http://bdtnp.lbl.gov/Fly-Net/bioimaging.jsp



RDIND

Berkeley Drosophila Transcription Network Project

About

3D Gene Expression

In Vivo DNA Binding



In Vitro DNA Binding

Transgenic Pro

3D Gene Expression Summary

Search Data Browse Data Previous Releases

Project Goals

Staining & Mounting

Probe Constructs

PointCloudXplore PointCloudToolBox

PointCloudAlign

Overview: Summary

Methods:

Staging

Imaging

Software:

This database allows search and retrieval of two file types describing gene expression and embryo morphology in 3D at cellular resolution: Single PointClouds and Virtual PointClouds. An analysis tool, **PointCloudXplore**, allows visualization and analysis of the data in these files. Meta-data associated with each file is also provided, including detailed information on embryo collection, staining, imaging, gene probes and antibodies used, protocols, quality estimators etc.

The data are produced as follows: Embryos are collected at the desired developmental stage, fixed, and **fluorescently stained** to label nuclei and the protein or mRNA expression patterns of several genes, each labeled in a different color. The **developmental stage** of embryos is judged under phase contrast microscopy. Multi-photon confocal microscopy is used to collect a **3D image stack** of each labeled embryo. Automated **image analysis methods** then determine the location and extent of each nuclei. This information is used to generate Single PointCloud files that contain geometric data for each nucleus (position, volume, etc.), and the measured levels of gene expression in a single embryo. To allow comparison between the expression patterns of more than two or three genes, **registration methods** are used to place gene expression data from many embryos into a Virtual PointCloud file.

Currently, our **project's goals** are focused on the gene expression network regulated by 37 principal transcription factors in the pregastrula embryo. A **Browse Data** page allows you to browse the data through a summary of the data available for given genes, developmental stages, genotypes and species. The **Search Data** page allows selection of user defined subsets of files and their associated meta-data. Data for **previous releases** of our datasets are available also.

Note that because of their large size (300 - 500 Mb) the original 3D confocal image stack files are not available from this public database, but are available by **request**.