Meeting: 1002, Pittsburgh, Pennsylvania, SS 15A, Special Session on PDE-Based Methods in Imaging and Vision

1002-35-122 **Alberto Bartesaghi*** (abarte@ece.umn.edu), 4-174 EE/CSci BLDG, 200 Union Street S.E., Minneapolis, MN 55455, and **Guillermo Sapiro**, **Stanton Lee**, **Jon Lefman**, **Sharon Wahl**, **Sriram Subramaniam** and **Jan Orenstein**. *A new approach for 3D segmentation of cellular tomograms obtained using three-dimensional electron microscopy.*

Electron tomography allows determination of the three-dimensional structures of cells and tissues at resolutions significantly higher than is possible with optical microscopy. Electron tomograms contain, in principle, vast amounts of information on the locations and architectures of large numbers of subcellular assemblies and organelles. The development of reliable quantitative approaches for interpretation of features in tomograms, is an important problem, but is a challenging prospect because of the low signal-to-noise ratios that are inherent to biological electron microscopic images. As a first step in this direction, we report methods for the automated statistical analysis of HIV particles and selected cellular compartments in electron tomograms recorded from fixed, plastic-embedded sections derived from HIV-infected human macrophages. Individual features in the tomogram are segmented using a novel, robust algorithm that finds their boundaries as global minimal surfaces in a metric space defined by image features. Our expectation is that such methods will provide tools for semi-automated detection and statistical evaluation of HIV particles at different stages of assembly in the cells, and present opportunities for correlation with biochemical markers of HIV infection. (Received September 10, 2004)