Dr. Qi Li
Department of Computer Science

• Data mining
• Machine Learning
• Bioinformatics
• Appearance based recognition
  – Classification of drosophila embryonic developmental stages based on gene expression pattern images
    • *In Situ* staining of a target mRNA during the development of a drosophila embryo gives a detailed spatial-temporal view of the expression pattern of a given gene.
    • It also allows the capture of spatial gene interactions based on computational analysis of images
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- Spatial-temporal view of expression patterns

(a-e) Series of five embryos stained with a probe (bgm)
(f-j) Series of five embryos stained with a probe (CG4829)
With the increased availability of expression images, the challenge is how to fully utilize them to:

- find other genes with overlapping or complementary patterns of gene expression.
- infer developmental pathways
- understand how regulation of concurrent and sequential gene expression patterns leads to the development of embryos and adult structures.

• The computational approach for answering the above questions automatically involves:
  – Image analysis
    • Standardization or size and orientation
    • Registration of corresponding cells and tissues as organism grows and develops
  – Machine learning
  – Informational retrieval
  – Database management