Reconstructing a Developmental Time Series of 3D Gene Expression Patterns in Drosophila Embryos

BDTNP
Berkeley Drosophila Transcription Network Project

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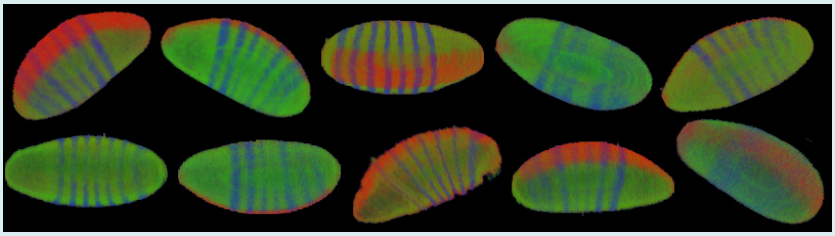
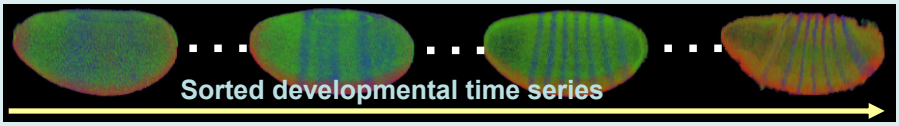
Problem

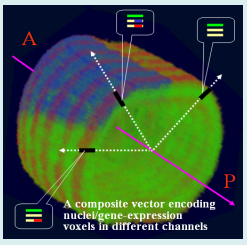


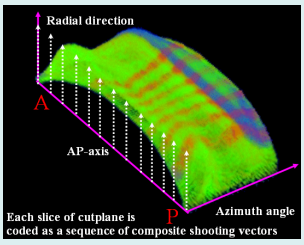
How can we accurately characterize the morphological change of gene expression patterns over time? To address this question we are analyzing randomly sampled 3D RNA *in situ* images, such as those at the left, to establish an ordered time series that describes with fine detail the temporal dynamics of expression.

Method

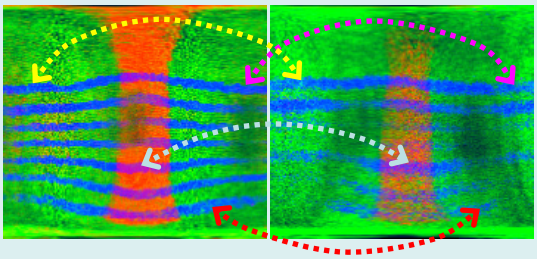
These images are sorted into their temporal order automatically by our new computational approach.

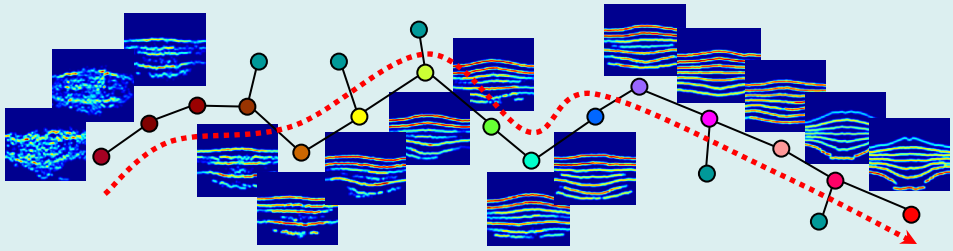






- **Unfolded embryo around the AP-axis and the "grid" representations of gene expression patterns.**
- **A dynamic programming method for comparing and registering these patterns.**





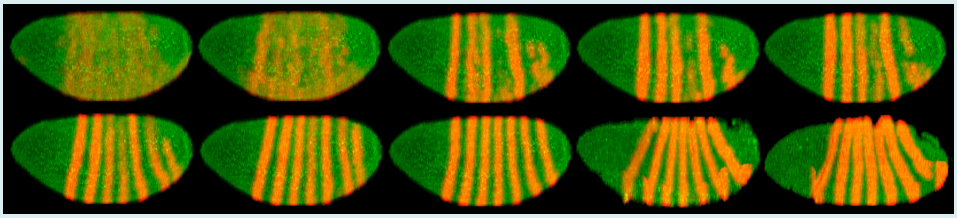
The core-graph (red) of minimum spanning tree indicates the temporal sequence of pattern development.

- **Distance score matrix between all pairs of embryos.**
- **A graph algorithm to sort the embryos temporally, by solving a special Traveling Salesman Problem (TSP) based on the inter-embryo distances. In our case, this is simplified as finding the core line graph in a minimum spanning tree.**

Results

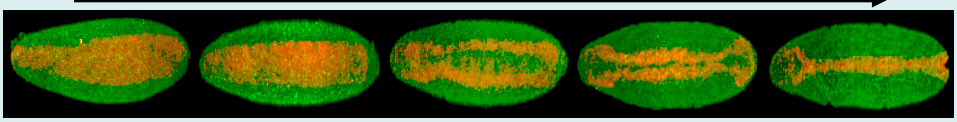
Computer reconstructed time series of blastoderm and gastrulating embryos, spanning an approximately 60-minute period. Background noise in these images has been suppressed.

- **The *ftz* pattern onsets as a broad band. Gradually, three, five, six, and seven stripes emerge and become sharp. When the gastrulation begins, these stripes move closer dorsally, while the morphology of the embryo undergoes a dramatic change.**



Sorted developmental time series of gene *ftz*

- **During gastrulation, the ventral furrow appears and the *snail* pattern opens in the middle, then closes again together with the ventral furrow.**



Sorted developmental time series of gene *snail*