

EPICViz : An interactive *C. elegans* embryogenesis and gene expression visualization

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C. elegans and gene regulation

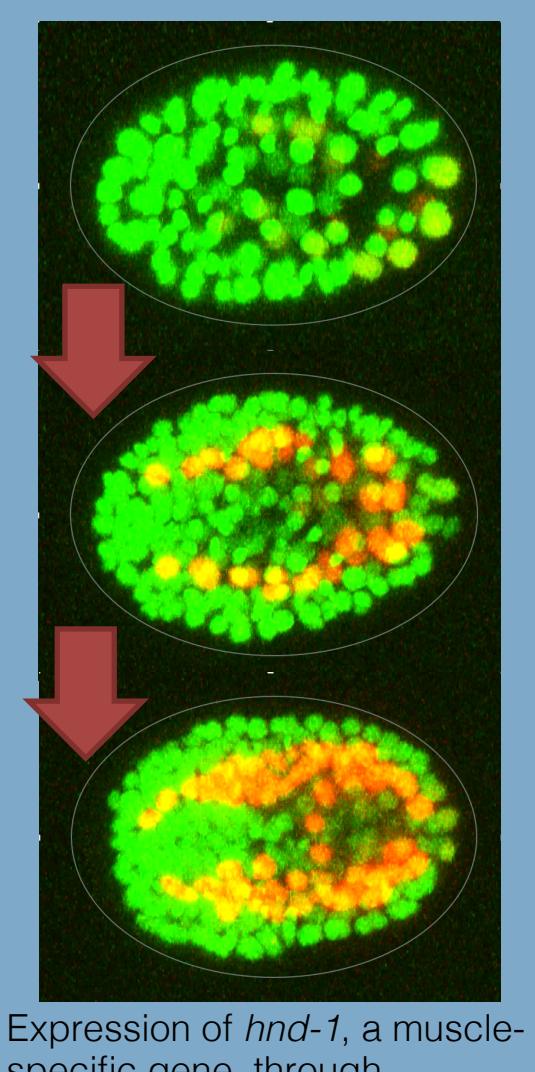
- *Caenorhabditis elegans* (*C. elegans*) is a small roundworm used widely as a model organism in genetics and genomics. Each worm takes around 14 hours to grow from a single fertilized cell to a hatched larvae with 558 cells.
- Embryonic development proceeds due to the tightly choreographed expression of several genes. These patterns of gene expression contribute to cell identity.
- Location of cells during embryogenesis is also important, as cell-cell interactions can influence gene regulation.



An adult *C. elegans* specimen.

Dataset

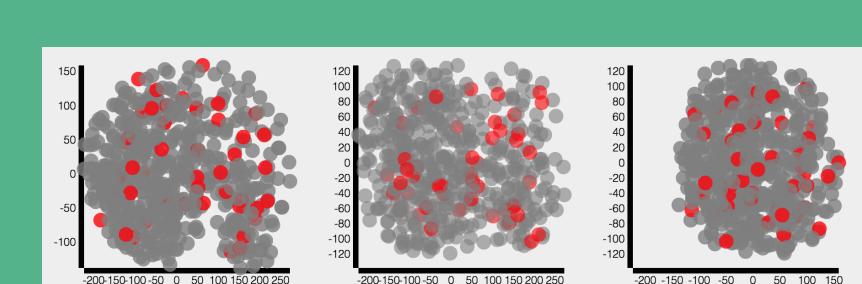
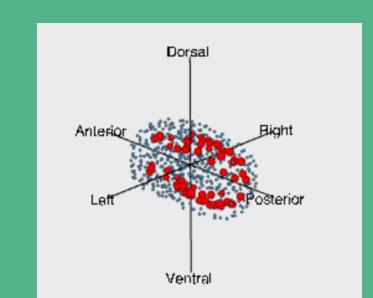
- The Expression Patterns In *C. elegans* (EPIC – <http://epic2.gs.washington.edu/Epic2>) project has generated a dataset that describes the spatial orientation of every cell during *C. elegans* embryogenesis, its developmental lineage and cell fate, and expression measurements for a set of about 227 genes.
- These data provide an expansive view of gene expression in the *C. elegans* embryo; however, to derive insights into gene expression patterns in different cells across time we need a tool to integrate and allow interactive exploration of the data.



Types of data
Spatial orientation and diameter of cells
Cell types and lineages
Gene expression for ~250 genes in each cell

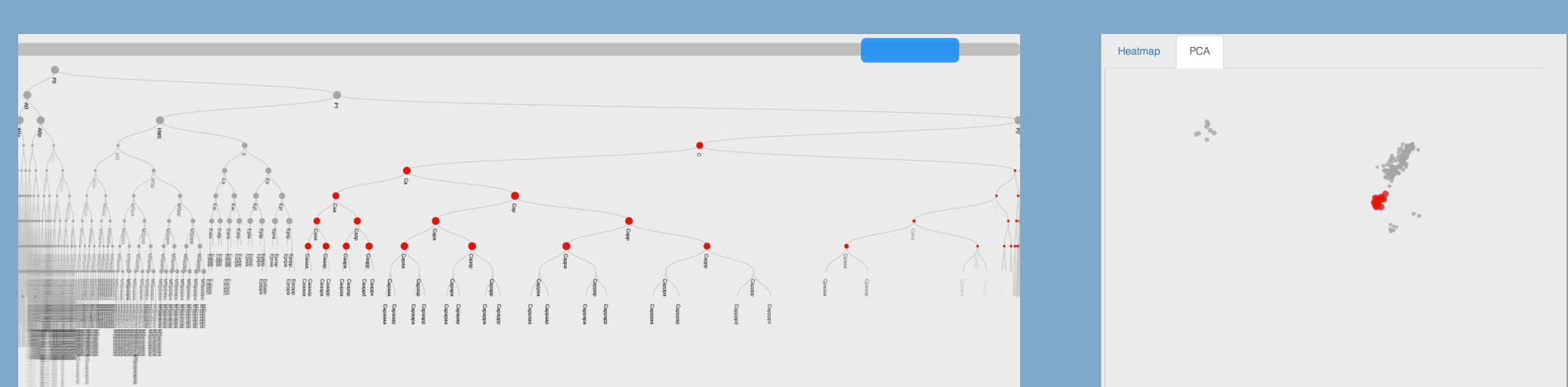
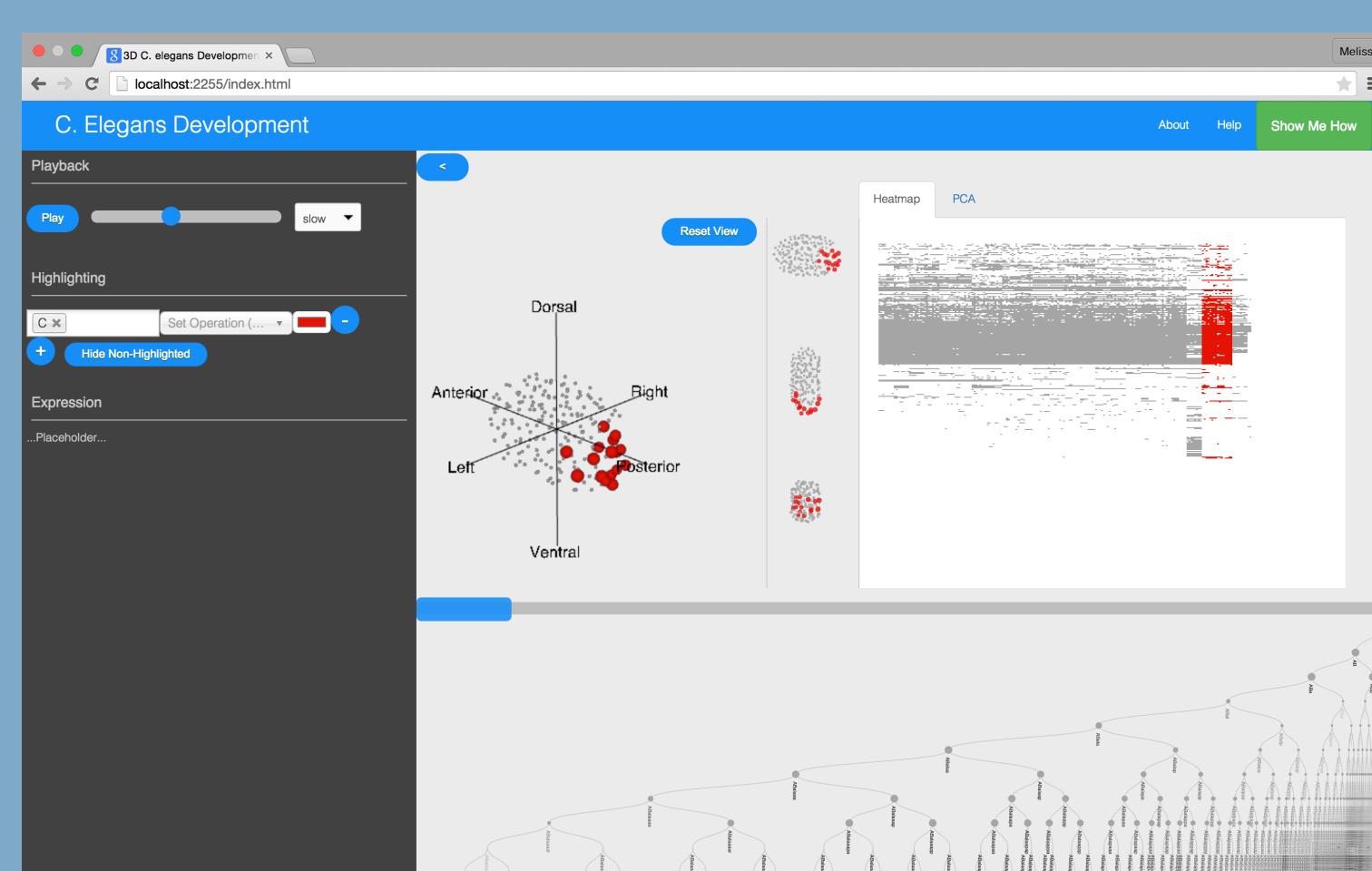
Features

- Based on user selection, specific lineages and cell types can be highlighted in color.
- The user can track development in 3D and in 2D small multiple projections.
- Genes of interest can be selected from the heat map for further study.

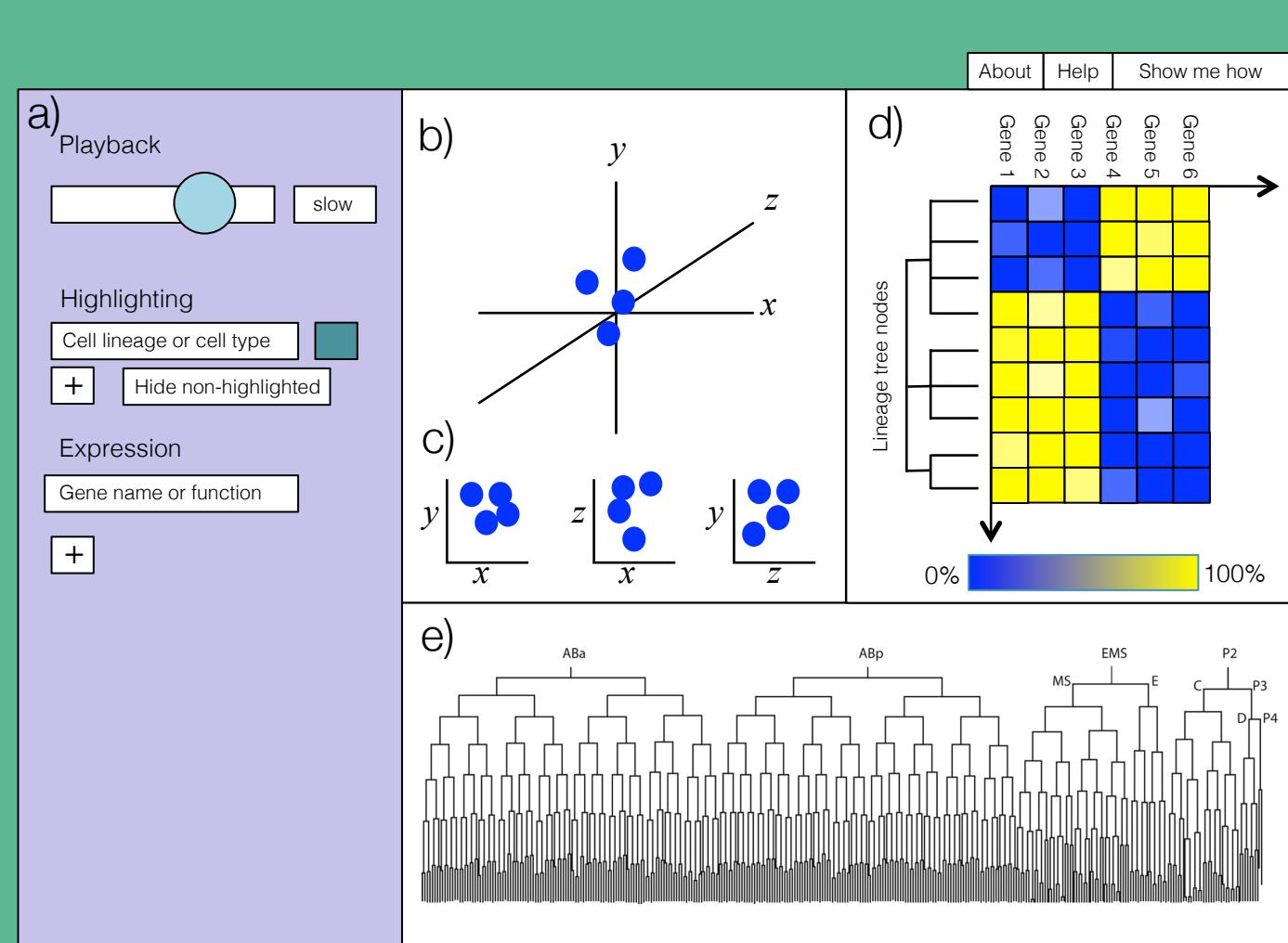


Preliminary study of 3D plot with 2D small multiples.

Results



Highlighting can be tracked in the lineage tree (left panel). In addition to a heatmap of gene expression, shown in the screenshot above, we added a PCA plot of cells based on their gene expression patterns (right panel).



A prototype of our visualization. We strived to combine a) user selections for cell lineage, cell type, and gene expression, b) a 3D plot of embryo development, c) small multiple projections of that 3D plot, d) a heat map of gene expression values, and e) the lineage tree.

Future Work

- Expand logical control of selections
- Add selection criteria for gene function
- Display histogram of expression among lineages upon selection in heatmap or PCA plot