PointCloudXplore: Visual Analysis of 3D Gene Expression Data Using Physical Views and Parallel Coordinates

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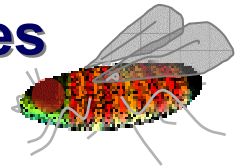
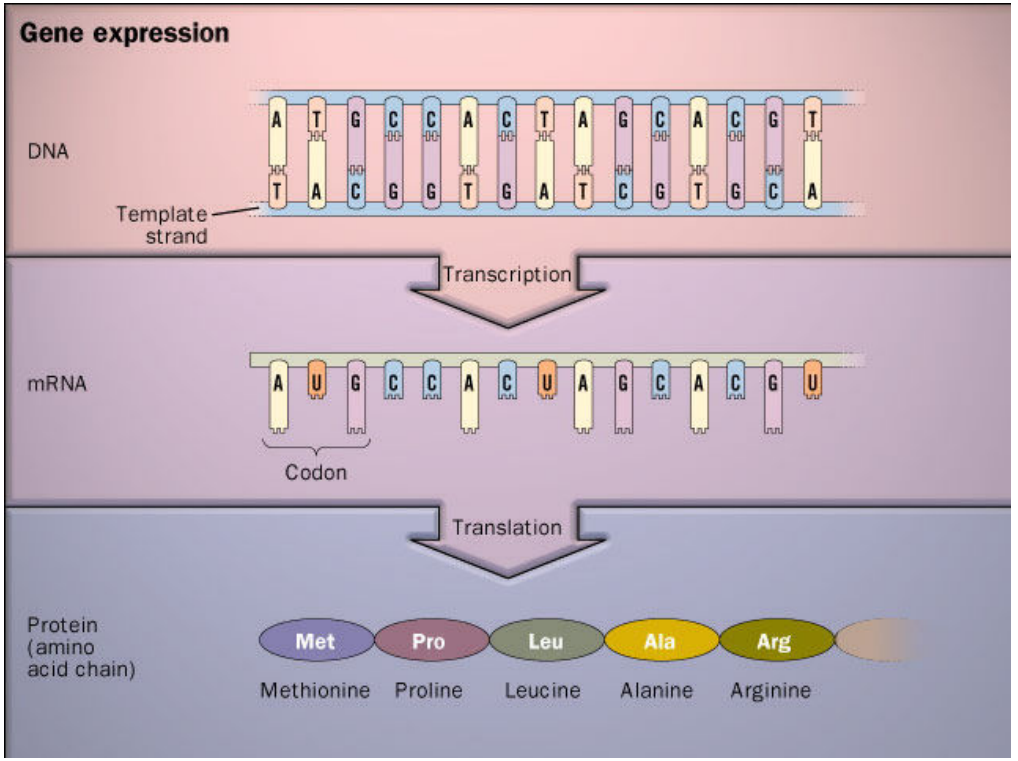


1. Genetic Fundamentals
2. Data- and Visualization Pipeline
3. Basic Principles
4. Visualization of Gene Expression in Physical Space
   - 4.1 Defining Embryo Orientation and Position
   - 4.2 Orthographic Views
   - 4.3 Unrolled View
   - 4.4 Expression Surfaces
5. Visualization in Gene Expression Space Using Parallel Coordinates
   - 5.1 Varying Line Properties
   - 5.2 Line Trace Highlighting and Animation
   - 5.3 Extending Parallel Coordinate View to 3D
   - 5.4 Brushing in Parallel Coordinate Views
6. Conclusions and Future Work

1. Genetic Fundamentals



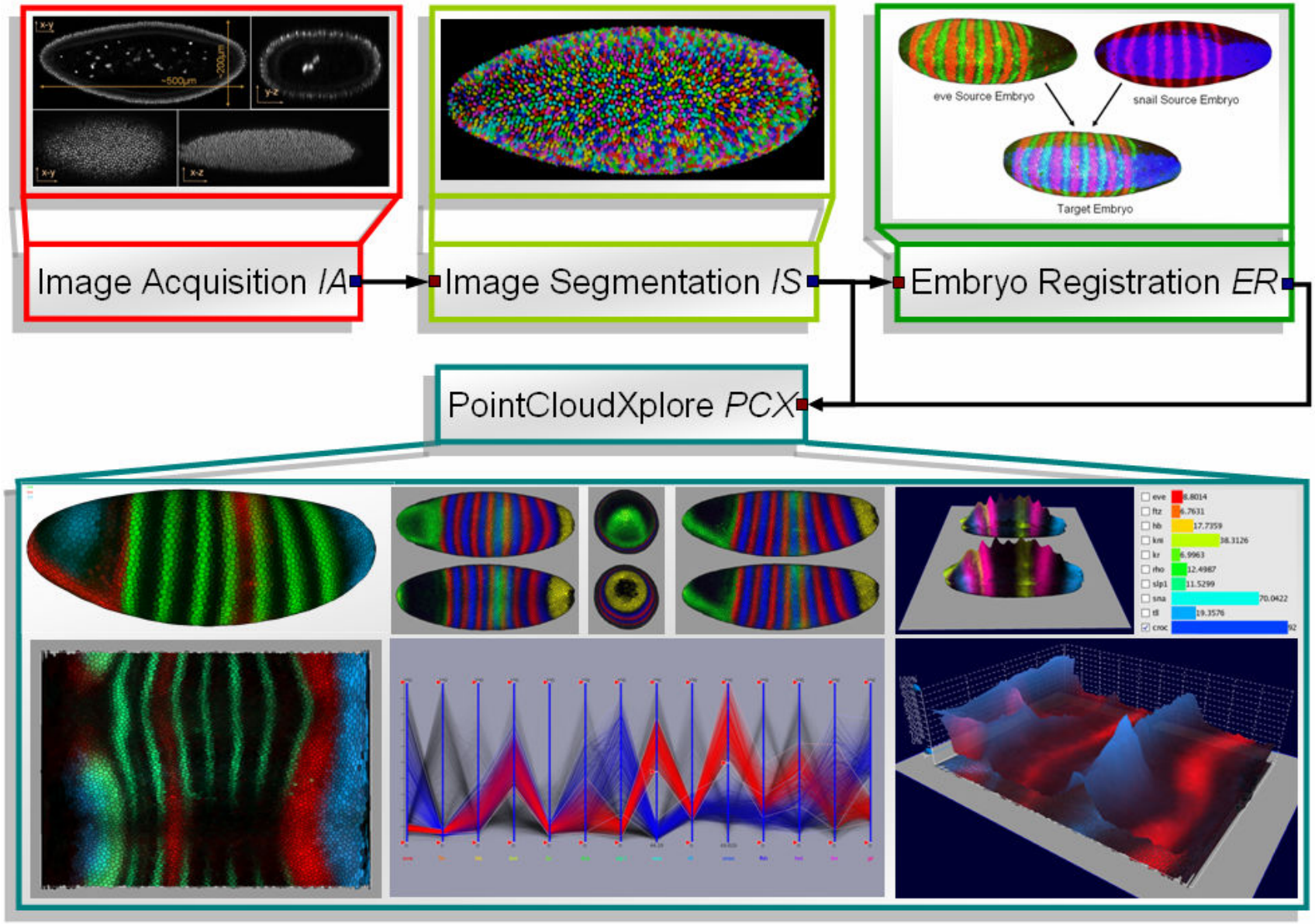
Gene Expression is the amount of protein produced inside a cell using the genetic information of one gene.

Proteins are involved in practically every function performed by a cell e.g. as enzymes, structural proteins or as regulatory proteins.

Regulatory proteins are responsible for regulation of gene expression.

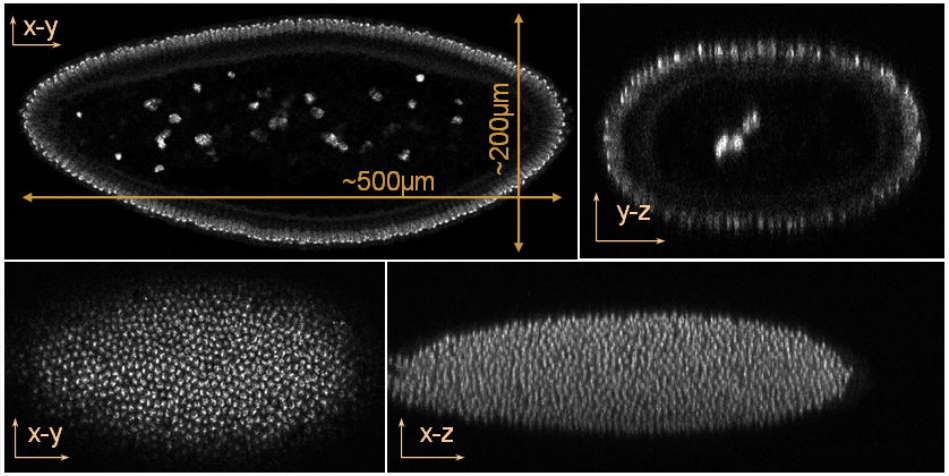
Development of any organism is guided by complex **genetic regulatory networks.**

2. Dataset- and Visualization Pipeline

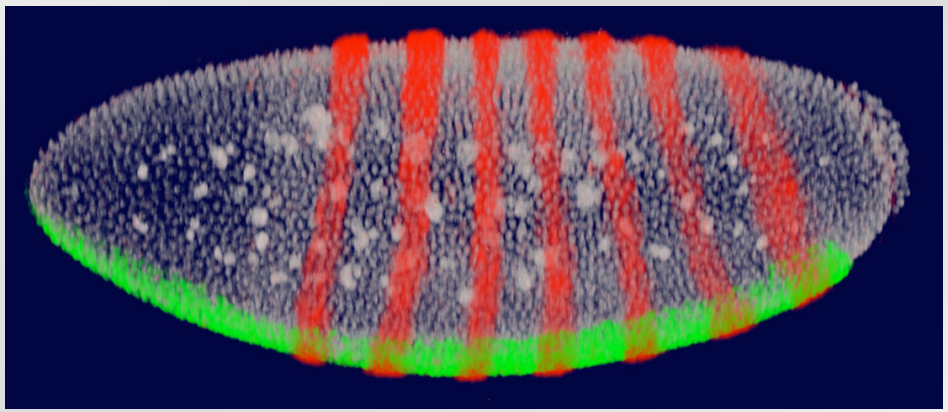


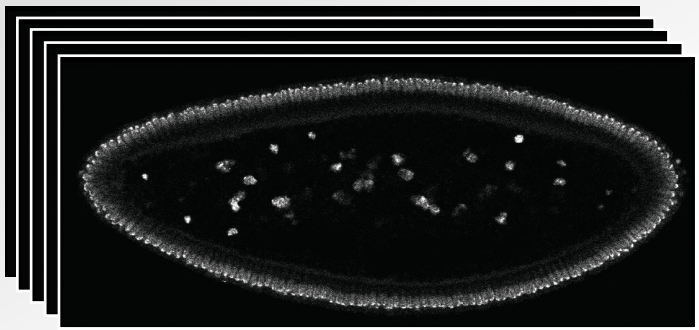
2.1 Image Acquisition

Image Acquisition → Image Segmentation → Embryo Registration



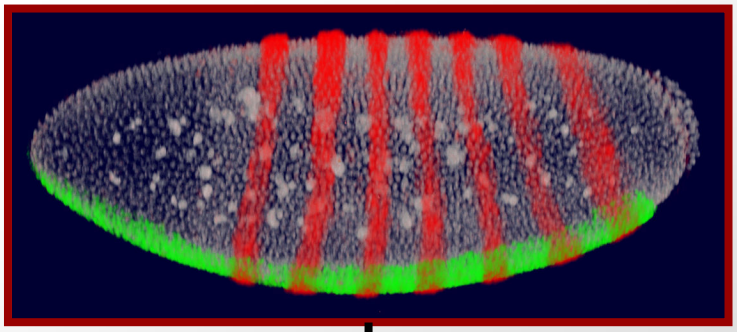
- Embryo is *mounted* and *stained* for nuclear DNA and two genes.
- Image the embryo using 2-photon fluorescent confocal microscopy.
- One image contains the whole embryo with enough resolution to segment individual nuclei.
- One image stack is about 0.5 GB.

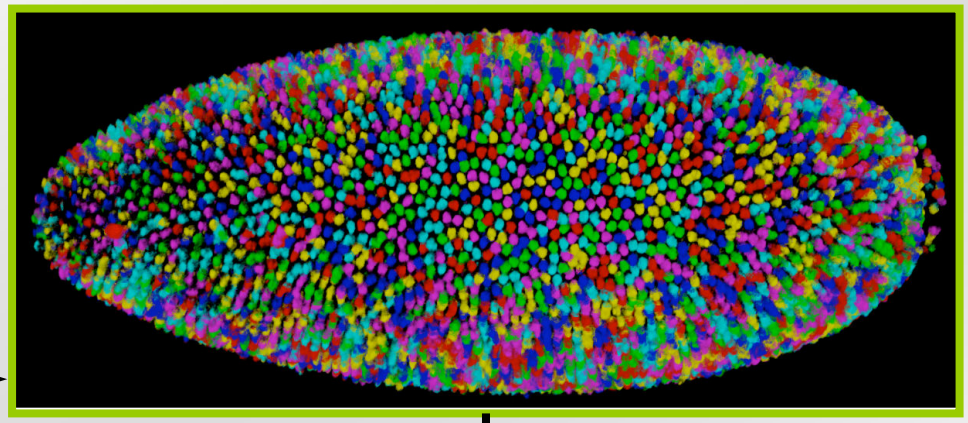




2.2 Image Segmentation

Image Acquisition → Image Segmentation → Embryo Registration

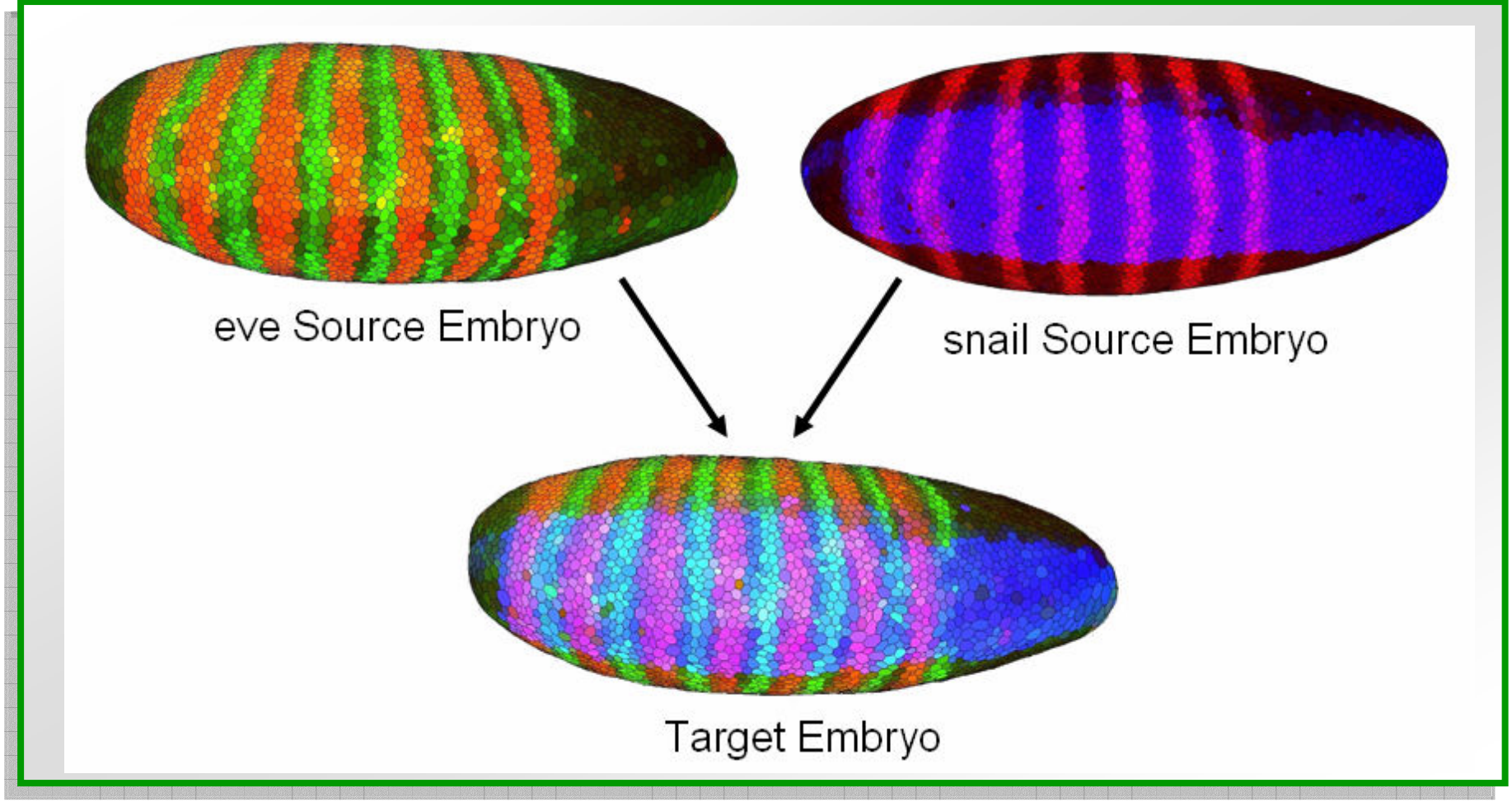




id,	x,	y,	z,	Nx,	Ny,	Nz,	Vn,	Vc,	Sytox,	Cy3_n,	Cy3_a,	Cy3_b,	Cy3_g,	Cou_n,	Cou_a,	Cou_b,	Cou_g
1,	102.36,	142.14,	112.00,	-0.396,	0.851,	0.344,	207.96,	605.36,	52.18,	23.55,	18.76,	22.55,	22.10,	11.95,	8.13,	28.01,	12.04
2,	264.63,	172.01,	79.36,	0.103,	0.972,	-0.208,	281.73,	599.90,	82.12,	31.67,	34.97,	15.95,	31.93,	21.06,	12.56,	41.40,	19.12
3,	225.91,	174.99,	88.65,	-0.030,	0.999,	-0.015,	185.79,	418.35,	85.32,	35.63,	31.27,	14.77,	34.00,	19.59,	20.53,	38.80,	21.35
4,	318.42,	48.34,	138.91,	0.095,	-0.744,	0.660,	182.46,	464.19,	37.61,	19.31,	15.15,	12.47,	17.55,	21.01,	13.78,	26.87,	17.53
5,	110.18,	34.40,	109.65,	-0.186,	-0.913,	0.362,	127.81,	432.01,	55.78,	24.12,	23.53,	12.19,	19.71,	13.81,	7.57,	28.16,	12.40
6,	340.48,	73.79,	37.548,	0.205,	-0.299,	-0.931,	208.26,	607.49,	80.23,	33.04,	26.75,	21.24,	28.91,	31.48,	20.69,	50.45,	26.96
		.	.	.	.	.	.										

2.3 Embryo Registration

Image Acquisition → Image Segmentation → Embryo Registration



Multiple Views

- Different views emphasize different data properties.
- Viewing data from different perspectives supports detailed data analysis.

Brushing and Linking

- **Brushing:** Allow selection of data and emphasize selected data parts.
- **Linking:** Indicate visually which parts of one data display correspond to that shown in another display.

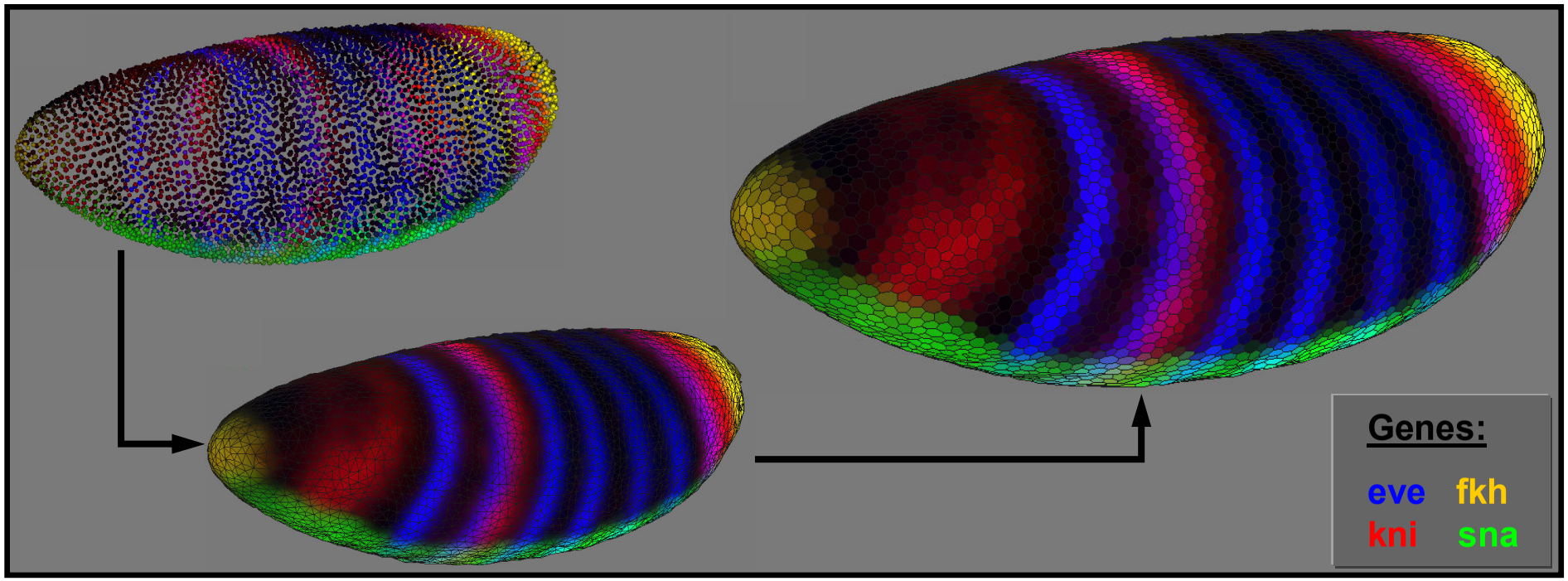
Fundamental idea

Mark interesting data parts according to data properties visualized in one view and look for other properties of selected data in other views.

➔ One can use different ways to select data parts using different type of brushes, but all brushes can be displayed in all views.

[BMMS91] BUJA A., MCDONALD J. A., MICHALAK J., STUETZLE W.: Interactive data visualization using focusing and linking. In IEEE Visualization 1991 (1991), IEEE Computer Society Press, pp. 156–163.
[HLD02] HAUSER H., LEDERMANN F., DOLEISCH H.: Angular brushing of extended parallel coordinates. In IEEE Symposium on Information Visualization (Info-Vis'02) (2002), IEEE Computer Society Press, pp. 127–130.
[KSH04] KOSARA R., SAHLING G. N., HAUSER H.: Linking scientific and information visualization with interactive 3d scatterplots. In Short Communication Papers Proceedings of the 12th International Conference in Central Europe on Computer Graphics, Visualization, and Computer Vision (WSCG) (2004), pp. 133–140.
[**GRW00]** GRESH D. L., ROGOWITZ B. E., WINSLOW R. L., SCOLLAN D. F., YUNG C. K.: WEAVE: A system for visually linking 3-d and statistical visualizations, applied to ardiac simulation and measurement data. In IEEE Visualization 2000 (2000), IEEE Computer Society Press, pp. 489–492.

4. Visualization of Gene Expression in Physical Space



Mapping gene expression to color:

$$color_{ij} = HSV\left(geneColor_j \ , \ 1.0 \ , \ value_{ij}\right)$$

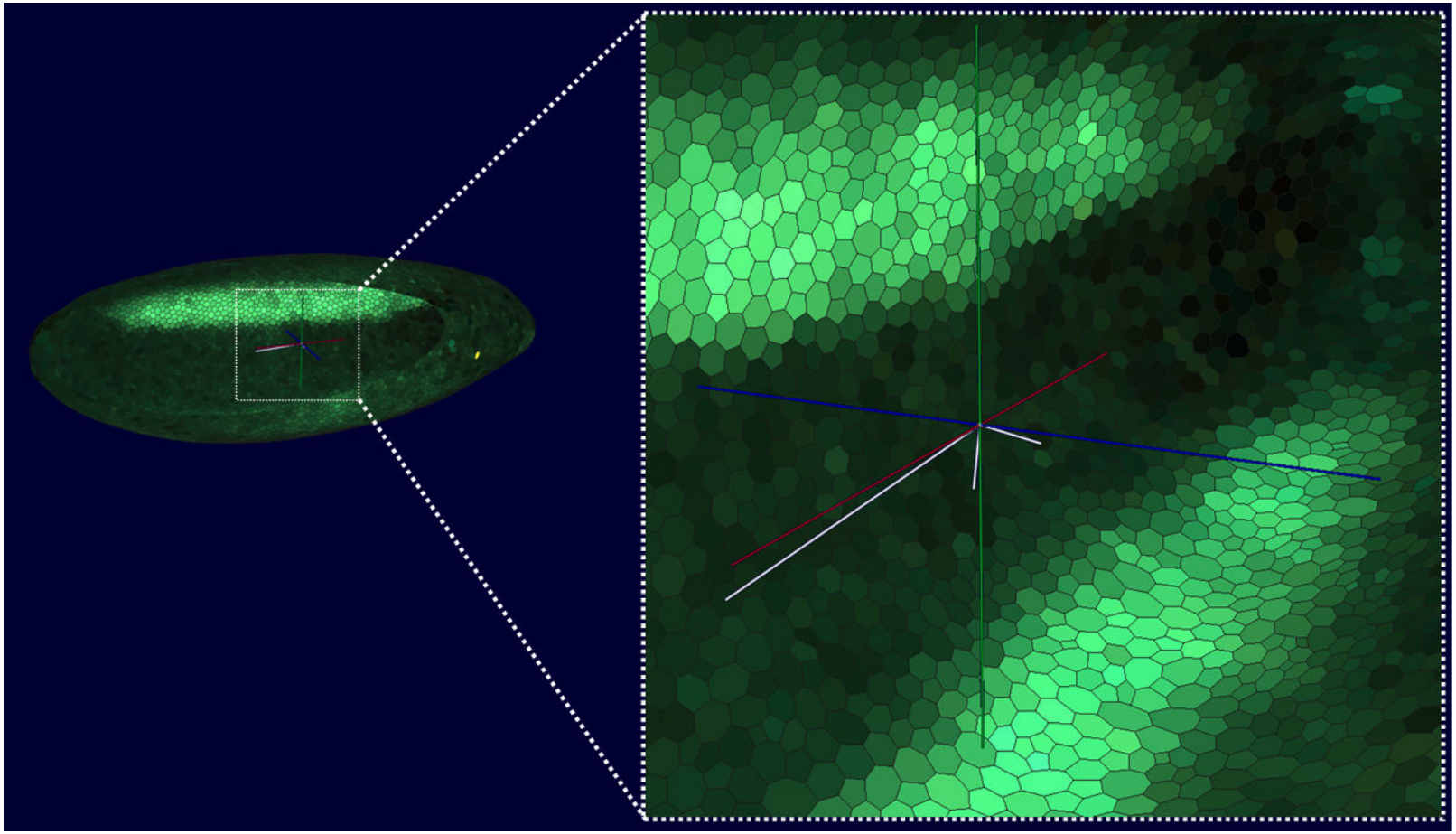
$$value_{ik} = \begin{cases} 0 & : exprLevel_{ij} < minDisp_j \\ \dfrac{exprLevel_{ij} - minDisp_j}{maxDisp_j - minDisp_j} & : minDisp_j \le exprLevel_{ij} \le maxDisp_j \\ 1.0 & : exprLevel_{ij} > maxDisp_j \end{cases}$$

$$color_{ik} = HSV\left(brushColor_{ik} \ , \ 1.0 \ , \ brushValue_{ik} \right)$$

Color of cell with index i : $color_i = \sum_{j=1}^{n} (color_{ij} * displayWeight_j) + \sum_{k=1}^{m} (color_{ik} * displayWeight_k)$

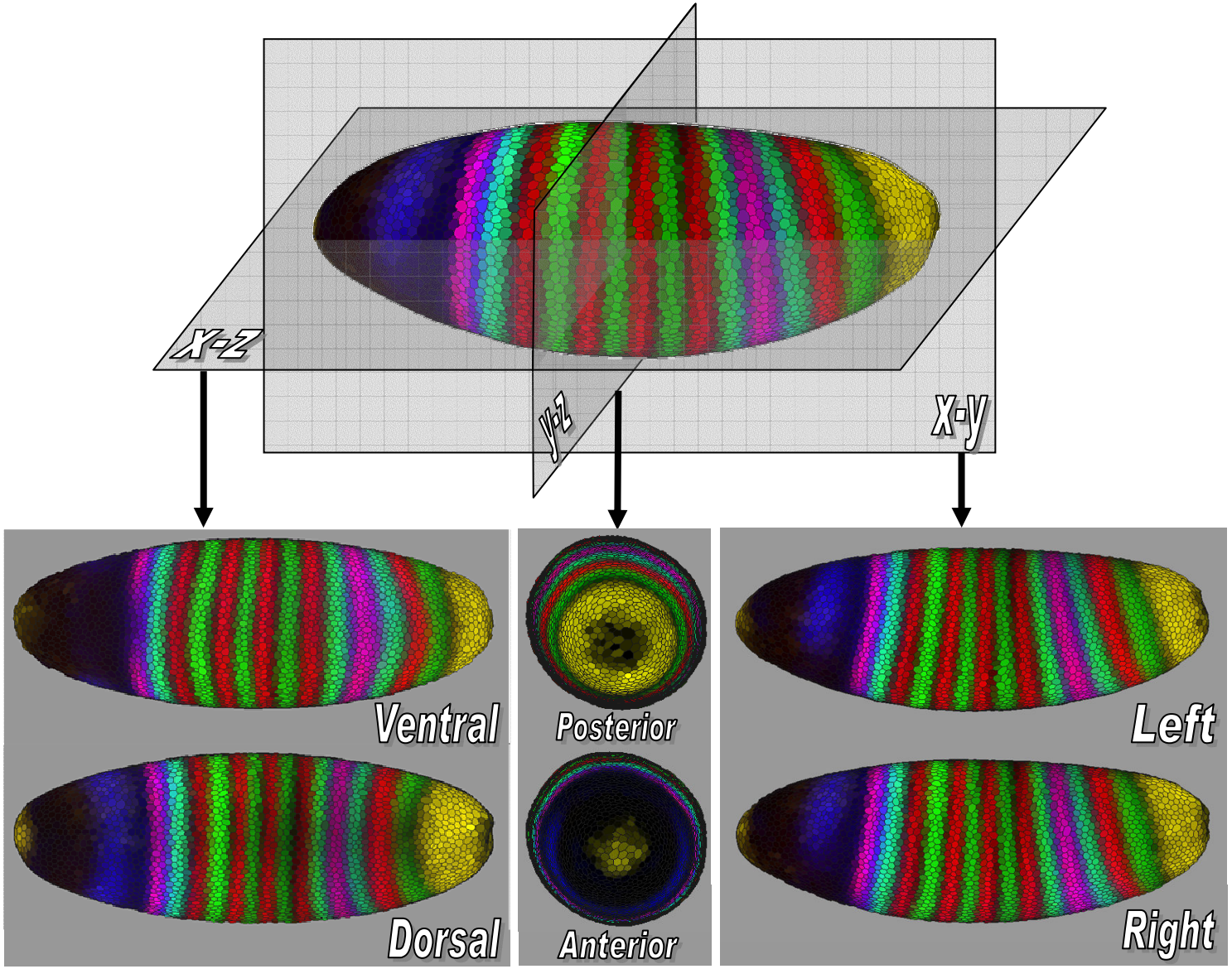
[KSO04] KOLLURI R., SHEWCHUK J. R., O'BRIEN J. F.: Spectral surface reconstruction from noisy point clouds. In Symposium on Geometry Processing (July 2004), ACM Press, pp. 11–21.

4.1 Defining Embryo Orientation and Position

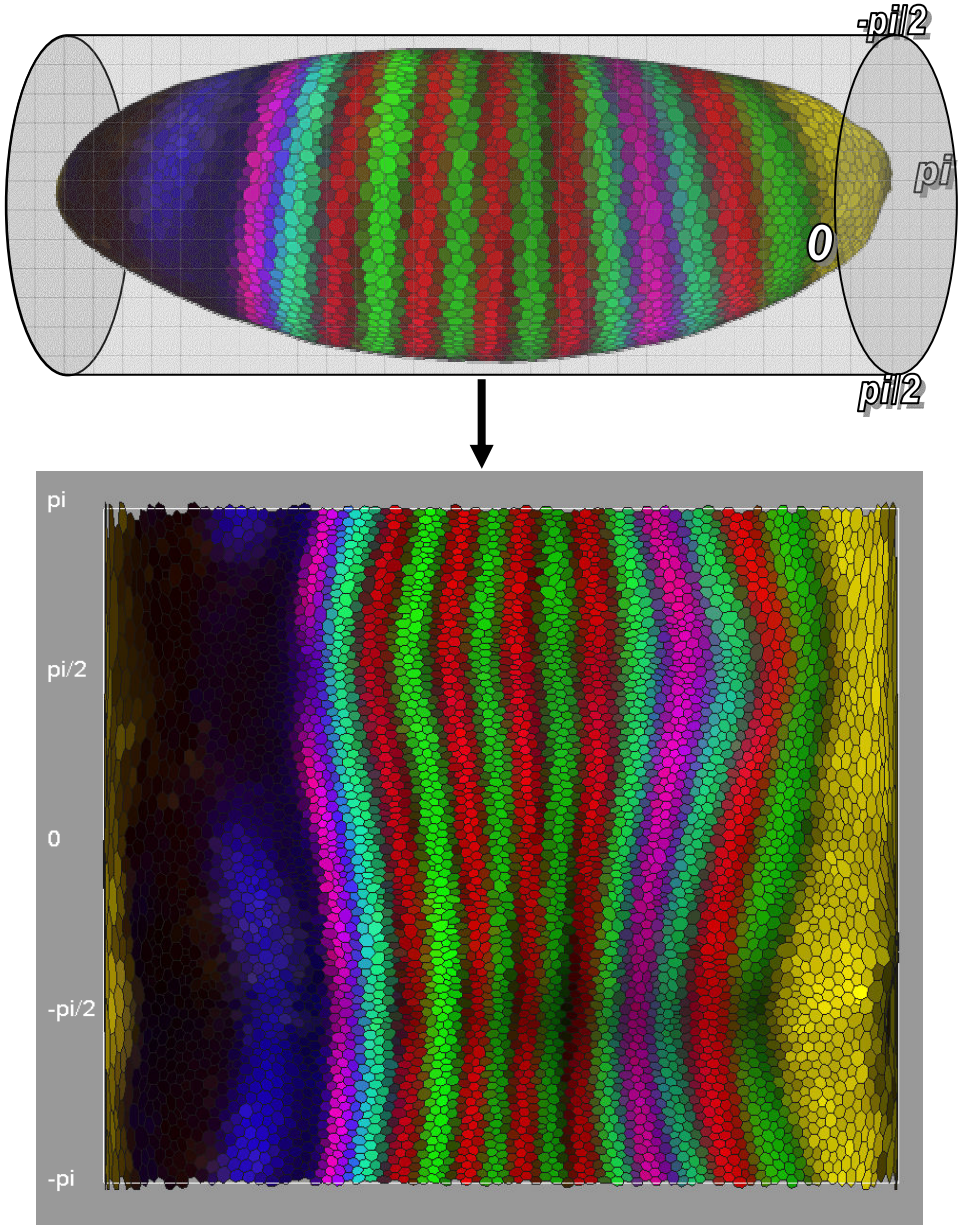


- Translate embryo into the point of origin of the world coordinate system by using the mean point of the PointCloud as reference point.
- Use principal component analysis to define the orientation of the PointCloud.

4.2 Orthographic Views



4.3 Unrolled View



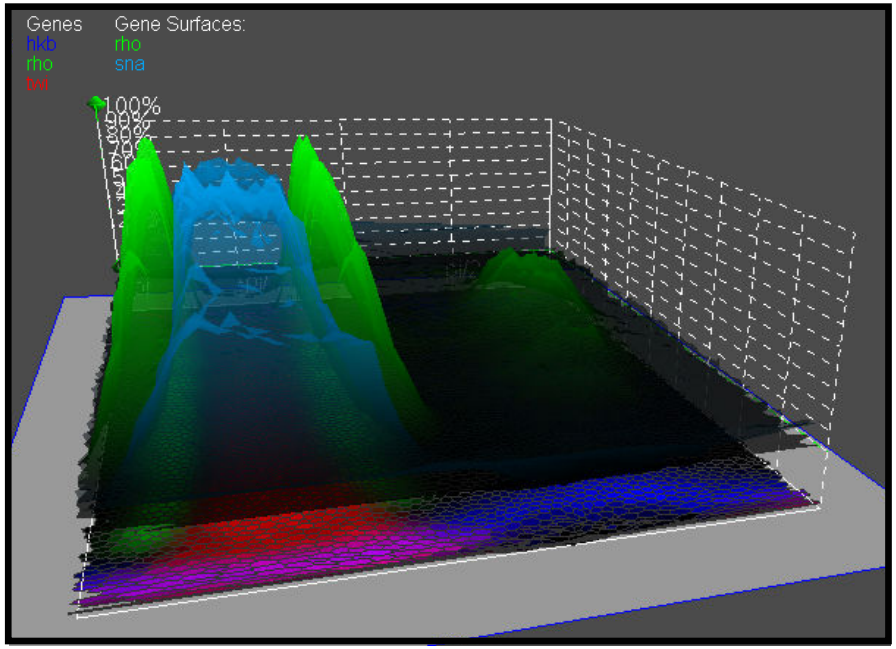
Interacting with Embryo Views:

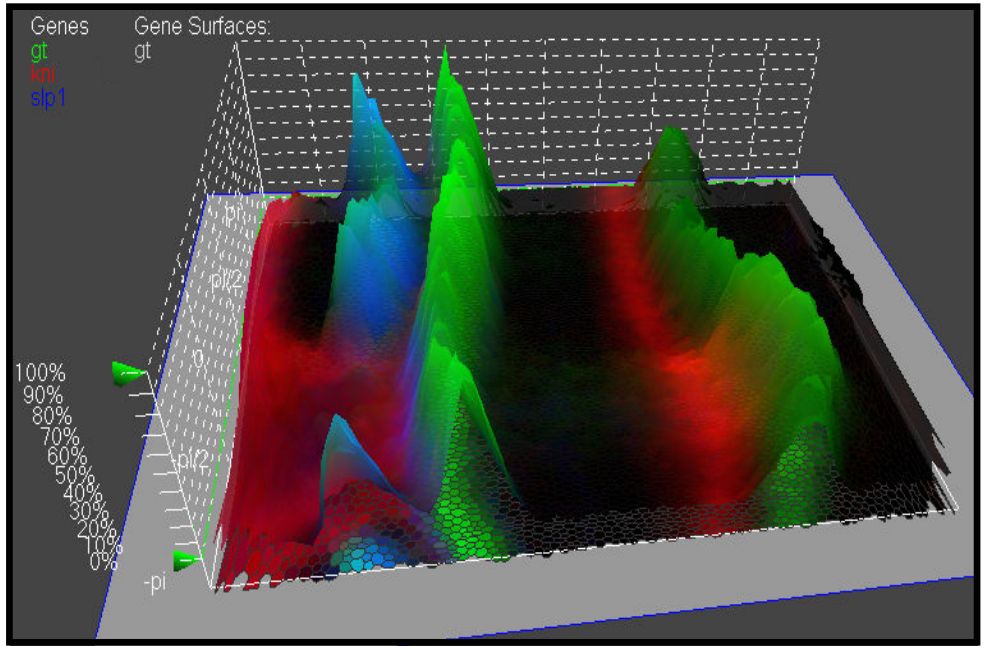
- Interactive zooming, panning, and rotation
- Selection of cells made possible via drawing on the embryo surface

Advantages

- Qualitative analysis of gene expression values
- Analysis and comparison of spatial gene expression pattern
- Information about cell size and density
- Selection of cells according to cell positions

4.4 Expression Surfaces

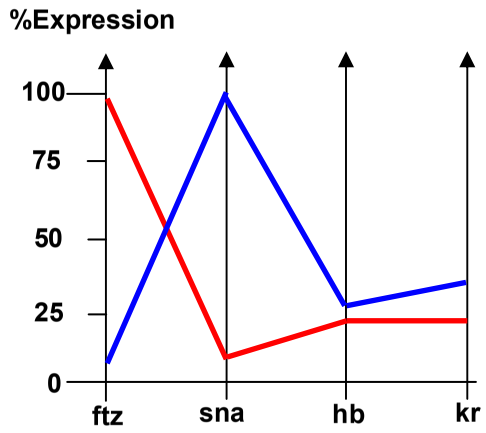




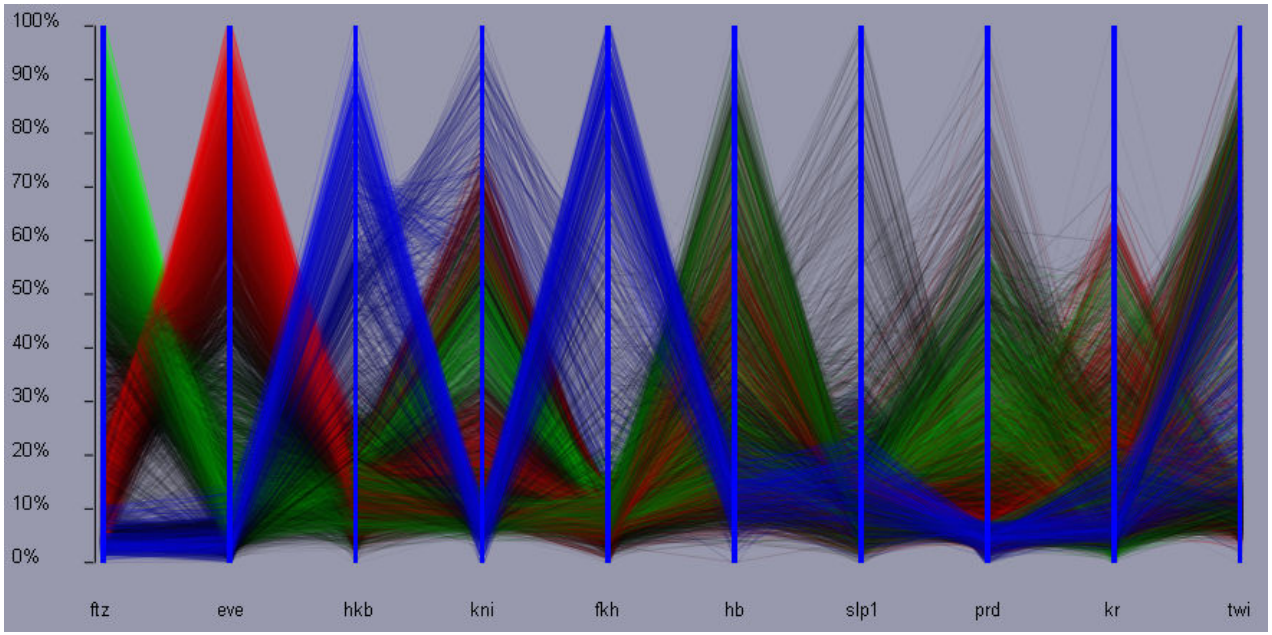
Advantages

- Quantitative analysis of gene expression values
- Detailed view of data without losing overall context
- Spatial information preserved

5 Visualization in Gene Expression Space Using Parallel Coordinates



	ftz	sna	hb	kr
Cell 1	100	8	22	22
Cell 2	8	100	25	30



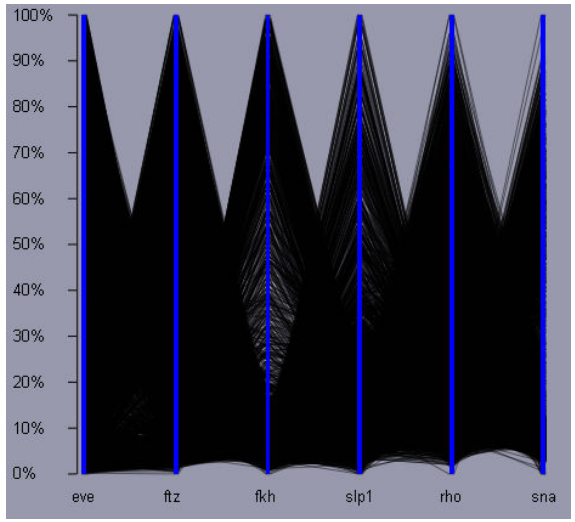
Advantages

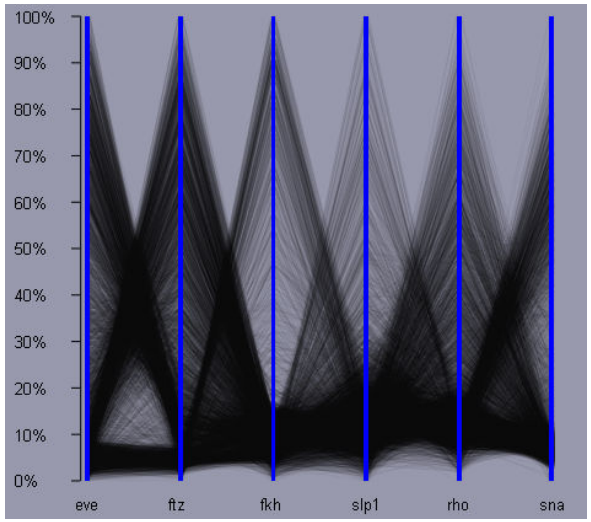
- Overview of expression values of many genes, all cells
- Identification of possible correlations between genes
- Visual identification of line clusters
- Data selection in many data dimensions possible

[Ins84] INSELBERG A.: Parallel coordinates for multidimensional displays. In Spatial Information Technologies for Remote Sensing Today and Tomorrow, The Ninth William T. Pecora Memorial Remote Sensing Symposium (1984), IEEE Computer Society Press, pp. 312–324.
[Weg90] WEGMAN E. J.: Hyperdimensional data analysis using parallel coordinates. Journal of the American Statistical Association 85, 411 (Sept. 1990), 664–675.
[FWR99] FUA Y.-H., WARD M. O., RUNDENSTEINER E. A.: Hierarchical parallel coordinates for exploration of large datasets. In IEEE Visualization 1999 (1999), IEEE Computer Society Press, pp. 43–50.

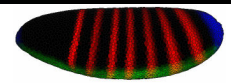
5.1 Varying Line Properties

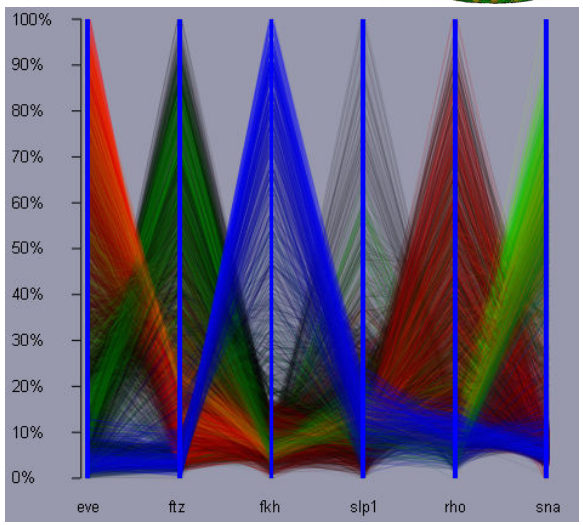
Line transparency



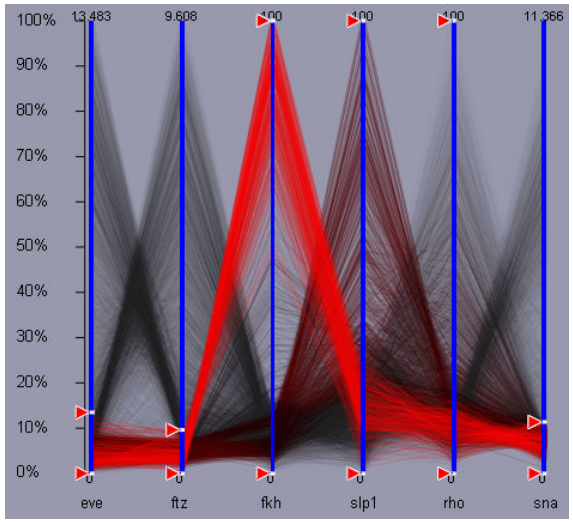


Embryo Coloring

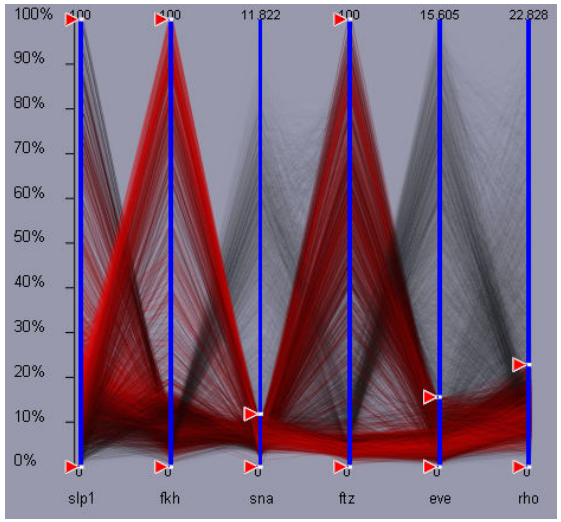




AP/DV Coloring



Distance to the first average

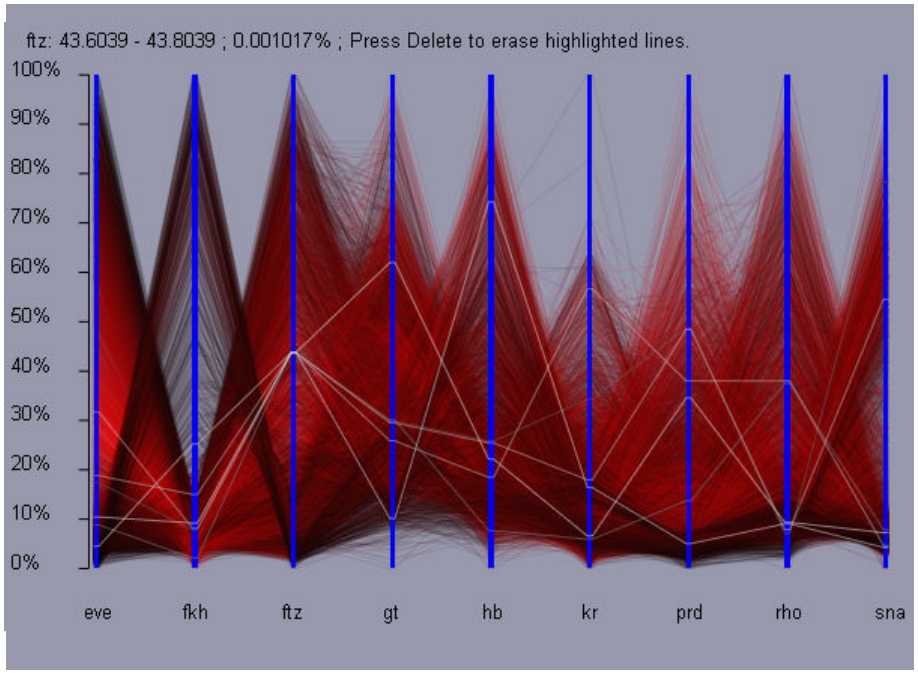


- Transparent data lines support detection of dense clusters in the data.
- Color helps in tracing the topology of data lines and highlights line clusters.

[WL97] WEGMAN E. J., LUO Q.: High dimensional clustering using parallel coordinates and the grand tour. Computing Science and Statistics 28 (1997), 361–368.

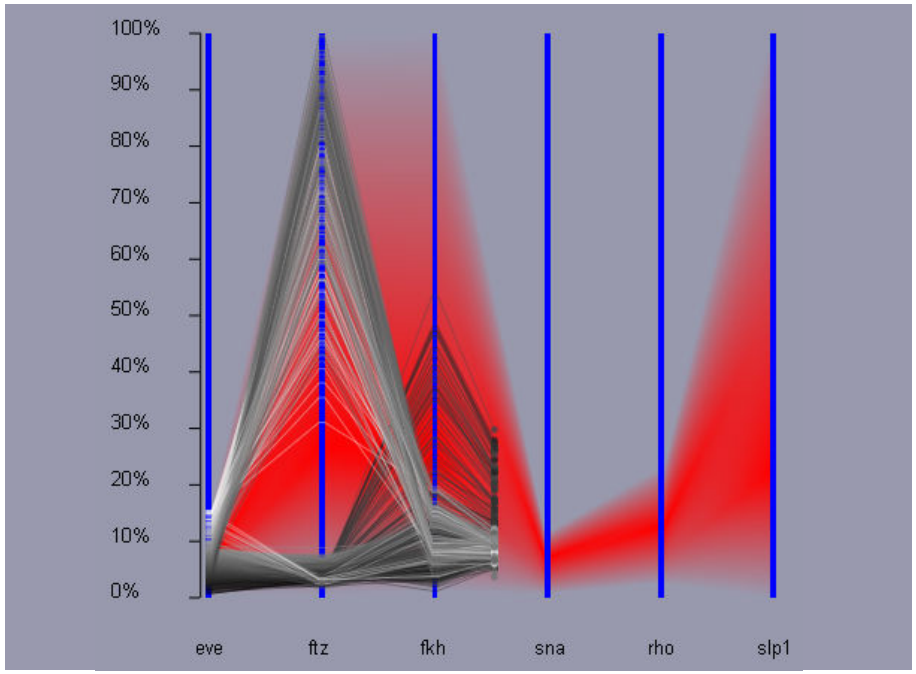
5.2 Line Trace Highlighting and Animation

Line Trace Highlighting



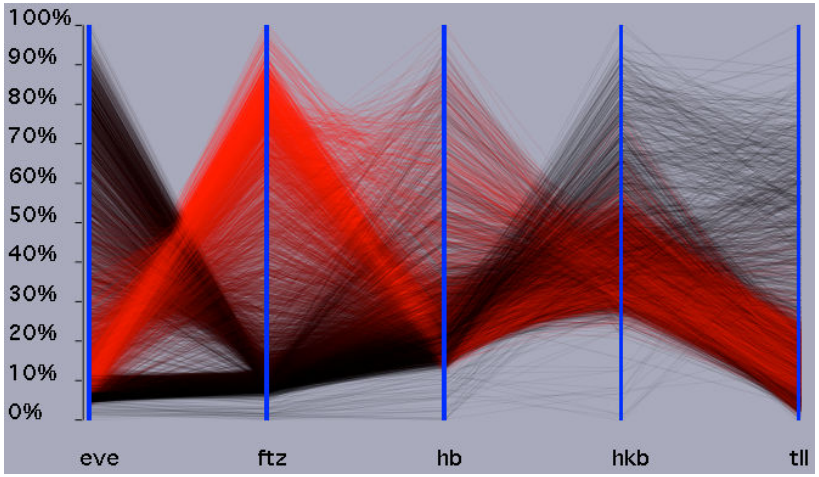
- Possible to follow the topology of single data lines
- Moving the cursor along a parallel coordinate axis reveals information about the data line density and line distribution along that axis.

Line Trace Animation



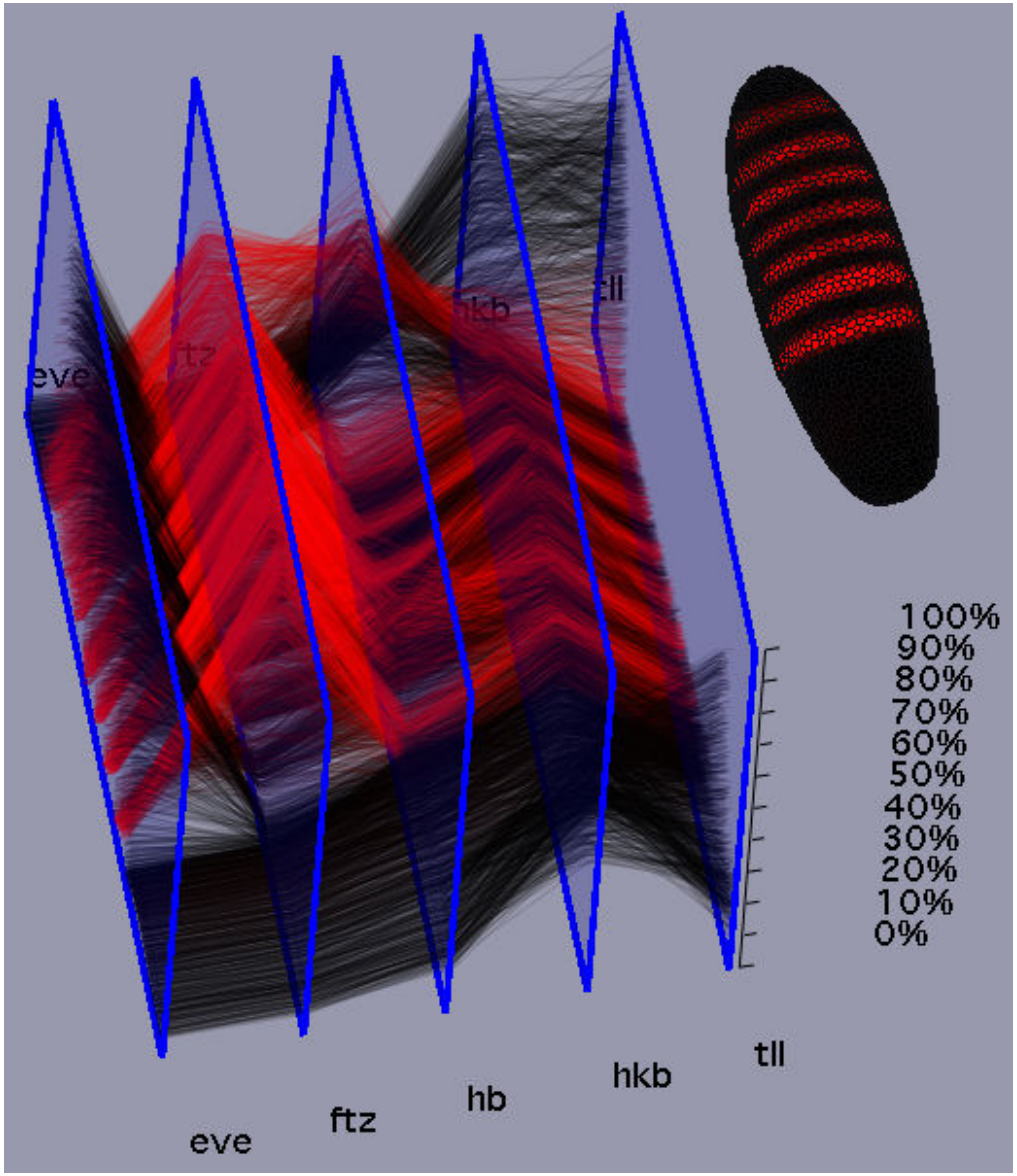
- Subset of lines to be animated is defined by the user
- User can stop and pause the animation and also define the current time step of the animation.

5.3 Extending Parallel Coordinate View to 3D



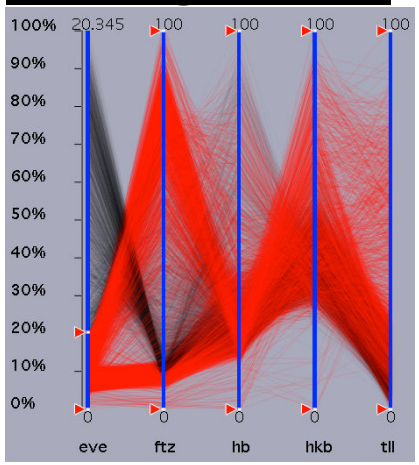
Advantage

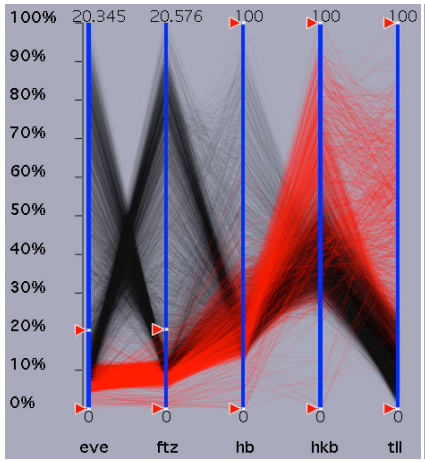
- Spatial dimensions are clearly separated from gene expression dimensions.
- Character of gene expression patterns are preserved in one dimension.
- Additional information about gene expression patterns and their relationships are revealed.



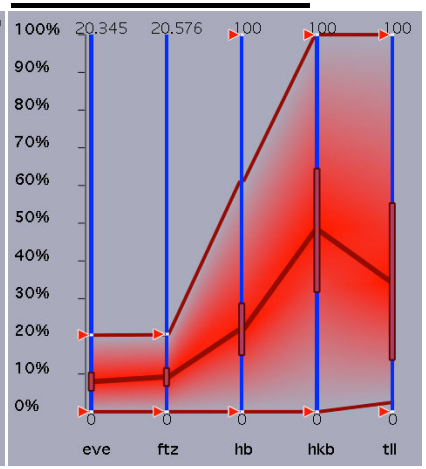
5.4 Brushing in Parallel Coordinate Views

Defining a Brush

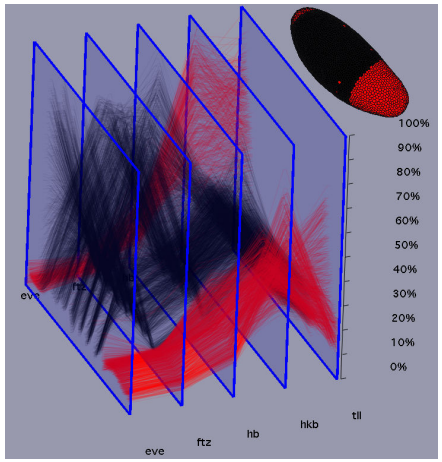




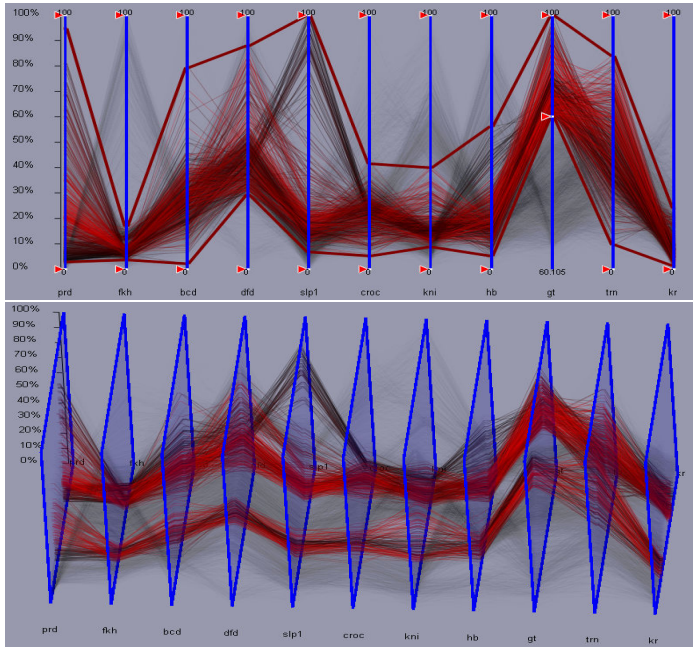
Brush Bands

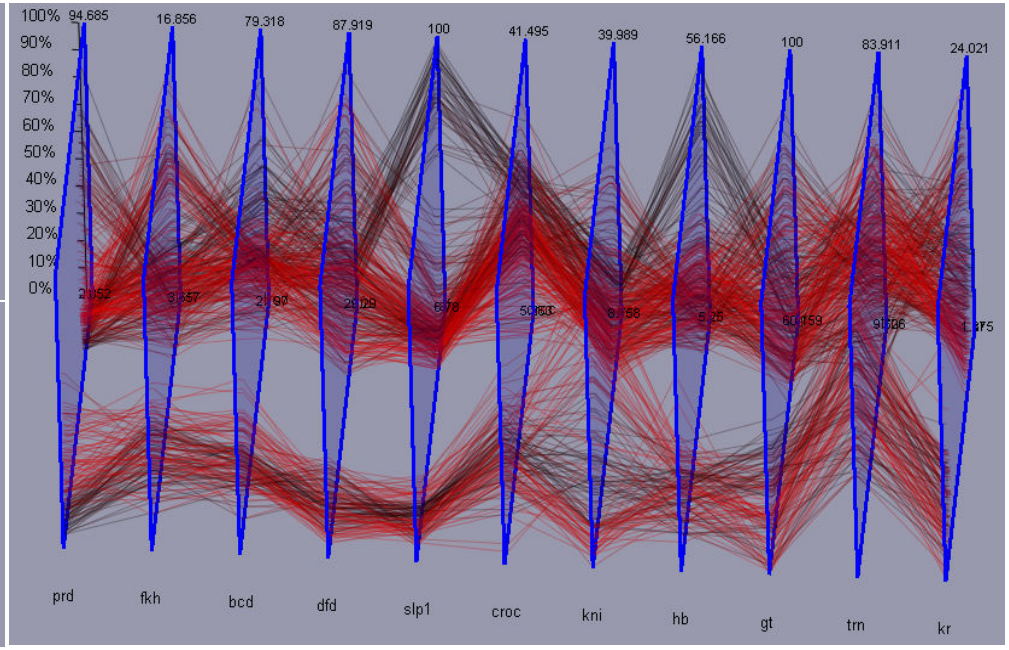


3D View

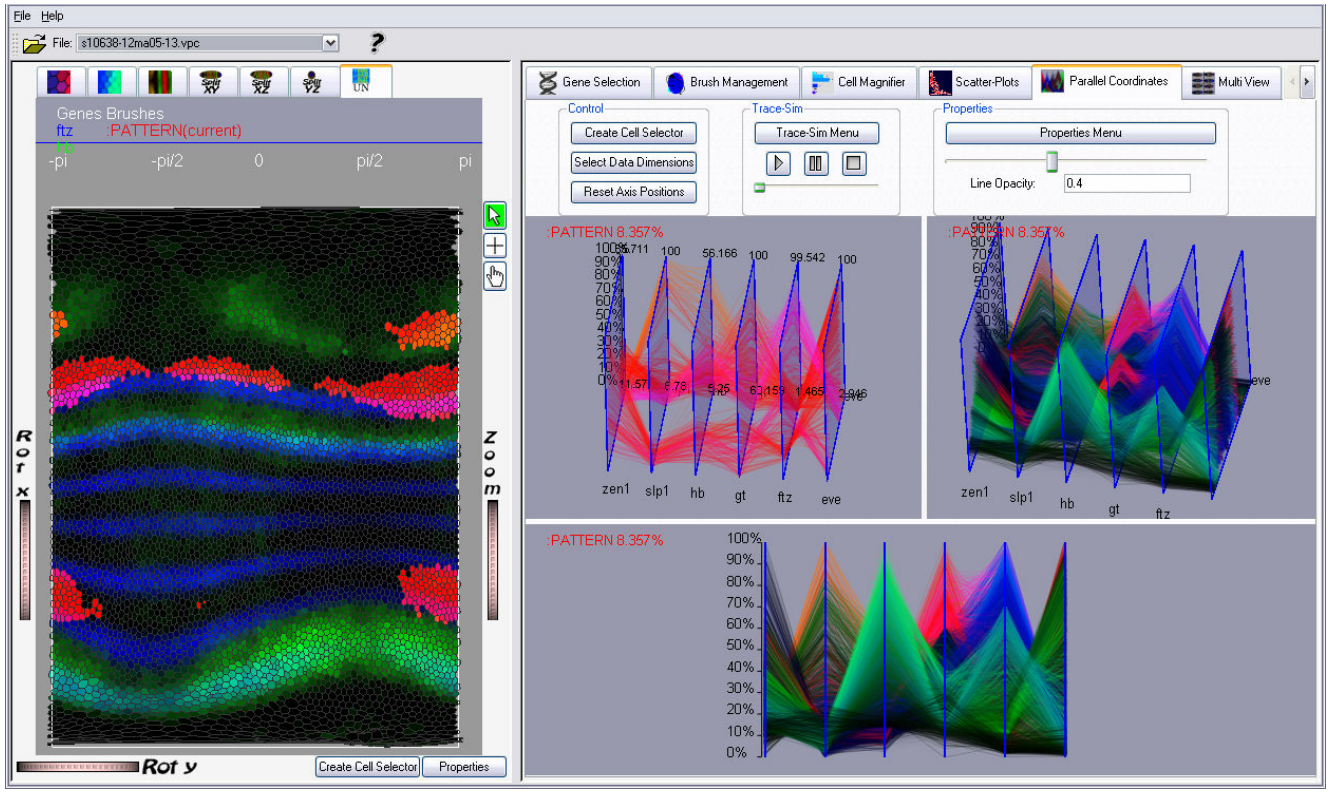


3D Dimensional Zoom





Conclusions and Future Work



Future Work

- Integration of additional information visualization techniques, e.g. scatter plots
- Integration of automatic data analysis methods, e.g.,
  - unsupervised clustering
  - singular value decomposition (SVD)

Acknowledgements

http://graphics.idav.ucdavis.edu/research/vistools3dgeneexpression

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- Computer Science Division, UC Berkeley
- Visualization Group at the Lawrence Berkeley National Laboratory
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