



Image processing for cryo electron tomography

We are looking for a motivated master student to develop and implement algorithms for 3d graphics and computer vision. Application field is molecular biology, with the ultimate goal of detection and visualization of biomolecules in their native environment.

Cryo electron tomography (CET) is a novel biophysical method to study the three dimensional structure of biological macromolecules in their native state at molecular resolution. Our lab C-CINA is equipped with high-end equipment to perform CET. The quality of the resulting reconstructions is limited by a number of distortions and low signal to noise ratio. Our laboratory develops image processing methods to extract as much information as possible from electron microscope data.

The project includes recovery of information in noisy images by a new approach being developed in our lab. Once the method is implemented and tested we have a number of exciting structural biological questions to investigate.

The candidate should have a strong background in physics, mathematics, programming or a related field. Knowledge of biology would be an advantage but is not required. Development will be performed in Matlab environment. Project may be started any time. You can find more about C-CINA at <http://www.c-cina.unibas.ch/> or write an email to Misha Kudryashev mikhail.kudryashev@unibas.ch