ABSTRACT

VISUALIZATION AND EXTRACTION OF STRUCTURAL COMPONENTS FROM RECONSTRUCTED VOLUMES

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Algorithms for image reconstruction from projections have expanded our ability to visualize the structure of objects. Image reconstruction covers a wide range of physical applications from electron microscopy of molecular structures to radio astronomy of cosmic structures. In this work we will focus on molecular structures, namely biological macromolecules imaged by a transmission electron microscope (*TEM*) and then reconstructed from such images.

Biological macromolecules are the main structural components from which living matter is built. This group of molecules consists of four broad subclasses: proteins, nucleic acids, polysaccharides and lipids. All of these macromolecules exhibit a complex structure which determines the interaction of the macromolecule with itself or with others. In particular, proteins have a functional role which is not present in the other three macromolecules. Different proteins carry out their diverse functions due to the extremely wide range of configurations they can exhibit. Indeed, it is believed that this specialization is largely due to the structure they possess.

TEM technology has been commonly used to obtain reconstructions of macromolecu-

lar structures because of the meaningful information this technology produces. Algebraic Reconstruction Techniques (*ART*) are methods for the reconstruction of macromolecular complexes in TEM. The process of reconstructing a macromolecular complex yields three-dimensional arrays of real numbers representing the macromolecular complex. After reconstruction, the approximation of the macromolecular complex is generally corrupted by noise, resulting from the noise in the data collection, and by errors inherent in the reconstruction algorithm. As a result, the reconstruction is typically an imprecise approximation of the macromolecular complex. Consequently, this approximation has to be further processed to obtain an accurate representation of the macromolecule.

Reconstructions with ART produce volumes expressed as linear combinations of some basis functions. Recently, spherically symmetric functions (*blobs*) have been introduced as efficacious basis functions for reconstruction. In this dissertation we propose a method of selecting blob parameters to obtain accurate reconstructions and visual representations of the three-dimensional structure of macromolecular complexes.

ART produces as output the set of weights for the basis functions, that we refer to as the set of coefficients. In order to produce fast and accurate visual representations of macromolecules we first propose a method that takes advantage of the properties of ART and blobs, together with simple thresholding of the set of coefficients that provides a "good" estimate of those blobs that contribute to the formation of the object of interest and, thus, simplifying the search for significant blobs. Furthermore, we also take advantage of the

various ways of placing the blobs in the three-dimensional space to produce more accurate visual representations and reduce the number of coefficients.

One characteristic of biological macromolecules, which distinguishes them from specimens used in other fields, is that they very frequently present some kind of symmetry. In fact, the functional form of many biological macromolecules is obtained by merging or joining several copies of one or several subunits. We propose to take advantage of the repetitive presence of subunits to improve the signal-to-noise ratio of the reconstruction of a macromolecular complex.