

# A Process Flow for Classification and Clustering of Fruit Fly Gene Expression Patterns

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# Outline

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## Gene expression images

- Background and motivation

## The elaborated Processing Pipeline

- Embryo Shape Segmentation
- Allignement / Registration
- GEP Extraction
- GEP Classification / Representation
- GEP Clustering

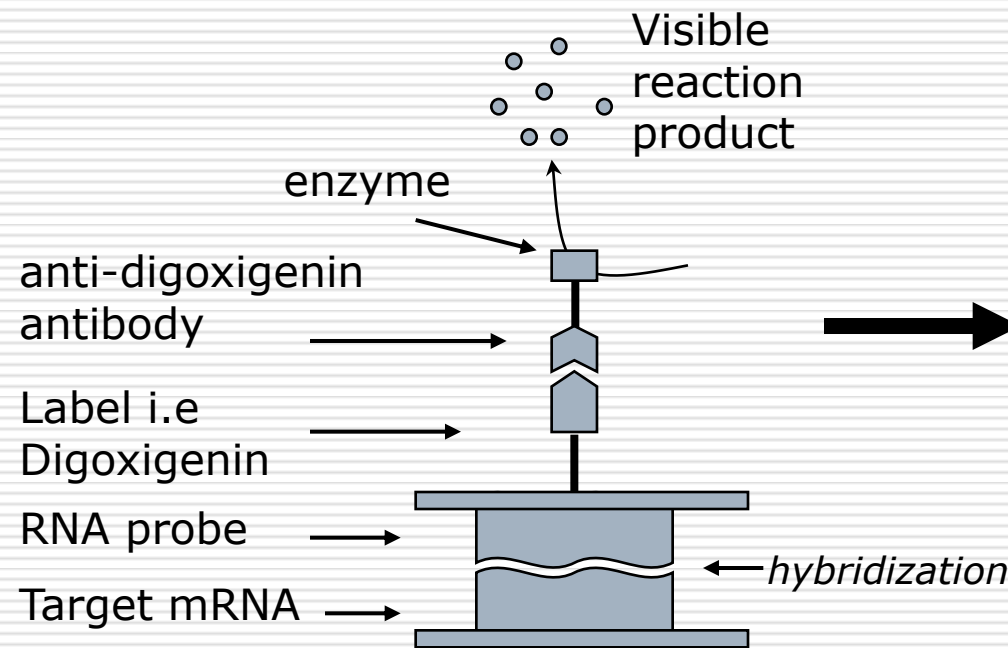
## Conclusion

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# Drosophila melanogaster Gene Expression Patterns (GEP)

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## □ whole-mount mRNA In situ hybridization



Gene example: Slp1 (Stage 4)



# Drosophila GEP Projects

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## Data management, storage, access, and integration:

- Berkeley Drosophila Genome Project
- FlyBase
- ...

## Data processing, analysis and observation:

- FlyExpress
  - ...
  - Our Approach
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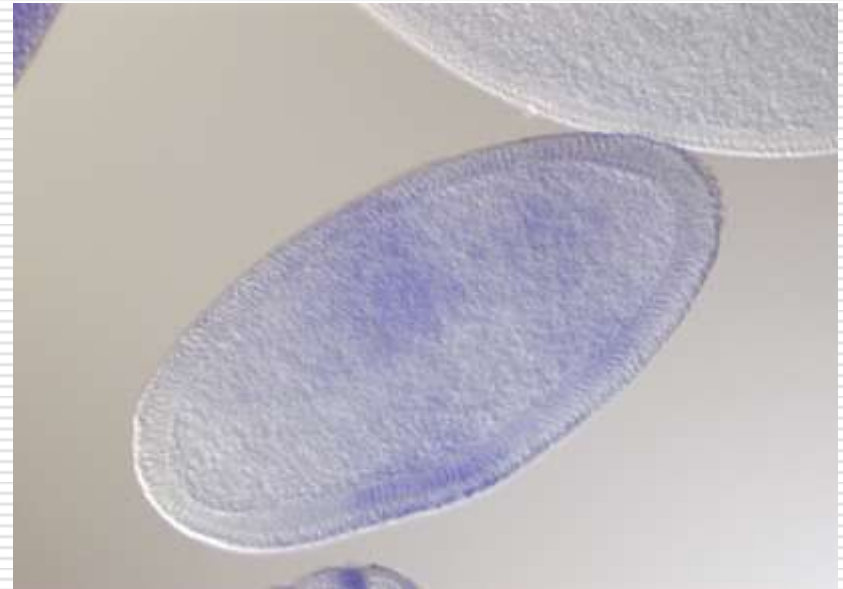
# Imaging Complications

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poor contrast &  
background shading

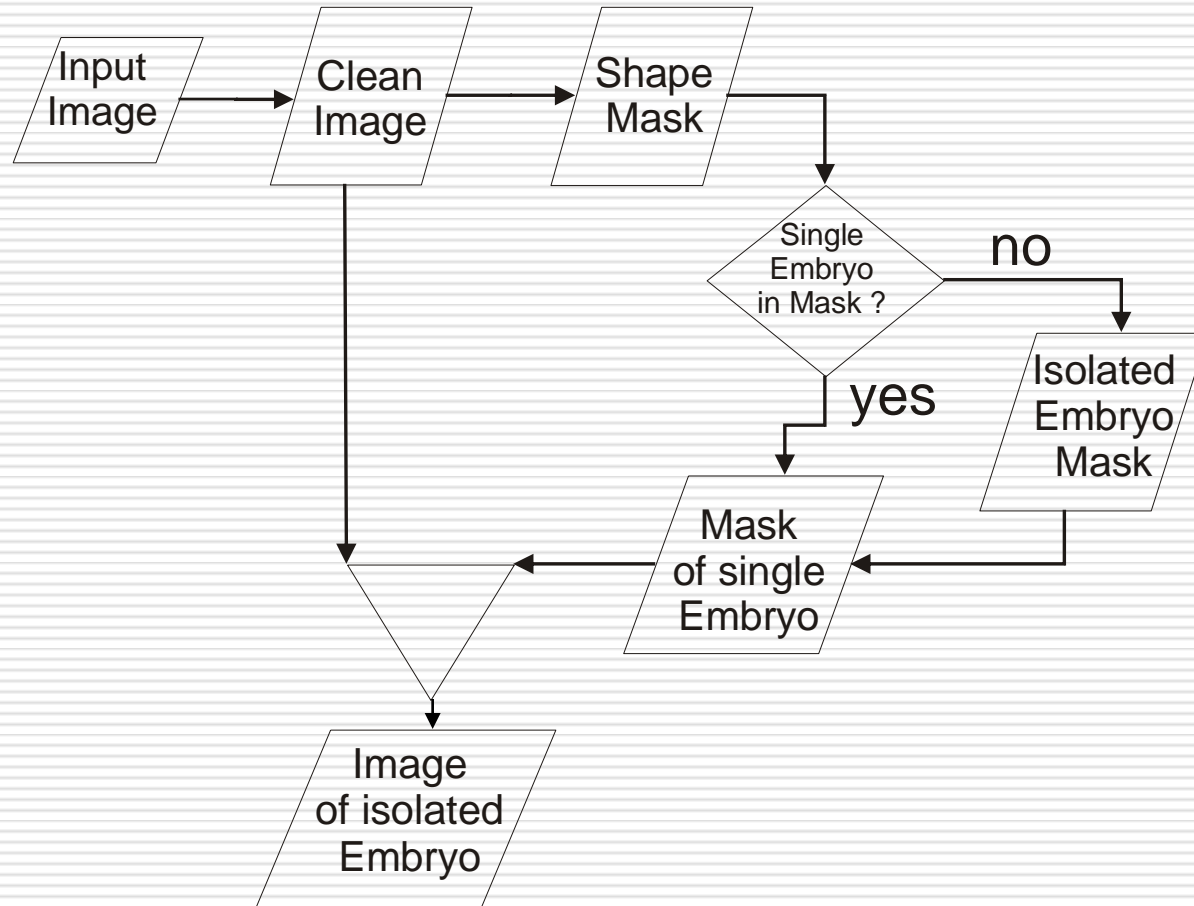


coherent partial embryos



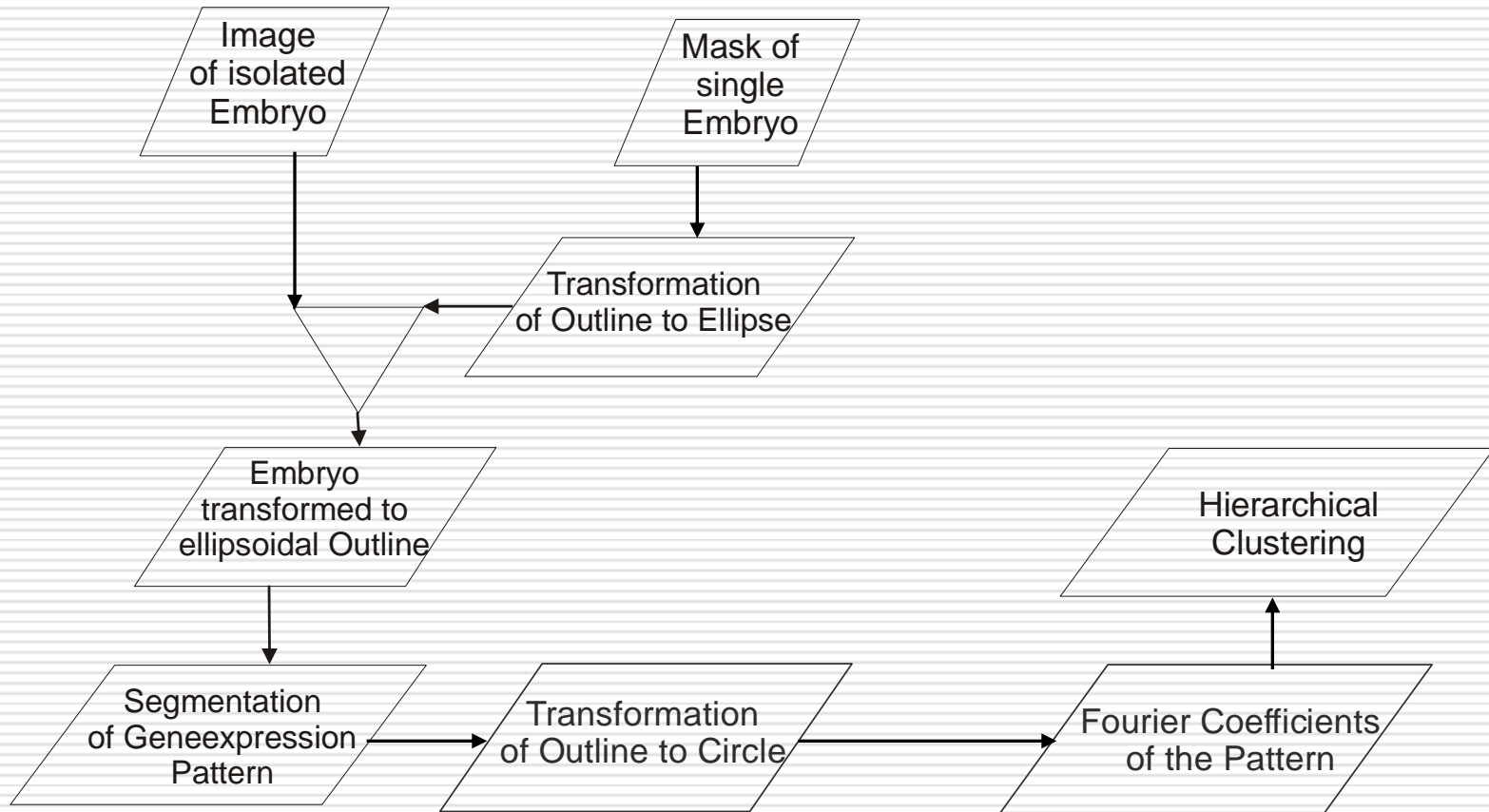
# Processing Pipeline Overview

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# Processing Pipeline Overview

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# Preprocessing

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- ❑ Shading correction
- ❑ Contrast optimization





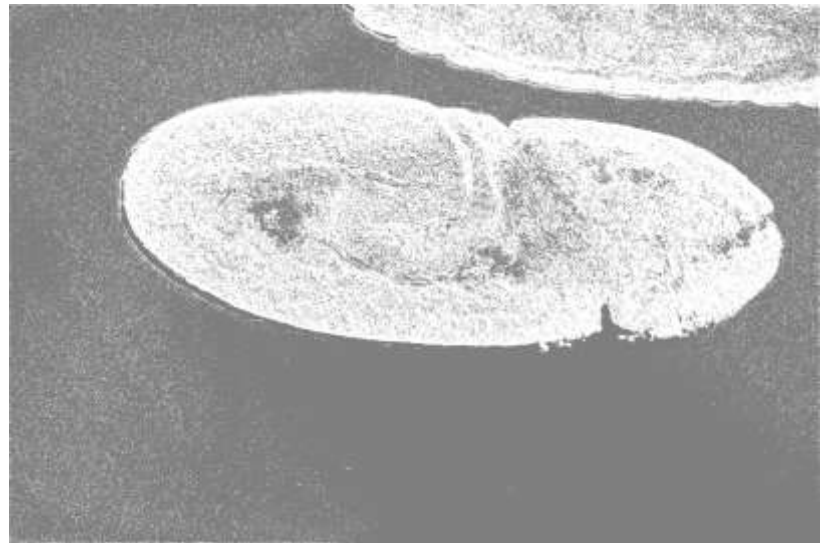
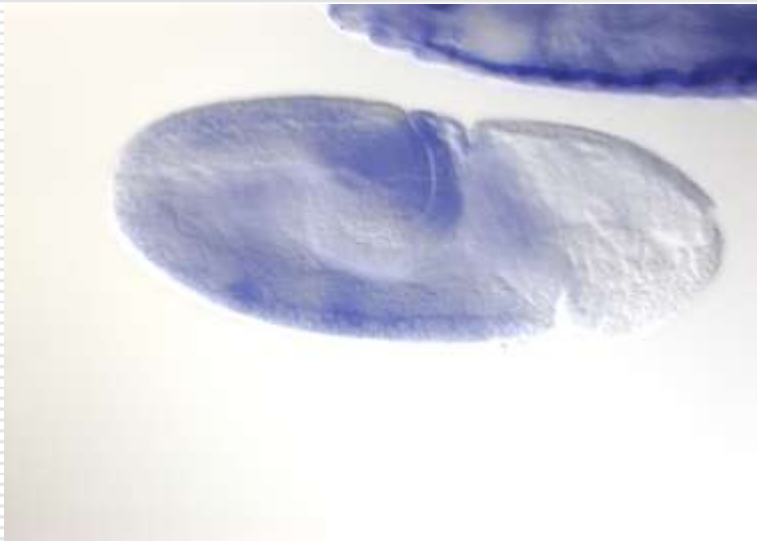
# Shape Segmentation

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□ Feature space:  
gradient magnitude

□ Method:

Estimating Gaussian Mixture Densities with EM



# Shape Segmentation

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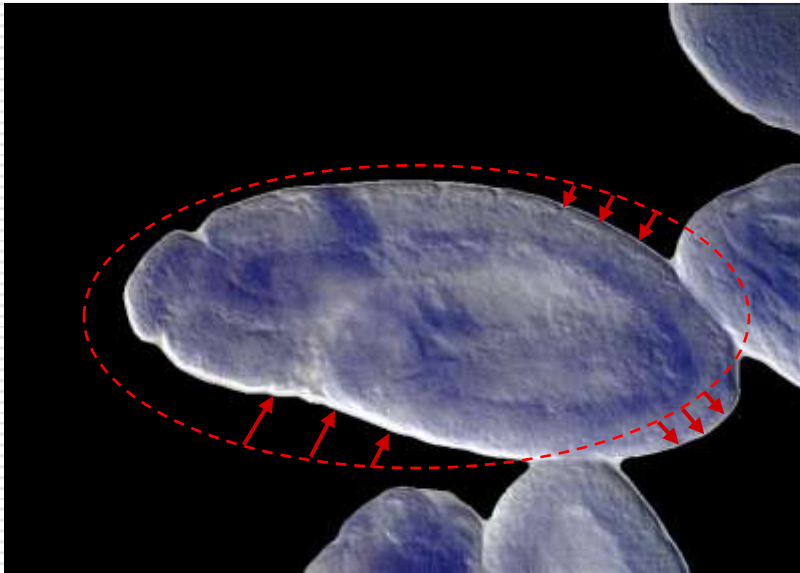
- ❑ Denoising: Total variation filter
- ❑ Close holes
- ❑ Remove other partial embryos



# Shape Segmentation - Isolate Coherent Embryos

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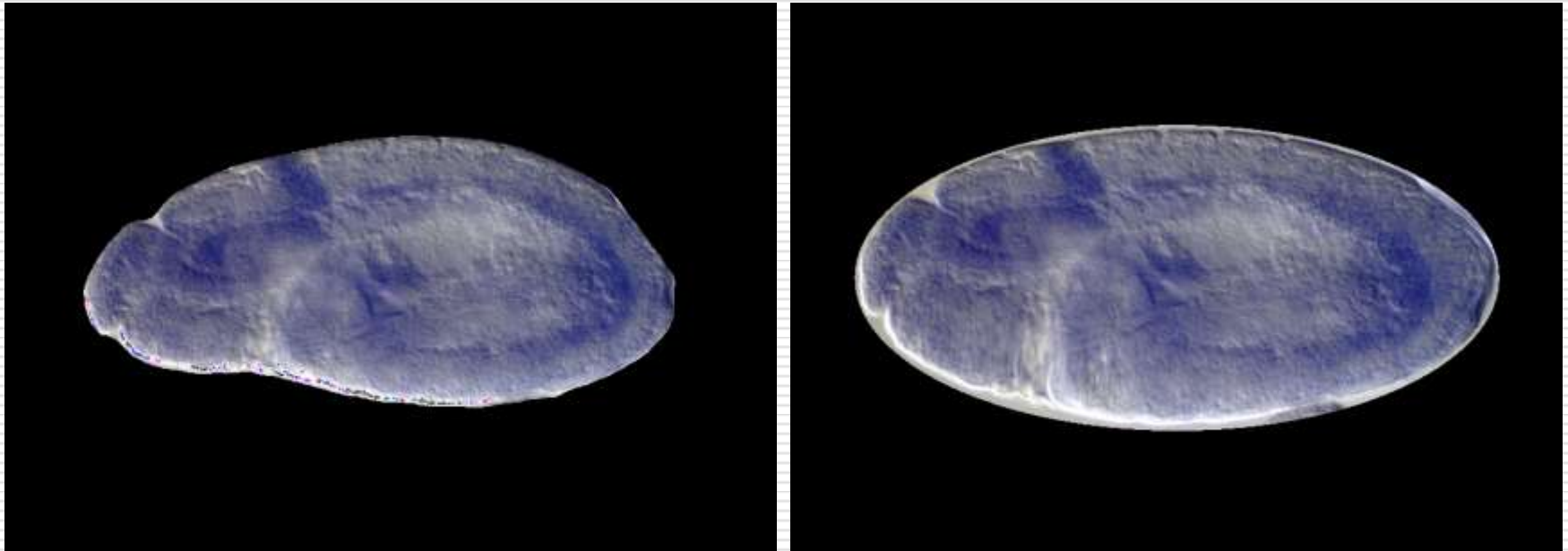
- Active Contour Approach - Snake Segmentation
- Marker particles are placed along an initial ellipsoidal contour.
  - -> Evolution toward maximum gradient regions



# Transformation of Outline to Ellips

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- ❑ Rigid Registration
- ❑ curvature based Nonlinear Registration



# Segmentation of the GEP

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## □ HSV Colorspace Transformation

V-channel,  $T=20\%$



# GEP Classification

## Fourier Coefficients

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- The patterns are described by a set of Fourier coefficients.

$$\mathcal{P}(r, \phi) = \sum_{j=1}^{\infty} \sum_{k=0}^{\infty} a_{j,k} \psi_{j,k}(r, \phi)$$

- As basis, the eigenfunctions of the Laplace operator on a circle of radius  $l$  are used.

$$\psi_{j,k}(r, \phi) \equiv N_{j,k} e^{ik\phi} J_k \left( \frac{r j_{k,j}}{l} \right)$$

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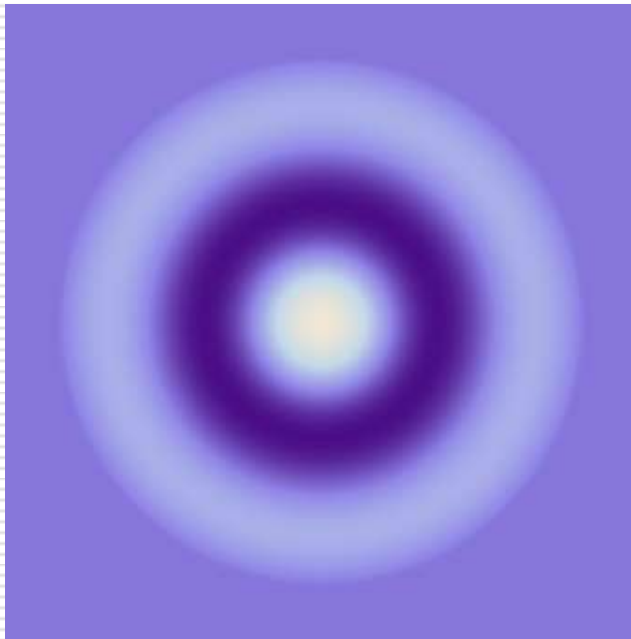
# Complete orthonormal system

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$$\psi_{j,k}(r, \phi) \equiv N_{j,k} e^{ik\phi} J_k \left( \frac{r j_{k,j}}{\ell} \right)$$

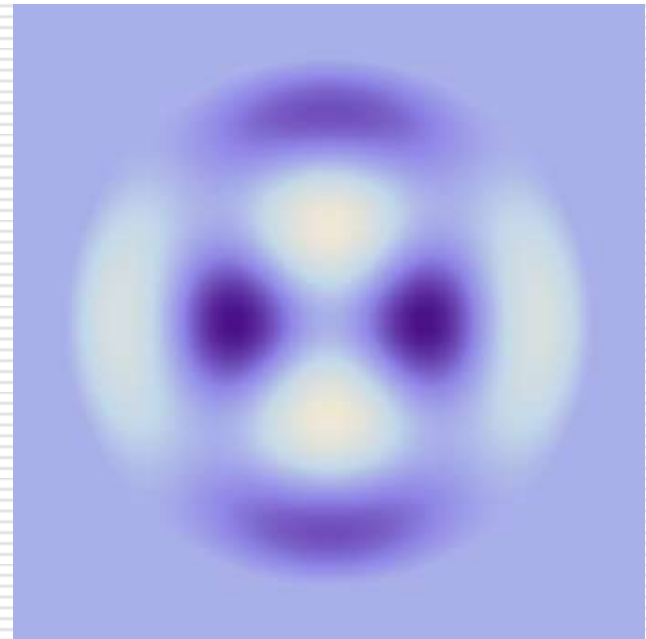
$k=0$

$j=3$



$k=2$

$j=2$



# Representation with a set of 420 Fourier coefficients

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$$a_{j,k} = \int_0^{\ell} \int_0^{2\pi} \psi_{j',k'}^*(r, \phi) g(r, \phi) r \, d\phi \, dr$$

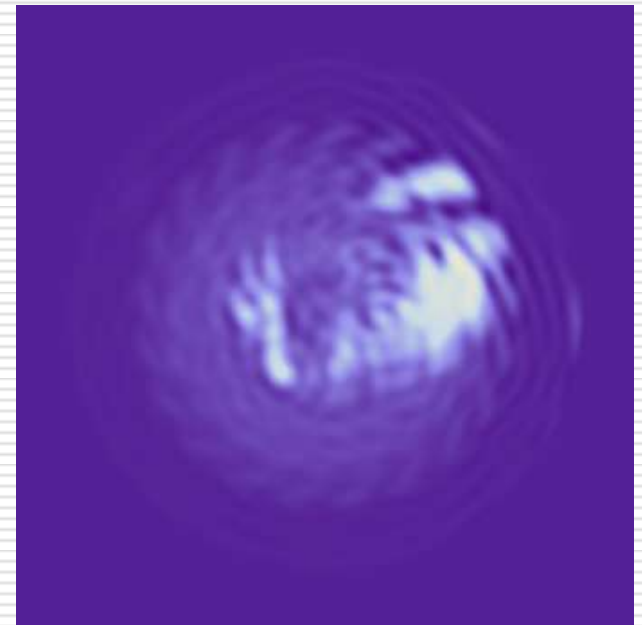


420 Fourier  
Coefficients



$k \in [0, \dots, 20]$

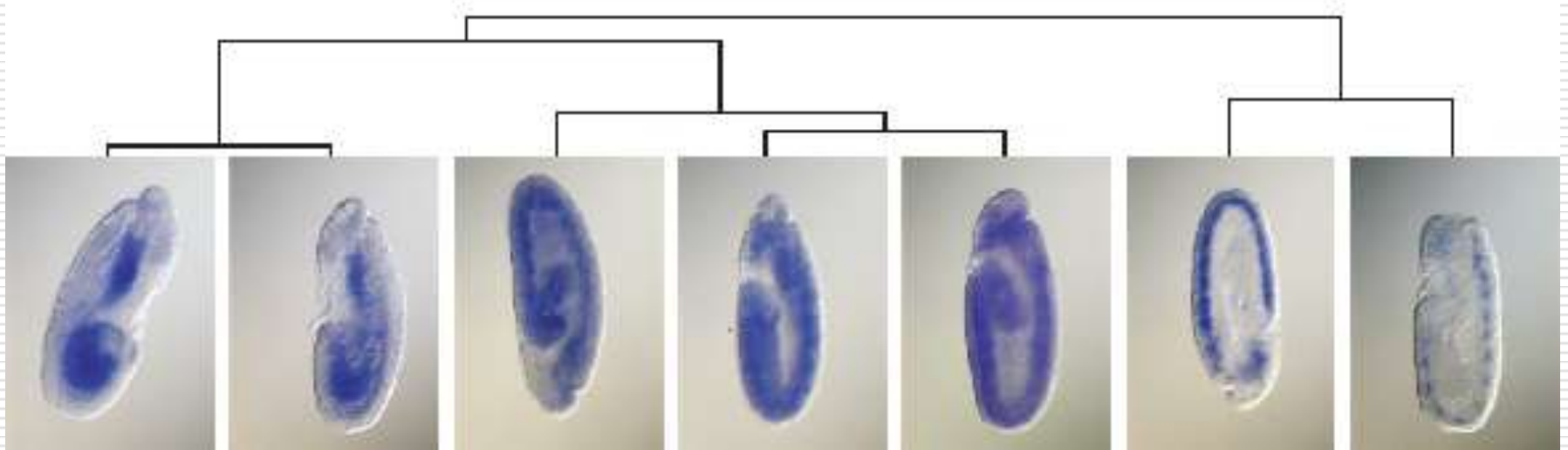
$j \in [1, \dots, 20]$





# GEP Clustering

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- Hierarchical clustering of the absolute values of the coefficient sets using Euclidean norm.
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# Conclusion

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- ❑ Clustering results show agreement with the visual expectation
  - ❑ The snake segmentation accuracy can be improved
  - ❑ The “orientation problem” should be solved
  - ❑ Future Work:  
Investigate biological relevance of the results
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# Thank you for your attention!

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[1] "Bdgp: Berkeley drosophila genome project," <http://www.fruitfly.org/>

[2] "Flybase: A database of drosophila genes and genomes," <http://flybase.bio.indiana.edu/>

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