Connectomics is the complete mapping of all individual neurons and their synaptic contacts in a region to create its canonical network map, also known as a connectome. While an important motivation is providing anatomical ground truth for neural circuit models, the ability to decipher neural wiring maps at the individual cell level is also important in studies of many neurodegenerative diseases. Connectomics requires the analysis of very large microscopy datasets including confocal and serial-section electron microscopy. This analysis entails several image processing and pattern recognition challenges including image alignment (Luke Hogrebe), cell membrane detection (Mojtaba Seyedhosseini, Liz Jurrus) and structure tracking (Ting Liu).

Visualization of Connectome data sets

Luke Hogrebe: In our work we align serial sections of confocal microscopy axonal image stacks using registration landmarks derived from in-section traces. Tissue deformations make it necessary to account for local warping in addition to the global rotation and translation of sections in the process of restoring axon continuity.

Mojtaba Seyedhosseini: Automated neural circuit reconstruction through electron microscopy (EM) images is a challenging problem. The main idea is to build a framework which is capable of extracting information about cell membranes from a large contextual area of an EM image in a computationally efficient way. We work on a novel method that exploits multi-scale contextual information together to learn a series of discriminative models.

Ting Liu: To help neuroscientists better study the spatial structure of neural systems, the work focuses on 3D neural structure tracking. Given 2D segmentation of microscopic images, combinatorial algorithms such as graph cuts are adopted for 3D structure reconstruction.

Student projects:

Luke Hogrebe: Automated axon alignment

Mojtaba Seyedhosseini: Automated neural circuit reconstruction through electron microscopy (EM) images is a challenging problem. The main idea is to build a framework which is capable of extracting information about cell membranes from a large contextual area of an EM image in a computationally efficient way. We work on a novel method that exploits multi-scale contextual information together to learn a series of discriminative models.

Ting Liu: To help neuroscientists better study the spatial structure of neural systems, the work focuses on 3D neural structure tracking. Given 2D segmentation of microscopic images, combinatorial algorithms such as graph cuts are adopted for 3D structure reconstruction.

Electron microscopy image segmentation.

Mark Ellisman, NCMIR, UCSD

The influence of visual context in natural image processing in the primary visual cerebral cortex.

Alessandra Angelucci, U. of Utah

Model-based Reconstruction for Dynamic MRI.

Edward Di Bella, University of Utah

High-Dimensional, Nonparametric Density Estimation for the Analysis of Images and Shapes.

Ross Whitaker, University of Utah

Parametrization of the manifold coordinates of a brain data set.

Collaborations:

A computational framework for mapping long range genetic circuits.

Julie Korenberg, Brain Institute, University of Utah

Automated axon alignment

Electron microscopy image segmentation.

Mark Ellisman, NCMIR, UCSD

Retinal Network

Model-based Reconstruction for Dynamic MRI.

Edward Di Bella, University of Utah

Single cell images of a sagittal slice of human breast, using different reconstruction methods.

Ross Whitaker, University of Utah

Parametrization of the manifold coordinates of a brain data set.