533c Data Integration and Bioinformatics in the Analysis of Developing Tissues

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We are interested in the mechanisms by which cell-cell interactions generate functional tissues and organs. Experimental systems in which cell communication pathways can be perturbed and monitored across spatiotemporal scales are crucial for exploring tissue- and organogenesis.[1] Egg development (oogenesis) of the fruit fly *Drosophila melanogaster* is an excellent system for this purpose. The development of living tissues requires tight spatiotemporal control of gene expression by cell communication pathways.[2] We are using genome-wide transcriptional profiling assays in combination with genetic perturbations to identify the transcriptional responses to cell communication pathways in *Drosophila* oogenesis. Our goals are threefold: 1) to identify all the genes responding to two cell communication pathways that have been identified as the key regulators in patterning of the *Drosophila* egg, 2) to uncover the spatiotemporal patterns of expression of these genes, and 3) to determine their role in establishing the three dimensional eggshell morphology. Because of the scale of this experimental effort and the amount of generated data, we are developing database systems to store, track, integrate, and visualize the emerging heterogeneous datasets.[3] In addition, we are working towards the elucidation of the sequence-specific regulatory patterns that underlie the observed dynamics of gene expression. This talk will describe the bioinformatics and data integration efforts associated with this project.

[1] S. Y. Shvartsman, Aiche Journal 51 (5), 1312-1318 (2005).

[2] A. Martinez-Arias and A. Stewart, Molecular principles of animal development. (Oxford University Press, New York, 2002).

[3] N. Yakoby, C. A. Bristow, R. Kalifa, I. Guzman, M. P. Rossi, Y. Gogotsi, T. Schupbach, and S. Y. Shvartsman, Systems Biology, in press (2005).