

**TITLE: BUILDING AN ATLAS OF GENE EXPRESSION IN DROSOPHILA
MELANOGASTER IMAGINAL DISCS**

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Dipteran imaginal discs are the primordial tissues that generate important parts of the adult insect exoskeleton, such as the eyes, wings, and legs. Intricate patterns of regulation of gene expression, in both time and space, are used to pattern the Imaginal disc and to guide cell fate decisions. Many genes are known to have interesting non-trivial spatial expression patterns in imaginal discs. Existing methods are limited in either resolution, as in the case of microarrays, which while able to operate on large numbers of genes provide little information about where genes are expressed, or in throughput, as in the case of in situ hybridization, which yields precise spatial information, but only for a single gene. To elucidate and explore the spatial patterns of a large number of genes with previously uncharacterized patterns, we have built a pipeline for mass-isolation of imaginal discs, for using gene expression microarrays to identify candidate genes likely to have interesting patterns, for generating probes for individual genes, for imaging discs stained with those probes and for the computational analysis of these patterns. We have built a common-lisp-based image processing package that learns imaginal disc shapes from a few manually segmented training examples and uses these learned shapes to automatically segment and align imaginal discs from images from a microscope and to produce a representation of the spatial pattern of gene expression for these genes. The process, while manually assisted in the training phase, proceeds automatically, enabling its use in a high-throughput pipeline. We have applied the pipeline to over 1000 images from over 100 different genes and have generated tens of non-trivial patterns.