \leq n,1 \leq i \leq m}(m_{i,j})\). In Method LAK1,

\[ x_j^{(k+1)} = \begin{cases} 
x_j^{(k)} \left( 1 + \frac{q_i}{s_i} \alpha_j \right), & \text{if } q_i \geq s_i, \\
x_j^{(k)} \left( 1 + \frac{q_i}{s_i} \alpha_j \right), & \text{if } q_i < s_i.
\end{cases} \]

In Method LAK2,

\[ x_j^{(k+1)} = \begin{cases} 
x_j^{(k)} \left[ 1 + \frac{q_i}{s_i} \alpha_j (1 + \frac{1}{2} \frac{q_i}{s_i} (\alpha_j + 1)) \right], & \text{if } q_i \geq s_i, \\
x_j^{(k)} \left[ 1 + \frac{q_i}{s_i} \alpha_j (1 + \frac{1}{2} \frac{q_i}{s_i} (\alpha_j - 1)) \right], & \text{if } q_i < s_i.
\end{cases} \]
This completes the description of a single step of a MART algorithm. One SNARK14 iteration of the algorithm (see Section 6.1) consists of kount steps. (If kount \leq 0, it is treated as if its value was PRJNUM \times SNRAYS if SELECT SNARK was specified or PRJNUM \times USRAYS if SELECT USER was specified (see Section 5.6). The contents of the \texttt{recon} array at the end of the iteration with iteration number iter are described by \( x^{(k)} \), with \( k = \text{iter} \times \text{kount} \), unless NORMAL is specified and \( \sum_{j=1}^{n} x^{(k)}_j > \text{ZERO} \). In that case, prior to returning control to exalg the MART subroutine multiplies each entry of \texttt{recon} by AVEDEN/\( \sum_{j=1}^{n} x^{(k)}_j \). If another iteration is called, the initial value for the new iteration will be the contents of \texttt{recon} at the end of the last iteration.

If ENTROPY is specified, SNARK14 will print at the end of an iteration by MART the value of the function

\[
- \sum_{j=1}^{n} \frac{\text{recon}[j-1]}{\text{TOTAL}} \times \ln \left( \frac{\text{recon}[j-1]}{\text{TOTAL}} \right),
\]

provided that \( \text{TOTAL} = \sum_{j=1}^{n} \text{recon}[j-1] > \text{ZERO} \).

### 7.9 QUADRATIC

\[ > \text{algorithm delta-flag d-flag min-eigen period toler delta gamma} \]

 Restrictions: See Table 7.1.

This is an implementation of the quadratic optimization techniques as described in [4, 34]. Roughly speaking, the algorithm minimizes a quadratic function on the vector of basis function densities with an iterative process of the type

\[
x^{(k+1)} = x^{(k)} + \delta^{(k)} g^{(k)},
\]

where \( x^{(0)} \) is an initial guess, and \( \delta^{(k)} \) and \( g^{(k)} \) are a scalar and a vector that depend on the particular quadratic function and minimization algorithm.

For the more precise description we adapt the definitions given in Section 7.6 for \( n, m, x^{(k)}, p, \) and \( m_i \). We use \( M \) to denote the \( m \times n \) matrix whose \( i \)-th row is the transpose of \( m_i \). The reconstruction aims at finding an \( x^* \) that minimizes

\[
k(x) = a(p - M x)^T A (p - M x) + (x - \bar{x})^T (b B^l + c C^{-l}) (x - \bar{x}),
\]

and if more than one \( x \) minimizes \( k(x) \), then \( x^* \) is the one among all the ones that minimize \( k(x) \) that also minimizes \( \|D^{-1} x\| \). Here \( A, B, C, \) and \( D \) are matrices, \( \bar{x} \) is a vector, \( a, b, c, \) and \( d \) are scalars, and \( l \) is an integer, which will be discussed later. We use \( Z^T \) to denote the transpose of the matrix \( Z \). The algorithm minimizes \( k(x) \) by attempting to find a solution to an equivalent problem, which can be stated as follows. Find the minimum norm solution \( y^* \) of

\[ Py = f, \]

where

\[
P = \begin{cases} \begin{cases} a C^{l/2} M^T A M C^{l/2} + b C^{l/2} B^l C^{l/2} + c C^{l-1}, & \text{if } b + c > 0, \\ D M^T A D, & \text{if } b + c = 0, \end{cases} \\ \end{cases} \]

\[ f = \begin{cases} \begin{cases} a C^{l/2} M^T A (p - M \bar{x}), & \text{if } b + c > 0, \\ D M^T A p, & \text{if } b + c = 0. \end{cases} \end{cases} \]

It has been shown that

\[
x^* = \begin{cases} \begin{cases} C^{l/2} y^* + \bar{x}, & \text{if } b + c > 0, \\ D y^*, & \text{if } b + c = 0. \end{cases} \end{cases}
\]

Our description of the algorithm will be in terms of a sequence \( y^{(0)}, y^{(1)}, y^{(2)}, \ldots \). This is purely a descriptive device; the contents of \texttt{recon} at the end of the \( k \)-th iteration are the components of \( x^{(k)} \), where

\[
x^{(k)} = \begin{cases} \begin{cases} C^{l/2} y^{(k)} + \bar{x}, & \text{if } b + c > 0, \\ D y^{(k)}, & \text{if } b + c = 0. \end{cases} \end{cases}
\]

The description consists of three parts: the basic method for getting from \( y^{(k)} \) to \( y^{(k+1)} \) (choosing the algorithm), the way the function \( k(x) \) is determined (defining the function), and additional features that can be incorporated into the quadratic optimization reconstruction procedures.
### 7.9.1 Choosing the algorithm

The choice of algorithm depends on the values of the integer modifiers `algorithm`, `delta-flag`, `min-eigen`, `period` and the floating point modifiers `toler`, `delta`, and `gamma`, as well as the integer modifiers `order` and `split`, which appear on the next line. Since the seventeen modifiers appearing on those two lines are likely to be confusing, a summary of their use appears in Table 7.1.

> order error-type exp-value split normalize print error minv interp

**Restrictions**: See Table 7.1.

In defining the sequence of $y^{(k)}$s our descriptions make use of sequences of other vectors and scalars. All the different algorithms use an $n$-dimensional vector $g^{(k)}$ and a scalar $\delta^{(k)}$. Other vectors and scalars will be introduced as and when they are needed.

If algorithm = 1 or algorithm = 2, the sequences are defined as follows.

$$
\begin{align*}
g^{(0)} & = f - Py^{(0)}, \\
g^{(k+1)} & = f - Py^{(k+1)} - \delta^{(k)}y^{(k)}, \\
g^{(k+1)} & = \begin{cases} 
   f - Py^{(k+1)}, & \text{if algorithm=1}, \\
   g^{(k)} - \delta^{(k)}Py^{(k)}, & \text{if algorithm=2}.
\end{cases}
\end{align*}
$$

The value of $\delta^{(k)}$ is defined as follows. (Restriction: In what follows $\delta^{(k)}$ is defined as a fraction. Except in the case delta-flag = 3, all values of $\delta^{(k)}$ that are needed during the iterative process are calculated before the first iteration. The denominator in the definition of all of these $\delta^{(k)}$s must be greater than ZERO.)

If delta-flag = 0, then $\delta^{(k)} = \text{delta}$.

If delta-flag = 1, then $\delta^{(k)} = 2/(\lambda + \overline{\lambda})$, where $\lambda$ and $\overline{\lambda}$ are supposed to be estimates of the largest and smallest eigenvalues of $P$. These are estimated by the iterative procedure described in [34]. That procedure gives a sequence of upper bounds and lower bounds for $\lambda$. The procedure stops when the difference between these bounds is less than toler times the upper bound. The estimate provided for $\overline{\lambda}$ is replaced by 0 if min-eigen = 0.

If delta-flag = -1, then $\delta^{(k)} = 2/(\overline{\lambda} + \lambda)$, where $\overline{\lambda}$ = delta and $\lambda$ = gamma.
If \( \delta^{(k)} \) is defined the same way as in the case \( \delta^{(k)} = 2 \), except that \( \bar{\lambda} = \delta \) and \( \lambda = \gamma \).

If \( \delta^{(k)} = 3 \), then

\[
\delta^{(k)} = \frac{2}{\lambda + \lambda - (\lambda - \lambda) \cos((2q(k) - 1) \times \pi/2N)},
\]

where \( \bar{\lambda} \) and \( \lambda \) are defined as in the case \( \delta^{(k)} = 1 \), \( N \) is the value of the integer modifier period and \( q \) is a function whose definition depends on the integer modifier order. In any case, \( q(k) = \sigma(i) \), where \( 0 \leq i < N - 1 \) and \( k = jN + i \) for some integer \( j \). If order = 1, then \( \sigma(i) = i + 1 \). If order = 2, the values of \( \sigma(i) \) are given on a (sequence of) line(s) in the INPUT file.

\[
\text{Restrictions: This line is absent unless algorithm is 1 or 2, delta-flag is -2 or 2 and order is 2. For 0 \leq i \leq N - 1, 1 \leq \sigma(i) \leq N.}
\]

If algorithm = 3 or algorithm = 4, we need an additional \( n \)-dimensional vector \( r^{(k)} \) and additional scalar \( \gamma^{(k)} \). The sequences are defined as follows.

\[
\gamma^{(0)} = r^{(0)} = f - Py^{(0)},
\]

\[
\gamma^{(k+1)} = \frac{\langle r^{(k)}, r^{(k)} \rangle}{\langle g^{(k)}, Py^{(k)} \rangle},
\]

\[
\delta^{(k)} = \frac{\langle g^{(k)}, g^{(k)} \rangle}{\langle g^{(k)}, Py^{(k)} \rangle},
\]

The values of \( \delta^{(k)} \) and \( \gamma^{(k)} \) are defined as follows. (Restriction: If algorithm is 3 or 4, delta-flag must be 0 or 3.)

If delta-flag = 0, then \( \delta^{(k)} = \delta \) and \( \gamma^{(k)} = \gamma \).

If delta-flag = 3, then

\[
\delta^{(k)} = \frac{\langle r^{(k)}, r^{(k)} \rangle}{\langle g^{(k)}, Py^{(k)} \rangle},
\]

\[
\gamma^{(k)} = \frac{\langle r^{(k+1)}, r^{(k+1)} \rangle}{\langle r^{(k)}, r^{(k)} \rangle}.
\]
If the denominator in the definition of either $\delta^{(k)}$ or $\gamma^{(k)}$ is less than ZERO, no iterative step past the $k$th step will be carried out. 

All these techniques may possibly be accelerated by the method of splitting or scaling. This means that instead of solving $Py = f$ we solve $P'y' = f'$, where $P' = SPS$, $y' = S^{-1}y$, and $f' = Sf$ and then setting $y = Sy'$. If split = 0, then $S = I$. If split > 0, $S$ is an $m \times m$ diagonal matrix whose $j$th entry is the $j$th component of the array SV returned by the user supplied procedure:

if split = 1:

void quad_class::seset(REAL* sv, INTEGER* list, REAL* weight, BOOLEAN* alg);

if split = 2:

void quad_class::sset(REAL* sv, INTEGER* list, REAL* weight, BOOLEAN* alg);

where list and weight are defined in Section 6.2. alg is a logical variable whose value is set to TRUE if, and only if, the subroutine fails to calculate the value of sv for some reason.

7.9.2 Defining the functional

We now discuss how the matrices $A$, $B$, $C$, $D$, the vector $\bar{x}$, the scalars $a$, $b$, $c$, and the integers $l$ and $t$ are specified for the definition of the function $k$, the matrix $P$ and the vector $f$.

$A$ is an $m \times m$ diagonal matrix whose definition depends on the integer modifier error-type and floating point modifiers error and minv. (Restrictions: $1 \leq$ error-type $\leq 3$, error $> 0$, and minv $> 0$.) If error-type = 1, then every diagonal element of $A$ is equal to error. If error-type = 2, the $i$th diagonal entry of $A$ is $1/\max\{\minv, v\}$ where $v$ is defined by the formulas on page 92. If error-type = 3, then the value of the $i$th diagonal element of $A$ is the reciprocal of the value returned by a user supplied procedure:

REAL quad::uerror(INTEGER np, INTEGER nr, REAL pd, BOOLEAN* alg);

where $i = np \times N\text{RAYS} + nr + 1$, $pd = p$, and alg is a logical variable whose value is set to TRUE if, and only if, the function fails to calculate the value of uerror for some reason. Warning: It is the user’s responsibility to insure that the value returned by this function is greater than ZERO.

$D$ is an $n \times n$ diagonal matrix that is needed only if $b + c = 0$. Its definition depends on the value of the integer modifier d-flag. (Restriction: $1 \leq$ d-flag $\leq 4$.) If d-flag = 1, then the $j$th diagonal element of $D$ is given by

$$
\left( \sum_{i=1}^{m} m_{i,j}^2 / \sigma_i^2 \right)^{-1/2},
$$

where $\sigma_i$ is the $i$th diagonal element of the matrix $A$ defined above. (Restriction: If d-flag is 1 or 2, then for every $j$, such that $1 \leq j \leq n$, there is at least one $i$, such that $m_{i,j} \neq 0$.)

If d-flag = 2, then the $j$th diagonal element of $D$ is given by

$$
\left( \sum_{i=1}^{n} [M^T M]_{j,i} \right)^{-1/2},
$$

where $[M^T M]_{j,i}$ denotes the $(j, i)$th element of the matrix $M^T M$.

If d-flag = 3, then the $j$th diagonal element of $D$ is the $j$th component of the array dv returned by a user supplied procedure:

void quad::dset(REAL* dv, INTEGER* list, REAL* weight, BOOLEAN* alg);

where list and weight are defined in Section 6.2, and alg is a logical variable whose value is set to TRUE if, and only if, the function fails to calculate the value of dset for some reason.

If d-flag = 4, $D$ is the $n \times n$ identity matrix.

$\bar{x}$ is an $n$-dimensional vector whose definition depends on the integer modifiers exp-value and interp. (Restrictions: $1 \leq$ exp-value $\leq 5$, $-1 \leq$ interp $\leq 6$)
If exp-value = 1, \( \bar{x}_j = 0 \), for \( 1 \leq j \leq n \).
If exp-value = 2, \( \bar{x}_j = \text{AVEDEN} \), for \( 1 \leq j \leq n \).
If exp-value = 3, \( \bar{x} \) is the picture of size \( n \), which is related to an \( \text{NELEM}\times\text{NELEM} \) picture in the following way. In the pixel case, \( \bar{x} \) is the picture that would be produced from the given projection data by

**EXECUTE BACKPROJECTION**

name-of-the-execution

**DISCRETE MULTIPLICATIVE**

(see Section 7.1), with the usual indexing convention (described in Section 6.2). In the blob case, \( \bar{x} \) is the picture returned by pix2blob (see Section 6.3.4.2) when it is given the picture defined above.

If exp-value = 4, \( \bar{x} \) is the picture of size \( n \), which is related to an \( \text{NELEM}\times\text{NELEM} \) picture in the following way. In the pixel case, \( \bar{x} \) is the picture that would be produced from the given projection data by

**EXECUTE BACKPROJECTION**

name-of-the-execution

**CONTINUOUS interp MULTIPlicative**

In the blob case, \( \bar{x} \) is the picture returned by pix2blob (see Section 6.3.4.2) when it is given the picture defined above.

If exp-value = 5, then \( \bar{x} = x^{(0)} \), the contents of the recon array prior to the first iteration of the reconstruction procedure (see Section 5.8).

If d-flag is 1, 2 or 3, then \( a = 1 \) and \( b = c = 0 \). If d-flag is 4, then the constants \( a \), \( b \), and \( c \) are given the values of the floating point modifiers \( a \), \( b \), and \( c \), which appear on the next line in the file INPUT.

\[ \begin{bmatrix} a \\ b \\ c \end{bmatrix} \]

R**estrictions**: \( a \geq 0 \), \( b \geq 0 \), and \( c \geq 0 \). This line is absent unless d-flag = 4.

\( B \) is an \( n \times n \) matrix, determined by the values on the next line in the file INPUT.

\[ > \quad l \ bw1 \ bw2 \ bw3 \ \begin{cases} \text{SNARK} \\ \text{SAJZ} \\ \text{SAJC} \\ \text{KAMI} \end{cases} \]

R**estriction**: This line is absent unless d-flag = 4. The value of the integer modifier \( l \) is assigned to the \( l \) in the definition (7.2) of the function \( b \) (restriction: \( l > 0 \)). The matrix \( B \) is defined based on the floating point modifiers \( bw1 \), \( bw2 \), and \( bw3 \) and the following word (SNARK, SAJZ, SAJC, or KAMI) so that the vector represents a picture that is a smoothed version of the picture represented by the vector \( x \). Smoothing pixel and blob images are different enough to require separate explanations.

For pixel pictures, we make use of the notation \( V_1, \ldots, V_9, W_1, W_2, W_3 \) introduced in Section 5.8, with \( W_1, W_2, \) and \( W_3 \) equal to the values of the floating modifiers \( bw1 \), \( bw2 \) and \( bw3 \), respectively. Also, the smoothing operates in such a way as if the threshold were so large that \( |V_i - V_j| \leq \text{threshold} \) is always satisfied. If SNARK is specified, the smoothing performed by \( B \) is exactly the smoothing described in Section 5.8. (Restriction: If SNARK is specified, then \( W_1 > \text{ZERO} \), \( W_2 \geq 0.0 \) and \( W_3 \geq 0.0 \).) If SAJZ is specified, the smoothing performed by \( B \) is the same as the smoothing described in Section 5.8, except that the denominator in the formula on page 46 is replaced by 1. If SAJC is specified, the smoothing operates as follows. Put an extra layer of pixels all around the digitized picture. Assign to every boundary pixel the density in the nearest interior pixel. Apply the smoothing described in the case SAJZ to the extended picture, and then remove all the boundary pixels. The resulting picture is represented by the vector \( Bx \). If KAMI is specified, the smoothing operates as follows. (Restriction: KAMI is not allowed unless, \( l = 1 \).) Apply the smoothing described in the case SAJZ. Set the density in every boundary pixel to 0.0. Apply again the smoothing described in the case SAJZ.

For blob pictures only the weights \( bw1 \) and \( bw2 \) are used. If SNARK is specified, the value of each blob is replaced with the weighted average of the central blob and the up to six surrounding blobs, where the weight of the central blob is \( bw1 \) and the weight of the surrounding blobs is \( bw2 \). If SAJZ is specified, the smoothing is the weighted sum of the central blob and the surrounding blobs. This differs from the SNARK case in that the resulting value is not scaled by the sum of the weights. If SAJC is specified, the smoothing operates as follows. Put an extra layer of blobs all around the digitized picture. Each boundary blob is closest to 1, 2, or 3 image blobs. Assign to each boundary blob the average of the nearest image
CHAPTER 7. BUILT-IN RECONSTRUCTION ALGORITHMS

blobs. Apply the smoothing described by SAJZ to the extended picture, then remove the boundary pixels. If KAMI is specified, apply the smoothing described in the case SAJZ, set the density in each boundary blob to 0.0, and apply the smoothing described in the case SAJZ again. (Restriction: KAMI is not allowed unless, \( l = 1 \).)

\( C \) is an \( n \times n \) matrix, determined by the values on the next line in the file INPUT.

\[
> \quad t \ cw1 \ cw2 \ cw3 \left\{ \begin{array}{l}
SNARK \\
SAJZ \\
SAJC \\
KAMI
\end{array} \right. 
\]

Restriction: This line is absent unless d-flag = 4. If the value of the integer modifier \( t = 0 \), \( C \) is taken to be the identity matrix. Otherwise, the value of the integer modifier \( t \) is assigned to the \( t \) in the definitions of the function \( k \), the matrix \( P \) and the vector \( f \) on page 97. (Restrictions: \( t \geq 0 \). If algorithm > 1 or delta = 3, \( t \) must be even.) If \( t > 0 \), the matrix \( C \) is defined based on the floating point modifiers \( cw1 \), \( cw2 \), and \( cw3 \) and the word modifier in exactly the same way as the matrix \( B \) was defined above based on \( bw1 \), \( bw2 \), \( bw3 \) and its word modifier.

7.9.3 Additional features

One SNARK14 iteration of the QUADRATIC algorithm (see Section 6.1) consists of a single step of the kind described in Section 7.9.1. The contents of the \textit{recon} array at the end of the iteration with iteration number \( k \) are obtained from \( x^{(k)} \) in a way that depends on the value of the integer modifier normalize. (Restriction: The value normalize is 0 or 1.) This is best described by the following C++ like code.

```c
double total = 0.0;
for (int i = 0; i < n; ++i) {
    double v = recon[i];
    if (lofl) v = max(v, lower);
    if (upfl) v = min(v, upper);
    total += v;
    recon[i] = v;
}
if (normalize != 0) {
    if (abs(total) > Consts.zero) factor = nelem*nelem*aveden/total;
    // factor is not needed if condition is not met.
    for (int i = 0; i < n; ++i) {
        recon[i] = (abs(total) > Consts.zero) ? recon[i]* factor : aveden;
    }
}
```

The user may obtain information about the progress of the iterative procedure by the use of the integer modifier print. (Restriction: \( 0 \leq \) print \( \leq 2 \).) If print \( \geq 1 \), the following information is reported on the file OUTPUT. If delta-flag is 1 or 2, then the estimates of \( \lambda \) and \( \bar{\lambda} \) calculated by the program are reported. At the end of each iteration the following values are also reported: \( ||f - Py^{(k)}||^2 \) (provided algorithm\( \neq 1 \)), factor (defined by the code given above, provided it is calculated), \( ||\delta^{(k-1)}g^{(k-1)}||, \delta^{(k-1)} \) and \( ||g^{(k-1)}|| \). If print = 2 and \( t = 0 \), the value of \( k(x^{(k)}) \) is also reported. (If d-flag\( \neq 4 \), \( t \) is not read in and defaults to the value 0.)

7.10 SIRT

\[
> \quad \text{METHOD} \left\{ \begin{array}{l}
\text{GSIRT} \\
\text{LSIRT} \ \text{type}
\end{array} \right. \text{[START [BACKPROJECTED] [NORMAL]]}
\]

This is an implementation of four generalized and modified versions of the (additive) Simultaneous Iterative Reconstruction Technique (SIRT) of [17]. The generalizations are presented in [51]. In our description we shall follow, as closely as possible, the notation of [33]. (Restriction: This SIRT routine is applicable
only to PARALLEL STRIP projection data. The QUADRATIC routine contains a SIRT-type algorithm for other types of projection data, see Section 7.9.)

SIRT is an iterative procedure that, starting from an initial estimate of the picture to be reconstructed, updates the estimate through a sequence of steps. Roughly speaking, the correction at each update is the discrete backprojection of a set of “projection error data” that consists of the differences between all the estimated ray sums and corresponding pseudo ray sums from the current estimate of the image. In addition, there are some scaling operations involved in the update step that will be discussed in detail, as they are the distinguishing features of the different versions of the SIRT algorithm.

For the more detailed description we adopt the definitions in Section 7.6 for \( n, m, x^{(k)}, p, m_i, \text{ and } m_{i,j} \). In addition, for \( 1 \leq j \leq n \), we define a set of integers \( R_j \) as follows.

The set \( R_j \) depends on the most recently executed SELECT command (see Section 5.6). If no SELECT command has been executed,

SELECT EFFICIENT

is assumed.

We define two variables \( F \) and \( L \) as follows. If USER is specified by SELECT, \( F = FUSRAY \) and \( L = LUSRAY \). If SNARK is specified by SELECT, \( F = FSNRAY \) and \( L = LSNRAY \) (see Section 2.5).

An integer \( i \) is in \( R_j \) if it satisfies the following conditions: (a) \( i \) is of the form \( np \times NRRAYS + nr + 1 \) with \( F \leq nr \leq L \). (b) \( m_{i,j} \neq 0 \). (c) \( d_i \leq c_i - (w_i/1000) \), where \( d_i \) denotes the distance of the central line of the \( nr \)th ray of the \( np \)th projection from the origin, \( w_i \) denotes the width of the rays in the \( np \)th projection, and \( c_i \) is the distance from the origin to a line \( A \) that is defined as follows. \( A \) is parallel to the rays of the \( np \)th projection, it goes through a vertex of the reconstruction region, and among the (up to four) lines that have these properties, \( A \) is the one that is furthest from the origin. The purpose of this last condition is to ensure that, for \( i \in R_j \), the central line of the \( nr \)th ray of the \( np \)th projection properly intersects the reconstruction region.

At the beginning of the \( (k+1) \)st step of a SIRT algorithm, \( x^{(k)} \) is stored in the \texttt{recon} array. Then \( x^{(k+1)} \) is defined to be the \( n \)-dimensional column vector whose \( j \)th component is \( x_j^{(k+1)} \), where

\[
x_j^{(k+1)} = \begin{cases} 
  x_j^{(k)} + r \left[ b_j - \sum_{i \in R_j} f_i \sum_{t=1}^n m_{i,t} x_t^{(k)} \right], & \text{if } d_j \neq 0, \\
  x_j^{(k)}, & \text{if } d_j = 0,
\end{cases}
\]

and

\[
w = \begin{cases} 
  (\text{PIXISIZ})^2, & \text{in the pixel case}, \\
  \sqrt{3 \times (\text{DELTA})^2}/2, & \text{in the blob case}.
\end{cases}
\]

Here \( b \) and \( d \) are \( n \)-dimensional vectors and \( f \) is an \( m \)-dimensional vector. The precise definition, to be given below, of the components \( b_j, d_j, \) and \( f_i \) is what distinguishes the different versions of SIRT. The variable \( r \) denotes a relaxation parameter that is defined as follows.

If RELAX is specified, \( r \) is assigned the value of the floating point modifier relax. If SIGMA is specified, \( r \) is assigned the reciprocal of the value of the floating point modifier sigma. (Restrictions: relax > ZERO and sigma > ZERO.) If neither RELAX nor SIGMA is specified, \( r \) is assigned the value 1.0.

We now define the vectors \( b, d, \) and \( f \). In order to do this we need two auxiliary \( m \)-dimensional vectors \( n \) and \( a \), whose \( i \)th components are defined as follows. Let \( np \) and \( NR \) be such that \( i = np \times NRRAYS + nr + 1 \) with \( 0 \leq nr < NRRAYS \). Then \( n_i \) is the value of \texttt{numb} returned by either

\[
\text{ray}(np, nr, \text{list}, \text{weight}, &\texttt{numb}, &\texttt{snorm});
\]

in the pixel case or

\[
\text{Blob.bray}(np, nr, \text{list}, \text{weight}, &\texttt{numb}, &\texttt{snorm});
\]

in the blob case.

The value of \( a_i \) approximates the “area” of the \( nr \)th ray of the \( np \)th projection; it is the width of this ray multiplied by the length of intersection of the central line of the ray with the reconstruction region.
If GSIRT is specified, then
\[
b_j = \sum_{i \in R_j} \frac{p_i}{a_i},
\]
\[
d_j = \sum_{i \in R_j} n_i,
\]
\[
f_i = 1.
\]

If LSIRT is specified, the exact algorithm depends on the value of the integer modifier type. \textit{Restriction:} \(1 \leq \text{type} \leq 3\).

If \(\text{type} = 1\), then
\[
b_j = \left(\sum_{i \in R_j} \frac{n_i p_i}{a_i}\right) / \sum_{i \in R_j} n_i,
\]
\[
d_j = \sum_{i \in R_j} n_i,
\]
\[
f_i = 1.
\]

If \(\text{type} = 2\), then
\[
b_j = \frac{\sum_{i \in R_j} (p_i/a_i)}{d_j},
\]
\[
d_j = \sum_{i \in R_j} 1,
\]
\[
f_i = 1/n_i.
\]
(Note that \(f_i\) need not be defined unless \(i \in R_j\), in which case \(n_i \geq 1\)).

If \(\text{type} = 3\), then
\[
b_j = \frac{\sum_{i \in R_j} (p_i/(n_i \times a_i))}{\sum_{i \in R_j} (1/n_i)},
\]
\[
d_j = \sum_{i \in R_j} (1/n_i),
\]
\[
f_i = 1/n_i^2.
\]

The choice of \(x^{(0)}\) is determined by the keywords \textbf{START} or \textbf{START BACKPROJECTED}. If either of these options is chosen, then \(x^{(0)}\) is set to the vector \(b\). Otherwise the initialization option on the \textbf{EXECUTE} line (Section 5.8) is in effect.

One SNARK14 iteration of the SIRT algorithm (see Section 6.1) consists of a single step. The contents of the \texttt{recon} array at the end of the iteration with iteration number \(k\) are described by \(x^{(k)}\), unless the following conditions are met: \textbf{NORMAL} is specified, \texttt{AREA}×\texttt{AVEDEN} > \texttt{ZERO}, and \(|\sum_{j=1}^{n} x_j^{(k)}| > \texttt{ZERO}\). If all three conditions are satisfied, then, prior to returning control to \texttt{exalg}, the SIRT routine multiplies each entry of \texttt{recon} by \(\texttt{AVEDEN}/\sum_{j=1}^{n} x_j^{(k)}\). If another iteration is called, the initial value of \(x_j^{(k)}\) for the new iteration will be the contents of \(\texttt{recon}[j-1]\) at end of the last iteration.

### 7.11 EMAP

\(\texttt{gamma [EVAL]}\)

This is a general implementation of a maximum \textit{a posteriori} probability (MAP) algorithm for PET based on a modified expectation-maximization (EM) algorithm \cite{30,67}.

The MAP approach implemented by SNARK14 is the problem of finding an image vector \(x\) that maximizes the log-posterior functional (called the log-likelihood functional if \(\gamma = 0\))

\[
\ln P(x|y) = \sum_{i=1}^{l} \left[ y_i \ln \left( \sum_{j=1}^{J} l_{ij} x_j \right) - \sum_{j=1}^{J} l_{ij} x_j \right] - \frac{\gamma}{2} x^T S x,
\]  

\[ (7.3) \]
where \( x_j \) is the \( j \)th basis function of the image vector \( x \) \((1 \leq j \leq J)\), \( y_i \) is the \( i \)th component of the measurement vector \( y \) \((1 \leq i \leq I)\) and \( l_{ij} \) is the length of intersection of the \( i \)th measurement line with the \( j \)th basis function. **Restriction:** \( \gamma \) must be 0.0 in the blob case.

In view of this restriction the matrix \( S \) is defined only in the pixel case. It has the property that

\[
x^T S x = \sum_{r \in N} \left( x_r - \frac{1}{8} \sum_{j \in N_r} x_j \right)^2,
\]

where \( N \) is the set of indices \( r \) for that the \( r \)th basis function is not on the border of the picture region, \( N_r \) \((1 \leq r \leq N)\) is the set of indices associated with those at most eight basis functions that share a vertex with the \( r \)th basis function. If \( N \) is the empty set, the sum is 0. The entries of \( S \) are defined by

\[
S_{uv} = \sum_{r \in N} s_{ru} s_{rv}, \text{ for } 1 \leq u, v \leq J,
\]

where

\[
s_{rj} = \begin{cases} 1, & \text{if } j = r, \\ -\frac{1}{8}, & \text{if } j \in N_r, \\ 0, & \text{otherwise}. \end{cases}
\]

In case the floating-point modifier \( \text{gamma} \) in the follow-up command line is strictly greater than 0.0, its value is assigned to \( \gamma \) in (7.3). In this case, application of De Pierro’s modified EM algorithm to the MAP problem \([30]\) leads to the following iterative solution. Let \( x^{(k)} \) be the image vector whose \( j \)th component, \( x^{(k)}_j \), is \( \text{recon}[j - 1] \) after the \( k \)th iteration of the algorithm. Then

\[
x^{(k+1)}_j = \frac{1}{2} \left( -p^{(k)}_j + \sqrt{\left( p^{(k)}_j \right)^2 + 4q^{(k)}_j} \right),
\]

where

\[
p^{(k)}_j = \frac{W_{ij}}{\gamma(9S_{jj})} - x^{(k)}_j + \frac{1}{9S_{jj}} \sum_{u=1}^{J} S_{ju} x^{(k)}_u,
\]

\[
q^{(k)}_j = \frac{x^{(k)}_j}{\gamma(9S_{jj})} \sum_{i=1}^{J} \frac{l_{ij}y_i}{\sum_{n=1}^{J} l_{in}x^{(k)}_n},
\]

\[
W_{jj} = \sum_{i=1}^{I} l_{ij}.
\]

If \( \text{gamma} = 0.0 \), the MAP EM algorithm reduces to the maximum likelihood (ML) EM algorithm \([67]\) and the image vector is computed iteratively as follows (this option is available for blobs as well as for pixels):

\[
x^{(k+1)}_j = \frac{x^{(k)}_j}{W^{(k)}_{jj} \sum_{i=1}^{I} \frac{l_{ij}y_i}{\sum_{n=1}^{J} l_{in}x^{(k)}_n}}.
\]

If \( \text{EVAL} \) is specified, the log-likelihood functional and, if \( \text{gamma} > 0.0 \), the log-posterior functional are evaluated at each iteration and the results are written to a file named “MAPuser1”.

### 7.12 LINO

\[
> \begin{array}{c} \text{BANDLIMITING} \\ \text{SINC} \\ \text{COSINE} \end{array} \{ \text{cutoff} \}
\]

This is a general implementation of the linogram method \([13, 14]\). The reader is referred to \([14]\) for a step-by-step description of the algorithm and its implementation.
The filter name and the floating point modifier cutoff define a filter function used to filter the projection data. \((\text{Restriction: } 0 < \text{cutoff} \leq 1)\).

Warning: Note that during collection of sinogram data the detector array is always perpendicular to the ray direction. On the other hand, during collection of linogram data the detector array lies fixed along the x-axis for projection angles \(-\frac{\pi}{4} < \theta < \frac{\pi}{4}\), and lies fixed along the y-axis for projection angles \(\frac{\pi}{4} < \theta < \frac{3\pi}{4}\). The consequence of this is that to simulate linogram data collection with SNARK14 it is necessary to use the LINOGRAH geometry (Section 5.3.3, Set 6).

In SNARK14 the linogram program assumes the following relationship between the object size, the number of projections and the number of rays per projection. Let \(2N + 1\) be the (odd) number of pixels along a side of the digitized picture of the object. Then there are a total of \(2(4N + 3)\) projections with \(4N + 3\) rays per projection. Moreover, the \(2(4N + 3)\) projections are generated over two sets of angles as follows:

\[
\theta \in \left\{ \arctan \left( \frac{2i}{4N + 3} \right) \mid -(2N + 1) \leq i \leq (2N + 1) \right\} \cup \left\{ \arctan \left( \frac{2i}{4N + 3} \right) + \frac{\pi}{2} \mid -(2N + 1) \leq i \leq (2N + 1) \right\}.
\]

Thus for the first set of angles we have \(-\frac{\pi}{4} < \theta < \frac{\pi}{4}\) and for the second set of angles we have \(\frac{3\pi}{4} < \theta < \frac{5\pi}{4}\). These angles are generated by SNARK14 when the user specifies the LINOGRAH option of the GEOMETRY command (Section 5.3.3, Set 6). \(\text{Note: }\) The relationship between the angle THETA generated by SNARK14 (and defined in Figure 2.2) and the projection angle above is the following: \(\text{THETA} = \theta + \frac{\pi}{2}\).
Chapter 8

SNARK EXPERIMENTER

8.1 Introduction

In medical imaging an enormous variety of algorithms have been proposed to reconstruct a cross-section of the human body. It is therefore often desirable to evaluate the relative efficacy of two or more reconstruction methods for a specific medical task in a manner that is statistically sound [8, 15, 40, 41, 43]. Such an evaluation, therefore, must be done using a sample set that is large enough to provide us with a statistically significant result [43].

Performing this evaluation on mathematical phantoms requires a means of running the competing algorithms on projection data obtained from a large number of randomly generated phantoms. Thereafter, various numerical measures of agreement between the reconstructed images and the original phantoms may be used to reach a conclusion that has some statistical substance [43]. A straightforward way of achieving this goal with SNARK14 is to provide a front-end or driver program that contains all the requisite commands that may be fed to SNARK14 to generate as many phantoms as needed (plus their projection data); to implement the desired reconstruction algorithms on these data; and to evaluate the reconstructed images. Such a driver program is provided by SNARK experimenter. The method used in the comparative evaluation of the algorithms consists of the following procedures [15]:

- generation of random samples from a statistically described ensemble of phantoms and their projection data (see Sections 8.2.2-8.2.4);
- reconstruction from the projection data by each of the algorithms to be compared (Section 8.2.5);
- assignment of a figure of merit (FOM) to each reconstructed image. The FOM should be a measure of image quality for solving the specified task (Section 8.2.6);
- calculation of the statistical significance, based on the FOMs for all reconstructions, at which we can reject the hypothesis that the methods are equally helpful for solving the task (Section 8.4).

SNARK experimenter has been designed to be very easy to use once a working knowledge of the SNARK14 commands is attained. This chapter describes the SNARK experimenter commands and provides several examples of the use of SNARK experimenter. The notation used here follows the convention described in Sections 4.3-4.5.

8.2 SNARK experimenter commands

SNARK experimenter reads input from UNIXs standard input or a file. This means that the input lines may be manually entered after the SNARK experimenter executable file is evoked, or they may be stored in a file. For example, if file.in is the file containing the SNARK experimenter commands, then SNARK experimenter is executed when the user enters the following line at the UNIX command prompt:

snark14 -e file.in
If file.in is missing, then SNARK14 experimenter will expect the INPUT to be entered as the standard input, which typically means entering the INPUT on the console line-by-line. If the SNARK14 experimenter makes use of user-defined algorithms and/or criteria, then the user-defined executable (i.e., snark14UserDefined) should be placed inside the current directory. In such a case, the experimenter should be invoked using the command:

```
snark14UserDefined -e file.in
```

(Note: Since SNARK experimenter drives SNARK14, it evokes the SNARK14 executable file. Warning: If the current directory contains the executable file snark14UserDefined, that version of SNARK14 will be used, otherwise, the version found in the PATH environment variable will be used.)

A single execution of SNARK experimenter requires an input sequence consisting of the following seven command lines (the first command is optional):

```
[SEED seed_value ]
ENSEMBLE file-specification
EXPERIMENT nexp exp-flag nelem pixel-size navel nrun_1 [nphan_2 nrun_2]
DATA file-specification
RECONSTRUCTION file-specification
ANALYSIS file-specification
END
```

A typical input file for a single execution of SNARK experimenter is:

```
SEED -1
ENSEMBLE b.9.virus.ens
EXPERIMENT 1 0 95 1.6 7 18 30
DATA b.9.projection.ss
RECONSTRUCTION b.9.recon.ss
ANALYSIS b.9.compare.ss
END
```

Multiple executions of SNARK experimenter may be achieved by repeating the first five command lines. The END command signals termination of the SNARK experimenter input stream. In the following sections we describe in detail the first five command lines.

### 8.2.1 SEED

```
> SEED seed_value
```

In this optional command line seed_value is the value used to seed the random number generation in SNARK experimenter. The random number generator is used in three places in SNARK experimenter: 1) to choose the phantom from the ensemble of phantoms (see 8.2.2), 2) to generate the seed used for generation of optional inhomogeneity in the phantom (see description of SCALE in 8.2.2), and 3) to generate the seed used for generation of optional noise in projection data (see description of MEASUREMENT in 8.2.4). If seed_value \( \geq 0 \), that number is used to seed the random number generator (the entire experiment can be repeated with the same results, as long as the same random number generator is used). If seed_value < 0, the current time is used to seed the random number generator (each time the experiment is run, the results will be different).

If this line is not provided, the current time is used to seed the random number generator.

### 8.2.2 ENSEMBLE

```
> ENSEMBLE file-specification
```

In this command line file-specification is the name of an ensemble data file that contains a list of n phantom file names. The format of an ensemble data file is:

```
> phantom_file_1
```
In the example input file listed in Section 8.2 the file b.9.virus.ens is a typical ensemble data file that contains a list of 18 phantom file names as follows:

```
  virus_24_1_0.96_0.6.atl
  virus_24_1_0.96_0.7.atl
  virus_24_1_0.96_0.8.atl
  virus_24_1_0.97_0.6.atl
  virus_24_1_0.97_0.7.atl
  virus_24_1_0.97_0.8.atl
  virus_26_1_0.96_0.6.atl
  virus_26_1_0.96_0.7.atl
  virus_26_1_0.96_0.8.atl
  virus_26_1_0.97_0.6.atl
  virus_26_1_0.97_0.7.atl
  virus_26_1_0.97_0.8.atl
  virus_28_1_0.96_0.6.atl
  virus_28_1_0.96_0.7.atl
  virus_28_1_0.96_0.8.atl
  virus_28_1_0.97_0.6.atl
  virus_28_1_0.97_0.7.atl
  virus_28_1_0.97_0.8.atl
```

Each phantom file should start with one or two lines describing the spectrum of the x-ray beam in the manner specified by 5.3.3, Set 2. This is followed by a description of the phantom itself, it contains keywords and a series of follow-up lines that describe the elemental objects that make up the phantom:

```
> SINGLE
> [shape c_x c_y u v ang den(1)]
> [DENSITY den(2) . . . den(NERGY)]
...
> PAIR
> [shape c_x c_y u v ang den1(1) den2(1) prob]
> [DENSITY den1(2) . . . den1(NERGY)]
> [DENSITY den2(2) . . . den2(NERGY)]
...
> DUMMY
> [shape c_x c_y u v ang den(1)]
> [DENSITY den(2) . . . den(NERGY)]
...
> SCALE
> scale [ sd]
```

Restriction: The lines starting with the keyword DENSITY are absent in the monochromatic case or if NERGY = 1.

The keywords SINGLE, PAIR and DUMMY may be followed by one or more follow-up lines that describe an elemental object, or structure, that makes up the phantom. In these follow-up lines shape is one of the following: ELIPSE, RECTANGLE, TRIANGLE, SEGMENT, or SECTOR (see Section 5.3.3, Set 3). c_x, c_y, u, v, ang, and den(1) ... den(NERGY) are all floating point modifiers that, together with shape, define the elemental object (see Section 5.3.3, Set 3).

For each follow-up line after the SINGLE keyword a single structure of type described by shape is generated.

For each follow-up line after the PAIR keyword a pair of structures of type described by shape is generated. One structure is generated at coordinate (c_x, c_y) and its mirror image is generated at coordinate (−c_x, c_y).
with a rotation of \(-\ang\). The floating-point modifier \(\text{prob}\) is the probability of randomly assigning densities \(\text{den1}(1) \ldots \text{den1}(\text{ENERGY})\) to the structure at location \((c_x, c_y)\) and \(\text{den2}(1) \ldots \text{den2}(\text{ENERGY})\) to the structure at location \((-c_x, c_y)\). Equivalently, \((1-\text{prob})\) is the probability of randomly assigning densities \(\text{den1}(1) \ldots \text{den1}(\text{ENERGY})\) to the structure at location \((-c_x, c_y)\) and \(\text{den2}(1) \ldots \text{den2}(\text{ENERGY})\) to the structure at location \((c_x, c_y)\). \text{Restriction}: \text{den1}(i) \neq \text{den2}(i)\) for all \(i\). The current time (using the Linux system call “time”) is used as the seed of the random number generator. Multiple runs of SNARK experimenter with the same input files will generate different phantoms.

For each follow-up line after the DUMMY keyword a single structure of type described by shape is generated. However this structure is not used in calculating the figures of merit described in Section 8.2.6.

\text{Note}: In case a SINGLE, PAIR or DUMMY structure is not desired the corresponding follow-up line is left blank.

scale is a floating-point modifier that scales all previously defined densities. It may be optionally followed by local inhomogeneity specification using sd. These are identical to the scale and sd that follows the LAST keyword of the SNARK14 CREATE input sequence (see Section 5.3.3, Set 3). \text{Note}, that the seed value that follows the LAST keyword of the SNARK14 CREATE input sequence is generated automatically by SNARK experimenter; it should not be provided on the line following SCALE.

The contents of a typical phantom file are given below:

```
SPECTRUM MONOCHROMATIC 60
SINGLE
  elip 0 0 29.72 29.72 0 0
PAIR
  elip 4.14 63.19 3.89 3.89 0 1 0.97 0.5
  elip 12.36 62.11 3.89 3.89 0 1 0.97 0.5
  elip 20.36 59.97 3.89 3.89 0 1 0.97 0.5
  elip 28.01 56.80 3.89 3.89 0 1 0.97 0.5
  elip 35.18 52.66 3.89 3.89 0 1 0.97 0.5
  elip 41.76 47.61 3.89 3.89 0 1 0.97 0.5
  elip 47.61 41.76 3.89 3.89 0 1 0.97 0.5
  elip 52.66 35.18 3.89 3.89 0 1 0.97 0.5
  elip 56.80 28.01 3.89 3.89 0 1 0.97 0.5
  elip 59.97 20.36 3.89 3.89 0 1 0.97 0.5
  elip 62.11 12.36 3.89 3.89 0 1 0.97 0.5
  elip 63.19 4.14 3.89 3.89 0 1 0.97 0.5
  elip 63.19 -4.14 3.89 3.89 0 1 0.97 0.5
  elip 62.11 -12.36 3.89 3.89 0 1 0.97 0.5
  elip 59.97 -20.36 3.89 3.89 0 1 0.97 0.5
  elip 56.80 -28.01 3.89 3.89 0 1 0.97 0.5
  elip 52.66 -35.18 3.89 3.89 0 1 0.97 0.5
  elip 47.61 -41.76 3.89 3.89 0 1 0.97 0.5
  elip 41.76 -47.61 3.89 3.89 0 1 0.97 0.5
  elip 35.18 -52.66 3.89 3.89 0 1 0.97 0.5
  elip 28.01 -56.80 3.89 3.89 0 1 0.97 0.5
  elip 20.36 -59.97 3.89 3.89 0 1 0.97 0.5
  elip 12.36 -62.11 3.89 3.89 0 1 0.97 0.5
  elip 4.14 -63.19 3.89 3.89 0 1 0.97 0.5
DUMMY
  elip 0 0 59.44 59.44 0 0.8
SCALE
  1
```

This input file may generate the following SNARK14 command lines that describe the objects to be generated:

```
OBJECTS
  elip 0 0 29.72 29.72 0 0
```
elip 4.140000 63.189999 3.890000 3.890000 0.000000 1.000000
elip -4.140000 63.189999 3.890000 3.890000 -0.000000 0.970000
elip 12.360000 62.110001 3.890000 3.890000 0.000000 1.000000
elip -12.360000 62.110001 3.890000 3.890000 -0.000000 0.970000
elip 20.360001 59.970001 3.890000 3.890000 0.000000 0.970000
elip -20.360001 59.970001 3.890000 3.890000 -0.000000 1.000000
elip 28.010000 56.799999 3.890000 3.890000 0.000000 1.000000
elip -28.010000 56.799999 3.890000 3.890000 -0.000000 0.970000
elip 35.180000 52.660000 3.890000 3.890000 0.000000 0.970000
elip -35.180000 52.660000 3.890000 3.890000 -0.000000 1.000000
elip 41.759998 47.610001 3.890000 3.890000 0.000000 0.970000
elip -41.759998 47.610001 3.890000 3.890000 -0.000000 1.000000
elip 47.610001 41.759998 3.890000 3.890000 0.000000 0.970000
elip -47.610001 41.759998 3.890000 3.890000 -0.000000 1.000000
elip 52.660000 35.180000 3.890000 3.890000 0.000000 0.970000
elip -52.660000 35.180000 3.890000 3.890000 -0.000000 1.000000
elip 56.799999 28.010000 3.890000 3.890000 0.000000 0.970000
elip -56.799999 28.010000 3.890000 3.890000 -0.000000 1.000000
elip 59.970001 20.360001 3.890000 3.890000 0.000000 1.000000
elip -59.970001 20.360001 3.890000 3.890000 -0.000000 0.970000
elip 62.110001 12.360000 3.890000 3.890000 0.000000 0.970000
elip -62.110001 12.360000 3.890000 3.890000 -0.000000 1.000000
elip 63.189999 4.140000 3.890000 3.890000 0.000000 1.000000
elip -63.189999 4.140000 3.890000 3.890000 -0.000000 0.970000
elip 63.189999 -4.140000 3.890000 3.890000 0.000000 0.970000
elip -63.189999 -4.140000 3.890000 3.890000 -0.000000 1.000000
elip 62.110001 -12.360000 3.890000 3.890000 0.000000 1.000000
elip -62.110001 -12.360000 3.890000 3.890000 -0.000000 0.970000
elip 59.970001 -20.360001 3.890000 3.890000 0.000000 0.970000
elip -59.970001 -20.360001 3.890000 3.890000 -0.000000 1.000000
elip 56.799999 -28.010000 3.890000 3.890000 0.000000 0.970000
elip -56.799999 -28.010000 3.890000 3.890000 -0.000000 1.000000
elip 52.660000 -35.180000 3.890000 3.890000 0.000000 0.970000
elip -52.660000 -35.180000 3.890000 3.890000 -0.000000 1.000000
elip 47.610001 -41.759998 3.890000 3.890000 0.000000 0.970000
elip -47.610001 -41.759998 3.890000 3.890000 -0.000000 1.000000
elip 41.759998 -47.610001 3.890000 3.890000 0.000000 1.000000
elip -41.759998 -47.610001 3.890000 3.890000 -0.000000 0.970000
elip 35.180000 -52.660000 3.890000 3.890000 0.000000 0.970000
elip -35.180000 -52.660000 3.890000 3.890000 -0.000000 1.000000
elip 28.010000 -56.799999 3.890000 3.890000 0.000000 1.000000
elip -28.010000 -56.799999 3.890000 3.890000 -0.000000 1.000000
elip 20.360001 -59.970001 3.890000 3.890000 0.000000 1.000000
elip -20.360001 -59.970001 3.890000 3.890000 -0.000000 0.970000
elip 12.360000 -62.110001 3.890000 3.890000 0.000000 1.000000
elip -12.360000 -62.110001 3.890000 3.890000 -0.000000 0.970000
elip 4.140000 -63.189999 3.890000 3.890000 0.000000 0.970000
elip -4.140000 -63.189999 3.890000 3.890000 -0.000000 1.000000
elip 0 0 59.44 59.44 0 0.8
last 1

### 8.2.3 EXPERIMENT

> EXPERIMENT nexp exp-flag nelem pixel-size nave1 nphan-1 nrun-1 [nphan-2 nrun-2]
nexp is an integer modifier that equals the number of experiments to be performed. Restriction: $1 \leq nexp \leq 2$. When $nexp = 2$, the experiment described in the reconstruction phase (see Section 8.2.5) is performed twice.

exp-flag is an integer modifier used to control the phantom-file set used in each experiment as follows: if exp-flag = 0 the same set of phantom files is available for use in all experiments; if exp-flag = 1 then the phantom files used in the first experiment are excluded in the second experiment.

nelem, pixel-size, and nave1 are modifiers that are described by Set 4 of the SNARK14 CREATE input sequence (see Section 5.3.3).

nphan-i is an integer modifier that determines the number of phantom files used for experiment i.

nrun-i is an integer modifier that determines the number of runs for experiment i. Note: nphan-2 and nrun-2 are present only if nexp=2.

Restriction: nphan_i > 0; nrun_i > 0.

Note: The current time (using the Linux system call “time”) is used as the seed for the random number generator to select which phantoms of the ensemble are used in an experiment and which structure of a pair has the higher density. Multiple runs of snark experimenter will use different sets of phantoms from the ensemble and generate different structure pairs.

### 8.2.4 DATA

> DATA file-specification

In this command line file-specification is the name of a file that contains information about generation of the projection data. The input lines of this file have the same syntax as Sets 5-8 of the SNARK14 CREATE input sequence (see Section 5.3.3 and Sections 5.4-5.5); i.e.

> RAYSUM (Section 5.3.3, Set 5)
> GEOMETRY (Section 5.3.3, Set 6)
> MEASUREMENT (Section 5.3.3, Set 7)
> RUN (Section 5.3.3, Set 8)
> PICTURE (Section 5.4)
> PROJECTION (Section 5.5)

The file b.9.projection.ss that follows the DATA command in Section 8.2 is a typical file containing information about the generation of the projection data as follows:

```
raysum average 1
1
geometry
divergent arc 153 306
rays user 101 detector spacing 3.2
angles 300 equally spaced
0 358.8
measurement noisy
quantum 0.0 0.0 calibr 4
multiplicative 1.0 0.1
seed
background 0.0
run
picture test
projection real
```

Note: If quantum noise is simulated (see Section 5.3.3, Set 7), the seed value is automatically generated by SNARK experimenter; it should not be provided on this line (it is ignored if provided).

### 8.2.5 RECONSTRUCTION

> RECONSTRUCTION file-specification
In this command line file-specification is the name of the file that contains information about the reconstruction process. The input lines of this file have the same syntax as discussed in Sections 5.6-5.8; i.e.

> [SELECT (Section 5.6)]
> [BASIS (Section 5.7)]
> [STOP (Section 5.9)]
> EXECUTE algorithm-1 (Section 5.8)
> key1: name-of-execution-1
> algorithm-1 parameters
>
> [SELECT (Section 5.6)]
> [BASIS (Section 5.7)]
> [STOP (Section 5.9)]
> EXECUTE algorithm-n (Section 5.8)
> key-n: name-of-execution-n
> algorithm-n parameters

The follow-up string after each EXECUTE command is a string as described in Section 5.8. As explained in that section, SNARK14 merely echos this string on all outputs produced during the analysis phase of a SNARK14 run. The first 4 characters of each follow-up string after an EXECUTE command should be unique since they are used as keywords by SNARK experimenter to identify the two reconstruction algorithms being compared during the SNARK experimenter analysis phase (see Section 8.2.6). The lines described by algorithm-i parameters refer to the input command line(s) required by algorithm-i for execution. The file b.9.recon.ss that follows the RECONSTRUCTION command in Section 8.2 is a typical file containing information about the reconstruction process as follows:

```
stop iteration 15
execute average emap
alg1: testing super snark with ML
gamma is 0.0
execute average emap
alg2: testing super snark with MAP
gamma is 10.0
```

Here we note that after, each EXECUTE command, the first 4 characters of the follow-up string form a unique keyword (e.g., alg1 or alg2) that identify each reconstruction algorithm. Section 8.2.6 illustrates how these keywords are used in comparing two algorithms.

### 8.2.6 ANALYSIS

> ANALYSIS file-specification

In this command line file-specification is the name of the file containing information about the algorithms being compared. The format of this file is:

```
> fileout
> [MODE highden lowden]
> COMPARE key1 key2 FOM-1 [FOM-2 [FOM-3 [FOM-4]]]n
> iteration-number-1 iteration-number-2
> iteration-number-3 iteration-number-4
>
> [MODE highden lowden]
> COMPARE keyn keym FOM-1 [FOM-2 [FOM-3 [FOM-4]]]n
> iteration-number-1 iteration-number-2
> iteration-number-3 iteration-number-4
>
> END
```
Note that multiple comparisons may be achieved by repeating all but the first and last lines. The END command signals termination of this file.

fileout is the prefix of the file name that stores the significance results based on the FOMs discussed below. These results are stored in a text file whose name is of the form fileout.exp where exp is the experiment number (Section 8.2.3).

The MODE command line is an optional line whose function is discussed in Section 8.2.6.2.

In the first COMPARE command line key1 and key2 are unique keywords that identify the two algorithms being compared. These keys are the same as the first 4 characters of the follow-up strings discussed in Section 8.2.5. FOM-i is the FOM to be computed and may assume the following values: STRU, POIN, HITR, IROI, KLDS, USR1, USR2, USR3, USR4 and USR5. These FOMs are discussed below.

Following the COMPARE command line is a two-column list of iteration numbers to be compared. For example, the reconstructions from the algorithm identified by key-1 at iterations iteration-number-1, iteration-number-3, ... are compared to the reconstructions from the algorithm identified by key-2 at iterations iteration-number-2, iteration-number-4, respectively. Note: If an algorithm is noniterative then iteration-number-i should be set to 1. If iteration-number-i is set to 0, then the final iteration of that algorithm, whichever number that happens to be, will be compared.

In the example of Appendix A.9, the file b.9.compare.ss that follows the ANALYSIS command in Section 8.2 is a typical file containing the following instructions to compare the algorithms in the sample file b.9.recon.ss listed in Section 8.2.5:

```
testem
COMPARE alg1 alg2 HITR USR1
  1  1
  3  3
  6  6
  9  9
 12 12
 15 15
END
```

SNARK experimenter reads the MODE command lines and the list of iteration numbers from this file and combines these with the information contained in the files discussed in Sections 8.2.2-8.2.5 to generate a SNARK14 INPUT file (Chapter 3). SNARK experimenter then initiates a SNARK14 run with this file as input. The listing below illustrates a typical INPUT file generated by SNARK experimenter.

```
CREATE
  virus_24.1_0.97_0.8.atl, seed used in phantom generation= 1126459725
SPECTRUM MONOCHROMATIC 511
OBJECTS
  elip 0 0 29.72 29.72 0 0
  elip 4.140000 63.189999 3.890000 3.890000 0.000000 1.000000
  elip -4.140000 63.189999 3.890000 3.890000 -0.000000 0.970000
  elip 12.360000 62.110001 3.890000 3.890000 0.000000 1.000000
  elip -12.360000 62.110001 3.890000 3.890000 -0.000000 0.970000
  elip 20.360001 59.970001 3.890000 3.890000 0.000000 0.970000
  elip -20.360001 59.970001 3.890000 3.890000 0.000000 1.000000
  elip 28.010000 56.799999 3.890000 3.890000 0.000000 1.000000
  elip -28.010000 56.799999 3.890000 3.890000 -0.000000 0.970000
  elip 35.180000 52.660000 3.890000 3.890000 0.000000 1.000000
  elip -35.180000 52.660000 3.890000 3.890000 -0.000000 0.970000
  elip 41.759998 47.610001 3.890000 3.890000 0.000000 0.970000
  elip -41.759998 47.610001 3.890000 3.890000 -0.000000 1.000000
  elip 47.610001 41.759998 3.890000 3.890000 0.000000 0.970000
  elip -47.610001 41.759998 3.890000 3.890000 -0.000000 1.000000
  elip 52.660000 35.180000 3.890000 3.890000 0.000000 1.000000
```
elip -52.660000 35.180000 3.890000 3.890000 -0.000000 0.970000
elip 56.799999 28.010000 3.890000 3.890000 0.000000 0.970000
elip -56.799999 28.010000 3.890000 3.890000 -0.000000 1.000000
elip 59.970001 20.360001 3.890000 3.890000 0.000000 1.000000
elip -59.970001 20.360001 3.890000 3.890000 -0.000000 0.970000
elip 62.110001 12.360000 3.890000 3.890000 0.000000 0.970000
elip -62.110001 12.360000 3.890000 3.890000 -0.000000 1.000000
elip 63.189999 20.360001 3.890000 3.890000 0.000000 1.000000
elip -63.189999 20.360001 3.890000 3.890000 -0.000000 0.970000
elip 63.189999 -28.010000 3.890000 3.890000 0.000000 1.000000
elip -63.189999 -28.010000 3.890000 3.890000 -0.000000 0.970000
elip 62.110001 -12.360000 3.890000 3.890000 0.000000 1.000000
elip -62.110001 -12.360000 3.890000 3.890000 -0.000000 0.970000
elip 59.970001 -20.360000 3.890000 3.890000 0.000000 0.970000
elip -59.970001 -20.360000 3.890000 3.890000 -0.000000 1.000000
elip 56.799999 -28.010000 3.890000 3.890000 0.000000 0.970000
elip -56.799999 -28.010000 3.890000 3.890000 -0.000000 1.000000
elip 52.660000 -35.180000 3.890000 3.890000 0.000000 0.970000
elip -52.660000 -35.180000 3.890000 3.890000 -0.000000 1.000000
elip 47.610001 -41.759998 3.890000 3.890000 0.000000 0.970000
elip -47.610001 -41.759998 3.890000 3.890000 -0.000000 1.000000
elip 41.759998 -47.610001 3.890000 3.890000 0.000000 0.970000
elip -41.759998 -47.610001 3.890000 3.890000 -0.000000 1.000000
elip 35.180000 -52.660000 3.890000 3.890000 0.000000 0.970000
elip -35.180000 -52.660000 3.890000 3.890000 -0.000000 1.000000
elip 28.010000 -56.799999 3.890000 3.890000 0.000000 0.970000
elip -28.010000 -56.799999 3.890000 3.890000 -0.000000 1.000000
elip 20.360001 -59.970001 3.890000 3.890000 0.000000 1.000000
elip -20.360001 -59.970001 3.890000 3.890000 -0.000000 0.970000
elip 12.360000 -62.110001 3.890000 3.890000 0.000000 1.000000
elip -12.360000 -62.110001 3.890000 3.890000 -0.000000 0.970000
elip 4.140000 -63.189999 3.890000 3.890000 0.000000 0.970000
elip -4.140000 -63.189999 3.890000 3.890000 -0.000000 1.000000
elip 0 0 59.44 59.44 0 0.8
last 1
phantom average 7
95 1.600000
raysum average 1
1
gamma
divergent arc 153 306
rays user 101 detector spacing 3.2
angles 300 equally spaced
0 358.8
measurement noisy
quantum 0.0 0.0 calibr 4
multiplicative 1.0 0.1
seed 1126459725
background 0.0
run
picture test
projection real
stop iteration 15
execute average emap
alg1: testing super snark with ML experiment= 1 run= 1
gamma is 0.0
execute average emap
alg2: testing super snark with MAP experiment= 1 run= 1
gamma is 10.0
EVALUATE RESOLUTION
experimenter evaluation 1
SELECTIVE
elip 0.000000 0.000000 29.719999 29.719999 0.000000
elip 4.140000 63.189999 3.890000 3.890000 0.000000
elip -4.140000 63.189999 3.890000 3.890000 -0.000000
elip 12.360000 62.110001 3.890000 3.890000 0.000000
elip -12.360000 62.110001 3.890000 3.890000 -0.000000
elip 20.360001 59.970001 3.890000 3.890000 0.000000
elip -20.360001 59.970001 3.890000 3.890000 -0.000000
elip 28.010000 56.799999 3.890000 3.890000 0.000000
elip -28.010000 56.799999 3.890000 3.890000 -0.000000
elip 35.180000 52.660000 3.890000 3.890000 0.000000
elip -35.180000 52.660000 3.890000 3.890000 -0.000000
elip 41.759998 47.610001 3.890000 3.890000 0.000000
elip -41.759998 47.610001 3.890000 3.890000 -0.000000
elip 47.610001 41.759998 3.890000 3.890000 0.000000
elip -47.610001 41.759998 3.890000 3.890000 -0.000000
elip 52.660000 35.180000 3.890000 3.890000 0.000000
elip -52.660000 35.180000 3.890000 3.890000 -0.000000
elip 56.799999 28.010000 3.890000 3.890000 0.000000
elip -56.799999 28.010000 3.890000 3.890000 -0.000000
elip 59.970001 20.360000 3.890000 3.890000 0.000000
elip -59.970001 20.360000 3.890000 3.890000 -0.000000
elip 62.110000 12.360000 3.890000 3.890000 0.000000
elip -62.110000 12.360000 3.890000 3.890000 -0.000000
elip 63.189999 4.140000 3.890000 3.890000 0.000000
elip -63.189999 4.140000 3.890000 3.890000 -0.000000
elip 63.189999 -4.140000 3.890000 3.890000 0.000000
elip -63.189999 -4.140000 3.890000 3.890000 -0.000000
elip 62.110001 -12.360000 3.890000 3.890000 0.000000
elip -62.110001 -12.360000 3.890000 3.890000 -0.000000
elip 59.970001 -20.360001 3.890000 3.890000 0.000000
elip -59.970001 -20.360001 3.890000 3.890000 -0.000000
elip 56.799999 -28.010000 3.890000 3.890000 0.000000
elip -56.799999 -28.010000 3.890000 3.890000 -0.000000
elip 52.660000 -35.180000 3.890000 3.890000 0.000000
elip -52.660000 -35.180000 3.890000 3.890000 -0.000000
elip 47.610001 -41.759998 3.890000 3.890000 0.000000
elip -47.610001 -41.759998 3.890000 3.890000 -0.000000
elip 41.759998 -47.610001 3.890000 3.890000 0.000000
elip -41.759998 -47.610001 3.890000 3.890000 -0.000000
elip 35.180000 -52.660000 3.890000 3.890000 0.000000
elip -35.180000 -52.660000 3.890000 3.890000 -0.000000
elip 28.010000 -56.799999 3.890000 3.890000 0.000000
elip -28.010000 -56.799999 3.890000 3.890000 -0.000000
elip 20.360001 -59.970001 3.890000 3.890000 0.000000
elip -20.360001 -59.970001 3.890000 3.890000 -0.000000
elip 12.360000 -62.110001 3.890000 3.890000 0.000000
Since this input file contains the SNARK14 EVALUATE command, several quantitative measures of agreement between the phantom and the reconstructions are written to the eval file (Section 5.11). At the end of the SNARK14 run SNARK experimenter accesses the eval file and uses the various quantitative measures stored there to compute the FOMs discussed in Sections 8.2.6.1-8.2.6.7. These FOMs are then stored in a text file whose name is of the form fomfil.exp where exp is the experiment number (Section 8.2.3). This file is then used in the calculation of statistical significance.

8.2.6.1 STRU

If STRU is specified the FOM structural accuracy $[41]$ is calculated. This FOM is computed as follows.

Consider a phantom that contains a total of $N$ structures. (Recall from Section 8.2.2 that the SINGLE command generates one structure for each elemental object and the PAIR command generates two structures for each elemental object.) For a reconstruction at iteration $q$, let $A_k^{(q)}$ be the average pixel value for those pixels whose centers are within structure $k$. Let $A_k^{(0)}$ be the average pixel value of the corresponding structure in the phantom.

We define the structural accuracy of a reconstruction at iteration $q$ as

$$-\frac{1}{N} \sum_{k=1}^{N} |A_k^{(q)} - A_k^{(0)}|.$$  

8.2.6.2 POIN

If POIN is specified the FOM pointwise accuracy $[41]$ is calculated. The pointwise accuracy is defined as the negative of the normalized root mean square distance, $\delta^q$ (defined in Section 5.11) between a reconstruction and the phantom. It is sometimes desirable to compute the pointwise accuracy when both the phantom and the reconstruction are clipped to a specified density (for CT) or activity (for PET) range. If such clipping is desired then the COMPARE command line should be preceded by a command line of the form

> MODE lowden highden

When this command is present, both the phantom and the reconstruction are clipped to a density (for CT) or activity (for PET) range specified by the lowden and highden values of the MODE command (see Section 5.2 for a description of the MODE command).

Notes:

- The clipping caused by the MODE command (if it is present) only affects the calculation of pointwise accuracy. The other figures of merit are not affected.

- If no clipping is desired in the calculation of pointwise accuracy then the MODE command is absent.

- If POIN is specified in more than one COMPARE command line and the MODE command appears at least once, then the clip values set by the most recent preceding MODE command are used in the calculation of the pointwise accuracy.
8.2.6.3 HITR

If HITR is specified the FOM hit-ratio [41] is computed. This FOM is calculated only for those phantoms containing structures generated by the PAIR command. (Note: such paired structures must have unequal densities as noted in Section 8.2.2.) These structures form symmetric pairs in a phantom. For such pairs a hit occurs if the structure in the pair with the higher average density in the phantom is also the structure in the pair with the higher average density in the reconstruction. The hit-ratio for a reconstruction is the number of hits divided by the total number of pairs.

8.2.6.4 IROI

If IROI is specified, the FOM imagewise-region-of-interest [59] is computed. This FOM is calculated only for phantoms that contain structures generated by the PAIR command. Such paired structures must have unequal densities with one of the structures having non-zero density (we refer to it as the tumor) and the other having density zero. (Warning: As usual, in case of a polychromatic spectrum, density here refers to the value of den(1).) The pairs of structures are numbered from 1 to B. For 1 ≤ b ≤ B, let \( \alpha^r_t(b) \) (respectively, \( \alpha^r_n(b) \)) denote the average density in the phantom of the structure of the \( b \)th pair that is (respectively, is not) the tumor. We specify similarly \( \alpha^r_t(b) \) (respectively, \( \alpha^r_n(b) \)) for the reconstruction. The IROI figure of merit is defined by

\[
IROI = \frac{\sum_{b=1}^{B} (\alpha^r_t(b) - \alpha^r_n(b))}{\sqrt{\sum_{b=1}^{B} \left( \alpha^r_n(b) - \frac{1}{B} \sum_{b'=1}^{B} \alpha^r_n(b') \right)^2}} / \frac{\sum_{b=1}^{B} (\alpha^p_t(b) - \alpha^p_n(b))}{\sqrt{\sum_{b'=1}^{B} \left( \alpha^p_n(b') - \frac{1}{B} \sum_{b'=1}^{B} \alpha^p_n(b') \right)^2}}
\]

If the reconstruction is perfect (in the sense of being identical to the phantom), then IROI=1.

8.2.6.5 KLDS

If KLDS is specified, then the Kullback-Leibler distance KL, which has been previously specified in Section 5.9 (5.17), is computed as the FOM.

8.2.6.6 WSQD

If WSQD is specified, then the weighted squared distance WS, which has been previously specified in Section 5.9 (5.18), is computed as the FOM.

8.2.6.7 USR1, USR2, USR3, USR4, USR5

If one of the five FOMs, USR1, USR2, USR3, USR4 or USR5, is specified, then a user-defined FOM is computed. To calculate this FOM, SNARK experimenter provides the user with the C subroutine, for example user_fom1, which exchanges information with the calling program via the parameters in the parameter list of the subroutine. The subroutine contains the following statements and may be modified as indicated below. (An example illustrating the use of a user-defined FOM is given in Appendix A, Section A.9.)
first algorithm.
itr2 - array of length niters containing the iteration numbers for the
second algorithm.
niters - number of iterations to be compared
keywrd1 - string containing the keyword that defines the first algorithm.
keywrd2 - string containing the keyword that defines the second algorithm.
OUTPUTS:
user1 - array of length niters containing the user defined figure of
merit for the first algorithm.
user2 - array of length niters containing the user defined figure of
merit for the second algorithm.
*/
void user_fom1(int* itr1, int* itr2, int niters,
    char* keywrd1, char* keywrd2,
    double* user1, double* user2)
{
    double *phantom,*recon1,*recon2;
    int *regions,numstr,i,j,*strarea;
    float totarea=0.0,avgarea;

    /* Read in abnormality index and area for phantom structures.
    The program that does this is read_eval_phantom1.c.
    NOTE: the only information to be used is the value
    numstr (which is the number of structures in the phantom) */
    read_eval_phantom1(&regions,&numstr,&phantom,&strarea);

    /* allocate memory to store abnormality indexes and area
(i.e number of pixels) for structures in the
reconstructions */
    recon1 = (double *) malloc(numstr*sizeof(double));
    recon2 = (double *) malloc(numstr*sizeof(double));

    for(i=0;i < niters;i++) {
        /* read in variance for structures in
the reconstructions. Initialize the arrays
that will store the user FOM */

        read_eval_recon3(itr1[i],keywrd1,numstr,recon1);
        read_eval_recon3(itr2[i],keywrd2,numstr,recon2);
        /* the variance of the SINGLE structure to be
used is the first in the array. The FOM value
is 1-variance */
        user1[i]=1-recon1[0];
        user2[i]=1-recon2[0];
    }

    free(phantom); /* free memory for next function call */
    free(recon1);
    free(recon2);
    free(strarea);
}
8.3 Running in DEBUG mode

It is often useful to be able to look at individual runs of SNARK14 that are part of an experiment. SNARK experimenter saves the SNARK14 input and output files from the very last run in files snark_e.in and snark_e.out respectively. If this is not enough, and the record of input and output files from all the runs is desired, the user can run SNARK experimenter in the DEBUG mode. In order to do this, the environment variable SNARK_EXP should be set to DEBUG, before SNARK experimenter is run. To do so, type on the Linux/Unix command line:

```
export SNARK_EXP=DEBUG
```

(Note, there should be no spaces around equal sign.) and then run SNARK experimenter as usual.

The input files will be saved with names snark_e1.in ... snark_eN.in, the corresponding output files will be saved with names snark_e1.out ... snark_eN.out, and recfil files from each run will be saved with names recfil1 ... recfilN.

*Warning:* The recfil files may be very large and consume a lot of space on your system.

To disable this mode, type on the Linux/Unix command line:

```
export SNARK_EXP=
```

(nothing follows the equal sign).

8.4 Statistical significance level at which the null hypothesis can be rejected

In Section 8.1 the final step in the four-step evaluation procedure is the calculation of statistical significance. The FOMs defined in Section 8.2.6 indicate how good a particular reconstruction is for a given task. An algorithm with a higher average FOM is judged to be more appropriate for the given task than the one with a lower average FOM [43]. If we find, based on this FOM, that one method is more appropriate than another for the task at hand, we still need to determine if our finding is statistically significant. To determine this, we assign a level of statistical significance to rejecting the null-hypothesis that two reconstruction methods are equally good (from the point of view of the FOM), in favor of the hypothesis that the one with the higher average FOM is better, as follows [9, 15].

Let \( \psi_m(q) \) and \( \phi_m(r) \) be the FOMs of the reconstructions from the mth of altogether M data sets at iterations q and r, as reconstructed by the two methods, respectively. Then, according to the null-hypothesis, \( \psi_m(q) - \phi_m(r) \) is a sample of a zero-mean random variable. It follows, for large enough M (\( M \geq 30 \)), that

\[
\sum_{m=1}^{M} (\psi_m(q) - \phi_m(r))
\]

is a sample from a normally distributed random variable with zero mean and variance [41]

\[
\sum_{m=1}^{M} (\psi_m(q) - \phi_m(r))^2.
\]

We can thus use the normal distribution to calculate significance [58].

Listed below is the output file generated by SNARK experimenter that contains the computed significance levels based on the analysis file listed in Section 8.2.6.
Appendix A

EXAMPLES

A.1 Daisy pattern

In this example a test phantom consisting of ellipses, segments and a triangle is generated. Divergent projection data are simulated for 60 projections and the data are reconstructed using DCONV. In addition to the analysis output file both punch and recfil files are produced. From the recfil, images of phantom and reconstruction are produced by the display program snark14Display (see Figure A.1). It is also possible to produce these images from the file punch.

Figure A.1: Half-tone displays from Example A.1.

A.1.1 SNARK14 INPUT file

* EXAMPLE 1
* DAISY PATTERN
* CREATION OF PHANTOM AND DIVERGENT PROJECTION DATA
* RECONSTRUCTION WITH DCON
* ANALYSIS
CREATE
EXAMPLE 1 DAISY
SPECTRUM MONOCHROMATIC 75
OBJECTS
TRIA 1.9 -3.7 0.5 4.1 20.0 2.5
SEGM 4.0 0.1 2.9 4.3 47.0 2.2
SEGM -2.1 -2.1 3.1 3.0 -15.0 2.2
ELIP 0.0 2.5 1.0 1.0 0.0 1.5
A.1.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<<> EXAMPLE 1
<<> DAISY PATTERN
<<> CREATION OF PHANTOM AND DIVERGENT PROJECTION DATA
<<> RECONSTRUCTION WITH DCON
<<> ANALYSIS
<<> CREATE
EXAMPLE 1 DAISY

<&#> SPECTRUM MONOCHROMATIC 75
energy spectrum is monochromatic at energy level 75

<&#> OBJECTS
description of objects

density at levels

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<th>y-coord</th>
<th>x-length</th>
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<th>angle</th>
<th>av dens</th>
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<td>-3.7000</td>
<td>0.5000</td>
<td>4.1000</td>
<td>20.000</td>
<td>2.5000</td>
<td>2.5000</td>
</tr>
<tr>
<td>2</td>
<td>segm</td>
<td>4.0000</td>
<td>0.1000</td>
<td>2.9000</td>
<td>4.3000</td>
<td>47.000</td>
<td>2.2000</td>
<td>2.2000</td>
</tr>
<tr>
<td>4</td>
<td>elip</td>
<td>0.0000</td>
<td>2.5000</td>
<td>1.0000</td>
<td>1.0000</td>
<td>0.0000</td>
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<td>1.5000</td>
</tr>
<tr>
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<td>1.2000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
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<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>7</td>
<td>elip</td>
<td>-1.0000</td>
<td>1.5000</td>
<td>1.3000</td>
<td>1.1000</td>
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<td>1.0000</td>
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scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<&#> PHANTOM AVERAGE 3

this run will generate a phantom
density in each pixel is obtained as the average of 3 x 3 points

<&#> 31 0.4
picture size 31 x 31, pixel size 0.4000

<&#> RAYSUM AVERAGE 1
this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<&#> GEOMETRY
APPENDIX A. EXAMPLES

<<#> DIVERGENT ARC 20.0 10000.0
rays are divergent from point sources
source to origin distance 20.0000
the detectors lie on an arc with source to detector distance = 10000.0000

<<#> RAYS USER 65 150.0
number of rays per projection 65
at detector spacing 150.0000

<<#> ANGLES 60 EQUALLY SPACED
total number of projections 60

<<#> MEASUREMENT PERFECT
projection data are noiseless

<<#> BACKGROUND 0.0
at levels 75
background absorption 0.0000

<<#> RUN
0.001 seconds phantom creation
0.004 seconds projection data creation
0.005 seconds used for processing command crea

<<>
<<#> PICTURE TEST
EXAMPLE 1 DAISY

<<#> spec mono 75
energy spectrum is monochromatic at energy level 75

<<#> obje
description of objects
density at levels
APPENDIX A. EXAMPLES

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
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<th>av dens</th>
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<td>1.2000</td>
<td>1.2000</td>
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</tbody>
</table>

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> phan aver 3

density in each pixel is obtained as the average of 3 x 3 points

<#> pixe 31 size 0.4000
picture size 31 x 31, pixel size 0.4000

test picture read
EXAMPLE 1 DAISY
0.001 seconds used for processing command pict

<#> PROJECTION REAL

EXAMPLE 1 DAISY

<#> spec mono 75
energy spectrum is monochromatic at energy level 75

<#> obje
description of objects

density at levels
numb type x-coord y-coord x-length y-length angle av dens 75
APPENDIX A. EXAMPLES

1 tria  1.9000 -3.7000  0.5000  4.1000  20.0000  2.5000  2.5000
2 segm  4.0000  0.1000  2.9000  4.3000  47.0000  2.2000  2.2000
4 elip  0.0000  2.5000  1.0000  1.0000  0.0000  1.5000  1.5000
5 elip  0.1000  4.3000  1.3000  1.2000  0.0000  1.0000  1.0000
6 elip -2.0000  3.5000  1.3000  1.3000  0.0000  1.0000  1.0000
7 elip -1.0000  1.5000  1.3000  1.1000  0.0000  1.0000  1.0000
8 elip  1.5000  1.6000  1.5000  1.3000  0.0000  1.0000  1.0000
9 elip  1.8000  3.3000  1.2000  1.2000  0.0000  1.0000  1.0000

scale factor multiplying object densities  1.0000
seed set to 0
inhomogeneity set to 0.0000

<#> rays aver 1
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights  1

<#> geom

<#> dive arc source at 20.0000 det dist10000.0000
rays are divergent from point sources
source to origin distance  20.0000
the detectors lie on an arc with source to detector distance = 10000.0000

<#> rays user 65 spacing 150.0000
number of rays per projection  65
snark computed number of rays  63
at detector spacing  150.0000

<#> angl 60
total number of projections  60

projection angles  0.0000  5.9746  11.9492  17.9237  23.8983  29.8729  35.8475
  59.7458  65.7203  71.6949  77.6695  83.6441  89.6186  95.5932 101.5678
 107.5424 113.5169 119.4915 125.4661 131.4407 137.4153 143.3898 149.3644
 155.3390 161.3136 167.2881 173.2627 179.2373 185.2119 191.1864 197.1610
 203.1356 209.1102 215.0847 221.0593 227.0339 233.0085 238.9831 244.9576
 250.9322 256.9068 262.8814 268.8559 274.8305 280.8051 286.7797 292.7542
APPENDIX A. EXAMPLES

<#> meas  perf
projection data are noiseless

<#> back 0.0000
at levels
75
background absorption 0.0000

estimate of totlen = 31273.639204
estimate of totden = 11129.885164
estimate of average density = 0.3559
projection data read
EXAMPLE 1 DAISY
0.003 seconds used for processing command proj

<*> EXECUTE DCON

EXAMPLE 1 DIVERGENT CONVOLUTION FROM 60 VIEWS

<#> -1 1 -1 0.5 0
  cubic spline interpolation
  one out of every 1 projection(s) used for reconstruction
  64 points used on each side of convolution
  pre-smoothing weight on center ray = 0.5000
  pre-smoothing weight on side rays = 0.2500
  accurate back-projection

<#> BANDLIMITING
  band-limiting filter
  total time for obtaining smoothed projection data was 0.000
  total time for convoluting projection data was 0.000
  total time for back-projecting was 0.005
  algorithm executed in iteration 1
  0.006 seconds for the execution of the algorithm
  reconstruction completed after iteration 1
  0.006 seconds for this iteration
  0.010 seconds used for processing command exec

<*> LINES SCALE 100.0 COLUMN 16

last iteration

lines display of reconstruction using DCON iter 1
phantom name: EXAMPLE 1 DAISY
projection data: EXAMPLE 1 DAISY
execution name: EXAMPLE 1 DIVERGENT CONVOLUTION FROM 60 VIEWS
scaling factor = 100.00000

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<tr>
<td>18</td>
<td>0.00000</td>
</tr>
<tr>
<td>19</td>
<td>0.00000</td>
</tr>
<tr>
<td>20</td>
<td>0.00000</td>
</tr>
<tr>
<td>21</td>
<td>0.00000</td>
</tr>
<tr>
<td>22</td>
<td>122.22222</td>
</tr>
<tr>
<td>23</td>
<td>97.77778</td>
</tr>
<tr>
<td>24</td>
<td>0.00000</td>
</tr>
<tr>
<td>25</td>
<td>0.00000</td>
</tr>
<tr>
<td>26</td>
<td>0.00000</td>
</tr>
<tr>
<td>27</td>
<td>0.00000</td>
</tr>
<tr>
<td>28</td>
<td>0.00000</td>
</tr>
<tr>
<td>29</td>
<td>0.00000</td>
</tr>
<tr>
<td>30</td>
<td>0.00000</td>
</tr>
</tbody>
</table>

0.001 seconds used for processing command line

<*> PUNCH PHANTOM

last iteration

reconstruction of EXAMPLE 1 DIVERGENT CONVOLUTION using DCON iter 1, EXAMPLE 1 DAISY
0.002 seconds used for processing command punc
A.2 Simple pattern and user subroutines

In this example we illustrate user written subroutines and multiple executions in the same run. A user written function \texttt{tset} is provided for an ART reconstruction with variable tolerance. A user written algorithm \texttt{alp1} is also provided. This algorithm incorporates an extrapolation feature into an ART-type reconstruction procedure. Parallel projection data are simulated for 30 projections and the data are reconstructed by both algorithms mentioned above. Analysis output is produced using EVALUATE and LINES.

A.2.1 User written \texttt{tset}

```c
#include <stdio.h>
#include "blkdta.h"
#include "uiod.h"
#include "art.h"

REAL art_class::tset(REAL* recon, INTEGER iter, INTEGER np, INTEGER nr,INTEGER i, REAL raysum, INTEGER* list, REAL* weight, BOOLEAN* flag)
{
    REAL tmp = raysum / ((REAL)(10 * iter));
    *flag = FALSE;
    if(trace >= 1) {
        fprintf(output, "\n TOLERANCE IS %19.10f \n", tmp);
    }
    return tmp;
}
```

A.2.2 User written \texttt{alp1}

```c
#include <stdio.h>
#include "blkdta.h"
#include "uiod.h"
#include "art.h"

REAL art_class::tset(REAL* recon, INTEGER iter, INTEGER np, INTEGER nr,INTEGER i, REAL raysum, INTEGER* list, REAL* weight, BOOLEAN* flag)
{
    REAL tmp = raysum / ((REAL)(10 * iter));
    *flag = FALSE;
    if(trace >= 1) {
        fprintf(output, "\n TOLERANCE IS %19.10f \n", tmp);
    }
    return tmp;
}
```
Figure A.2: Half-tone displays from Example A.2. The phantom is on top, the next three rows show the ART reconstruction at each iteration, and the last five rows show the reconstruction with the user defined algorithm at each iteration.
Example 2 user-written reconstruction function

```
#include <stdio.h>
#include <math.h>

#include "blkdta.h"
#include "pseudo.h"
#include "projfile.h"
#include "uid.h"
#include "consts.h"
#include "alp1.h"

void extrap(REAL* newrec, REAL* oldrec, REAL c, INTEGER area);
void itrun(REAL* recon, REAL* oldrec, REAL* proj, INTEGER* list, REAL* weight);

BOOLEAN alp1_class::Run(REAL* recon, INTEGER* list, REAL* weight, INTEGER iter) {

    static REAL* oldrec;
    static INTEGER curprj;
    static REAL* proj;
    INTEGER i;
    static REAL newdif;
    static REAL olddif;
    static REAL c;

    if(iter == 1) {

        oldrec = new REAL[GeoPar.area];

        proj = new REAL[GeoPar.nrays];

        for(i = 0; i < GeoPar.area; i++) {
            oldrec[i] = 0;
        }

        // The previous art iteration is in OLDREC
        itrun(recon, oldrec, proj, list, weight);

        for(i = 0; i < GeoPar.area; i++) {
            oldrec[i] = recon[i];
        }
    }
}
```
curprj = 1;
return FALSE;
}
else if(iter == 2) {
itrune(recon, oldrec, proj, list, weight);
newdif = 0.0;
curprj = 2;
for(i = 0; i < GeoPar.area; i++) {
    newdif += SQR(recon[i] - oldrec[i]);
    oldrec[i] = recon[i];
}
newdif = (REAL) sqrt(newdif);
return FALSE;
}
else if((iter/2)*2 != iter) {
curprj += 1;
itrune(recon, oldrec, proj, list, weight);
olddif = newdif;
newdif = 0.0;
for(i = 0; i < GeoPar.area; i++) {
    newdif += SQR(recon[i] - oldrec[i]);
}
newdif = (REAL) sqrt(newdif);
if(olddif <= Consts.zero * newdif) {
    fprintf(output, "\nCONVERGENCE DIFFERENCES %20.12e, %20.12e", olddif, newdif);
    return FALSE;
} 
c = newdif/olddif;
fprintf(output, "\n EXTRAPOLATION PARAMETER IN EXTRAP IS %20.12e", c);
return FALSE;
}
extrap(recon, oldrec, c, GeoPar.area);
return FALSE;

// NEWREC will contain extrapolated values
// OLDREC will contain the old values of NEWREC
void extrap(REAL* newrec, REAL* oldrec, REAL c, INTEGER area)
{
    REAL d, save;
    INTEGER i;

    if(fabs(1.0 - c) > Consts.zero) {
        fprintf(output, "\n EXTRAPOLATION PARAMETER IN EXTRAP IS %20.12e", c);
        d = c / ((REAL) 1.0 - c);
for(i = 0; i < area; i++) {
    save = newrec[i];
    newrec[i] += d * (newrec[i] - oldrec[i]);
    oldrec[i] = save;
} return;

fprintf(output, "\nEXTRAPOLATION PARAMETER IN EXTRAP IS %20.12e", c);

fprintf(output, "\nEXTRAPOLATION PARAMETER TOO CLOSE TO 1");

for(i = 0; i < area; i++) {
    oldrec[i] = newrec[i];
} return;

void itrun(REAL* recon, REAL* oldrec, REAL* proj, INTEGER* list, REAL* weight) {
    INTEGER i, nr, np, numb, j;
    REAL snorm, raysum;

    for(i = 0; i < GeoPar.area; i++) {
        recon[i] = oldrec[i];
    }

    for(np = 0; np < GeoPar.prjnum; np++) {
        ProjFile.ReadProj(np, proj, GeoPar.nrays);
        for(nr = 0; nr < GeoPar.nrays; nr++) {
            raysum = pseudo(recon, np, nr, list, weight, &numb, &snorm, TRUE, FALSE);

            for(i = 0; i < numb; i++) {
                j = list[i];
                recon[j] += (proj[nr]-raysum)* weight[i] * (REAL) 0.025 / snorm;
            }
        }
    }

    return;
}

A.2.3 SNARK14 INPUT file

**** EXAMPLE 2
* Creation of a small test pattern and projection data with execution of
* a user-defined reconstruction algorithm and analysis.
* CREATE
Example 2, A simple test pattern and projection data
SPECTRUM MONOCHROMATIC with energy at 75 KeV
OBJECTS cx cy u v ang den
APPENDIX A. EXAMPLES

ELIP 0.00 0.00 0.90 0.90 0.00 2.50
ELIP 0.00 0.00 0.80 0.60 0.00 -1.25
ELIP 0.00 0.00 0.21 0.25 0.00 0.10
LAST 1.00
PHANTOM AVERAGE 1 point for estimating pixel density
number of elements is 31 Size of a pixel is 0.07
RAYSUM AVERAGE 1 line for estimation of ray sum with weight
   1
GEOMETRY
PARALLEL UNIFORM LINE
RAY S USER-defined 63 rays per projection at spacing 0.05
ANGLES 30 EQUAL SPACING between the first and last angles which are
   0.0 174.0
MEASUREMENT PERFECT
BACKGROUND absorption is 0.0
RUN
* PICTURE TEST
* PROJECT REAL
* MODE LOWER constraint set at 0.0 UPPER constraint set at 2.5
* SELECT USER RAYSEQ
STEP projections by 10 and rays by 1
* STOP TERMINATION VARIANCE at 0.01
* EXECUTE AVERAGE ART SMOOTH
Example 2a underrelaxed art4 with variable tolerance
smoothing threshold is 0.2 Weights are 2.25 1.5 1.0
11111111111111111111111111111111111111111
ART4 RELAXATION CONSTANT = 0.025 TOLERANCE VARIABLE decreasing
CONSTRAINT BOUND CONRELAX CONSTANT = 0.5 NORMLIZE at each iteration
* STOP ITERATIONS = 30
* EXECUTE ALP1
Example 2b underrelaxed art with extrapolation
* * Reset mode to unconstrained
MODE
* EVALUATE RESOLUTION
Example 2a underrelaxed art4
WHOLEPIC
22222222222222222222222222222222222222222
* LINES COLUMNS 15 and 18 are to be printed
1 1 1 1
* END
A.2.4 SNARK14 OUTPUT file

snark14UserDefined.s170710 - A PICTURE RECONSTRUCTION PROGRAM

<<< *** EXAMPLE 2

<<< Creation of a small test pattern and projection data with execution of

<<< a user-defined reconstruction algorithm and analysis.

<<<

<<< CREATE

Example 2, A simple test pattern and projection data

<<< SPECTRUM MONOCHROMATIC with energy at 75 KeV

energy spectrum is monochromatic at energy level 75

<<< OBJECTS cx cy u v ang den
description of objects
density at levels

numb type x-coord y-coord x-length y-length angle av dens 75
1 elip 0.0000 0.0000 0.9000 0.9000 0.0000 2.5000 2.5000
2 elip 0.0000 0.0000 0.8000 0.6000 0.0000 -1.2500 -1.2500
3 elip 0.0000 0.0000 0.2100 0.2500 0.0000 0.1000 0.1000

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<<< PHANTOM AVERAGE 1 point for estimating pixel density

this run will generate a phantom
density in each pixel is obtained as the average of 1 x 1 points

<<< number of elements is 31 Size of a pixel is 0.07
picture size 31 x 31, pixel size 0.0700

<<< RAYSUM AVERAGE 1 line for estimation of ray sum with weight

this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<#> GEOMETRY

<#> PARALLEL UNIFORM LINE
rays are parallel with uniform spacing between rays
data collected along lines

<#> RAYS USER-defined 63 rays per projection at spacing 0.05
number of rays per projection 63
at detector spacing 0.0500

<#> ANGLES 30 EQUAL SPACING between the first and last angles which are
total number of projections 30
projection angles 0.0000 6.0000 12.0000 18.0000 24.0000 30.0000 36.0000
60.0000 66.0000 72.0000 78.0000 84.0000 90.0000 96.0000 102.0000 108.0000
114.0000 120.0000 126.0000 132.0000 138.0000 144.0000 150.0000 156.0000
162.0000 168.0000 174.0000

<#> MEASUREMENT PERFECT
projection data are noiseless

<#> BACKGROUND absorption is 0.0
at levels
background absorption 0.0000

<#> RUN
0.001 seconds phantom creation
0.001 seconds projection data creation
0.002 seconds used for processing command crea

<#>

<#> PICTURE TEST
Example 2, A simple test pattern and projection data

<#> spec mono 75
energy spectrum is monochromatic at energy level 75

<#> obje
description of objects
APPENDIX A. EXAMPLES

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>75</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.9000</td>
<td>0.9000</td>
<td>0.0000</td>
<td>2.5000</td>
<td>2.5000</td>
</tr>
<tr>
<td>2</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.8000</td>
<td>0.6000</td>
<td>0.0000</td>
<td>-1.2500</td>
<td>-1.2500</td>
</tr>
<tr>
<td>3</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.2100</td>
<td>0.2500</td>
<td>0.0000</td>
<td>0.1000</td>
<td>0.1000</td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> phan aver 1

density in each pixel is obtained as the average of 1 x 1 points

<#> pixe 31 size 0.0700
picture size 31 x 31, pixel size 0.0700

test picture read
Example 2, A simple test pattern and projection data
0.000 seconds used for processing command pict

<#> PROJECTION REAL

Example 2, A simple test pattern and projection data

<#> spec mono 75
energy spectrum is monochromatic at energy level 75

<#> obje
description of objects

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>75</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.9000</td>
<td>0.9000</td>
<td>0.0000</td>
<td>2.5000</td>
<td>2.5000</td>
</tr>
<tr>
<td>2</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.8000</td>
<td>0.6000</td>
<td>0.0000</td>
<td>-1.2500</td>
<td>-1.2500</td>
</tr>
<tr>
<td>3</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.2100</td>
<td>0.2500</td>
<td>0.0000</td>
<td>0.1000</td>
<td>0.1000</td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000
APPENDIX A. EXAMPLES

<#> rays aver 1

projection data are calculated by dividing each ray interval into 1 substrips

with aperture (substrip) weights 1

<#> geom

<#> para unif line
rays are parallel with uniform spacing between rays

data collected along lines

<#> rays user 63 spacing 0.0500
number of rays per projection 63
snark computed number of rays 63
at detector spacing 0.0500

<#> angl 30

total number of projections 30

projection angles 0.0000 6.0000 12.0000 18.0000 24.0000 30.0000 36.0000 42.0000 48.0000 54.0000

60.0000 66.0000 72.0000 78.0000 84.0000 90.0000 96.0000 102.0000 108.0000 114.0000

120.0000 126.0000 132.0000 138.0000 144.0000 150.0000 156.0000 162.0000 168.0000 174.0000

<#> meas perf
projection data are noiseless

<#> back 0.0000

at levels 75
background absorption 0.0000

estimate of totlen = 2823.757863
estimate of totden = 2677.896607
estimate of average density = 0.9483
projection data read
Example 2, A simple test pattern and projection data

0.001 seconds used for processing command proj

<#>

<#> MODE LOWER constraint set at 0.0 UPPER constraint set at 2.5
lower constraint set to 0.0000
upper constraint set to 2.5000
0.000 seconds used for processing command mode
SELECT USER RAYSEQ

STEP projections by 10 and rays by 1
  sequential ray selection with ray-step 1 and projection-step 10
  0.000 seconds used for processing command sele

STOP TERMINATION VARIANCE at 0.01
  termination test vari
  epsilon = 0.010000
  0.000 seconds used for processing command stop

EXECUTE AVERAGE ART SMOOTH

Example 2a underrelaxed art4 with variable tolerance

smoothing threshold is 0.2  Weights are 2.25 1.5 1.0
reconstruction is smoothed after

<table>
<thead>
<tr>
<th>iterations</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>11</td>
<td>12</td>
<td>13</td>
<td>14</td>
<td>15</td>
<td>16</td>
<td>17</td>
<td>18</td>
<td>19</td>
<td>20</td>
</tr>
<tr>
<td></td>
<td>21</td>
<td>22</td>
<td>23</td>
<td>24</td>
<td>25</td>
<td>26</td>
<td>27</td>
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<td>29</td>
<td>30</td>
</tr>
<tr>
<td></td>
<td>31</td>
<td>32</td>
<td>33</td>
<td>34</td>
<td>35</td>
<td>36</td>
<td>37</td>
<td>38</td>
<td>39</td>
<td>40</td>
</tr>
<tr>
<td></td>
<td>41</td>
<td>42</td>
<td>43</td>
<td>44</td>
<td>45</td>
<td>46</td>
<td>47</td>
<td>48</td>
<td>49</td>
<td>50</td>
</tr>
</tbody>
</table>

last iteration

threshold = 0.20000  w1 = 2.25000  w2 = 1.50000  w3 = 1.00000

ART4 RELAXATION CONSTANT = 0.025  TOLERANCE VARIABLE decreasing
  art4 method
  relaxation parameter is 0.0250
  tolerance is variable

CONSTRAINT BOUND CONRELAX CONSTANT = 0.5  NOMLIZE at each iteration
  constraint set to boundaries
  relax constraints with cr= 0.5000
  picture is normalized to 0.9483 after each iteration
  1890 rays are used for each iteration
  lower constraint = 0.0000
  upper constraint = 2.5000

algorithm executed in iteration 1
  0.002 seconds for the execution of the algorithm
iteration 1 completed
  0.002 seconds for this iteration
algorithm executed in iteration 2
0.002 seconds for the execution of the algorithm
iteration 2 completed
0.002 seconds for this iteration
algorithm executed in iteration 3
0.002 seconds for the execution of the algorithm
iteration 3 completed
0.002 seconds for this iteration
algorithm executed in iteration 4
0.002 seconds for the execution of the algorithm
iteration 4 completed
0.002 seconds for this iteration
algorithm executed in iteration 5
0.002 seconds for the execution of the algorithm
iteration 5 completed
0.002 seconds for this iteration
algorithm executed in iteration 6
0.002 seconds for the execution of the algorithm
iteration 6 completed
0.002 seconds for this iteration
algorithm executed in iteration 7
0.002 seconds for the execution of the algorithm
iteration 7 completed
0.002 seconds for this iteration
algorithm executed in iteration 8
0.002 seconds for the execution of the algorithm
iteration 8 completed
0.002 seconds for this iteration
algorithm executed in iteration 9
0.002 seconds for the execution of the algorithm
iteration 9 completed
0.002 seconds for this iteration
algorithm executed in iteration 10
0.002 seconds for the execution of the algorithm
iteration 10 completed
0.002 seconds for this iteration
algorithm executed in iteration 11
0.002 seconds for the execution of the algorithm
iteration 11 completed
0.002 seconds for this iteration
algorithm executed in iteration 12
0.002 seconds for the execution of the algorithm
iteration 12 completed
0.002 seconds for this iteration
algorithm executed in iteration 13
0.002 seconds for the execution of the algorithm
iteration 13 completed
0.002 seconds for this iteration
algorithm executed in iteration 14
0.002 seconds for the execution of the algorithm
iteration 14 completed
0.002 seconds for this iteration
algorithm executed in iteration 15
0.002 seconds for the execution of the algorithm
iteration 15 completed
0.002 seconds for this iteration
algorithm executed in iteration 16
0.002 seconds for the execution of the algorithm
iteration 16 completed
0.002 seconds for this iteration
algorithm executed in iteration 17
0.002 seconds for the execution of the algorithm
iteration 17 completed
0.002 seconds for this iteration
algorithm executed in iteration 18
0.002 seconds for the execution of the algorithm
iteration 18 completed
0.002 seconds for this iteration
algorithm executed in iteration 19
0.003 seconds for the execution of the algorithm
iteration 19 completed
0.003 seconds for this iteration
algorithm executed in iteration 20
0.002 seconds for the execution of the algorithm
iteration 20 completed
0.002 seconds for this iteration
algorithm executed in iteration 21
0.002 seconds for the execution of the algorithm
iterative process stops at iteration 21
the change in variance is less than 0.009852 of the variance
reconstruction completed after iteration 21
0.002 seconds for this iteration
0.039 seconds for all iterations
0.041 seconds used for processing command exec

<*> STOP ITERATIONS = 30
30 iterations
0.000 seconds used for processing command stop

<*> EXECUTE ALP1

Example 2b underrelaxed art with extrapolation
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
iteration 1 completed
0.001 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iteration 2 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 5.062718796778e-01
algorithm executed in iteration 3
0.001 seconds for the execution of the algorithm
iteration 3 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 5.062718796778e-01
algorithm executed in iteration 4
0.000 seconds for the execution of the algorithm
iteration 4 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 6.560964044719e-01
algorithm executed in iteration 5
0.001 seconds for the execution of the algorithm
iteration 5 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 6.560964044719e-01
algorithm executed in iteration 6
0.000 seconds for the execution of the algorithm
iteration 6 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 7.480594958675e-01
algorithm executed in iteration 7
0.001 seconds for the execution of the algorithm
iteration 7 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 7.480594958675e-01
algorithm executed in iteration 8
0.000 seconds for the execution of the algorithm
iteration 8 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 7.951514183812e-01
algorithm executed in iteration 9
0.001 seconds for the execution of the algorithm
iteration 9 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 7.951514183812e-01
algorithm executed in iteration 10
0.000 seconds for the execution of the algorithm
iteration 10 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.250655739411e-01
algorithm executed in iteration 11
0.001 seconds for the execution of the algorithm
iteration 11 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.250655739411e-01
algorithm executed in iteration 12
0.000 seconds for the execution of the algorithm
iteration 12 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.467169748437e-01
algorithm executed in iteration 13
0.000 seconds for the execution of the algorithm
iteration 13 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.467169748437e-01
algorithm executed in iteration 14
0.000 seconds for the execution of the algorithm
iteration 14 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.628058734349e-01
algorithm executed in iteration 15
0.000 seconds for the execution of the algorithm
iteration 15 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.628058734349e-01
algorithm executed in iteration 16
0.000 seconds for the execution of the algorithm
iteration 16 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.749346145383e-01
algorithm executed in iteration 17
0.001 seconds for the execution of the algorithm
iteration 17 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.749346145383e-01
algorithm executed in iteration 18
0.000 seconds for the execution of the algorithm
iteration 18 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.843623393369e-01
algorithm executed in iteration 19
0.002 seconds for the execution of the algorithm
iteration 19 completed
0.002 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.843623393369e-01
algorithm executed in iteration 20
0.000 seconds for the execution of the algorithm
iteration 20 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.920147280181e-01
algorithm executed in iteration 21
0.000 seconds for the execution of the algorithm
iteration 21 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.920147280181e-01
algorithm executed in iteration 22
0.000 seconds for the execution of the algorithm
iteration 22 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.985122210336e-01
algorithm executed in iteration 23
0.000 seconds for the execution of the algorithm
iteration 23 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 8.985122210336e-01
algorithm executed in iteration 24
0.000 seconds for the execution of the algorithm
iteration 24 completed
0.000 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 9.042443038619e-01
algorithm executed in iteration 25
0.001 seconds for the execution of the algorithm
iteration 25 completed
0.001 seconds for this iteration
EXTRAPOLATION PARAMETER IN EXTRAP IS 9.042443038619e-01
algorithm executed in iteration 26
0.000 seconds for the execution of the algorithm
iteration 26 completed
0.000 seconds for this iteration
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algorithm executed in iteration 27
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iteration 27 completed
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EXTRAPOLATION PARAMETER IN EXTRAP IS 9.094448804097e-01
algorithm executed in iteration 28
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algorithm executed in iteration 29
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iteration 29 completed
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EXTRAPOLATION PARAMETER IN EXTRAP IS 9.142500229503e-01
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reconstruction completed after iteration 30
0.000 seconds for this iteration
0.014 seconds for all iterations
0.015 seconds used for processing command exec

<<>

<<> Reset mode to unconstrained

<#> MODE
0.000 seconds used for processing command mode

<<>

<#> EVALUATE RESOLUTION

Example 2a underrelaxed art4

<#> WHOLEPIC
Region cx cy u v ang t1 t2

wholepic -1e+20 1e+20

iterations 1 2 3 4 5 6 7 8 9 10
11 12 13 14 15 16 17 18 19 20
residual calculation using line integration

0.061 seconds used for processing command eval

<*>  
<#> LINES COLUMNS 15 and 18 are to be printed

iterations 10 20 30

last iteration

lines display of reconstruction using ART iter 10

phantom name: Example 2, A simple test pattern and projection data
projection data: Example 2, A simple test pattern and projection data
execution name: Example 2a underrelaxed art4 with variable tolerance

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APPENDIX A. EXAMPLES

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10 1.25000  1.42731  0.17731  1.25000  1.34954  0.0954

lines display of reconstruction using ALP1 iter 10

phantom name:   Example 2, A simple test pattern and projection data
projection data: Example 2, A simple test pattern and projection data
execution name: Example 2b underrelaxed art with extrapolation
scaling factor = 1.00000

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 3  2.50000  2.23551 -0.26449  2.50000  2.01480 -0.48520
 4  2.50000  2.39456 -0.10544  2.50000  2.31508 -0.18492
 5  2.50000  2.44644 -0.05356  2.50000  2.45967 -0.04033
 6  2.50000  2.44977 -0.05023  2.50000  2.27692 -0.22308
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 9  0.00000  0.00161  0.00161  0.00000  0.02249  0.02249
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17 1.35000  1.32157 -0.02844  1.25000  1.26567  0.01657
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### APPENDIX A. EXAMPLES

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**lines display of reconstruction using ALP1 iter 20**

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**projection data:** Example 2, A simple test pattern and projection data  
**execution name:** Example 2b underrelaxed art with extrapolation  
**scaling factor =** 1.00000

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APPENDIX A. EXAMPLES

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APPENDIX A. EXAMPLES

A.2.5 SNARK14 eval file

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projection name: Example 2, A simple test pattern and projection data

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execution name: Example 2b underrelaxed art with extrapolation

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APPENDIX A. EXAMPLES

A.3 Realistic x-ray data

In this example we illustrate the capability of SNARK14 to simulate taking of x-ray projection data in a realistic fashion. The test phantom is very similar to the output of an actual CT scan. The data are collected for one projection according to a geometry similar to that of the rotational scanners. The polychromaticity, photon statistics and scatter of x-rays are all simulated, as well as the divergence of the beam between the source and the detector. In addition to the INPUT and OUTPUT files we give a listing of the file11 produced by this run.

A.3.1 SNARK14 INPUT file

```plaintext
* EXAMPLE 3
* CREATION OF HEAD PHANTOM. GENERATION OF POLychromatic
* PROJECTION DATA.
*
* CREATE A PHANTOM
* GENERATE PROJECTION DATA
CREATE
EXAMPLE 3 HEAD PHANTOM
SPECTRUM POLychromatic 5
40 10 50 30 80 20 100 10
OBJECTS
SEGM 1.375 -7.5 1.1 0.625 19.2 0.734
DENS -0.472 -0.288 -0.116 -0.029
SEGM 1.375 -7.5 1.1 4.32 19.2 0.734
DENS 0.472 0.288 0.116 0.029
ELIP 0.0 8.625 6.4687 90.0 1.0
```
A.3.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<*> EXAMPLE 3

<*> CREATION OF HEAD PHANTOM. GENERATION OF POLYCHROMATIC

<*> PROJECTION DATA.

<*> CREATE A PHANTOM

<*> GENERATE PROJECTION DATA
EXAMPLE 3 HEAD PHANTOM

ENERGY SPECTRUM POLYCHROMATIC 5

The energy spectrum is polychromatic with 5 energy levels, with the following photon distribution:

<table>
<thead>
<tr>
<th>Energy Level</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>40</td>
<td>10</td>
</tr>
<tr>
<td>50</td>
<td>30</td>
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<tr>
<td>60</td>
<td>30</td>
</tr>
<tr>
<td>80</td>
<td>20</td>
</tr>
<tr>
<td>100</td>
<td>10</td>
</tr>
</tbody>
</table>

OBJECTS

<table>
<thead>
<tr>
<th>Num</th>
<th>Type</th>
<th>X-Coord</th>
<th>Y-Coord</th>
<th>X-Length</th>
<th>Y-Length</th>
<th>Angle</th>
<th>AV Dens</th>
<th>40</th>
<th>50</th>
<th>60</th>
</tr>
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<tbody>
<tr>
<td>1</td>
<td>segm</td>
<td>1.3750</td>
<td>-7.5000</td>
<td>1.1000</td>
<td>0.6250</td>
<td>19.2000</td>
<td>-0.3275</td>
<td>-0.7340</td>
<td>-0.4720</td>
<td>-0.2880</td>
</tr>
<tr>
<td>2</td>
<td>segm</td>
<td>1.3750</td>
<td>-7.5000</td>
<td>1.1000</td>
<td>4.3200</td>
<td>19.2100</td>
<td>0.3275</td>
<td>0.7340</td>
<td>0.4720</td>
<td>0.2880</td>
</tr>
<tr>
<td>3</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>8.6250</td>
<td>6.4687</td>
<td>90.0000</td>
<td>0.5400</td>
<td>1.0000</td>
<td>0.7000</td>
<td>0.5000</td>
</tr>
<tr>
<td>4</td>
<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>7.8750</td>
<td>5.7187</td>
<td>90.0000</td>
<td>-0.3300</td>
<td>-0.7370</td>
<td>-0.4750</td>
<td>-0.2910</td>
</tr>
<tr>
<td>5</td>
<td>elip</td>
<td>0.0000</td>
<td>1.5000</td>
<td>0.3750</td>
<td>0.3000</td>
<td>90.0000</td>
<td>-0.0029</td>
<td>-0.0030</td>
<td>-0.0060</td>
<td>-0.0020</td>
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<tr>
<td>6</td>
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<td>-2.2500</td>
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<td>-0.0029</td>
<td>-0.0030</td>
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<tr>
<td>7</td>
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<td>3.7500</td>
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<td>0.5000</td>
<td>135.0000</td>
<td>-0.0029</td>
<td>-0.0030</td>
<td>-0.0060</td>
<td>-0.0020</td>
</tr>
<tr>
<td>8</td>
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<td>3.7500</td>
<td>1.0000</td>
<td>0.5000</td>
<td>225.0000</td>
<td>-0.0029</td>
<td>-0.0030</td>
<td>-0.0060</td>
<td>-0.0020</td>
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<tr>
<td>9</td>
<td>elip</td>
<td>0.6750</td>
<td>-0.7500</td>
<td>0.2250</td>
<td>0.1500</td>
<td>140.0000</td>
<td>0.0127</td>
<td>0.0250</td>
<td>0.0160</td>
<td>0.0100</td>
</tr>
<tr>
<td>10</td>
<td>elip</td>
<td>0.7500</td>
<td>1.5000</td>
<td>0.3750</td>
<td>0.2250</td>
<td>50.0000</td>
<td>0.0046</td>
<td>0.0050</td>
<td>0.0040</td>
<td>0.0040</td>
</tr>
<tr>
<td>11</td>
<td>tria</td>
<td>5.0250</td>
<td>3.7500</td>
<td>1.1250</td>
<td>0.5000</td>
<td>110.7500</td>
<td>0.3300</td>
<td>0.7370</td>
<td>0.4750</td>
<td>0.2910</td>
</tr>
</tbody>
</table>
APPENDIX A. EXAMPLES

12 tria -5.0250 3.7500 1.1250 0.5000 -110.7500 0.3300 0.7370 0.4750 0.2910 0.1180 0.0290

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> PHANTOM AVERAGE 1

this run will generate a phantom
density in each pixel is obtained as the average of 1 x 1 points

<#> 23 0.77
picture size 23 x 23, pixel size 0.7700

<#> RAYSUM AVERAGE 3

this run will generate projection data
projection data are calculated by dividing each ray interval into 3 substrips
with aperture (substrip) weights 1 1 1

<#> GEOMETRY

<#> DIVERGENT ARC 78.0 110.0
rays are divergent from point sources
source to origin distance 78.0000
the detectors lie on an arc with source to detector distance = 110.0000

<#> RAYS USER 159 0.213
number of rays per projection 159
at detector spacing 0.2130

<#> ANGLE 1

total number of projections 1

projection angles 0.0000

<#> MEASUREMENT NOISY

noise characteristics of projection data follow
nature characteristics

<#> QUANTUM 10000000.0 360.0 CALIBRATION 2

quantum mean number of photons in actual measurement 1.0000e+07
mean number of photons in calibration measurement is 360.0000
calibration is constant over all projections for any single ray
mean numbers of photons entering each substrip are
3.3333e+06  3.3333e+06  3.3333e+06

<#> SCATTER 0.24 0.4445
scatter the fraction scattered in line is 0.2400
scatter extends to a distance of 0.4445
dying linearly from the middle

<#> SEED 1
seed for random number generator is 1

<#> BACKGROUND 0.0 0.0 0.0 0.0 0.0
at levels

<table>
<thead>
<tr>
<th></th>
<th>40</th>
<th>50</th>
<th>60</th>
<th>80</th>
<th>100</th>
</tr>
</thead>
<tbody>
<tr>
<td>aos</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>aos</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
</tbody>
</table>

<#> RUN
0.001 seconds phantom creation
0.001 seconds projection data creation
0.002 seconds used for processing command crea

<#> END

A.3.3 SNARK14 file11

EXAMPLE 3 HEAD PHANTOM
spec poly 5
segm 1.3750 -7.5000 1.1000 0.6250 19.2000 -0.733999999999999986
dens -0.4720000000 -0.2880000000 -0.1160000000 -0.0290000000
segm 1.3750 -7.5000 1.1000 4.3200 19.2100 0.733999999999999986
dens 0.4720000000 0.2880000000 0.1160000000 0.0290000000
elip 0.0000 0.0000 8.6250 6.4687 90.0000 1.000000000000000000
dens -0.4720000000 -0.2880000000 -0.1160000000 -0.0290000000
elip 0.0000 0.0000 7.8750 5.7187 90.0000 -0.736999999999999988
dens -0.4750000000 -0.2910000000 -0.1180000000 -0.0290000000
elip 0.0000 1.5000 0.3750 0.3000 90.0000 -0.003000000000000000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
segm 0.0000 -2.2500 1.1250 0.3750 0.0000 -0.003000000000000000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
segm -1.0000 3.7500 1.0000 0.5000 135.0000 -0.003000000000000000
dens -0.0060000000 -0.0020000000 -0.0010000000 0.0000000000
segm 1.0000 3.7500 1.0000 0.5000 225.0000 -0.003000000000000000
dens -0.0060000000 -0.0020000000 -0.0010000000 0.0000000000
elip 0.6750 -0.7500 0.2250 0.1500 140.0000 0.025000000000000001
dens 0.0160000000 0.0100000000 0.0080000000 0.0080000000
elip 0.7500 1.5000 0.3750 0.2250 50.0000 0.005000000000000000
dens 0.0040000000 0.0040000000 0.0060000000 0.0050000000
tria 5.0250 3.7500 1.1250 0.5000 110.7500 0.736999999999999988
### APPENDIX A. EXAMPLES

<table>
<thead>
<tr>
<th>pixe</th>
<th>size</th>
<th>phan aver</th>
</tr>
</thead>
<tbody>
<tr>
<td>23</td>
<td>0.7700</td>
<td>1</td>
</tr>
</tbody>
</table>

<table>
<thead>
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<th>tria</th>
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<th>phan aver</th>
</tr>
</thead>
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<tr>
<td>0.47500000000000000000</td>
<td>-5.0250</td>
<td>1.0000</td>
<td>1</td>
</tr>
<tr>
<td>0.29100000000000000000</td>
<td>3.7500</td>
<td>0.0000</td>
<td></td>
</tr>
<tr>
<td>0.11800000000000000000</td>
<td>1.1250</td>
<td>0.0000</td>
<td></td>
</tr>
<tr>
<td>0.01800000000000000000</td>
<td>0.5000</td>
<td>0.0000</td>
<td></td>
</tr>
<tr>
<td>0.01800000000000000000</td>
<td>-10.7500</td>
<td>0.0000</td>
<td></td>
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<tr>
<td>0.02900000000000000000</td>
<td>0.73699999999999999999</td>
<td>0.0000</td>
<td></td>
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</tbody>
</table>

<table>
<thead>
<tr>
<th>dens</th>
<th>tria</th>
<th>last</th>
<th>phan aver</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.47500000000000000000</td>
<td>-5.0250</td>
<td>1.0000</td>
<td>1</td>
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<tr>
<td>0.29100000000000000000</td>
<td>3.7500</td>
<td>0.0000</td>
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<td>0.11800000000000000000</td>
<td>1.1250</td>
<td>0.0000</td>
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<tr>
<td>0.01800000000000000000</td>
<td>0.5000</td>
<td>0.0000</td>
<td></td>
</tr>
<tr>
<td>0.01800000000000000000</td>
<td>-10.7500</td>
<td>0.0000</td>
<td></td>
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<tr>
<td>0.02900000000000000000</td>
<td>0.73699999999999999999</td>
<td>0.0000</td>
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</table>
### EXAMPLE 3 HEAD PHANTOM

<table>
<thead>
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<th>spec</th>
<th>poly</th>
<th>5</th>
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<tbody>
<tr>
<td>40</td>
<td>10</td>
<td>50</td>
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<tr>
<td>obje</td>
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<td></td>
</tr>
<tr>
<td>segm</td>
<td>1.3750 &amp; -7.5000 &amp; 1.1000 &amp; 0.6250 &amp; 19.2000 &amp; -0.7339999999999986</td>
<td></td>
</tr>
<tr>
<td>dens</td>
<td>-0.4720000000 &amp; -0.2880000000 &amp; -0.1160000000 &amp; -0.0290000000</td>
<td></td>
</tr>
<tr>
<td>segm</td>
<td>1.3750 &amp; -7.5000 &amp; 1.1000 &amp; 4.3200 &amp; 19.2100 &amp; 0.7339999999999986</td>
<td></td>
</tr>
<tr>
<td>dens</td>
<td>0.4720000000 &amp; 0.2880000000 &amp; 0.1160000000 &amp; 0.0290000000</td>
<td></td>
</tr>
<tr>
<td>elip</td>
<td>0.0000 &amp; 0.0000 &amp; 8.6250 &amp; 6.4687 &amp; 90.0000 &amp; 1.0000000000000000</td>
<td></td>
</tr>
<tr>
<td>dens</td>
<td>0.7000000000 &amp; 0.5000000000 &amp; 0.3000000000 &amp; 0.2000000000</td>
<td></td>
</tr>
</tbody>
</table>
APPENDIX A. EXAMPLES

elip 0.0000 0.0000 7.8750 5.7187 90.0000 0.0000
dens -0.4750000000 -0.2910000000 -0.1180000000 -0.0290000000
elip 0.0000 1.5000 0.3750 0.3000 90.0000 0.0000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
segm 0.0000 -2.2500 1.1250 0.3750 90.0000 0.0000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
segm -1.0000 3.7500 1.0000 0.5000 135.0000 0.0000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
segm 1.0000 3.7500 1.0000 0.5000 225.0000 0.0000
dens -0.0060000000 -0.0020000000 -0.0010000000 -0.0000000000
elip 0.6750 -0.7500 0.2250 0.1500 140.0000 0.0250000000
dens 0.0160000000 0.0100000000 0.0080000000 0.0080000000
elip 0.7500 1.5000 0.3750 0.2250 50.0000 0.0050000000
dens 0.0040000000 0.0040000000 0.0060000000 0.0000000000
tria 5.0250 3.7500 1.1250 0.5000 110.7500 0.0250000000
dens 0.4750000000 0.2910000000 0.1180000000 0.0290000000
tria -5.0250 3.7500 1.1250 0.5000 -110.7500 0.0250000000
dens 0.4750000000 0.2910000000 0.1180000000 0.0290000000
last 1.0000 0 0.0000
rays aver 3
1 1 1
geom
dive arc source at 78.0000 det dist 110.0000
rays user 159 spacing 0.2130
angl 1
0.0000
meas nois
quan 10000000.0000 360.0000 cali 2
scat noise peak 0.2400000000 width 0.4445000000
seed 1
back 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000
0.00000000000000000000 0.00000000000000000000
-0.00007805279554173564 0.00004650918767980816 -0.00004473035394917833
-0.00075472753879972268 -0.00017424462354294768 -0.00012797762539250472
0.00021021831069931401 -0.00009455298249226776 0.00006385006732581148
-0.00032644267523053823 0.00089929757471288543 0.00012658356922487648
0.00006385006732581148 0.00053314583792116199 0.00009455298249226776
0.00012658356922487648 -0.00009455298249226776 0.00006385006732581148
0.00023324993034164262 0.0002459151306294491 0.00118821246111817777
0.02750129911112374089 0.33870223840002701391 1.08546976203441387777
1.51371216702628408335 1.6682459961816637602 1.80667866090861228834
1.89336338353435951198 1.91448622168842397251 1.9720178537812468441
2.04306084993126656840 2.09313602387015951223 2.13117505887408276166
2.16769439166981170430 2.20662677672364315740 2.2450781574611511630
2.28157818983265059387 2.3197472529811517660 2.35590760276760269321
2.3899565135634164095 2.42336651583670321884 2.457380027873954959
2.48922649053305659697 2.517051153614261958 2.5521443824605815981
2.5791372629166738710 2.6071774658142742349 2.6319287710821254848
2.65866836490095659329 2.68228778490192620865 2.7079317087967602620
2.7311461998925059665 2.7516805213055000456 2.7723847211504674601
2.7920538760598167613 2.81140730588376268095 2.830296211092319708
2.84629883402569872075 2.86183010574974705216 2.87870752255707676096
2.89094037834704886691 2.905699073629108397 2.9173919330117106452
2.92767866353370775911 2.94100719601768556544 2.95520648731837987100
A.4 Star pattern and pseudo projection data

In this example we illustrate the capability of SNARK14 to calculate pseudo projection data. The test phantom consists of six equally spaced sectors resembling a star test pattern. Pseudo data is taken for twelve views and is reconstructed using ART. The reconstruction is contoured, reproducing the test phantom perfectly.
A.4.1  SNARK14 INPUT file

******EXAMPLE 4
* STAR PATTERN WITH PSEUDO PROJECTION DATA
* RECONSTRUCTION BY ART
*
CREATE
EXAMPLE 4 STAR PATTERN
SPECTRUM MONOCHROMATIC 10
OBJECTS
SECT  0.0  -24.0  6.0  24.0  0.0  1.0
SECT  21.0  -12.0  6.0  24.0  60.0  1.0
SECT  21.0   12.0  6.0  24.0 120.0  1.0
SECT   0.0   24.0  6.0  24.0 180.0  1.0
SECT -21.0   12.0  6.0  24.0 240.0  1.0
SECT -21.0  -12.0  6.0  24.0 300.0  1.0
LAST  1.0
PHANTOM AVERAGE 1
25 PIXELS OF SIZE 2.0
RAYSUM
*
PICTURE TEST
*
PROJECTION PSEUDO
EXAMPLE 4 PSEUDO PROJECTION DATA FOR TWELVE VIEWS
GEOMETRY
PARALLEL VARIABLE STRIP
RAYS PROGRAM 25 2.0 DETECTOR SPACING AT 2.0
ANGLES 12 EQUALLY SPACED
0.0 165.0
MEASUREMENT PERFECT
BACKGROUND 50.0
APPENDIX A. EXAMPLES

* MODE LOWER CONSTRAINT IS SET TO 0.0 UPPER CONSTRAINT IS 1.0 *
* SELECT SNARK RAYSEQ STEP 3 1 *
* STOP ITERATION 9 *
* EXECUTE ART CONTOUR EXAMPLE 4 ART RECONSTRUCTION 0.5 0.0 1.0 1 ART3 CONSTRAINT BOUND STEPS 204 *
END

A.4.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<*> *******EXAMPLE 4
<*> STAR PATTERN WITH PSEUDO PROJECTION DATA
<*> RECONSTRUCTION BY ART
<*>
<#> CREATE

EXAMPLE 4 STAR PATTERN

<#> SPECTRUM MONOCHROMATIC 10
energy spectrum is monochromatic at energy level 10

<#> OBJECTS
description of objects
density at levels

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>sect</td>
<td>0.0000</td>
<td>-24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>2</td>
<td>sect</td>
<td>21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>60.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>3</td>
<td>sect</td>
<td>21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>120.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>4</td>
<td>sect</td>
<td>0.0000</td>
<td>24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>180.0000</td>
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<tr>
<td>5</td>
<td>sect</td>
<td>-21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>240.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>
APPENDIX A. EXAMPLES

6 sect -21.0000 -12.0000 6.0000 24.0000 300.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<## PHANTOM AVERAGE 1

this run will generate a phantom
density in each pixel is obtained as the average of 1 x 1 points

<## 25 PIXELS OF SIZE 2.0
picture size 25 x 25, pixel size 2.0000

<## RAYSUM

0.001 seconds phantom creation
0.001 seconds used for processing command crea

<**>

<## PICTURE TEST

EXAMPLE 4 STAR PATTERN

<## spec mono 10
energy spectrum is monochromatic at energy level 10

<## obje
description of objects
density at levels

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>10</th>
</tr>
</thead>
<tbody>
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<td>-24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
<tr>
<td>2 sect</td>
<td>21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>60.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
<tr>
<td>3 sect</td>
<td>21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>120.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
<tr>
<td>4 sect</td>
<td>0.0000</td>
<td>24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>180.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
<tr>
<td>5 sect</td>
<td>-21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>240.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
<tr>
<td>6 sect</td>
<td>-21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>300.0000</td>
<td>1.0000</td>
<td>1.0000</td>
<td></td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000
APPENDIX A. EXAMPLES

seed set to 0
inhomogeneity set to 0.0000

<#> phan aver 1
density in each pixel is obtained as the average of 1 x 1 points

<#> pixe 25 size 2.0000
picture size 25 x 25, pixel size 2.0000
test picture read
EXAMPLE 4 STAR PATTERN
0.000 seconds used for processing command pict

<>>

<#> PROJECTION PSEUDO
EXAMPLE 4 PSEUDO PROJECTION DATA FOR TWELVE VIEWS

<#> GEOMETRY

<#> PARALLEL VARIABLE STRIP
rays are parallel with variable spacing between rays
data collected along strips

<#> RAYS PROGRAM 25 2.0 DETECTOR SPACING AT 2.0
number of rays per projection 53
snark computed number of rays 53
at detector spacing 2.0000

<#> ANGLES 12 EQUALLY SPACED
total number of projections 12
projection angles 0.0000 15.0000 30.0000 45.0000 60.0000 75.0000 90.0000 105.0000 120.0000 135.0000 150.0000 165.0000

<#> MEASUREMENT PERFECT
projection data are noiseless

<#> BACKGROUND 50.0
at levels
10
background absorption 50.0000
APPENDIX A. EXAMPLES

estimate of totlen = 16985.417500
estimate of totden = 6066.137812
estimate of average density = 0.3571
projection data read
EXAMPLE 4 PSEUDO PROJECTION DATA FOR TWELVE VIEWS
           0.001 seconds used for processing command proj

<<>

<<# MODE LOWER CONSTRAINT IS SET TO 0.0 UPPER CONSTRAINT IS 1.0
lower constraint set to 0.0000
upper constraint set to 1.0000
       0.000 seconds used for processing command mode

<<>

<<# SELECT SNARK RAYSEQ

<<# STEP 3 1
sequential ray selection with ray-step 1 and projection-step 3
       0.000 seconds used for processing command sele

<<>

<<# STOP ITERATION 9
9 iterations
       0.000 seconds used for processing command stop

<<>

<<# EXECUTE ART CONTOUR
EXAMPLE 4 ART RECONSTRUCTION

<<# 0.5 0.0 1.0
reconstruction is contoured after last iteration
threshold = 0.50000   w1 = 0.00000   w2 = 1.00000   w3 = 0.00000

<<# ART3
art3 method
relaxation parameter is 1.0
norm is 2
tolerance is 0.0

<<# CONSTRAINT BOUND STEPS 204
constraint set to boundaries
picture is not normalized
204 rays are used for each iteration
lower constraint = 0.0000
upper constraint = 1.0000
algorithm executed in iteration 1
0.000 seconds for the execution of the algorithm
iteration 1 completed
0.000 seconds for this iteration
algorithm executed in iteration 2
0.000 seconds for the execution of the algorithm
iteration 2 completed
0.000 seconds for this iteration
algorithm executed in iteration 3
0.000 seconds for the execution of the algorithm
iteration 3 completed
0.000 seconds for this iteration
algorithm executed in iteration 4
0.000 seconds for the execution of the algorithm
iteration 4 completed
0.000 seconds for this iteration
algorithm executed in iteration 5
0.000 seconds for the execution of the algorithm
iteration 5 completed
0.000 seconds for this iteration
algorithm executed in iteration 6
0.000 seconds for the execution of the algorithm
iteration 6 completed
0.000 seconds for this iteration
algorithm executed in iteration 7
0.000 seconds for the execution of the algorithm
iteration 7 completed
0.000 seconds for this iteration
algorithm executed in iteration 8
0.000 seconds for the execution of the algorithm
iteration 8 completed
0.000 seconds for this iteration
algorithm executed in iteration 9
0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 9
0.000 seconds for this iteration
0.001 seconds for all iterations
0.002 seconds used for processing command exec

A.5 Star pattern with parallel projections

In this example we illustrate various algorithms that are appropriate for parallel projection data. The test phantom is the same as the one described in Section A.4. Parallel strip data is taken for 24 parallel strip projections between $0^\circ$ and $172.5^\circ$. Reconstructions are done using BACKPROJECTION, CONVOLUTION,
RFL, FOURIER, ART, MART, QUADRATIC, and SIRT. In each case the parameters have been set either at their default values or at simple values that are not likely to be optimal for the projection data in question. EVALUATE is used in the analysis phase.

![Half-tone displays from Example A.5. The phantom and the final reconstruction with each method is shown.](image)

**A.5.1 SNARK14 INPUT file**

```plaintext
*EXAMPLE 5
*STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS
*RECONSTRUCTION BY ALL APPROPRIATE ALGORITHMS WITH DEFAULT
*OR EASY OPTIONS.
*
CREATE
EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS
SPECTRUM MONOCHROMATIC 10
OBJECTS
SECT 0.0 -24.0 6.0 24.0 0.0 1.0
SECT 21.0 -12.0 6.0 24.0 60.0 1.0
SECT 21.0 12.0 6.0 24.0 120.0 1.0
SECT 0.0 24.0 6.0 24.0 180.0 1.0
SECT -21.0 12.0 6.0 24.0 240.0 1.0
SECT -21.0 -12.0 6.0 24.0 300.0 1.0
LAST 1.0
PHANTOM AVERAGE 5
25 PIXELS OF SIZE 2.0
RAYSUM AVERAGE 1
1
GEOMETRY
PARALLEL UNIFORM STRIP
RAYS USER 25 DETECTOR SPACING 2.0
ANGLES 24 EQUAL SPACING
0.0 172.5
MEASUREMENT PERFECT
BACKGROUND 0.0
RUN
```
APPENDIX A. EXAMPLES

* PICTURE TEST
* PROJECTION REAL
* EXECUTE BACKPROJECTION
EXAMPLE 5A CONTINUOUS BACKPROJECTION WITH LINEAR INTERPOLATION
CONTINUOUS 2 MULTIPLICATIVE
* EXECUTE CONVOLUTION
EXAMPLE 5B CONVOLUTION WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
BANDLIMITING 1.0 2
* EXECUTE RFL
EXAMPLE 5C RHO FILTERED LAYERGRAM WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
BANDLIMITING 1.0 2
* EXECUTE FOURIER
EXAMPLE 5D FOURIER WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
BANDLIMITING 1.0 3
* STOP TERMINATION VARIANCE = 0.1
* EXECUTE ART
EXAMPLE 5F ART WITH NO TRICKS
ART3
CONSTRAINT ART2 STEPS 888
* EXECUTE MART
EXAMPLE 5G MULTIPLICATIVE ART A LA LENT
METHOD LENT 888 1.0 0.0
* EXECUTE QUADRATIC
EXAMPLE 5H OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE
3 3 1 0 1 0.1 0.0 0.0
1 1 1 0 0 0 1.0 0.1 0
* EXECUTE SIRT
EXAMPLE 5I GENERALIZED SIMULTANEOUS ITERATIVE RECONSTRUCTION TECHNOLOGY
METHOD GSIRT
* EVALUATE
EXAMPLE 5 RECONSTRUCTION OF STAR PATTERN FROM PARALLEL PROJECTIONS
WHOLEPIC
11111111111
* END

A.5.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM
EXAMPLE 5

STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

RECONSTRUCTION BY ALL APPROPRIATE ALGORITHMS WITH DEFAULT OR EASY OPTIONS.

CREATE

EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

SPECTRUM MONOCHROMATIC 10
energy spectrum is monochromatic at energy level 10

OBJECTS
description of objects
density at levels
type x-coord y-coord x-length y-length angle av dens 10
1 sect 0.0000 -24.0000 6.0000 24.0000 0.0000 1.0000 1.0000
2 sect 21.0000 -12.0000 6.0000 24.0000 60.0000 1.0000 1.0000
3 sect 21.0000 12.0000 6.0000 24.0000 120.0000 1.0000 1.0000
4 sect 0.0000 24.0000 6.0000 24.0000 180.0000 1.0000 1.0000
5 sect -21.0000 12.0000 6.0000 24.0000 240.0000 1.0000 1.0000
6 sect -21.0000 -12.0000 6.0000 24.0000 300.0000 1.0000 1.0000
scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

PHANTOM AVERAGE 5
this run will generate a phantom
density in each pixel is obtained as the average of 5 x 5 points

25 PIXELS OF SIZE 2.0
picture size 25 x 25, pixel size 2.0000

RAYSUM AVERAGE 1
this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips with aperture (substrip) weights 1

<##> GEOMETRY

<##> PARALLEL UNIFORM STRIP
rays are parallel with uniform spacing between rays
data collected along strips

<##> RAYS USER 25 DETECTOR SPACING 2.0
number of rays per projection 25
at detector spacing 2.0000

<##> ANGLES 24 EQUAL SPACING
total number of projections 24
projection angles 0.0000 7.5000 15.0000 22.5000 30.0000 37.5000 45.0000 52.5000 60.0000 67.5000 75.0000 82.5000 90.0000 97.5000 105.0000 112.5000 120.0000 127.5000 135.0000 142.5000 150.0000 157.5000 165.0000 172.5000

<##> MEASUREMENT PERFECT
projection data are noiseless

<##> BACKGROUND 0.0
at levels 10
background absorption 0.0000

<##> RUN
0.000 seconds phantom creation
0.002 seconds projection data creation
0.002 seconds used for processing command crea

<##>

<##> PICTURE TEST
EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

<##> spec mono 10
energy spectrum is monochromatic at energy level 10
APPENDIX A. EXAMPLES

<#> obje
description of objects
density at levels

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>sect</td>
<td>0.0000</td>
<td>-24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>2</td>
<td>sect</td>
<td>21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>60.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>3</td>
<td>sect</td>
<td>21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>120.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>4</td>
<td>sect</td>
<td>0.0000</td>
<td>24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>180.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>5</td>
<td>sect</td>
<td>-21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>240.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>6</td>
<td>sect</td>
<td>-21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>300.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> phan aver 5
density in each pixel is obtained as the average of 5 x 5 points

<#> pixe 25 size 2.0000
picture size 25 x 25, pixel size 2.0000

test picture read
EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

0.001 seconds used for processing command pict

<#> PROJECTION REAL

EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

<#> spec mono 10
energy spectrum is monochromatic at energy level 10

<#> obje
description of objects
density at levels

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>10</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>sect</td>
<td>0.0000</td>
<td>-24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>2</td>
<td>sect</td>
<td>21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>60.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>
APPENDIX A. EXAMPLES

3 sect 21.0000 12.0000 6.0000 24.0000 120.0000 1.0000 1.0000
4 sect 0.0000 24.0000 6.0000 24.0000 180.0000 1.0000 1.0000
5 sect -21.0000 12.0000 6.0000 24.0000 240.0000 1.0000 1.0000
6 sect -21.0000 -12.0000 6.0000 24.0000 300.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> rays aver 1

projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<#> geom

<#> para unif stri
rays are parallel with uniform spacing between rays
data collected along strips

<#> rays user 25 spacing 2.0000
number of rays per projection 25
snark computed number of rays 37
at detector spacing 2.0000

<#> angl 24
total number of projections 24

projection angles 0.0000 7.5000 15.0000 22.5000 30.0000 37.5000 45.0000
75.0000 82.5000 90.0000 97.5000 105.0000 112.5000 120.0000 127.5000
135.0000 142.5000 150.0000 157.5000 165.0000 172.5000

<#> meas perf
projection data are noiseless

<#> back 0.0000
at levels 10
background absorption 0.0000
APPENDIX A. EXAMPLES

estimate of totlen = 28263.966195
estimate of totden = 10749.116539
estimate of average density = 0.3803
projection data read
EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS
  0.001 seconds used for processing command proj

<*> EXECUTE BACKPROJECTION

EXAMPLE 5A CONTINUOUS BACKPROJECTION WITH LINEAR INTERPOLATION

<#> CONTINUOUS 2 MULTIPLICATIVE
  continuous back-projection
  2 order lagrange interpolation
  multiplicative normalization
algorithm executed in iteration 1
  0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 1
  0.000 seconds for this iteration
  0.000 seconds used for processing command exec

<*>(<#>) EXECUTE CONVOLUTION

EXAMPLE 5B CONVOLUTION WITH BANDLIMITING FILTER & LINEAR INTERPOLATION

<#> BANDLIMITING 1.0 2
  convolution reconstruction algorithm
  using filter band
cutoff (or alpha) = 1.0000
  2 point lagrange interpolation
algorithm executed in iteration 1
  0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 1
  0.000 seconds for this iteration
  0.000 seconds used for processing command exec

<*>(<#>) EXECUTE RFL

EXAMPLE 5C RHO FILTERED LAYERGRAM WITH BANDLIMITING FILTER & LINEAR INTERPOLATION

<#> BANDLIMITING 1.0 2
  rho-filtered layergram reconstruction algorithm
  using filter band
cutoff (or alpha) = 1.0000
  2 point lagrange interpolation
backprojection is performed on a 26 x 26 region
algorithm executed in iteration 1
0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 1
0.000 seconds for this iteration
0.002 seconds used for processing command exec

<*><#> EXECUTE FOURIER

EXAMPLE 5D FOURIER WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
fourier reconstruction

strip projections
<#> BANDLIMITING 1.0 3
filter= 0
cutoff= 1.00
interp= 3
nsizel= 38
nsizel= 26
time for projection transforms : 0.000 seconds
time for interpolations : 0.000 seconds
time for backtransform : 0.000 seconds
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
reconstruction completed after iteration 1
0.001 seconds for this iteration
0.002 seconds used for processing command exec

<*><#> STOP TERMINATION VARIANCE = 0.1
termination test vari
epsilon = 0.100000
0.000 seconds used for processing command stop

<*><#> EXECUTE ART

EXAMPLE 5F ART WITH NO TRICKS
<#> ART3
art3 method
relaxation parameter is 1.0
norm is 2
tolerance is 0.0
<#> CONSTRAINT ART2 STEPS 888
constraint art2 way
picture is not normalized
888 rays are used for each iteration
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
iteration 1 completed
0.001 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iteration 2 completed
0.001 seconds for this iteration
algorithm executed in iteration 3
0.001 seconds for the execution of the algorithm
iterative process stops at iteration 3
the change in variance is less than 0.006869 of the variance
reconstruction completed after iteration 3
0.001 seconds for this iteration
0.003 seconds for all iterations
0.004 seconds used for processing command exec

<*> EXECUTE MART

EXAMPLE 5G MULTIPLICATIVE ART A LA LENT

METHOD LENT 888 1.0 0.0
multiplicative art version lent
no of rays used in each iteration 888
underrelaxation factor 1.00000
all projection data with values less than 1.0000000000e-20 are ignored
reconstruction not normalized
entropy functional not calculated
algorithm executed in iteration 1
0.002 seconds for the execution of the algorithm
iteration 1 completed
0.002 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iterative process stops at iteration 2
the change in variance is less than 0.009779 of the variance
reconstruction completed after iteration 2
0.001 seconds for this iteration
0.003 seconds for all iterations
0.004 seconds used for processing command exec

<*> EXECUTE QUADRATIC

EXAMPLE 5H OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE
3 3 1 0 1 0.1 0.0 0.0

1 1 1 0 0 0 1.0 0.1 0

the conjugate gradient algorithm

direct gradient computation

=================================
algorithm executed in iteration 1
0.002 seconds for the execution of the algorithm
iteration 1 completed
0.002 seconds for this iteration

algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iteration 2 completed
0.001 seconds for this iteration

algorithm executed in iteration 3
0.001 seconds for the execution of the algorithm
iteration 3 completed
0.001 seconds for this iteration

algorithm executed in iteration 4
0.001 seconds for the execution of the algorithm
iteration 4 completed
0.001 seconds for this iteration

algorithm executed in iteration 5
0.001 seconds for the execution of the algorithm
iterative process stops at iteration 5
the change in variance is less than 0.095803 of the variance
reconstruction completed after iteration 5
0.001 seconds for this iteration
0.006 seconds for all iterations
0.007 seconds used for processing command exec

EXECUTE SIRT

EXAMPLE 5I GENERALIZED SIMULTANEOUS ITERATIVE RECONSTRUCTION TECHNOLOGY
user rays selected

METHOD GSIRT
gsirt method
sigma = inverse of relaxation = 1.0000

this run is unconstrained sirt
this run is unnormalized sirt
starting picture is as in execute command
algorithm executed in iteration 1
0.002 seconds for the execution of the algorithm
iteration 1 completed
0.002 seconds for this iteration
algorithm executed in iteration 2
0.000 seconds for the execution of the algorithm
iteration 2 completed
0.000 seconds for this iteration
algorithm executed in iteration  3
0.000 seconds for the execution of the algorithm
iteration  3 completed
0.000 seconds for this iteration
algorithm executed in iteration  4
0.000 seconds for the execution of the algorithm
iteration  4 completed
0.000 seconds for this iteration
algorithm executed in iteration  5
0.000 seconds for the execution of the algorithm
iteration  5 completed
0.000 seconds for this iteration
algorithm executed in iteration  6
0.000 seconds for the execution of the algorithm
iteration  6 completed
0.000 seconds for this iteration
algorithm executed in iteration  7
0.000 seconds for the execution of the algorithm
iteration  7 completed
0.000 seconds for this iteration
algorithm executed in iteration  8
0.000 seconds for the execution of the algorithm
iteration  8 completed
0.000 seconds for this iteration
algorithm executed in iteration  9
0.000 seconds for the execution of the algorithm
iteration  9 completed
0.000 seconds for this iteration
algorithm executed in iteration 10
0.000 seconds for the execution of the algorithm
iteration 10 completed
0.000 seconds for this iteration
algorithm executed in iteration 11
0.000 seconds for the execution of the algorithm
iteration 11 completed
0.000 seconds for this iteration
algorithm executed in iteration 12
0.001 seconds for the execution of the algorithm
iterative process stops at iteration  12
the change in variance is less than  0.086811 of the variance
reconstruction completed after iteration 12
0.001 seconds for this iteration
0.007 seconds for all iterations
0.008 seconds used for processing command exec

<<>

<#> EVALUATE

EXAMPLE 5 RECONSTRUCTION OF STAR PATTERN FROM PARALLEL PROJECTIONS

<#> WHOLEPIC
Region  cx  cy  u  v  ang  t1  t2
wholepic  -1e+20  1e+20

iterations  1  2  3  4  5  6  7  8  9  10  11
last iteration

0.002 seconds used for processing command eval

<<>
<##> END

A.5.3 SNARK14 eval file

evaluation name: EXAMPLE 5 RECONSTRUCTION OF STAR PATTERN FROM PARALLEL PROJECTIONS

global resolution measures

phantom name: EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS
projection name: EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

metrics for test phantom
region  area  average distance  rel err  variance  std dev
0  625  0.3622  0.1860  0.4312

execution name: EXAMPLE 5A CONTINUOUS BACKPROJECTION WITH LINEAR INTERPOLATION
metrics for algorithm BACK
iter  area  average distance  rel err  variance  std dev
1  625  0.3803  0.8608  0.9469  0.0079  0.0889

execution name: EXAMPLE 5B CONVOLUTION WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
metrics for algorithm CONV
iter  area  average distance  rel err  variance  std dev
1  625  0.3482  0.3830  0.3383  0.2160  0.4647

execution name: EXAMPLE 5C RHO FILTERED LAYERGRAM WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
metrics for algorithm RFL
iter  area  average distance  rel err  variance  std dev
1  625  0.3803  0.4012  0.3383  0.2160  0.4647

execution name: EXAMPLE 5D FOURIER WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
metrics for algorithm FOUR
iter  area  average distance  rel err  variance  std dev
1  625  0.3803  0.4012  0.3383  0.2136  0.4622

execution name: EXAMPLE 5F ART WITH NO TRICKS
metrics for algorithm ART
iter  area  average distance  rel err  variance  std dev
1  625  0.3686  0.6318  0.6148  0.2842  0.5331
APPENDIX A. EXAMPLES

2 625 0.3645 0.6925 0.6650 0.3130 0.5595
3 625 0.3637 0.7017 0.6784 0.3109 0.5576

execution name: EXAMPLE 5G MULTIPLICATIVE ART A LA LENT
metrics for algorithm MART
iter  area  average  distance  rel err  variance  std dev
1  625  0.3653  0.8483  0.5747  0.3696  0.6079
2  625  0.3653  0.8313  0.5462  0.3660  0.6050

execution name: EXAMPLE 5H OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE
metrics for algorithm QUAD
iter  area  average  distance  rel err  variance  std dev
1  625  0.3696  0.8616  0.9410  0.0076  0.0870
2  625  0.3509  0.3743  0.3558  0.1763  0.4199
3  625  0.3599  0.4943  0.4726  0.2569  0.5068
4  625  0.3570  0.4943  0.4726  0.2569  0.5068
5  625  0.3582  0.5808  0.5616  0.2815  0.5305
6  625  0.3692  0.5642  0.5986  0.0487  0.2208
7  625  0.3681  0.5237  0.5475  0.0594  0.2437
8  625  0.3672  0.4942  0.5051  0.0698  0.2642
9  625  0.3665  0.4605  0.4694  0.0798  0.2825
10 625  0.3658  0.4363  0.4385  0.0894  0.2989
11 625  0.3653  0.4162  0.4117  0.0984  0.3137
12 625  0.3648  0.3997  0.3889  0.1070  0.3271

execution name: EXAMPLE 5I GENERALIZED SIMULTANEOUS ITERATIVE RECONSTRUCTION TECHNOLOGY
metrics for algorithm SIRT
iter  area  average  distance  rel err  variance  std dev
1  625  0.3788  0.8970  0.9925  0.0007  0.0254
2  625  0.3760  0.8082  0.8900  0.0009  0.0462
3  625  0.3738  0.7323  0.8016  0.0017  0.1323
4  625  0.3719  0.6673  0.7245  0.0027  0.1656
5  625  0.3704  0.6117  0.6570  0.0030  0.1949
6  625  0.3692  0.5642  0.5986  0.0047  0.2208
7  625  0.3681  0.5237  0.5475  0.0054  0.2437
8  625  0.3672  0.4894  0.5051  0.0069  0.2642
9  625  0.3665  0.4605  0.4694  0.0079  0.2825
10 625  0.3658  0.4363  0.4385  0.0089  0.2989
11 625  0.3653  0.4162  0.4117  0.0094  0.3137
12 625  0.3648  0.3997  0.3889  0.0107  0.3271

point by point resolution measures
phantom name: EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS
projection name: EXAMPLE 5 STAR PATTERN WITH 24 PARALLEL STRIP PROJECTIONS

execution name: EXAMPLE 5A CONTINUOUS BACKPROJECTION WITH LINEAR INTERPOLATION
align iter  e(0)  e(1)  e(2)  e(3)  e(4)
BACK 1  0.6022  0.5629  0.4543  0.0981  0.0045

execution name: EXAMPLE 5B CONVOLUTION WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
align iter  e(0)  e(1)  e(2)  e(3)  e(4)
CONV 1  1.5231  0.5371  0.1511  0.0693  0.0263

execution name: EXAMPLE 5C RHO FILTERED LAYERGRAM WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
align iter  e(0)  e(1)  e(2)  e(3)  e(4)
RFL 1  1.2289  0.3918  0.1144  0.0623  0.0227

execution name: EXAMPLE 5D FOURIER WITH BANDLIMITING FILTER & LINEAR INTERPOLATION
align iter  e(0)  e(1)  e(2)  e(3)  e(4)
FOUR 1  1.6646  0.5753  0.1553  0.0610  0.0266
A.6 Star pattern with divergent projections

In this example we illustrate various algorithms that are appropriate for divergent projection data. The test phantom is the same as the one described in Section A.4. Divergent projection data are taken for 24 equally spaced views between $0^\circ$ and $345^\circ$. Reconstructions are done using DCONV, ART, MART and QUADRATIC. In each case the parameters have been set either at their default values or at simple values that are not likely to be optimal for the projection data in question. EVALUATE is used in the analysis phase.

<table>
<thead>
<tr>
<th>execution name: EXAMPLE 5F ART WITH NO TRICKS</th>
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</thead>
<tbody>
<tr>
<td>alg</td>
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<tr>
<td>ART 1</td>
</tr>
<tr>
<td>ART 2</td>
</tr>
<tr>
<td>ART 3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>execution name: EXAMPLE 5G MULTIPLICATIVE ART A LA LENT</th>
</tr>
</thead>
<tbody>
<tr>
<td>alg</td>
</tr>
<tr>
<td>MART 1</td>
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<tr>
<td>MART 2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>execution name: EXAMPLE 5H OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE</th>
</tr>
</thead>
<tbody>
<tr>
<td>alg</td>
</tr>
<tr>
<td>QUAD 1</td>
</tr>
<tr>
<td>QUAD 2</td>
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<tr>
<td>QUAD 3</td>
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<tr>
<td>QUAD 4</td>
</tr>
<tr>
<td>QUAD 5</td>
</tr>
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</table>

<table>
<thead>
<tr>
<th>execution name: EXAMPLE 5I GENERALIZED SIMULTANEOUS ITERATIVE RECONSTRUCTION TECHNOLOGY</th>
</tr>
</thead>
<tbody>
<tr>
<td>alg</td>
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<tr>
<td>SIRT 1</td>
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<td>SIRT 6</td>
</tr>
<tr>
<td>SIRT 7</td>
</tr>
<tr>
<td>SIRT 8</td>
</tr>
<tr>
<td>SIRT 9</td>
</tr>
<tr>
<td>SIRT 10</td>
</tr>
<tr>
<td>SIRT 11</td>
</tr>
<tr>
<td>SIRT 12</td>
</tr>
</tbody>
</table>

Figure A.5: Half-tone displays from Example A.6. The phantom and the final reconstruction with each method is shown.
A.6.1 SNARK14 INPUT file

*EXAMPLE 6
*STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
*RECONSTRUCTION BY ALL APPROPRIATE ALGORITHMS WITH DEFAULT
*OR EASY OPTIONS.
*
CREATE
EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
SPECTRUM MONOCHROMATIC 10
OBJECTS
SECT 0.0 -24.0 6.0 24.0 0.0 1.0
SECT 21.0 -12.0 6.0 24.0 60.0 1.0
SECT 21.0 12.0 6.0 24.0 120.0 1.0
SECT 0.0 24.0 6.0 24.0 180.0 1.0
SECT -21.0 12.0 6.0 24.0 240.0 1.0
SECT -21.0 -12.0 6.0 24.0 300.0 1.0
LAST 1.0
PHANTOM AVERAGE 5
25 PIXELS OF SIZE 2.0
RAYSUM AVERAGE 1
1
GEOMETRY
DIVERGENT ARC 40.0 40.0
RAYS PROGRAM 25 2.0 DETECTOR SPACING 2.0
ANGLES 24 EQUAL SPACING
0.0 345.0
MEASUREMENT PERFECT
BACKGROUND 0.0
RUN
*
PICTURE TEST
*
PROJECTION REAL
*
EXECUTE DCONV
EXAMPLE 6A DIVERGENT BEAM CONVOLUTION WITH BANDLIMITING FILTER
2 1 25 1.0 0
BANDLIMITING
*
STOP TERMINATION VARIANCE = 0.1
*
EXECUTE ART
EXAMPLE 6C ART WITH NO TRICKS
ART3
CONSTRAINT ART2
*
EXECUTE MART
EXAMPLE 6D MULTIPLICATIVE ART A LA LENT
METHOD LENT 0 1.0 0.0
*
EXECUTE QUADRATIC
EXAMPLE 6E OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE GRADIENT
3 3 1 0 1 0.1 0.0 0.0
A.6.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<<< EXAMPLE 6

<<< STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

<<< RECONSTRUCTION BY ALL APPROPRIATE ALGORITHMS WITH DEFAULT OR EASY OPTIONS.

<<< CREATE

EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

<<< SPECTRUM MONOCHROMATIC 10
energy spectrum is monochromatic at energy level 10

<<< OBJECTS
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens 10
1 sect 0.0000 -24.0000 6.0000 24.0000 0.0000 1.0000 1.0000
2 sect 21.0000 -12.0000 6.0000 24.0000 60.0000 1.0000 1.0000
3 sect 21.0000 12.0000 6.0000 24.0000 120.0000 1.0000 1.0000
4 sect 0.0000 24.0000 6.0000 24.0000 180.0000 1.0000 1.0000
5 sect -21.0000 12.0000 6.0000 24.0000 240.0000 1.0000 1.0000
6 sect -21.0000 -12.0000 6.0000 24.0000 300.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000
APPENDIX A. EXAMPLES

<## PHANTOM AVERAGE 5

this run will generate a phantom
density in each pixel is obtained as the average of 5 x 5 points

<## 25 PIXELS OF SIZE 2.0

picture size 25 x 25, pixel size 2.0000

<## RAYSUM AVERAGE 1

this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips

with aperture (substrip) weights 1

<## GEOMETRY

<## DIVERGENT ARC 40.0 40.0

rays are divergent from point sources

source to origin distance 40.0000

the detectors lie on an arc with source to detector distance = 40.0000

<## RAYS PROGRAM 25 2.0 DETECTOR SPACING 2.0

number of rays per projection 45

at detector spacing 2.0000

<## ANGLES 24 EQUAL SPACING

total number of projections 24

projection angles 0.0000 15.0000 30.0000 45.0000 60.0000 75.0000 90.0000 105.0000 120.0000 135.0000 150.0000 165.0000 180.0000 195.0000 210.0000 225.0000 240.0000 255.0000 270.0000 285.0000 300.0000 315.0000 330.0000 345.0000

<## MEASUREMENT PERFECT

projection data are noiseless

<## BACKGROUND 0.0

at levels 10

background absorption 0.0000

<## RUN

0.001 seconds phantom creation
0.001 seconds projection data creation
0.003 seconds used for processing command create

<<>

<<#> PICTURE TEST

EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

<<#> spec mono 10
energy spectrum is monochromatic at energy level 10

<<#> obje
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens 10
1 sect 0.0000 -24.0000 6.0000 24.0000 0.0000 1.0000 1.0000
2 sect 21.0000 -12.0000 6.0000 24.0000 60.0000 1.0000 1.0000
3 sect 21.0000 12.0000 6.0000 24.0000 120.0000 1.0000 1.0000
4 sect 0.0000 24.0000 6.0000 24.0000 180.0000 1.0000 1.0000
5 sect 21.0000 12.0000 6.0000 24.0000 240.0000 1.0000 1.0000
6 sect 21.0000 12.0000 6.0000 24.0000 300.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

<<#> phan aver 5
density in each pixel is obtained as the average of 5 x 5 points

<<#> pixe 25 size 2.0000
picture size 25 x 25, pixel size 2.0000

test picture read
EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
0.001 seconds used for processing command pict

<<>

<<#> PROJECTION REAL

EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
spec mono 10
energy spectrum is monochromatic at energy level 10

obje
description of objects
density at levels

<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>10</th>
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<td>0.0000</td>
<td>-24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>0.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>2</td>
<td>sect</td>
<td>21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>60.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>3</td>
<td>sect</td>
<td>21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>120.0000</td>
<td>1.0000</td>
<td>1.0000</td>
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<tr>
<td>4</td>
<td>sect</td>
<td>0.0000</td>
<td>24.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>180.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>5</td>
<td>sect</td>
<td>-21.0000</td>
<td>12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>240.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
<tr>
<td>6</td>
<td>sect</td>
<td>-21.0000</td>
<td>-12.0000</td>
<td>6.0000</td>
<td>24.0000</td>
<td>300.0000</td>
<td>1.0000</td>
<td>1.0000</td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

rays aver 1
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

geom
dive arc source at 40.0000 det dist 40.0000
rays are divergent from point sources
source to origin distance 40.0000
the detectors lie on an arc with source to detector distance = 40.0000

rays user 45 spacing 2.0000
number of rays per projection 45
snark computed number of rays 45
at detector spacing 2.0000

angl 24
total number of projections 24
projection angles 0.0000 15.0000 30.0000 45.0000 60.0000 75.0000 90.0000 105.0000 120.0000 135.0000 150.0000 165.0000 180.0000 195.0000 210.0000 225.0000 240.0000 255.0000 270.0000 285.0000 300.0000 315.0000 330.0000 345.0000

meas perf

projection data are noiseless

back 0.0000

at levels 10

background absorption 0.0000

estimate of totlen = 32578.803295

estimate of totden = 11270.139500

estimate of average density = 0.3459

projection data read

EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

0.001 seconds used for processing command proj

EXECUTE DCONV

EXAMPLE 6A DIVERGENT BEAM CONVOLUTION WITH BANDLIMITING FILTER

2 1 25 1.0 0

2 point lagrange interpolation

one out of every 1 projection(s) used for reconstruction

25 points used on each side of convolution

pre-smoothing weight on center ray = 1.0000

pre-smoothing weight on side rays = 0.0000

accurate back-projection

BANDLIMITING

band-limiting filter

total time for obtaining smoothed projection data was 0.000

total time for convoluting projection data was 0.000

total time for back-projecting was 0.001

algorithm executed in iteration 1

0.001 seconds for the execution of the algorithm

reconstruction completed after iteration 1

0.001 seconds for this iteration

0.003 seconds used for processing command exec

STOP TERMINATION VARIANCE = 0.1

termination test vari

epsilon = 0.100000

0.000 seconds used for processing command stop
<*><*

<## EXECUTE ART

EXAMPLE 6C ART WITH NO TRICKS

<## ART3
art3 method
relaxation parameter is 1.0
norm is 2
tolerance is 0.0

<## CONSTRAINT ART2
constraint art2 way
relaxation constraints with cr = 1.0
picture is not normalized
1080 rays are used for each iteration
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
iteration 1 completed
0.001 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iterative process stops at iteration 2
the change in variance is less than 0.041353 of the variance
reconstruction completed after iteration 2
0.001 seconds for this iteration
0.001 seconds for all iterations
0.003 seconds used for processing command exec

<*><*

<## EXECUTE MART

EXAMPLE 6D MULTIPLICATIVE ART A LA LENT

<## METHOD LENT 0 1.0 0.0
multiplicative art version lent
no of rays used in each iteration 1080
underrelaxation factor 1.00000
all projection data with values less than 1.0000000000e-20 are ignored
reconstruction not normalized
entropy functional not calculated
algorithm executed in iteration 1
0.000 seconds for the execution of the algorithm
iteration 1 completed
0.000 seconds for this iteration
algorithm executed in iteration 2
0.000 seconds for the execution of the algorithm
iterative process stops at iteration 2
the change in variance is less than 0.026757 of the variance
reconstruction completed after iteration 2
0.000 seconds for this iteration
0.000 seconds for all iterations
0.001 seconds used for processing command exec

<#>

EXECUTE QUADRATIC

EXAMPLE 6E OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE GRADIENT

<#>

3 3 1 0 1 0.1 0.0 0.0

1 1 1 0 0 0 1.0 0.1 0

the conjugate gradient algorithm

direct gradient computation

=================================
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
iteration 1 completed
0.001 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iteration 2 completed
0.001 seconds for this iteration
algorithm executed in iteration 3
0.001 seconds for the execution of the algorithm
iteration 3 completed
0.001 seconds for this iteration
algorithm executed in iteration 4
0.001 seconds for the execution of the algorithm
iteration 4 completed
0.001 seconds for this iteration
algorithm executed in iteration 5
0.001 seconds for the execution of the algorithm
iterative process stops at iteration 5
the change in variance is less than 0.046725 of the variance
reconstruction completed after iteration 5
0.001 seconds for this iteration
0.004 seconds for all iterations
0.005 seconds used for processing command exec

<#>

EVALUATE

EXAMPLE 6 RECONSTRUCTION OF STAR PATTERN FROM DIVERGENT PROJECTIONS

WHOLEPIC

Region cx cy u v ang t1 t2
A.6.3 SNARK14 eval file

evaluation name: EXAMPLE 6 RECONSTRUCTION OF STAR PATTERN FROM DIVERGENT PROJECTIONS

global resolution measures

phantom name: EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
projection name: EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

metrics for test phantom
region area average distance rel err variance std dev
0 625 0.3622 0.1860 0.4312

execution name: EXAMPLE 6A DIVERGENT BEAM CONVOLUTION WITH BANDLIMITING FILTER
metrics for algorithm DCON
iter area average distance rel err variance std dev
1 625 0.1208 4.0003 1.9817 3.2118 1.7921

execution name: EXAMPLE 6C ART WITH NO TRICKS
metrics for algorithm ART
iter area average distance rel err variance std dev
1 625 0.3543 0.6235 0.5861 0.2149 0.4635
2 625 0.3525 0.5613 0.5098 0.2238 0.4730

execution name: EXAMPLE 6D MULTIPLICATIVE ART A LA LENT
metrics for algorithm MART
iter area average distance rel err variance std dev
1 625 0.3517 0.8027 0.5958 0.2824 0.5314
2 625 0.3533 0.7543 0.5662 0.2749 0.5243

execution name: EXAMPLE 6E OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE GRADIENT
metrics for algorithm QUAD
iter area average distance rel err variance std dev
1 625 0.3681 0.8683 0.9420 0.0095 0.0972
2 625 0.3542 0.5688 0.5600 0.1476 0.3842
3 625 0.3584 0.5546 0.5303 0.1779 0.4217
4 625 0.3564 0.5635 0.5279 0.1991 0.4462
5 625 0.3577 0.5685 0.5184 0.2084 0.4565

point by point resolution measures
APPENDIX A. EXAMPLES

phantom name: EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS
projection name: EXAMPLE 6 STAR PATTERN WITH 24 DIVERGENT PROJECTIONS

execution name: EXAMPLE 6A DIVERGENT BEAM CONVOLUTION WITH BANDLIMITING FILTER
align iter e(0) e(1) e(2) e(3) e(4)
DCON 1 16.9760 6.5672 2.0533 0.5332 0.1783

execution name: EXAMPLE 6C ART WITH NO TRICKS
align iter e(0) e(1) e(2) e(3) e(4)
ART 1 2.0575 0.7039 0.1127 0.0568 0.0294
ART 2 2.2177 0.6297 0.1291 0.0675 0.0352

execution name: EXAMPLE 6D MULTIPLICATIVE ART A LA LENT
align iter e(0) e(1) e(2) e(3) e(4)
MART 1 2.4042 0.5922 0.1526 0.0931 0.0415
MART 2 1.6089 0.4700 0.1179 0.0852 0.0424

execution name: EXAMPLE 6E OPTIMIZATION OF LEAST SQUARES FUNCTIONAL USING CONJUGATE GRADIENT
align iter e(0) e(1) e(2) e(3) e(4)
QUAD 1 0.6402 0.5899 0.4709 0.1040 0.0065
QUAD 2 1.2944 0.5751 0.1622 0.0753 0.0152
QUAD 3 1.5651 0.5930 0.1275 0.0497 0.0194
QUAD 4 1.8313 0.5988 0.1105 0.0547 0.0144
QUAD 5 2.0261 0.6589 0.1501 0.0406 0.0194

A.7 Simulating data collection and image reconstruction for PET

This example illustrates a SNARK14 run that simulates the collection of PET data and uses EMAP to reconstruct a test phantom. The test phantom was obtained from a computerized overlay atlas based on average anatomy of the brain [41]. In this phantom neuroanatomical structures are represented by various ellipses and rectangles at appropriate locations. The activity in the brain background is assigned 1.0 (in arbitrary units), while the activity in the neuroanatomical structures is either 1.95 or 2.0. A 95×95 digitization of this phantom is shown in Figure A.6.

To simulate data obtained from a PET system with a ring of 300 detectors and with each detector in coincidence with 101 detectors opposite it, we generate divergent projection data over 300 view angles with 101 rays per view. In this case we assume that the detectors are arranged on an arc. Poisson noise is introduced into the projection measurements and the phantom densities are scaled by a factor of 0.51 to yield a total photon count that is approximately 2,000,000 (note the actual parameter totden in the output file shown in Section A.7.2).

Figure A.6: A Brain Phantom
A.7.1 SNARK14 INPUT file

*******EXAMPLE 7
* MAP EM ALGORITHM FOR EMISSION TOMOGRAPHY. RECONSTRUCTION OF BRAIN
* PHANTOM. SIMULATING PET GEOMETRY WITH A RING OF 300 DETECTORS WITH
* EACH DETECTOR IN COINCIDENCE WITH 101 DETECTORS OPPOSITE IT.
* COEFFICIENT OF PENALTLY TERM IS SET TO 10.0
*
CREATE
EXAMPLE 7 Brain Phantom
SPECTRUM MONOCHROMATIC 511
OBJECTS
  1 elip -7.0 46.0 3.0 6.0 17.0 0.95 1.0
  2 elip  7.0 46.0 3.0 6.0 -17.0 1.0 0.95
  3 rect -12.0 64.0 7.5 4.5 5.0 1.0 1.0
  4 rect  12.0 64.0 7.5 4.5 -5.0 0.95 0.95
  5 rect -38.0 51.0 3.5 13.0 -39.0 0.95 1.0
  6 rect  38.0 51.0 3.5 13.0 39.0 1.0 0.95
  7 rect -46.0 24.0 6.5 6.0 -18.0 0.95 1.0
  8 rect  46.0 24.0 6.5 6.0 18.0 1.0 0.95
  9 rect -49.0 6.0 2.5 10.0 63.0 1.0 1.0
 10 rect  49.0 6.0 2.5 10.0 -63.0 0.95 0.95
 11 rect -52.0 -14.0 9.0 7.0 -14.0 0.95 1.0
 12 rect  52.0 -14.0 9.0 7.0 14.0 1.0 0.95
 13 rect -10.0 -56.0 5.5 10.0 -1.0 0.95 1.0
 14 rect  10.0 -56.0 5.5 10.0 1.0 1.0 0.95
 15 elip -40.0 -47.0 9.0 22.5 48.0 1.0 1.0
 16 elip  40.0 -47.0 9.0 22.5 -48.0 0.95 0.95
 17 elip -8.0 -22.0 3.5 15.5 -9.0 1.0 1.0
 18 elip  8.0 -22.0 3.5 15.5 9.0 0.95 0.95
 19 elip -27.0 -6.0 5.5 23.5 -5.0 0.95 1.0
 20 elip  27.0 -6.0 5.5 23.5 5.0 1.0 0.95
 21 elip -25.0 38.0 6.5 10.5 -14.0 1.0 1.0
 22 elip  25.0 38.0 6.5 10.5 14.0 0.95 0.95
 23 rect -8.0 32.0 1.5 6.5 38.0 1.0 1.0
 24 rect  8.0 32.0 1.5 6.5 -38.0 0.95 0.95
 25 rect -8.0 3.0 1.0 9.0 33.0 1.0 0.95
 26 rect  8.0 3.0 1.0 9.0 -33.0 0.95 1.0
 27 elip  0.0 0.0 66.5 74.0 0.0 1.0 1.0
LAST .51 1 0.05
PHANTOM AVERAGE 7
95 PIXELS OF SIZE 1.6
RAYSUM AVERAGE 1
A.7.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<<> *******EXAMPLE 7
<<> MAP EM ALGORITHM FOR EMISSION TOMOGRAPHY. RECONSTRUCTION OF BRAIN
<<> PHANTOM. SIMULATING PET GEOMETRY WITH A RING OF 300 DETECTORS WITH
<<> EACH DETECTOR IN COINCIDENCE WITH 101 DETECTORS OPPOSITE IT.
<<> COEFFICIENT OF PENALTY TERM IS SET TO 10.0
<<>
<<# CREATE

EXAMPLE 7 Brain Phantom

<<# SPECTRUM MONOCHROMATIC 511
   energy spectrum is monochromatic at energy level  511

<<# OBJECTS
   description of objects

   density at levels
<table>
<thead>
<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>511</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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APPENDIX A. EXAMPLES

27 elip 0.0000 0.0000 66.5000 74.0000 0.0000 1.0000 1.0000

scale factor multiplying object densities 0.5100

seed set to 1
inhomogeneity set to 0.0500

<##> PHANTOM AVERAGE 7

this run will generate a phantom
density in each pixel is obtained as the average of 7 x 7 points

<##> 95 PIXELS OF SIZE 1.6
picture size 95 x 95, pixel size 1.6000

<##> RAYSUM AVERAGE 1

this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<##> GEOMETRY

<##> divergent arc 153 306
rays are divergent from point sources
source to origin distance 153.0000
the detectors lie on an arc with source to detector distance = 306.0000

<##> RAYS USER 101 DETECTOR SPACING 3.2
number of rays per projection 101
at detector spacing 3.2000

<##> ANGLES 300 EQUAL SPACING
total number of projections 300

projection angles 0.0000 1.2000 2.4000 3.6000 4.8000 6.0000 7.2000
36.0000 37.2000 38.4000 39.6000 40.8000 42.0000 43.2000
48.0000 49.2000 50.4000 51.6000 52.8000 54.0000 55.2000
60.0000 61.2000 62.4000 63.6000 64.8000 66.0000 67.2000
72.0000 73.2000 74.4000 75.6000 76.8000 78.0000 79.2000
84.0000 85.2000 86.4000 87.6000 88.8000 90.0000 91.2000
<#> MEASUREMENT NOISY
noise characteristics of projection data follow
nature characteristics

<#> QUANTUM 1.0 1.0 CALIBRATION 4
Emission tomography

<#> SEED 0
seed for random number generator is 0

<#> BACKGROUND 0.0
at levels
511
background absorption 0.0000

<#> RUN
0.027 seconds phantom creation
0.106 seconds projection data creation
0.133 seconds used for processing command crea

<#>

<#> PICTURE TEST
EXAMPLE 7 Brain Phantom

<#> spec mono 511
energy spectrum is monochromatic at energy level 511
## APPENDIX A. EXAMPLES

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APPENDIX A. EXAMPLES

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27 elip  0.0000  0.0000  66.5000  74.0000  0.0000  0.5100  0.5100

scale factor multiplying object densities  0.5100

seed set to  1
inhomogeneity set to  0.0500

<#> phan aver 7
density in each pixel is obtained as the average of 7 x 7 points

<#> pixe  95  size  1.6000
picture size 95 x 95, pixel size 1.6000
test picture read
EXAMPLE 7 Brain Phantom
0.003 seconds used for processing command pict

<#> PROJECTION REAL

EXAMPLE 7 Brain Phantom

<#> spec mono 511
energy spectrum is monochromatic at energy level  511

<#> obje
description of objects
density at levels

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APPENDIX A. EXAMPLES

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18 elip  8.0000 -22.0000  3.5000  15.5000  9.0000  0.4845  0.4845
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25 rect -8.0000  3.0000  1.0000  9.0000 -33.0000  0.4845  0.4845
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27 elip  0.0000  0.0000  66.5000  74.0000  0.0000  0.5100  0.5100

scale factor multiplying object densities  0.5100

seed set to 1
inhomogeneity set to  0.0500

<#> rays aver  1

projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights  1

<#> geom
APPENDIX A. EXAMPLES

<<#> dive arc source at 153.0000 det dist 306.0000
rays are divergent from point sources
source to origin distance 153.0000
the detectors lie on an arc with source to detector distance = 306.0000

<<#> rays user 101 spacing 3.2000
number of rays per projection 101
snark computed number of rays 151
at detector spacing 3.2000

<<#> angl 300
total number of projections 300

projection angles  0.0000  1.2000  2.4000  3.6000  4.8000  6.0000  7.2000
36.0000 37.2000 38.4000 39.6000 40.8000 42.0000 43.2000
48.0000 49.2000 50.4000 51.6000 52.8000 54.0000 55.2000
60.0000 61.2000 62.4000 63.6000 64.8000 66.0000 67.2000
72.0000 73.2000 74.4000 75.6000 76.8000 78.0000 79.2000
84.0000 85.2000 86.4000 87.6000 88.8000 90.0000 91.2000
96.0000 97.2000 98.4000 99.6000 100.8000 102.0000 103.2000
108.0000 109.2000 110.4000 111.6000 112.8000 114.0000 115.2000
120.0000 121.2000 122.4000 123.6000 124.8000 126.0000 127.2000
132.0000 133.2000 134.4000 135.6000 136.8000 138.0000 139.2000
144.0000 145.2000 146.4000 147.6000 148.8000 150.0000 151.2000
156.0000 157.2000 158.4000 159.6000 160.8000 162.0000 163.2000
168.0000 169.2000 170.4000 171.6000 172.8000 174.0000 175.2000
192.0000 193.2000 194.4000 195.6000 196.8000 198.0000 199.2000
204.0000 205.2000 206.4000 207.6000 208.8000 210.0000 211.2000
228.0000 229.2000 230.4000 231.6000 232.8000 234.0000 235.2000
252.0000 253.2000 254.4000 255.6000 256.8000 258.0000 259.2000
264.0000 265.2000 266.4000 267.6000 268.8000 270.0000 271.2000
276.0000 277.2000 278.4000 279.6000 280.8000 282.0000 283.2000
300.0000 301.2000 302.4000 303.6000 304.8000 306.0000 307.2000
312.0000 313.2000 314.4000 315.6000 316.8000 318.0000 319.2000
324.0000 325.2000 326.4000 327.6000 328.8000 330.0000 331.2000
348.0000 349.2000 350.4000 351.6000 352.8000 354.0000 355.2000

<<#> meas nois
noise characteristics of projection data follow
nature characteristics

<<#> quan 1.0000 1.0000 cali 4
Emission tomography
APPENDIX A. EXAMPLES

seed 0
seed for random number generator is 0

back 0.0000
at levels 511
background absorption 0.0000

estimate of totlen = 4263169.769963
estimate of totden = 2020362.000000
estimate of average density = 0.4739
projection data read
EXAMPLE 7 Brain Phantom
0.012 seconds used for processing command proj

STOP ITERATION 20
20 iterations
0.000 seconds used for processing command stop

EXECUTE AVERAGE EMAP

Example 7 Illustrating the MAP EM algorithm for PET

gamma is 10.0 EVAL

maximum a-posteriori probability expectation maximization

algorithm executed in iteration 1
0.162 seconds for the execution of the algorithm
iteration 1 completed
algorithm executed in iteration 2
0.108 seconds for the execution of the algorithm
iteration 2 completed
algorithm executed in iteration 3
0.104 seconds for the execution of the algorithm
iteration 3 completed
algorithm executed in iteration 4
  0.095 seconds for the execution of the algorithm
iteration 4 completed
  0.095 seconds for this iteration
algorithm executed in iteration 5
  0.095 seconds for the execution of the algorithm
iteration 5 completed
  0.095 seconds for this iteration
algorithm executed in iteration 6
  0.095 seconds for the execution of the algorithm
iteration 6 completed
  0.095 seconds for this iteration
algorithm executed in iteration 7
  0.095 seconds for the execution of the algorithm
iteration 7 completed
  0.095 seconds for this iteration
algorithm executed in iteration 8
  0.095 seconds for the execution of the algorithm
iteration 8 completed
  0.095 seconds for this iteration
algorithm executed in iteration 9
  0.095 seconds for the execution of the algorithm
iteration 9 completed
  0.095 seconds for this iteration
algorithm executed in iteration 10
  0.104 seconds for the execution of the algorithm
iteration 10 completed
  0.104 seconds for this iteration
algorithm executed in iteration 11
  0.100 seconds for the execution of the algorithm
iteration 11 completed
  0.100 seconds for this iteration
algorithm executed in iteration 12
  0.105 seconds for the execution of the algorithm
iteration 12 completed
  0.105 seconds for this iteration
algorithm executed in iteration 13
  0.105 seconds for the execution of the algorithm
iteration 13 completed
  0.105 seconds for this iteration
algorithm executed in iteration 14
  0.100 seconds for the execution of the algorithm
iteration 14 completed
  0.100 seconds for this iteration
algorithm executed in iteration 15
  0.100 seconds for the execution of the algorithm
iteration 15 completed
  0.100 seconds for this iteration
algorithm executed in iteration 16
  0.100 seconds for the execution of the algorithm
iteration 16 completed
  0.100 seconds for this iteration
algorithm executed in iteration 17
  0.100 seconds for the execution of the algorithm
iteration 17 completed
0.100 seconds for this iteration
algorithm executed in iteration 18
0.097 seconds for the execution of the algorithm
iteration 18 completed
0.097 seconds for this iteration
algorithm executed in iteration 19
0.097 seconds for the execution of the algorithm
iteration 19 completed
0.097 seconds for this iteration
algorithm executed in iteration 20
0.095 seconds for the execution of the algorithm
reconstruction completed after iteration 20
0.095 seconds for this iteration
2.048 seconds for all iterations
2.101 seconds used for processing command exec

A.7.3 SNARK14 MAPUser1 file

<table>
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<th>log-likelihood</th>
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<td>6721050.941879908</td>
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<td>6735133.991341705</td>
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<td>6772295.791661046</td>
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</table>

A.8 Linogram reconstruction

This example illustrates the use of the linogram algorithm in reconstructing the head phantom described in [29, Section 4.3]. A 115 × 115 digitization of the phantom is shown in Figure A.8. (Note: in the notation in Section 7.12, N=57 for this phantom.) Parallel projection data are collected with variable ray spacing to
provide us with a total of 462 projections and 231 rays per projection. The reconstructions obtained using both the linogram and the filtered backprojection methods are shown in Figures A.9 and A.10, respectively.

Figure A.8: Head phantom

Figure A.9: Linogram reconstruction

Figure A.10: Filtered backprojection reconstruction

A.8.1 SNARK14 INPUT file

******* EXAMPLE 8
* RECONSTRUCTION OF HEAD PHANTOM USING LINOGRAM AND FILTERED
* BACKPROJECTION METHODS. SINC FILTER FOR LINOGRAM AND COSINE
* FILTER FOR FBP.
*
create
EXAMPLE 8 LINOGRAM RECONSTRUCTION
spectrum monochromatic 75
objects cx cy u v ang den
APPENDIX A. EXAMPLES

elip 0.000 0.000 8.625 6.4687 90.00 0.416
elip 0.000 0.000 7.875 5.7187 90.00 -0.206
elip 0.000 0.000 0.375 0.3000 90.00 -0.003
elip 0.675 -0.750 0.225 0.1500 140.00 0.010
elip 0.750 1.500 0.375 0.2250 50.00 0.003
segm 1.375 -7.500 1.100 0.6250 19.20 -0.204
segm 1.375 -7.500 1.100 4.3200 19.21 0.204
segm 0.000 -2.250 1.125 0.3750 0.00 -0.003
segm 0.000 -2.250 1.125 3.0000 0.00 0.003
segm -1.000 3.750 1.000 0.5000 135.00 -0.003
segm -1.000 3.750 1.000 3.0000 135.00 0.003
segm 1.000 3.750 1.000 0.5000 225.00 -0.003
segm 1.000 3.750 1.000 3.0000 225.00 0.003
tria 5.025 3.750 1.125 0.5000 110.75 0.206
tria -5.025 3.750 1.125 0.9000 -110.75 0.206
last 1.0
phantom average 5
115 0.1504
raysum average 1
1
geometry
linogram
measurement perfect
background absorption is 0.0
run
picture test
projection real
execute lino
EXAMPLE 8a LINOGRAM METHOD
sinc 1.0
execute conv
EXAMPLE 8b FILTERED BACKPROJECTION
cosine 1.0 2
end

A.8.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<<< ******* EXAMPLE 8

<<< RECONSTRUCTION OF HEAD PHANTOM USING LINOGRAM AND FILTERED

<<< BACKPROJECTION METHODS. SINC FILTER FOR LINOGRAM AND COSINE

<<< FILTER FOR FBP.

<<<

# create

EXAMPLE 8 LINOGRAM RECONSTRUCTION
<#> spectrum monochromatic 75
energy spectrum is monochromatic at energy level 75

<#> objects cx cy u v ang den
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens
density at levels 75

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<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
<th>75</th>
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<td>6.4687</td>
<td>90.0000</td>
<td>0.4160</td>
<td>0.4160</td>
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<td>elip</td>
<td>0.0000</td>
<td>0.0000</td>
<td>7.8750</td>
<td>5.7187</td>
<td>90.0000</td>
<td>-0.2060</td>
<td>-0.2060</td>
</tr>
<tr>
<td>3</td>
<td>elip</td>
<td>0.0000</td>
<td>1.5000</td>
<td>0.3750</td>
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<td>0.2060</td>
</tr>
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</table>

scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> phantom average 5
this run will generate a phantom
density in each pixel is obtained as the average of 5 x 5 points

<#> 115 0.1504
picture size 115 x 115, pixel size 0.1504
APPENDIX A. EXAMPLES

<#> raysum average 1

this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<#> geometry

<#> linogram
rays are parallel with variable spacing between rays
data collected along lines

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APPENDIX A. EXAMPLES

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172.1131 172.6004 173.0888 173.5782 174.0685 174.5597 175.0517 175.5444 176.0378 176.5318
177.0263 177.5212 178.0165 178.5121 179.0080 179.5039 180.0000 180.4961 180.9920 181.4879
181.9835 182.4788 182.9737 183.4682 183.9622 184.4556 184.9483 185.4403 185.9315 186.4218
186.9112 187.3996 187.8869 188.3730 188.8580 189.3416 189.8239 190.3048 190.7843 191.2622
196.4030 196.8584 197.3116 197.7627 198.2114 198.6579 199.1020 199.5438 199.9831 200.4200
200.8545 201.2864 201.7158 202.1427 202.5670 202.9887 203.4078 203.8243 204.2381 204.6492
205.0576 205.4633 205.8664 206.2666 206.6642 207.0590 207.4510 207.8403 208.2267 208.6105
208.9914 209.3695 209.7449 210.1174 210.4872 210.8542 211.2184 211.5798 211.9384 212.2943
216.0274 216.3505 216.6710 216.9888 217.3039 217.6165 217.9265 218.2338 218.5386 218.8408
219.1405 219.4377 219.7323 220.0244 220.3141 220.6013 220.8860 221.1684 221.4483 221.7258
222.0009 222.2737 222.5441 222.8122 223.0780 223.3416 223.6028 223.8618 224.1186 224.3732
224.6255 224.8757

<##> measurement perfect
projection data are noiseless

<##> background absorption is 0.0
at levels
    75
background absorption 0.0000

<##> run
0.007 seconds phantom creation
0.117 seconds projection data creation
0.125 seconds used for processing command crea

<##> picture test

EXAMPLE 8 LINOGRAM RECONSTRUCTION

<##> spec  mono  75
energy spectrum is monochromatic at energy level 75

<##> obje
description of objects
density at levels

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<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
<th>angle</th>
<th>av dens</th>
</tr>
</thead>
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<td>0.0000</td>
<td>8.6250</td>
<td>6.4687</td>
<td>90.0000</td>
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<td>0.0000</td>
<td>7.8750</td>
<td>5.7187</td>
<td>90.0000</td>
<td>-0.2060</td>
</tr>
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<td>elip</td>
<td>0.0000</td>
<td>1.5000</td>
<td>0.3750</td>
<td>0.3000</td>
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<td>-0.0030</td>
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<td>-0.7500</td>
<td>0.2250</td>
<td>0.1500</td>
<td>140.0000</td>
<td>0.0100</td>
</tr>
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</table>
scale factor multiplying object densities 1.0000

seed set to 0
inhomogeneity set to 0.0000

<#> phan aver 5

density in each pixel is obtained as the average of 5 x 5 points

<#> pixe 115 size 0.1504
picture size 115 x 115, pixel size 0.1504

test picture read
EXAMPLE 8 LINOGRAM RECONSTRUCTION
0.004 seconds used for processing command pict

<#> projection real

EXAMPLE 8 LINOGRAM RECONSTRUCTION

<#> spec mono 75
energy spectrum is monochromatic at energy level 75

<#> obje
description of objects

density at levels
numb type x-coord y-coord x-length y-length angle av dens 75
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<th>0.0000</th>
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<th>6.4687</th>
<th>90.0000</th>
<th>0.4160</th>
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</thead>
<tbody>
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<td>0.0000</td>
<td>0.0000</td>
<td>7.8750</td>
<td>5.7187</td>
<td>90.0000</td>
<td>-0.2060</td>
<td>-0.2060</td>
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<td>0.0000</td>
<td>1.5000</td>
<td>0.3750</td>
<td>0.3000</td>
<td>90.0000</td>
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<td>-0.0030</td>
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<td>-0.7500</td>
<td>0.2250</td>
<td>0.1500</td>
<td>140.0000</td>
<td>0.0100</td>
<td>0.0100</td>
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<td>elip</td>
<td>0.7500</td>
<td>1.5000</td>
<td>0.3750</td>
<td>0.2250</td>
<td>50.0000</td>
<td>0.0030</td>
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<td>-7.5000</td>
<td>1.1000</td>
<td>0.6250</td>
<td>19.2000</td>
<td>-0.2040</td>
<td>-0.2040</td>
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<td>-7.5000</td>
<td>1.1000</td>
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<td>19.2100</td>
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<td>9</td>
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<td>0.0000</td>
<td>-2.2500</td>
<td>1.1250</td>
<td>3.0000</td>
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<td>0.0030</td>
<td>0.0030</td>
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<td>segm</td>
<td>-1.0000</td>
<td>3.7500</td>
<td>1.0000</td>
<td>0.5000</td>
<td>135.0000</td>
<td>-0.0030</td>
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<td>3.7500</td>
<td>1.0000</td>
<td>3.0000</td>
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<td>0.0030</td>
<td>0.0030</td>
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<tr>
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<td>segm</td>
<td>1.0000</td>
<td>3.7500</td>
<td>1.0000</td>
<td>0.5000</td>
<td>225.0000</td>
<td>-0.0030</td>
<td>-0.0030</td>
</tr>
<tr>
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<td>segm</td>
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<td>3.7500</td>
<td>1.0000</td>
<td>3.0000</td>
<td>225.0000</td>
<td>0.0030</td>
<td>0.0030</td>
</tr>
<tr>
<td>14</td>
<td>tria</td>
<td>5.0250</td>
<td>3.7500</td>
<td>1.1250</td>
<td>0.5000</td>
<td>110.7500</td>
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<td>0.2060</td>
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<tr>
<td>15</td>
<td>tria</td>
<td>-5.0250</td>
<td>3.7500</td>
<td>1.1250</td>
<td>0.9000</td>
<td>-110.7500</td>
<td>0.2060</td>
<td>0.2060</td>
</tr>
</tbody>
</table>

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

<#> rays aver 1

projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<#> geom

<#> lino
rays are parallel with variable spacing between rays
data collected along lines

number of rays per projection 231
snark computed number of rays 233
at detector spacing 0.1504
### APPENDIX A. EXAMPLES

<table>
<thead>
<tr>
<th>total number of projections</th>
<th>462</th>
</tr>
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<tbody>
<tr>
<td>projection angles</td>
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<td>50.5623</td>
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<td>57.0023</td>
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<td>222.0009</td>
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</tr>
<tr>
<td>224.6255</td>
<td></td>
</tr>
</tbody>
</table>

projection data are noiseless
EXAMPLE 8 LINOGRAM RECONSTRUCTION

0.044 seconds used for processing command proj

EXAMPLE 8a LINOGRAM METHOD

sinc 1.0
linogram reconstruction algorithm
using filter sinc
cutoff = 1.0000
algorithm executed in iteration 1
0.061 seconds for the execution of the algorithm
reconstruction completed after iteration 1
0.061 seconds for this iteration
0.192 seconds used for processing command exec

EXAMPLE 8b FILTERED BACKPROJECTION

cosine 1.0 2
convolution reconstruction algorithm
using filter cosi
cutoff (or alpha) = 1.0000
2 point lagrange interpolation
algorithm executed in iteration 1
0.109 seconds for the execution of the algorithm
reconstruction completed after iteration 1
0.109 seconds for this iteration
0.240 seconds used for processing command exec

A.9 Using a user-defined figure of merit in SNARK experimenter

This example illustrates the use of a user-written subroutine to compute a user-defined figure of merit in SNARK experimenter (see Section 8.2.6.7). A user written subroutine is provided in the file user_fom1.c. This subroutine computes a figure of merit defined by

\[ 1 - \nu^q, \]
where $v^q$ is defined in Section 5.11 with $S$ as the set of pixels whose center lies in a circle centered at the origin with a radius of 29.72. A listing of the user-written subroutine is given in Section A.9.1. This FOM demonstrates that one can reject the null hypotheses that the EM algorithm produces similarly noisy images whether or not the likelihood term is complemented by a regularizing term, in favor of the alternative hypothesis that the regularizing term reduces the noise in the reconstructions. Section A.9.2 shows a listing of the SNARK experimenter input file. In this listing the files b.9.virus.ens and b.9.projection.ss are identical to those listed in Sections 8.2.2 and 8.2.4, respectively. The files b.9.recon.ss and b.9.compare.ss are listed in Sections A.9.6 and A.9.7, respectively. The output file containing the significance results is listed in Section A.9.8.

### A.9.1 User-defined figure of merit

```c
#include <malloc.h>
#include "experimenter.h"
#include "read_eval_phantom1.h"
#include "read_eval_recon3.h"
#include "user_fom1.h"

/* ----------------------------- user_fom1.c -----------------------------
This function illustrates the use of a user-defined figure of merit.

**INPUTS:****
itr1 - array of length niters containing the iteration numbers for the first algorithm.
itr2 - array of length niters containing the iteration numbers for the second algorithm.
niters - number of iterations to be compared
keywrd1 - string containing the keyword which defines the first algorithm.
keywrd2 - string containing the keyword which defines the second algorithm.

**OUTPUTS:****
user1 - array of length niters containing the user defined figure of merit for the first algorithm.
user2 - array of length niters containing the user defined figure of merit for the second algorithm.

*/

void user_fom1(int* itr1, int* itr2, int niters, char* keywrd1, char* keywrd2, double* user1, double* user2)
{
    double *phantom,*recon1,*recon2;
    int *regions,numstr,i,j,*strarea;
    float totarea=0.0,avgarea;

    /* Read in abnormality index and area for phantom structures.
The program which does this is read_eval_phantom1.c.
NOTE: the only information to be used is the value 'numstr' (which is the number of structures in the phantom) */
    read_eval_phantom1(&regions,&numstr,&phantom,&strarea);
```
/* allocate memory to store abnormality indexes and area 
(i.e number of pixels) for structures in the 
reconstructions */
recon1 = (double *) malloc(numstr*sizeof(double));
recon2 = (double *) malloc(numstr*sizeof(double));

for(i=0;i < niters;i++) {
/* read in variance for structures in 
the reconstructions. Initialize the arrays 
which will store the user FOM */

//printf("*** about to read variance\n"); /* TEST (JD) */
read_eval_recon3(itr1[i],keywrd1,numstr,recon1);
read_eval_recon3(itr2[i],keywrd2,numstr,recon2);
/* the variance of the 'SINGLE' structure to be 
used is the first in the array. The FOM value 
is 1-variance */
user1[i]=1-recon1[0];
user2[i]=1-recon2[0];
}

free(phantom); /* free memory for next function call */
free(recon1);
free(recon2);
free(strarea);
}

A.9.2 SNARK14Experimenter input file

SEED -1
ENSEMBLE b.9.virus.ens
EXPERIMENT 1 0 95 1.6 7 18 30
DATA b.9.projection.ss
RECONSTRUCTION b.9.recon.ss
ANALYSIS b.9.compare.ss
END

A.9.3 SNARK14Experimenter virus.ens file

virus_24_1_0.96_0.6.atl
virus_24_1_0.96_0.7.atl
virus_24_1_0.96_0.8.atl
virus_24_1_0.97_0.6.atl
virus_24_1_0.97_0.7.atl
virus_24_1_0.97_0.8.atl
virus_26_1_0.96_0.6.atl
virus_26_1_0.96_0.7.atl
virus_26_1_0.96_0.8.atl
virus_26_1_0.97_0.6.atl
virus_26_1_0.97_0.7.atl
virus_26_1_0.97_0.8.atl
virus_28_1_0.96_0.6.atl
virus_28_1_0.96_0.7.atl
virus_28_1_0.96_0.8.atl
virus_28_1_0.97_0.6.atl
virus_28_1_0.97_0.7.atl
virus_28_1_0.97_0.8.atl

A.9.4 SNARK14Experimenter virus_24_1_0.96_0.6.atl file

SPECTRUM MONOCHROMATIC 60
SINGLE
elip 0 0 29.72 29.72 0 0
PAIR
elip 4.14 63.19 3.89 3.89 0 1 0.96 0.5
elip 12.36 62.11 3.89 3.89 0 1 0.96 0.5
elip 20.36 59.97 3.89 3.89 0 1 0.96 0.5
elip 28.01 56.80 3.89 3.89 0 1 0.96 0.5
elip 35.18 52.66 3.89 3.89 0 1 0.96 0.5
elip 41.76 47.61 3.89 3.89 0 1 0.96 0.5
elip 47.61 41.76 3.89 3.89 0 1 0.96 0.5
elip 52.66 35.18 3.89 3.89 0 1 0.96 0.5
elip 56.80 28.01 3.89 3.89 0 1 0.96 0.5
elip 59.97 20.36 3.89 3.89 0 1 0.96 0.5
elip 62.11 12.36 3.89 3.89 0 1 0.96 0.5
elip 63.19 4.14 3.89 3.89 0 1 0.96 0.5
elip 63.19 -4.14 3.89 3.89 0 1 0.96 0.5
elip 62.11 -12.36 3.89 3.89 0 1 0.96 0.5
elip 59.97 -20.36 3.89 3.89 0 1 0.96 0.5
elip 56.80 -28.01 3.89 3.89 0 1 0.96 0.5
elip 52.66 -35.18 3.89 3.89 0 1 0.96 0.5
elip 47.61 -41.76 3.89 3.89 0 1 0.96 0.5
elip 41.76 -47.61 3.89 3.89 0 1 0.96 0.5
elip 35.18 -52.66 3.89 3.89 0 1 0.96 0.5
elip 28.01 -56.80 3.89 3.89 0 1 0.96 0.5
elip 20.36 -59.97 3.89 3.89 0 1 0.96 0.5
elip 12.36 -62.11 3.89 3.89 0 1 0.96 0.5
elip 4.14 -63.19 3.89 3.89 0 1 0.96 0.5
DUMMY
elip 0 0 59.44 59.44 0 0.6
SCALE
1

A.9.5 SNARK14Experimenter projection.ss file

raysum average 1
1
gometry
divergent arc 153 306
rays user 101 detector spacing 3.2
angles 300 equally spaced
0 358.8
measurement noisy
quantum 0.0 0.0 calibr 4
multiplicative 1.0 0.1
seed
background 0.0
run
picture test
projection real

A.9.6 SNARK14Experimenter recon.ss file

stop iteration 15
execute average emap
alg1: testing super snark with ML
gamma is 0.0
execute average emap
alg2: testing super snark with MAP
gamma is 10.0

A.9.7 SNARK14Experimenter compare.ss file

testem
COMPARE alg1 alg2 HITR USR1
1 1
3 3
6 6
9 9
12 12
15 15
END

A.9.8 SNARK14Experimenter output file (testem.1)

FIGURE OF MERIT: Hit-ratio
alg1  mean  alg2  mean  significance level
1  0.66720085470085477297  1  0.66857448107448103070  0.2632687146066866014
3  0.66709401709401705549  3  0.67362637362637343562  0.01279497859528494486
6  0.66570512820512817154  6  0.66739926739926735966  0.28449303561745276081
9  0.67206959706959712442  9  0.67136752136752131381  0.41681030593677706
12 0.66701770451770436843  12 0.66829975579975575695  0.38225459735271893891
15 0.66312576312576299031  15 0.65789072039072016285  0.12231587153007145163

FIGURE OF MERIT: User-defined-1
alg1  mean  alg2  mean  significance level
1  0.999983333333333517  1  1.00000000000000000000  0.01267365933873415562
3  0.999706666666667645  3  0.9997766666666697992  0.000022964165589588
6  0.9989533333333291570  6  0.999240000000000012811  0.00004817048354644
9  0.9978466666666699264  9  0.9984466666666670451  0.0000000544455583539
12 0.9964533333333352410  12 0.997510000000000000778  0.00000005198049951582
15 0.9947866666666681895  15 0.996443333333335961  0.00000005097848687630

A.10 Reconstruction using blobs

This example illustrates reconstructing a simple image using both blob and pixel basis elements.
A.10.1 SNARK14 INPUT file

*******EXAMPLE 10
* ROTATED RECTANGLE WITH PSEUDO PROJECTION DATA
* RECONSTRUCTION BY ART WITH BLOB BASIS
*
*TRACE 1
CREATE
EXAMPLE 10 ROTATED RECTANGLE
SPECTRUM MONOCHROMATIC 10
OBJECTS
RECT 0.0 0.0 2.0 10.0 -30.0 1.0
LAST 1.0
PHANTOM AVERAGE 1
25 PIXELS OF SIZE 1.0
RAYSUM
RUN
*
PICTURE TEST
*
PROJECTION PSEUDO
EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS
GEOMETRY
PARALLEL UNIFORM LINE
RAYS PROGRAM 25 2.0 DETECTOR SPACING AT 2.0
ANGLES 12 EQUALLY SPACED
0.0 165.0
MEASUREMENT PERFECT
BACKGROUND 50.0
*
BASIS BLOB
*
SELECT SNARK RAYSEQ
STEP 3 1
*
STOP ITERATION 10
*
EXECUTE AVERAGE ART
ART WITH BLOB BASIS
ART3
CONSTRAINT ART2
*
BASIS PIXEL
EXECUTE AVERAGE ART
ART WITH PIXEL BASIS
ART3
CONSTRAINT ART2
*
EVALUATE BOTH
COMPARING BLOB AND PIXEL BASIS
WHOLEPIC
2222222222
END
A.10.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<<> *******EXAMPLE 10
<<> ROTATED RECTANGLE WITH PSEUDO PROJECTION DATA
<<> RECONSTRUCTION BY ART WITH BLOB BASIS
<<>
<<> TRACE 1
<#> CREATE

EXAMPLE 10 ROTATED RECTANGLE

<#> SPECTRUM MONOCHROMATIC 10
energy spectrum is monochromatic at energy level 10

<#> OBJECTS
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens 10
1 rect 0.0000 0.0000 2.0000 10.0000 -30.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

<#> PHANTOM AVERAGE 1
this run will generate a phantom
density in each pixel is obtained as the average of 1 x 1 points

<#> 25 PATS OF SIZE 1.0
picture size 25 x 25, pixel size 1.0000

<#> RAYSUM
0.000 seconds phantom creation
0.001 seconds used for processing command crea

<<> RUN
APPENDIX A. EXAMPLES

<<>

<<# PICTURE TEST

EXAMPLE 10 ROTATED RECTANGLE

<<# spec mono 10
energy spectrum is monochromatic at energy level 10

<<# obje
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens 10
1 rect 0.0000 0.0000 2.0000 10.0000 -30.0000 1.0000 1.0000

scale factor multiplying object densities 1.0000
seed set to 0
inhomogeneity set to 0.0000

<<# phan aver 1
density in each pixel is obtained as the average of 1 x 1 points

<<# pixe 25 size 1.0000
picture size 25 x 25, pixel size 1.0000

test picture read
EXAMPLE 10 ROTATED RECTANGLE
0.000 seconds used for processing command pict

<<>

<<# PROJECTION PSEUDO

EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS

<<# GEOMETRY

<<# PARALLEL UNIFORM LINE
rays are parallel with uniform spacing between rays
data collected along lines
RAYS PROGRAM 25 2.0 DETECTOR SPACING AT 2.0
number of rays per projection 37
snark computed number of rays 19
at detector spacing 2.0000

ANGLES 12 EQUALLY SPACED
total number of projections 12
projection angles 0.0000 15.0000 30.0000 45.0000 60.0000 75.0000 90.0000 105.0000 120.0000 135.0000 150.0000 165.0000

MEASUREMENT PERFECT
projection data are noiseless

BACKGROUND 50.0
at levels 10
background absorption 50.0000
estimate of totlen = 3776.330760
estimate of totden = 498.725717
estimate of average density = 0.1321
projection data read
EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS
EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS
0.000 seconds used for processing command proj

BASIS BLOB
hexagonal grid: there are 25 rows, the middle row has 21 grid points and the row next to the middle one has 22 grid points
blob basis with parameters: support = 2.0629 shape = 11.2829 delta = 1.1547 0.078 seconds used for processing command basi

SELECT SNARK RAYSEQ
STEP 3 1
sequential ray selection with ray-step 1 and projection-step 3 0.000 seconds used for processing command sele

STOP ITERATION 10
10 iterations 0.000 seconds used for processing command stop
APPENDIX A. EXAMPLES

EXECUTE AVERAGE ART

ART WITH BLOB BASIS

ART3
art3 method
relaxation parameter is 1.0
norm is 2
tolerance is 0.0

CONSTRAINT ART2
constraint art2 way
relaxation constraints with cr = 1.0
picture is not normalized
228 rays are used for each iteration
algorithm executed in iteration 1
0.001 seconds for the execution of the algorithm
iteration 1 completed
0.001 seconds for this iteration
algorithm executed in iteration 2
0.001 seconds for the execution of the algorithm
iteration 2 completed
0.001 seconds for this iteration
algorithm executed in iteration 3
0.001 seconds for the execution of the algorithm
iteration 3 completed
0.001 seconds for this iteration
algorithm executed in iteration 4
0.001 seconds for the execution of the algorithm
iteration 4 completed
0.001 seconds for this iteration
algorithm executed in iteration 5
0.001 seconds for the execution of the algorithm
iteration 5 completed
0.001 seconds for this iteration
algorithm executed in iteration 6
0.001 seconds for the execution of the algorithm
iteration 6 completed
0.001 seconds for this iteration
algorithm executed in iteration 7
0.001 seconds for the execution of the algorithm
iteration 7 completed
0.001 seconds for this iteration
algorithm executed in iteration 8
0.001 seconds for the execution of the algorithm
iteration 8 completed
0.001 seconds for this iteration
algorithm executed in iteration 9
0.001 seconds for the execution of the algorithm
iteration 9 completed
0.001 seconds for this iteration
algorithm executed in iteration 10
0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 10
0.001 seconds for this iteration
0.009 seconds for all iterations
0.010 seconds used for processing command exec

<<>
<<#> BASIS PIXEL
  pixel basis
  0.000 seconds used for processing command basis

<<#> EXECUTE AVERAGE ART
  ART WITH PIXEL BASIS
<<#> ART3
  art3 method
  relaxation parameter is 1.0
  norm is 2
  tolerance is 0.0
<<#> CONSTRAINT ART2
  constraint art2 way
  relaxation constraints with cr = 1.0
  picture is not normalized
  228 rays are used for each iteration
  algorithm executed in iteration 1
  0.000 seconds for the execution of the algorithm
  iteration 1 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 2
  0.000 seconds for the execution of the algorithm
  iteration 2 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 3
  0.000 seconds for the execution of the algorithm
  iteration 3 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 4
  0.000 seconds for the execution of the algorithm
  iteration 4 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 5
  0.000 seconds for the execution of the algorithm
  iteration 5 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 6
  0.000 seconds for the execution of the algorithm
  iteration 6 completed
  0.000 seconds for this iteration
  algorithm executed in iteration 7
0.000 seconds for the execution of the algorithm
iteration 7 completed
0.000 seconds for this iteration
algorithm executed in iteration 8
0.000 seconds for the execution of the algorithm
iteration 8 completed
0.000 seconds for this iteration
algorithm executed in iteration 9
0.000 seconds for the execution of the algorithm
iteration 9 completed
0.000 seconds for this iteration
algorithm executed in iteration 10
0.000 seconds for the execution of the algorithm
reconstruction completed after iteration 10
0.000 seconds for this iteration
0.001 seconds for all iterations
0.002 seconds used for processing command exec

<<>

<#> EVALUATE BOTH

COMPARING BLOB AND PIXEL BASIS

<#> WHOLEPIC
Region cx cy u v ang t1 t2
wholepic -1e+20 1e+20

iterations 1 2 3 4 5 6 7 8 9
last iteration

residual calculation using line integration
0.004 seconds used for processing command eval

<#> END

A.10.3 SNARK14 eval file

evaluation name: COMPARING BLOB AND PIXEL BASIS

global resolution measures

phantom name: EXAMPLE 10 ROTATED RECTANGLE
projection name: EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS

metrics for test phantom
region area average distance rel err variance std dev residual
0 625 0.1328 0.1152 0.3394 0.0000
### APPENDIX A. EXAMPLES

#### execution name: ART WITH BLOB BASIS

**metrics for algorithm ART**

<table>
<thead>
<tr>
<th>iter</th>
<th>area</th>
<th>average distance</th>
<th>rel err</th>
<th>variance</th>
<th>std dev</th>
<th>residual</th>
</tr>
</thead>
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<td>0.2669</td>
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<tr>
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<td>625</td>
<td>0.1305</td>
<td>0.4957</td>
<td>0.7881</td>
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<td>0.2663</td>
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<tr>
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<td>625</td>
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<tr>
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<td>625</td>
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<td>0.7928</td>
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<td>0.2655</td>
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<tr>
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<td>0.7951</td>
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<td>0.2647</td>
</tr>
</tbody>
</table>

#### execution name: ART WITH PIXEL BASIS

**metrics for algorithm ART**

<table>
<thead>
<tr>
<th>iter</th>
<th>area</th>
<th>average distance</th>
<th>rel err</th>
<th>variance</th>
<th>std dev</th>
<th>residual</th>
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<td>0.6932</td>
<td>1.1917</td>
<td>0.0598</td>
<td>0.2446</td>
</tr>
</tbody>
</table>

#### point by point resolution measures

**phantom name: EXAMPLE 10 ROTATED RECTANGLE**

**projection name: EXAMPLE 10 PSEUDO PROJECTION DATA FOR TWELVE VIEWS**

#### execution name: ART WITH BLOB BASIS

**metrics for alignment ART**

<table>
<thead>
<tr>
<th>align</th>
<th>iter</th>
<th>e(0)</th>
<th>e(1)</th>
<th>e(2)</th>
<th>e(3)</th>
<th>e(4)</th>
</tr>
</thead>
<tbody>
<tr>
<td>ART</td>
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<td>0.6508</td>
<td>0.4348</td>
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<td>0.0191</td>
<td>0.0026</td>
</tr>
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<td>0.4530</td>
<td>0.1313</td>
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<td>0.4445</td>
<td>0.1427</td>
<td>0.0172</td>
<td>0.0030</td>
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<tr>
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</table>

#### execution name: ART WITH PIXEL BASIS

**metrics for alignment ART**

<table>
<thead>
<tr>
<th>align</th>
<th>iter</th>
<th>e(0)</th>
<th>e(1)</th>
<th>e(2)</th>
<th>e(3)</th>
<th>e(4)</th>
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<td>0.0154</td>
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</tbody>
</table>
A.11 Simulating data collection and superiorized image reconstruction for PET

The basic setup of this example is very similar to example A.7. The following adjustments have been made in order to improve visibility: the digitization has been increased to 381 x 381 pixels, the view angles have been increased to 500 and the rays per view have been increased to 301. Superiorization is applied with the following settings: N = 16, a = 0.999, b = 1. SMOO is used as secondary optimization criterion and the stopping criterion has been changed from 20 iterations to the Kullback-Leibler distance of getting below 100,000, resulting in 12 iterations.

Figure A.11: A Brain Phantom

Figure A.12: Superiorized MAP EM reconstruction after 24 iterations
A.11.1 SNARK14 INPUT file

********EXAMPLE 11
* SUPERIORIZED MAP EM ALGORITHM FOR EMISSION TOMOGRAPHY. RECONSTRUCTION
* OF BRAIN PHANTOM. SIMULATING PET GEOMETRY WITH A RING OF 300 DETECTORS
* WITH EACH DETECTOR IN COINCIDENCE WITH 101 DETECTORS OPPOSITE IT.
* COEFFICIENT OF PENALTLY TERM IS SET TO 0
*
CREATE
EXAMPLE 11 Brain Phantom
SPECTRUM MONOCHROMATIC 511
OBJECTS
  1 elip -7.0 46.0 3.0 6.0 17.0 0.95 1.0
  2 elip 7.0 46.0 3.0 6.0 -17.0 1.0 0.95
  3 rect -12.0 64.0 7.5 4.5 5.0 1.0 1.0
  4 rect 12.0 64.0 7.5 4.5 -5.0 0.95 0.95
  5 rect -38.0 51.0 3.5 13.0 -39.0 0.95 1.0
  6 rect 38.0 51.0 3.5 13.0 39.0 1.0 0.95
  7 rect -46.0 24.0 6.5 6.0 -18.0 0.95 1.0
  8 rect 46.0 24.0 6.5 6.0 18.0 1.0 0.95
  9 rect -49.0 6.0 2.5 10.0 -63.0 0.95 0.95
 10 rect 49.0 6.0 2.5 10.0 63.0 1.0 1.0
 11 rect -52.0 -14.0 9.0 7.0 -14.0 0.95 1.0
 12 rect 52.0 -14.0 9.0 7.0 14.0 1.0 0.95
 13 rect -10.0 -56.0 5.5 10.0 -1.0 0.95 1.0
 14 rect 10.0 -56.0 5.5 10.0 1.0 1.0 0.95
 15 elip -40.0 -47.0 9.0 22.5 48.0 1.0 1.0
 16 elip 40.0 -47.0 9.0 22.5 -48.0 0.95 0.95
 17 elip 8.0 -22.0 3.5 15.5 9.0 0.95 0.95
 18 elip -27.0 -6.0 5.5 23.5 -5.0 0.95 1.0
 19 elip 27.0 -6.0 5.5 23.5 5.0 1.0 0.95
 20 elip -25.0 38.0 6.5 10.5 -14.0 1.0 1.0
 21 elip 25.0 38.0 6.5 10.5 14.0 0.95 0.95
 22 elip -8.0 32.0 1.5 6.5 38.0 1.0 1.0
 23 rect 8.0 32.0 1.5 6.5 -38.0 0.95 0.95
 24 rect -8.0 3.0 1.0 9.0 -33.0 0.95 1.0
 25 rect 8.0 3.0 1.0 9.0 33.0 1.0 0.95
 27 elip 0.0 0.0 66.5 74.0 0.0 1.0 1.0
LAST .51 1 0.05
PHANTOM AVERAGE 7
381 PIXELS OF SIZE 0.4
RAYSUM AVERAGE 1
1
GEOMETRY
divergent arc 153 306
RAYS USER 301 DETECTOR SPACING 1.1
ANGLES 500 EQUAL SPACING
0.0 358.8
MEASUREMENT NOISY
QUANTUM 1.0 1.0 CALIBRATION 4
SEED 0
BACKGROUND 0.0
RUN
APPENDIX A. EXAMPLES

* PICTURE TEST
* PROJECTION REAL
* STOP TERMINATION KLDS 100000 RPRT
* SUPERIORIZE 16 0.999 1 SMOO RPRT
EXECUTE AVERAGE EMAP
Example 11 Illustrating the Superiorized MAP EM algorithm for PET
gamma is 0 EVAL
*
END

A.11.2 SNARK14 OUTPUT file

snark14.s171029 - A PICTURE RECONSTRUCTION PROGRAM

<*> *******EXAMPLE 11
<*> SUPERIORIZED MAP EM ALGORITHM FOR EMISSION TOMOGRAPHY. RECONSTRUCTION
<*> OF BRAIN PHANTOM. SIMULATING PET GEOMETRY WITH A RING OF 300 DETECTORS
<*> WITH EACH DETECTOR IN COINCIDENCE WITH 101 DETECTORS OPPOSITE IT.
<*> COEFFICIENT OF PENALTLY TERM IS SET TO 0
<*> CREATE

EXAMPLE 11 Brain Phantom

<#> SPECTRUM MONOCHROMATIC 511
energy spectrum is monochromatic at energy level 511

<#> OBJECTS
description of objects

density at levels

<table>
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<tr>
<th>numb</th>
<th>type</th>
<th>x-coord</th>
<th>y-coord</th>
<th>x-length</th>
<th>y-length</th>
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<td>46.0000</td>
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<td>-17.0000</td>
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<tr>
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<td>4.5000</td>
<td>-5.0000</td>
<td>0.9500</td>
<td>0.9500</td>
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</table>
APPENDIX A. EXAMPLES

scale factor multiplying object densities 0.5100

seed set to 1
inhomogeneity set to 0.0500

<#> PHANTOM AVERAGE 7

this run will generate a phantom
density in each pixel is obtained as the average of 7 x 7 points

<#> 381 PIXELS OF SIZE 0.4
picture size 381 x 381, pixel size 0.4000

<#> RAYSUM AVERAGE 1
this run will generate projection data
projection data are calculated by dividing each ray interval into 1 substrips
with aperture (substrip) weights 1

<#> GEOMETRY
<#> divergent arc 153 306
rays are divergent from point sources
source to origin distance 153.0000
the detectors lie on an arc with source to detector distance = 306.0000

<#> RAYS USER 301 DETECTOR SPACING 1.1
number of rays per projection 301
at detector spacing 1.1000

<#> ANGLES 500 EQUAL SPACING
total number of projections 500
projection angles 0.0000 0.7190 1.4381 2.1571 2.8762 3.5952 4.3142
35.9519 36.6709 37.3900 38.1090 38.8281 39.5471 40.2661
43.1423 43.8613 44.5804 45.2994 46.0184 46.7375 47.4565
50.3327 51.0517 51.7707 52.4898 53.2088 53.9279 54.6469
57.5230 58.2421 58.9611 59.6802 60.3992 61.1182 61.8373
64.7134 65.4325 66.1515 66.8705 67.5896 68.3086 69.0277
71.9038 72.6228 73.3419 74.0609 74.7800 75.4990 76.2180
79.0942 79.8132 80.5323 81.2513 81.9703 82.6894 83.4084
86.2846 87.0036 87.7226 88.4417 89.1607 89.8798 90.5988
93.4749 94.1940 94.9130 95.6321 96.3511 97.0701 97.7892
100.6653 101.3844 102.1034 102.8224 103.5415 104.2605 104.9796
107.8557 108.5747 109.2938 110.0128 110.7319 111.4509 112.1699
115.0461 115.7651 116.4842 117.2032 117.9222 118.6413 119.3603
122.2365 122.9556 123.6745 124.3936 125.1126 125.8317 126.5507
129.4269 130.1459 130.8649 131.5840 132.3030 133.0220 133.7411
136.6172 137.3363 138.0553 138.7743 139.4934 140.2124 140.9315
143.8076 144.5267 145.2457 145.9647 146.6838 147.4028 148.1218
150.9980 151.7170 152.4361 153.1551 153.8741 154.5932 155.3122
APPENDIX A. EXAMPLES

158.1884 158.9074 159.6265 160.3455 161.0645 161.7836 162.5026 163.2216 163.9407 164.6597
165.3788 166.0978 166.8168 167.5359 168.2549 168.9739 169.6930 170.4120 171.1311 171.8501
172.5691 173.2882 174.0072 174.7263 175.4453 176.1643 176.8834 177.6024 178.3214 179.0405
186.9499 187.6689 188.3880 189.1070 189.8261 190.5451 191.2641 191.9832 192.7022 193.4212
194.1403 194.8593 195.5784 196.2974 197.0164 197.7355 198.4545 199.1735 199.8926 200.6116
201.3307 202.0497 202.7687 203.4878 204.2068 204.9259 205.6449 206.3639 207.0830 207.8020
208.5210 209.2401 209.9591 210.6782 211.3972 212.1162 212.8353 213.5543 214.2733 214.9924
215.7114 216.4305 217.1495 217.8685 218.5876 219.3066 220.0257 220.7447 221.4637 222.1828
222.9018 223.6208 224.3399 225.0589 225.7780 226.4970 227.2160 227.9351 228.6541 229.3731
237.2826 238.0016 238.7206 239.4397 240.1587 240.8778 241.5968 242.3158 243.0349 243.7539
244.4729 245.1920 245.9110 246.6301 247.3491 248.0681 248.7872 249.5062 250.2253 250.9443
251.6633 252.3824 253.1014 253.8204 254.5395 255.2585 255.9776 256.6966 257.4156 258.1347
258.8537 259.5727 260.2918 261.0108 261.7299 262.4489 263.1679 263.8870 264.6060 265.3251
266.0441 266.7631 267.4822 268.2012 268.9202 269.6393 270.3583 271.0774 271.7964 272.5154
273.2345 273.9535 274.6725 275.3916 276.1106 276.8297 277.5487 278.2677 279.0868 279.8058
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287.6152 288.3343 289.0533 289.7723 290.4914 291.2104 291.9295 292.6485 293.3675 294.0866
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316.3768 317.0958 317.8148 318.5339 319.2529 319.9719 320.6910 321.4100 322.1291 322.8481
323.5671 324.2862 325.0052 325.7242 326.4433 327.1623 327.8814 328.6004 329.3194 330.0385
330.7575 331.4766 332.1956 332.9146 333.6337 334.3527 335.0717 335.7908 336.5098 337.2289
337.9479 338.6669 339.3860 340.1050 340.8240 341.5431 342.2621 342.9812 343.7002 344.4192
345.1383 345.8573 346.5764 347.2954 348.0144 348.7335 349.4525 350.1715 350.8906 351.6096
352.3287 353.0477 353.7667 354.4858 355.2048 355.9238 356.6429 357.3620 358.0810 358.8000

<##> MEASUREMENT NOISY
noise characteristics of projection data follow nature characteristics

<##> QUANTUM 1.0 1.0 CALIBRATION 4
Emission tomography

<##> SEED 0
seed for random number generator is 0

<##> BACKGROUND 0.0
at levels 511
background absorption 0.0000

<##> RUN
0.361 seconds phantom creation
1.177 seconds projection data creation
1.539 seconds used for processing command crea

<<*>>
### EXAMPLE 11 Brain Phantom

**Example Description:**
- **Spec:** mono 511
- Energy spectrum is monochromatic at energy level 511

#### Description of Objects

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<tr>
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<th>x-length</th>
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<th>density at levels</th>
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APPENDIX A. EXAMPLES

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22 elip 25.0000 38.0000 6.5000 10.5000 14.0000 0.4845 0.4845
23 rect -8.0000 32.0000 1.5000 6.5000 38.0000 0.5100 0.5100
24 rect 8.0000 32.0000 1.5000 6.5000 -38.0000 0.4845 0.4845
25 rect -8.0000 3.0000 1.0000 9.0000 -33.0000 0.4845 0.4845
26 rect 8.0000 3.0000 1.0000 9.0000 33.0000 0.5100 0.5100
27 elip 0.0000 0.0000 66.5000 74.0000 0.0000 0.5100 0.5100

scale factor multiplying object densities 0.5100
seed set to 1
inhomogeneity set to 0.0500
<#> phan aver 7
density in each pixel is obtained as the average of 7 x 7 points

<#> pixe 381 size 0.4000
picture size 381 x 381, pixel size 0.4000
test picture read
EXAMPLE 11 Brain Phantom
0.039 seconds used for processing command pict

<<>

<#> PROJECTION REAL
EXAMPLE 11 Brain Phantom

<#> spec mono 511
energy spectrum is monochromatic at energy level 511

<#> obje
description of objects
density at levels
numb type x-coord y-coord x-length y-length angle av dens
1 elip -7.0000 46.0000 3.0000 6.0000 17.0000 0.4845 0.4845
2 elip 7.0000 46.0000 3.0000 6.0000 -17.0000 0.5100 0.5100
3 rect -12.0000 64.0000 7.5000 4.5000 5.0000 0.5100 0.5100
APPENDIX A. EXAMPLES

scale factor multiplying object densities  0.5100
seed set to 1
inhomogeneity set to 0.0500
APPENDIX A. EXAMPLES

1 rays aver 1

projection data are calculated by dividing each ray interval into 1 substrips

with aperture (substrip) weights 1

1 geom

1 dive arc source at 153.0000 det dist 306.0000

rays are divergent from point sources

source to origin distance 153.0000

the detectors lie on an arc with source to detector distance = 306.0000

1 rays user 301 spacing 1.1000

number of rays per projection 301

snark computed number of rays 437

at detector spacing 1.1000

1 angl 500

total number of projections 500

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APPENDIX A. EXAMPLES

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208.5210 209.2401 209.9591 210.6782 211.3972 212.1162 212.8353 213.5543 214.2733 214.9924 
215.7114 216.4305 217.1495 217.8685 218.5876 219.3066 220.0257 220.7447 221.4637 222.1828 
222.9018 223.6208 224.3399 225.0589 225.7780 226.4970 227.2160 227.9351 228.6541 229.3731 
237.2826 238.0016 238.7206 239.4397 240.1587 240.8778 241.5968 242.3158 243.0349 243.7539 
244.4729 245.1920 245.9110 246.6301 247.3491 248.0681 248.7872 249.5061 250.2252 250.9443 
251.6633 252.3824 253.1014 253.8204 254.5395 255.2585 255.9776 256.6966 257.4156 258.1347 
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279.4248 280.1439 280.8629 281.5820 282.3010 283.0200 284.7391 285.4581 286.1772 286.8962 
287.6152 288.3343 289.0533 289.7723 290.4914 291.2104 291.9295 292.6485 293.3675 294.0866 
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337.9479 338.6669 339.3860 340.1050 340.8240 341.5431 342.2621 342.9811 343.7002 344.4192 
345.1383 345.8573 346.5764 347.2954 348.0144 348.7335 349.4526 350.1716 350.8906 351.6096 
352.3287 353.0477 353.7667 354.4858 355.2048 355.9238 356.6429 357.3619 358.0810 358.8000 

Meas. Noise

Characteristics of projection data follow the nature characteristics.

Quant 1.0000 1.0000 cali 4

Emission tomography

Seed 0

Seed for random number generator is 0

Back 0.0000

At levels 511

Background absorption 0.0000

Estimate of totalen = 20962469.574466
Estimate of totden = 9802000.000000
Estimate of average density = 0.4676

Projection data read

Example 11 Brain Phantom

0.051 seconds used for processing command proj

Stop termination klds 100000 rpert

Termination test klds

Reporting is enabled

Reporting file: RPRTklds
reporting on every iteration
epsilon = 100000
   0.000 seconds used for processing command stop

<<>

<#> SUPERIORIZE 16 0.999 1 SMOO RPRT
Superiorization is enabled
N = 16
a = 0.999
b = 1
secondary criterion: smoo
reporting is enabled
reporting file: RPRTsuperiorization
reporting on every iteration
   0.000 seconds used for processing command supe

<#> EXECUTE AVERAGE EMAP

Example 11 Illustrating the Superiorized MAP EM algorithm for PET

<#> gamma is 0 EVAL

-----------------------------------------------------------
maximum a-posteriori probability expectation maximization

   gamma: 0.000
   evaluation flag is set

-----------------------------------------------------------

   value of l: 15
   value of phi before algorithm operator: 4.42622e-28
   value of phi after algorithm operator: 3.14467
algorithm executed in iteration 1
   3.333 seconds for the execution of the algorithm
current epsilon (KL distance) = 638282
iteration 1 completed
   4.308 seconds for this iteration
   value of l: 31
   value of phi before algorithm operator: 0.429607
   value of phi after algorithm operator: 1.65065
algorithm executed in iteration 2
   2.215 seconds for the execution of the algorithm
current epsilon (KL distance) = 446785
iteration 2 completed
   3.228 seconds for this iteration
   value of l: 47
   value of phi before algorithm operator: 0.706119
   value of phi after algorithm operator: 2.49879
algorithm executed in iteration 3
2.225 seconds for the execution of the algorithm
current epsilon (KL distance) = 331430
iteration 3 completed
  3.246 seconds for this iteration
  value of l: 63
  value of phi before algorithm operator: 0.564997
  value of phi after algorithm operator: 2.14542
algorithm executed in iteration 4
  2.242 seconds for the execution of the algorithm
current epsilon (KL distance) = 257464
iteration 4 completed
  3.246 seconds for this iteration
  value of l: 79
  value of phi before algorithm operator: 0.577605
  value of phi after algorithm operator: 2.1505
algorithm executed in iteration 5
  2.293 seconds for the execution of the algorithm
current epsilon (KL distance) = 207738
iteration 5 completed
  3.347 seconds for this iteration
  value of l: 95
  value of phi before algorithm operator: 0.579469
  value of phi after algorithm operator: 2.11049
algorithm executed in iteration 6
  2.523 seconds for the execution of the algorithm
current epsilon (KL distance) = 173224
iteration 6 completed
  3.666 seconds for this iteration
  value of l: 111
  value of phi before algorithm operator: 0.581496
  value of phi after algorithm operator: 2.08666
algorithm executed in iteration 7
  2.553 seconds for the execution of the algorithm
current epsilon (KL distance) = 148708
iteration 7 completed
  4.322 seconds for this iteration
  value of l: 127
  value of phi before algorithm operator: 0.587932
  value of phi after algorithm operator: 2.07545
algorithm executed in iteration 8
  3.349 seconds for the execution of the algorithm
current epsilon (KL distance) = 130971
iteration 8 completed
  4.363 seconds for this iteration
  value of l: 143
  value of phi before algorithm operator: 0.598034
  value of phi after algorithm operator: 2.07283
algorithm executed in iteration 9
  2.207 seconds for the execution of the algorithm
current epsilon (KL distance) = 117930
iteration 9 completed
  3.191 seconds for this iteration
  value of l: 159
  value of phi before algorithm operator: 0.610951
value of phi after algorithm operator:  2.07635
algorithm executed in iteration  10
 2.381 seconds for the execution of the algorithm
current epsilon (KL distance) = 108196
iteration  10 completed
 3.380 seconds for this iteration
value of l:  175
value of phi before algorithm operator:  0.625866
value of phi after algorithm operator:  2.08405
algorithm executed in iteration  11
 2.345 seconds for the execution of the algorithm
current epsilon (KL distance) = 100827
iteration  11 completed
 3.616 seconds for this iteration
value of l:  191
value of phi before algorithm operator:  0.64192
value of phi after algorithm operator:  2.09414
algorithm executed in iteration  12
 2.838 seconds for the execution of the algorithm
current epsilon (KL distance) = 95173.6
reconstruction completed after iteration  12
 3.922 seconds for this iteration
43.835 seconds for all iterations
43.992 seconds used for processing command exec

<!--

A.11.3 SNARK14 RPRTsuperiorization file

superiorization reporting output

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<td>3.144667097</td>
</tr>
<tr>
<td>2</td>
<td>31</td>
<td>0.429607167</td>
<td>1.650648486</td>
</tr>
<tr>
<td>3</td>
<td>47</td>
<td>0.706118937</td>
<td>2.498788058</td>
</tr>
<tr>
<td>4</td>
<td>63</td>
<td>0.564997126</td>
<td>2.145424127</td>
</tr>
<tr>
<td>5</td>
<td>79</td>
<td>0.577604758</td>
<td>2.150495034</td>
</tr>
<tr>
<td>6</td>
<td>95</td>
<td>0.579469392</td>
<td>2.110487832</td>
</tr>
<tr>
<td>7</td>
<td>111</td>
<td>0.581496172</td>
<td>2.086655912</td>
</tr>
<tr>
<td>8</td>
<td>127</td>
<td>0.587931709</td>
<td>2.075449463</td>
</tr>
<tr>
<td>9</td>
<td>143</td>
<td>0.598033798</td>
<td>2.072629250</td>
</tr>
<tr>
<td>10</td>
<td>159</td>
<td>0.610951264</td>
<td>2.076351897</td>
</tr>
<tr>
<td>11</td>
<td>175</td>
<td>0.625866008</td>
<td>2.084050951</td>
</tr>
<tr>
<td>12</td>
<td>191</td>
<td>0.641919981</td>
<td>2.094143205</td>
</tr>
</tbody>
</table>

-->
Appendix B

FILE11: A TOOL FOR ENTERING USER DATA

SNARK14 is capable of reconstructing objects using user-supplied data. To do that, you must first create a file11 containing the user data. That file is an ASCII file consisting of the CREATE command Sets 1, 2, 3, 5, 6, and 7 (see Section 5.3.3) followed by the user data. In Set 6 be sure to use the USER option of the RAYS command. Each projection of the user data starts a command line containing the projection angle in both radians and degrees. These angles must be in the same order and agree with the angles specified in CREATE command Set 6. The next lines contain the projection data. The order of the rays within a projection is illustrated in Figures 2.1 and 2.2. The SNARK14 program reads lines until it finds user-rays (the values specified on the RAYS USER command line) values. This is repeated for each projection angle. The SNARK14 commands to reconstruct images from this data should omit the CREATE sequence. The first commands should be:

\[
\text{PICTURE RECONSTRUCTION } nelem \text{ pixel-size} \\
\text{PROJECTION REAL}
\]

where \textit{nelem} and \textit{pixel-size} describe the reconstruction geometry. These are followed the commands needed for the desired reconstruction algorithm and outputs.
Appendix C

STRUCTURE OF PRJFIL AND RECFIL

Both prjfil and recfil consist of XML headers followed by binary data. The XML header files are described by schema files PRJFIL.xsd and RECFIL.xsd, respectively. Familiarity with XML and XSD schemas is necessary to understand these files. There are many books that can provide that understanding. Users without such understanding can still use files prjfil and recfil, by creating them using the standard SNARK14 commands PICTURE and PROJECTION (Sections 5.4 and 5.5). For those users who wish to create such files themselves, the schema files can be obtained by the following sequence of clicks (starting on the Desktop of the Virtual Machine):

Computer⇒usr⇒local⇒snark14⇒src⇒snark14⇒schema

C.1 PRJFIL.xsd

```xml
<?xml version = "1.0" ?>

<xsd:schema
    xmlns:xsd="http://www.w3.org/2001/XMLSchema">

    <!-- documentation of schema file -->
    <xsd:annotation>
        <xsd:documentation xml:lang="en">
            This is a SNARK09 prjfil schema file.
            See PRJFIL.xml for an instance file of this type,
            it will clear up how such a file should look.
            Version: $Revision: 1.2 $
            Last Updated: $Date: 2008/09/06 22:22:46 $
        </xsd:documentation>
    </xsd:annotation>

    <xsd:element name="DIG_DATA">
        <xsd:complexType>
            <xsd:sequence>
                <xsd:element name="main_header">
                    <xsd:complexType>
                        <xsd:sequence>
                            <xsd:element name="comments" type="xsd:string" minOccurs="0"/>
                            <xsd:element name="dimensions">
                                <xsd:complexType>
                                    <!-- dimension is the vector (USRAYS, 1, 1) -->
                                </xsd:complexType>
                            </xsd:element>
                        </xsd:sequence>
                    </xsd:complexType>
                </xsd:element>
            </xsd:sequence>
        </xsd:complexType>
    </xsd:element>
</xsd:schema>
```
<xsd:attribute name="x" type="oddPositiveInteger" use="required"/>
<xsd:attribute name="y" type="xsd:positiveInteger" fixed="1"/>
<xsd:attribute name="z" type="xsd:positiveInteger" fixed="1"/>
</xsd:complexType>
</xsd:element> <!-- dimensions -->
<xsd:element name="sampling_rate_x">
<xsd:complexType> <!-- sampling_rate_x is the vector (PINC, 0, 0) -->
<xsd:attribute name="x" type="positiveReal" use="required"/>
<xsd:attribute name="y" type="nonNegativeReal" fixed="0.0"/>
<xsd:attribute name="z" type="nonNegativeReal" fixed="0.0"/>
</xsd:complexType>
</xsd:element> <!-- sample_rate_x -->
<xsd:element name="sampling_rate_y">
<xsd:complexType> <!-- sampling_rate_y is the vector (0, 0, 0) -->
<xsd:attribute name="x" type="nonNegativeReal" fixed="0.0"/>
<xsd:attribute name="y" type="nonNegativeReal" fixed="0.0"/>
<xsd:attribute name="z" type="nonNegativeReal" fixed="0.0"/>
</xsd:complexType>
</xsd:element> <!-- sampling_rate_y -->
<xsd:element name="sampling_rate_z">
<xsd:complexType> <!-- sampling_rate_z is the vector (0, 0, 0) -->
<xsd:attribute name="x" type="nonNegativeReal" fixed="0.0"/>
<xsd:attribute name="y" type="nonNegativeReal" fixed="0.0"/>
<xsd:attribute name="z" type="nonNegativeReal" fixed="0.0"/>
</xsd:complexType>
</xsd:element> <!-- sampling_rate_z -->
</xsd:sequence>
<xsd:attribute name="type" use="required">
<xsd:simpleType>
<xsd:restriction base="xsd:string">
<xsd:pattern value="SNARK09 prjfil"/>
</xsd:restriction>
</xsd:simpleType>
</xsd:attribute> <!-- type -->
<xsd:attribute name="title" type="xsd:string" use="required"/>
<xsd:attribute name="channels" use="required">
<xsd:simpleType>
<xsd:restriction base="xsd:positiveInteger">
<xsd:pattern value="1"/>
</xsd:restriction>
</xsd:simpleType>
</xsd:attribute> <!-- channels -->
<xsd:attribute name="number_of_arrays" type="xsd:positiveInteger" use="required"/>
<xsd:attribute name="number_of_array_sets" type="xsd:positiveInteger" use="required"/>
<xsd:attribute name="endian" use="required">
<xsd:simpleType>
<xsd:restriction base="xsd:string">
<xsd:pattern value="little|big"/>
</xsd:restriction>
</xsd:simpleType>
</xsd:attribute> <!-- endian -->
<xsd:attribute name="value_type" use="required"/>
<xsd:complexType>
  <xsd:sequence>
  </xsd:sequence>
</xsd:complexType>
<xsd:element name="detector_type">
  <xsd:simpleType>
    <xsd:restriction base="xsd:string">
      <xsd:pattern value="tangent|arc"/>
    </xsd:restriction>
  </xsd:simpleType>
</xsd:element> <!-- detector_type -->
</xsd:sequence>
<xsd:element> <!-- divergent -->
  <xsd:complexType>
    <xsd:sequence>
      <xsd:element name="detector_type">
        <xsd:simpleType>
          <xsd:restriction base="xsd:string">
            <xsd:pattern value="uniform|variable"/>
          </xsd:restriction>
        </xsd:simpleType>
      </xsd:element> <!-- detector_type -->
      <xsd:element name="projection_type">
        <xsd:simpleType>
          <xsd:restriction base="xsd:string">
            <xsd:pattern value="strip|line"/>
          </xsd:restriction>
        </xsd:simpleType>
      </xsd:element> <!-- projection_type -->
    </xsd:sequence>
  </xsd:complexType>
</xsd:element> <!-- parallel -->
</xsd:choice>
</xsd:complexType>
</xsd:element> <!-- geometric_header -->
</xsd:element name="noise_header">
  <xsd:complexType>
    <xsd:sequence>
      <xsd:element name="quantum" minOccurs="0" maxOccurs="1">
        <xsd:complexType>
          <xsd:attribute name="mean" type="xsd:decimal" use="required"/>
          <xsd:attribute name="calibration_measurement" type="xsd:decimal" use="required"/>
          <xsd:attribute name="gantry_arrangement" use="required"/>
        </xsd:complexType>
      </xsd:element>
    </xsd:sequence>
  </xsd:complexType>
</xsd:element> <!-- noise_header -->
APPENDIX C. STRUCTURE OF PRJFIL AND RECFL

</xsd:simpleType>
</xsd:attribute> <!-- gantry_arrangement -->
</xsd:complexType>
</xsd:element> <!-- quantum -->
<xsd:element name="scatter" minOccurs="0" maxOccurs="1">
<xsd:complexType>
  <xsd:attribute name="peak" type="positiveReal"
    use="required"/> <!-- value of SCTNPK -->
  <xsd:attribute name="width" type="positiveReal"
    use="required"/> <!-- value of SCTNWD -->
</xsd:complexType>
</xsd:element> <!-- scatter -->
<xsd:element name="additive" minOccurs="0" maxOccurs="1">
<xsd:complexType>
  <xsd:attribute name="mean" type="xsd:decimal"
    use="required"/> <!-- value of ADDNMN -->
  <xsd:attribute name="standard_deviation"
    type="xsd:decimal" use="required"/> <!-- value of ADDNSD -->
</xsd:complexType>
</xsd:element> <!-- additive -->
<xsd:element name="multiplicative" minOccurs="0" maxOccurs="1">
<xsd:complexType>
  <xsd:attribute name="mean" type="xsd:decimal"
    use="required"/> <!-- value of MULTNMN != 0 -->
  <xsd:attribute name="standard_deviation"
    type="xsd:decimal" use="required"/> <!-- value of MULTNSD -->
</xsd:complexType>
</xsd:element> <!-- multiplicative -->
</xsd:sequence>
</xsd:complexType>
</xsd:element> <!-- noise_header -->
</xsd:element>
</xsd:complexType>
</xsd:element> <!-- spectrum_header -->
</xsd:complexType>
</xsd:sequence>
<xsd:element name="energy_level" minOccurs="1" maxOccurs="7">
<xsd:complexType> <!-- should occur number_of_energies times -->
  <xsd:attribute name="energy" type="xsd:integer"
    use="required"/> <!-- values of -->
  <xsd:attribute name="ratio" type="nonNegativeReal"
    use="required"/> <!-- values of PERCENT/100 -->
  <xsd:attribute name="background" type="xsd:decimal"
    use="required"/> <!-- values of backgr -->
</xsd:complexType>
</xsd:element> <!-- energy_level -->
</xsd:sequence>
</xsd:complexType>
</xsd:element> <!-- number_of_energies -->
</xsd:simpleType> <!-- value of NERGY -->
</xsd:complexType>
</xsd:element> <!-- number_of_energies -->
APPENDIX C. STRUCTURE OF PRJFIL AND RECFIL

C.2 RECFIL.xsd

<?xml version = "1.0" ?>

<xsd:schema
 xmlns:xsd="http://www.w3.org/2001/XMLSchema">

  <!-- documentation of schema file -->
  <xsd:annotation>
    <xsd:documentation xml:lang="en">
      This is an SNARK09 recfil schema file.
      See RECFIL.xml for an instance file of this type,
      it will clear up how such a file should look.
      Version: $Revision: 1.2 $
      Last Updated: $Date: 2008/09/06 22:22:46 $
    </xsd:documentation>
  </xsd:annotation>

  <xsd:element name="DIG_DATA">
    <xsd:complexType>
      <xsd:sequence>
        <xsd:element name="main_header">
          <xsd:complexType>
            <xsd:sequence>
              <xsd:element name="comments" type="xsd:string" minOccurs="0"/>
              <xsd:element name="dimensions">
                <xsd:complexType> <!-- dimensions is vector (NELEM, NELEM, 1) -->
                  <xsd:attribute name="x" type="oddPositiveInteger" use="required"/>
                  <xsd:attribute name="y" type="oddPositiveInteger" use="required"/>
                  <xsd:attribute name="z" type="oddPositiveInteger" fixed="1"/>
                </xsd:complexType>
              </xsd:element> <!-- dimensions -->
              <xsd:element name="sampling_rate_x">
                <xsd:complexType> <!-- sampling_rate_x is vector (PIXSIZ, 0, 0) -->
                  <xsd:attribute name="x" type="positiveReal" use="required"/>
                  <xsd:attribute name="y" type="nonNegativeReal" fixed="0"/>
                  <xsd:attribute name="z" type="nonNegativeReal" fixed="0"/>
                </xsd:complexType>
              </xsd:element> <!-- sampling_rate_x -->
              <xsd:element name="sampling_rate_y">
                <xsd:complexType> <!-- sampling_rate_y is vector (0, PIXSIZ, 0) -->
                  <xsd:attribute name="x" type="nonNegativeReal" fixed="0"/>
                  <xsd:attribute name="y" type="positiveReal" use="required"/>
                  <xsd:attribute name="z" type="nonNegativeReal" fixed="0"/>
                </xsd:complexType>
              </xsd:element> <!-- sampling_rate_y -->
            </xsd:sequence>
          </xsd:complexType>
        </xsd:element> <!-- main_header -->
      </xsd:sequence>
    </xsd:complexType>
  </xsd:element> <!-- DIG_DATA -->
</xsd:schema>
APPENDIX C. STRUCTURE OF PRJFIL AND RECFIL

</xsd:complexType>
</xsd:element> <!-- sampling_rate_y -->
<xsd:complexType> <!-- sampling_rate_z is vector (0, 0, 0) -->
    <xsd:attribute name="x" type="nonNegativeReal" fixed="0"/>
    <xsd:attribute name="y" type="nonNegativeReal" fixed="0"/>
    <xsd:attribute name="z" type="nonNegativeReal" fixed="0"/>
</xsd:complexType>
</xsd:element> <!-- sampling_rate_z -->
</xsd:sequence>
<xsd:attribute name="type" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:string">
            <xsd:pattern value="SNARK09 recfil"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- type -->
<xsd:attribute name="title" type="xsd:string" use="required"/>
<xsd:attribute name="channels" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:positiveInteger">
            <xsd:pattern value="1"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- channels -->
<xsd:attribute name="number_of_arrays" type="xsd:positiveInteger" use="required"/>
<xsd:attribute name="number_of_array_sets" type="xsd:positiveInteger" use="required"/>
<xsd:attribute name="endian" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:string">
            <xsd:pattern value="little|big"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- endian -->
<xsd:attribute name="value_type" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:string">
            <xsd:pattern value="real"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- value_type -->
<xsd:attribute name="data_type" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:string">
            <xsd:pattern value="double"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- data_type -->
<xsd:attribute name="data_format" use="required">
    <xsd:simpleType>
        <xsd:restriction base="xsd:string">
            <xsd:pattern value="binary"/>
        </xsd:restriction>
    </xsd:simpleType>
</xsd:attribute> <!-- data_format -->
<xsd:complexType>
  <xsd:attribute name="data_format" use="required">
    <xsd:simpleType>
      <xsd:restriction base="xsd:string">
        <xsd:pattern value="SC"/>
      </xsd:restriction>
    </xsd:simpleType>
  </xsd:attribute> <!-- data_format -->
  <xsd:attribute name="grid_type" use="required">
    <xsd:simpleType>
      <xsd:restriction base="xsd:string">
        <xsd:pattern value="SC"/>
      </xsd:restriction>
    </xsd:simpleType>
  </xsd:attribute> <!-- grid_type -->
  <xsd:attribute name="basis_function" use="required">
    <xsd:simpleType>
      <xsd:restriction base="xsd:string">
        <xsd:pattern value="voronoi"/>
      </xsd:restriction>
    </xsd:simpleType>
  </xsd:attribute> <!-- basis_function -->
  <xsd:attribute name="unit" use="required">
    <xsd:simpleType>
      <xsd:restriction base="xsd:string">
        <xsd:pattern value="unspecified"/>
      </xsd:restriction>
    </xsd:simpleType>
  </xsd:attribute> <!-- unit -->
  <xsd:attribute name="other_unit" use="optional">
    <xsd:simpleType>
      <xsd:restriction base="xsd:string">
        <xsd:pattern value=""/> <!-- other_unit -->
      </xsd:restriction>
    </xsd:simpleType>
  </xsd:attribute>
  <xsd:element name="main_header">
    <xsd:complexType>
      <xsd:sequence>
        <xsd:element name="comments" type="xsd:string" minOccurs="0"/>
        <xsd:element name="parameters" type="xsd:string" />
        <xsd:element name="array_header" minOccurs="1" maxOccurs="unbounded">
          <xsd:complexType>
            <xsd:sequence>
              <xsd:element name="comments" type="xsd:string" minOccurs="0"/> <!-- array_header -->
            </xsd:sequence>
            <xsd:attribute name="enumeration_number" type="xsd:nonNegativeInteger" use="required"/>
          </xsd:complexType>
        </xsd:element> <!-- array_header -->
      </xsd:sequence>
    </xsd:complexType>
  </xsd:element> <!-- main_header -->
</xsd:complexType>
C.3 Creating a prjfil or recfil

Some users may wish to create their own prjfil or recfil for use with snark14. Those files consist of an XML header following the appropriate schema, PRJFIL.xsd or RECFIL.xsd, immediately followed by the binary data. The data file is a raw binary file containing the data in any IEEE 754 representation in either big or little endian byte order. There are several ways in which to create the XML header. Two possibilities are:

1. extract the header from an existing prjfil or recfil and edit it to match the binary data,
2. create the header from scratch following the schema.

In either case, the header needs to be checked for validity. Although every effort has been made to ensure that SNARK14 will accept all valid XML headers, some invalid headers are known to cause SNARK14 to terminate in unexpected ways. One possible way to validate a user-generated XML header is to use an XML schema validator. In the prjfil case, another possibility is to use the CREATE sequence (see Section 5.3) with no objects to describe the data collection geometry and then the PROJECTION REAL command (see Section 5.5) to create a prjfil and then run the command

```
# tr -d '\000' < prjfil > prjfil.xml
```
to strip off the data.
If “data” is the file containing the projection data in the specified format, then they can be combined into a
prjfil by the command

    # cat prjfil.xml data > prjfil

A similar approach can be used to create a recfil from its XML header data.
Appendix D

SNARK14 SOURCE CODE AND SCRIPTS

D.1 SNARK14 source code

The SNARK14 source code can be obtained by the following sequence of clicks (starting on the Desktop of the Virtual Machine):
Computer⇒usr⇒local⇒snark14⇒src⇒snark14⇒snark

D.2 snark14GetExamples

Executing the snark14GetExamples script in a directory will create a copy of the inputs needed to recreate the eleven examples of Appendix A in a directory of the user’s choosing. The default is to create a directory called snark14Examples in the current directory and place the examples there. Each example includes a script called run that will execute SNARK14 and recreate the example. In addition, Example 2 contains a script called build that is used to recreate the SNARK14 executable containing the user-defined algorithm and Example 9 includes files needed for the experimenter run of that example.

D.3 snark14GetUserDefined

The snark14GetUserDefined script is located in the same directory where SNARK14 was installed, which, under normal circumstances, is Root/usr/local/snark14/bin. To get into Root you should click on Computer on the Virtual Machine Desktop. To use the script, you should first create a directory, here we refer to it as the current directory. All other directories referred to below are sub-directories of the current directory. Executing the script in the current directory will create a directory that can be used as a starting point for a user-written algorithm, one of the user-written functions described in the ART (Section 7.6) or QUADRATIC (Section 7.9) algorithms, or a user-defined FOM (Section 8.2.6.7). The default is to create a directory called snark14UserDefined in the current directory and place the skeleton files there. The src subdirectory contains the skeletons for the user-written algorithms: five algorithms that use pixels (ALP1, ALP2, ALP3, ALP4, ALP5), five algorithms that use blobs (ALB1, ALB2, ALB3, ALB4, ALB5), the skeletons for the ART and QUADRATIC user-written functions, and the skeleton for the user-defined figures of merit USR1, USR2, USR3, USR4 and USR5. These routines are found in their respective filenames (i.e., alp*.cpp, alp*.h, alb*.cpp, alb*.h, art*.cpp, quad*.cpp, user*.cpp and user*.h). The user may also place any additional .h and .cpp files into the src subdirectory that contain user-written auxiliary subroutines. For each .cpp file that the user adds, a new object with the same name needs to be added manually to the list of objects in the Makefile located inside the src subdirectory. In the directory snark14UserDefined the script snark14UserDefinedBuild will compile the source code and place a new SNARK14 executable in the bin.
directory. In order to minimize confusion between this executable and the standard SNARK14 executable, this version is named snark14UserDefined. Enter the command:

```
# ./bin/snark14UserDefined
```

while in the snark14UserDefined directory to execute this modified version of SNARK14.

**Warning:** The program snark14Input has a special provision that if it is run from a directory containing a bin/snark14UserDefined executable, it will use that version of SNARK14 instead of the standard version.

**Warning:** The files used by snark14getUserDefined are located in the SNARK14 installation directory. Do not create your user algorithm there. Those files should remain unmodified so that every user of snark14getUserDefined gets untouched copies of the skeleton files.

**Warning:** The files exalg.cpp, stopex.cpp, term.h and termtest.h in the snark14UserDefined directory should remain in their original form and should not be modified by the user.

### D.4 Building (a modified version of) SNARK14 from source code

The content of this subsection is intended for users who are familiar with C++ programming, building large projects and the make build automation tool; modifications made without such knowledge to the files described in this subsection may lead to unexpected results.

The following procedure creates a working copy of the programs snark14, snark14Input, and snark14Display as they have been built in the original distribution of SNARK14. To build these programs from source code, a user needs to invoke the following script

```
# snark14GetTrunk
```

The script snark14GetTrunk will create a directory, named snark14Trunk, containing the Makefiles and source-code files necessary for building the executable SNARK14 programs. When invoked, the script will ask for a location where to create the directory snark14Trunk; if the user does not provide a location, the script will create the directory snark14Trunk in the location where the script was invoked from.

The snark14Trunk directory contains a Makefile file already configured to successfully build the executable SNARK14 programs using the make build automation tool. Upon invoking the snark14GetTrunk script, the directory snark14Trunk will also contain the following three directories: src, include, and tools. The src directory contains files with the source code while the include directory contains header files necessary for building the executable SNARK14 program (i.e., snark14). In turn, the tools directory contains the directories Display and Input containing the source code for building snark14Display and snark14Input, respectively.

To build the executable SNARK14 programs, the user should get inside the recently created directory snark14Trunk and issue the following command

```
# make
```

This process will take some time to finish. In a normal case, after the building process is complete the process has created three extra directories inside the snark14Trunk directory: bin, build, and lib. The build directory contains the object-code files for building the final programs and, typically, a user would not want to access this directory. The lib directory contains the libraries libDIGFile, libDIGFileSnark, and libDIGRand; these are libraries containing routines necessary for the proper operation of SNARK14 programs and in normal circumstances a user would not want to modify neither the source code nor the libraries for these routines. It is worth noticing that similar libraries are already part of the original SNARK14 distribution and they are installed in the directory /usr/local/snark14/lib. Finally, the directory bin contains the executable SNARK14 programs. One may invoke any of the recently created programs by accessing the bin directory and invoking either snark14, snark14Input, or snark14Display.

An important note: A user may want to modify only the routines in the directory src/snark and, thus, is not necessary to modify the system-wide LD_LIBRARY_PATH variable. However, if a user modifies the behavior of any of the routines making up the libraries libDIGFile, libDIGFileSnark, or libDIGRand, this variable needs to point to the directory snark14Trunk/lib instead of the usual /usr/local/snark14/lib when executing any of the newly built executable SNARK14 programs.
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