Virtual Embryos As Tools For 3D Gene Expression Analyses

The Berkeley Drosophila Transcription Network Project (BDTNP) is a multidisciplinary collaboration studying the developmental regulatory network of Drosophila blastoderm embryos. One component of this project (Luengo et al., Genome Biology 7:R123, 2006) maps the full 3D blastoderm expression patterns of 37 principal developmental regulatory genes and hundreds of their targets at cellular resolution, and uses these data to model potential regulatory interactions. We have developed an automated pipeline and methods for producing these data. Both the algorithms and the data are freely available at:

http://bdtnp.lbl.gov/

Introduction

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Mutants & Other Species

Gene expression data in regulatory factor mutant embryos and other Drosophila species is also being collected.

Collecting the Data

The 3D, full blastoderm images are analyzed and accurately converted into PointCloud files by an automated algorithm.

Generating Virtual Embryos

Because each imaged embryo contains expression information of only two genes, expression data from hundreds of embryos are mapped onto a virtual embryo to allow many genes’ expression to be compared and modeled within each cohort. These virtual embryos contain nuclei placed to match the average density pattern and embryo shape for each cohort.

Uses of Virtual Embryos

The use of standardized virtual embryos allows temporal comparison within each nucleus between earlier expression of regulators in one cohort and the later expression of target gene patterns in another cohort, as well as better estimates of the developmental increase in complexity.

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Functions of Virtual Embryos

We currently have data for 24 of the principal regulators and over 80 putative target genes, the latter selected using BDTNP Chip-chip binding data and BDGP expression data.

PointClouds

Virtual Embryo

Density changes through time (Keränen et al., Genome Biology 7:R124, 2006)

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