# Recovery of Label Distributions

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Our long-term aim is to utilize electron micrographs of biological macromolecules to produce a tessellation of space into small volume elements (voxels), each labeled as containing ice, protein, or RNA. Traditional approaches to achieve this first assign to each voxel a gray value (associated with the density of atoms in the voxel) based on the micrographs and then threshold this gray value image to obtain a label image. A problem with this approach is that at higher resolutions (smaller voxels) the ranges of atom densities corresponding to different labels greatly overlap, and so the label image will need to be of low resolution in order to be reliable. Another difficulty is that, due to the distructive nature of the electron microscope, only a few projections can be taken. We propose to overcome these difficulties by first postulating some low level prior knowledge (based on the general nature of macromolecules) regarding the underlying label images, and then estimating directly a particular label image based on this prior distribution together with the micrographs. We also report on our first experiments aimed at evaluating this approach.