Cryo-electron microscopy and cryo-electron tomography have emerged as important methods for discovery of structure and function at the sub-cellular level. They are in effect bridging the gap between cellular and molecular biology. In this talk, I will first present a brief overview of these techniques, followed by my contributions and recent advances in ways to interpret the resulting 3-dimensional data. This includes methods for segmentation and fitting/building structural models. The methods aim to reveal structural components along with their dynamics and interactions, while integrating results from Cryo-EM/ET and other methods such as X-ray crystallography. Also, I will introduce a new system for sharing and visualizing 3-dimensional models of molecular components via the web and virtual reality, which aims to facilitate communication and collaboration in this quickly expanding field. Finally, I will reflect on the future of the field, highlighting where new methods are needed in order to allow us to better integrate and make use of the rich data coming out of these and other methods.