

## TECHNOLOGY

## Developmental networks in time and space

**DOI:**  
10.1038/nrg2055

**URLs**  
The Berkeley Drosophila  
Transcription Network  
Project: <http://bdtnp.lbl.gov/>  
Fly-Net

Ideas about the transcriptional control of development are largely based on two-dimensional snapshots of gene expression that ignore the continuously changing, three-dimensional nature of the embryo. A new high-throughput approach now brings us closer to a fuller understanding of how transcription-factor networks control fruitfly development in the context of embryonic morphology.

As part of the **Berkeley Drosophila Transcription Network Project**, Luengo Hendriks and colleagues developed a method that allows simultaneous quantitative visualization of gene expression and cellular-level morphological analysis in whole embryos. They focused their approach



on blastoderm-stage *Drosophila melanogaster* embryos, in which transcriptional regulatory networks have been thoroughly investigated. Fixed embryos were fluorescently stained for mRNA expression and nuclear location, sorted by developmental stage, and imaged from whatever orientation they happened to be lying in, allowing a three-dimensional profile to be built up.

Working with whole embryos presented challenges in generating high-quality images. Careful optimization of fixation, staining and mounting conditions was crucial to the success of the approach, as was the use of two-photon laser-scanning microscopy (which improves optical penetration and resolution, and reduces signal attenuation). Another important feature was the method that the authors used for image analysis. They converted the large data files for each image into a specially developed format that they termed a PointCloud, which compressed the file to a manageable size while retaining detailed information about morphology and gene expression.

Luengo Hendriks and colleagues initially tested their method on 1,282 embryos, looking at the mRNA levels of 22 developmental control genes, which form the first levels of the transcriptional hierarchy that governs anterior–posterior and dorsal–

ventral patterning. The authors have made their imaging data publicly available for others to use.

Together with an accompanying study by Keränen *et al.*, this work provides some interesting new insights into the developmental functioning of transcription factors. For example, the authors were able to model how a combination of morphological movements and regulatory interactions between genes determines the precise boundaries of pair-rule gene expression stripes and provides a basis for interaction between the two main body axes.

Despite focusing on a narrow developmental time window and a small number of genes that have already been well studied, this approach has provided new biological information. The extension of this method to many more genes and a wider range of embryonic stages should add another dimension to our understanding of development in the fruitfly.

Louisa Flintoft

**ORIGINAL RESEARCH PAPERS**

Luengo Hendriks, C. L. *et al.* 3D morphology and gene expression in the *Drosophila* blastoderm at cellular resolution I: data acquisition pipeline. *Genome Biol.* **7**, R123 (2006) | Keränen, S. V. E. *et al.* 3D morphology and gene expression in the *Drosophila* blastoderm at cellular resolution II: dynamics. *Genome Biol.* **7**, R124 (2006)

**WEB SITE**

The Berkeley Drosophila Transcription Network Project: <http://bdtnp.lbl.gov/Fly-Net>