BERKELEY DROSOPHILA TRANSCRIPTION NETWORK PROJECT: MORPHOLOGY AND GENE EXPRESSION ATLAS

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The Berkeley Drosophila Transcription Network Project (bdtnp.lbl.gov) is conducting a system-wide analysis of the transcription network in the early Drosophila embryo. As part of this multidisciplinary effort, we have developed a suite of imaging, image analysis and visualization methods that provide the first quantitative three-dimensional description of Drosophila blastoderm morphology and gene expression at cellular resolution. To date we have computationally registered around 2000 high-resolution fluorescence images of blastoderm embryos to create an atlas of over 100 early-acting genes at multiple time points. Our methods provide a new spatio-temporal coordinate framework for studying three-dimensional patterns of gene expression. They reveal previously undetected morphological movements, as well as regulatory interactions between the networks controlling the two major body axes. We have also compared the expression patterns of specific genes in different Drosophila species. The results imply that the expression of a large percent of genes differ quantitatively between species. We are now using all of these different data to computationally model the early transcription network, and are extending our techniques to capture Drosophila morphology and gene expression right through embryogenesis.
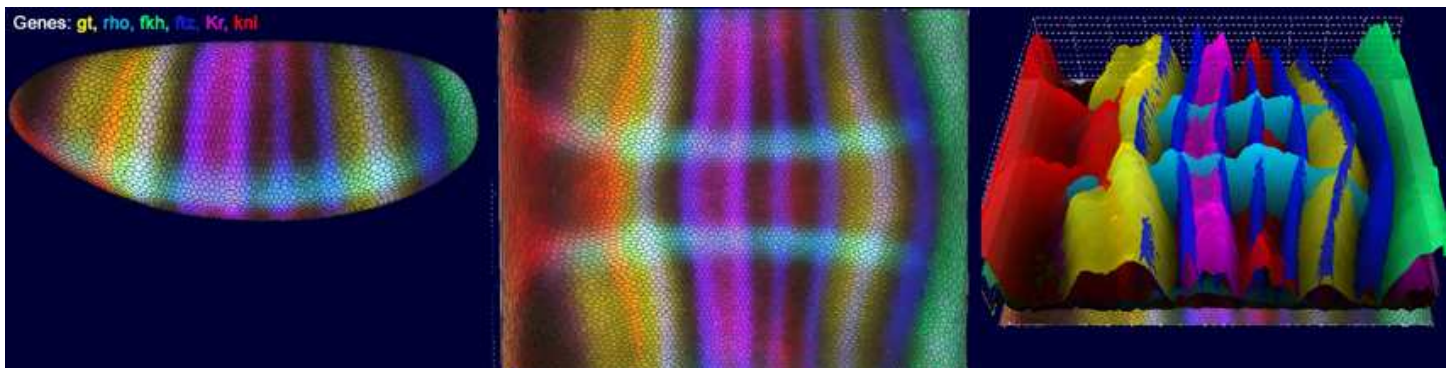
BDTNP's blastoderm morphology and gene expression atlas. This figure shows expression patterns of *gt, rho, fkh, ftz, kr* and *kni* from our blastoderm atlas. The patterns can be visualized on a virtual embryo, which can be rotated to any angle, (left) or on its unrolled surface to reveal patterns in a single view (middle). This view can then be also rotated and to show height-maps of the relative expression for each gene (right).