Toward Automatic Annotation of *in situ* mRNA Expression Patterns of Drosophila Embryos

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Abstract

The in situ mRNA hybridization gene expression pattern images of Drosophila melanogaster in the course of embryogenesis provide spatial-temporal information of the expression patterns of a target gene. This information is critical for understanding the roles of genes during the development of embryos. Currently, the annotation of these images is often done by manually assigning a subset of image ontology terms to the images. This approach is time consuming and depends heavily on the consistency of the experts. Alternatively, if the annotation process can be automated or semi-automated, efficiency and consistency are likely to be greatly enhanced. We formulate this task as a pattern classification problem, and present preliminary results. We consider both the template-based global matching and the multiobjective classification based on neural networks (e.g. multi-layer perceptron). We develop a method to combine them to optimize efficiency and accuracy. This method has been applied to the gene expression pattern image database generated by the Berkeley Drosophila Genome Project.