Miriah Meyer

Assistant Professor, School of Computing

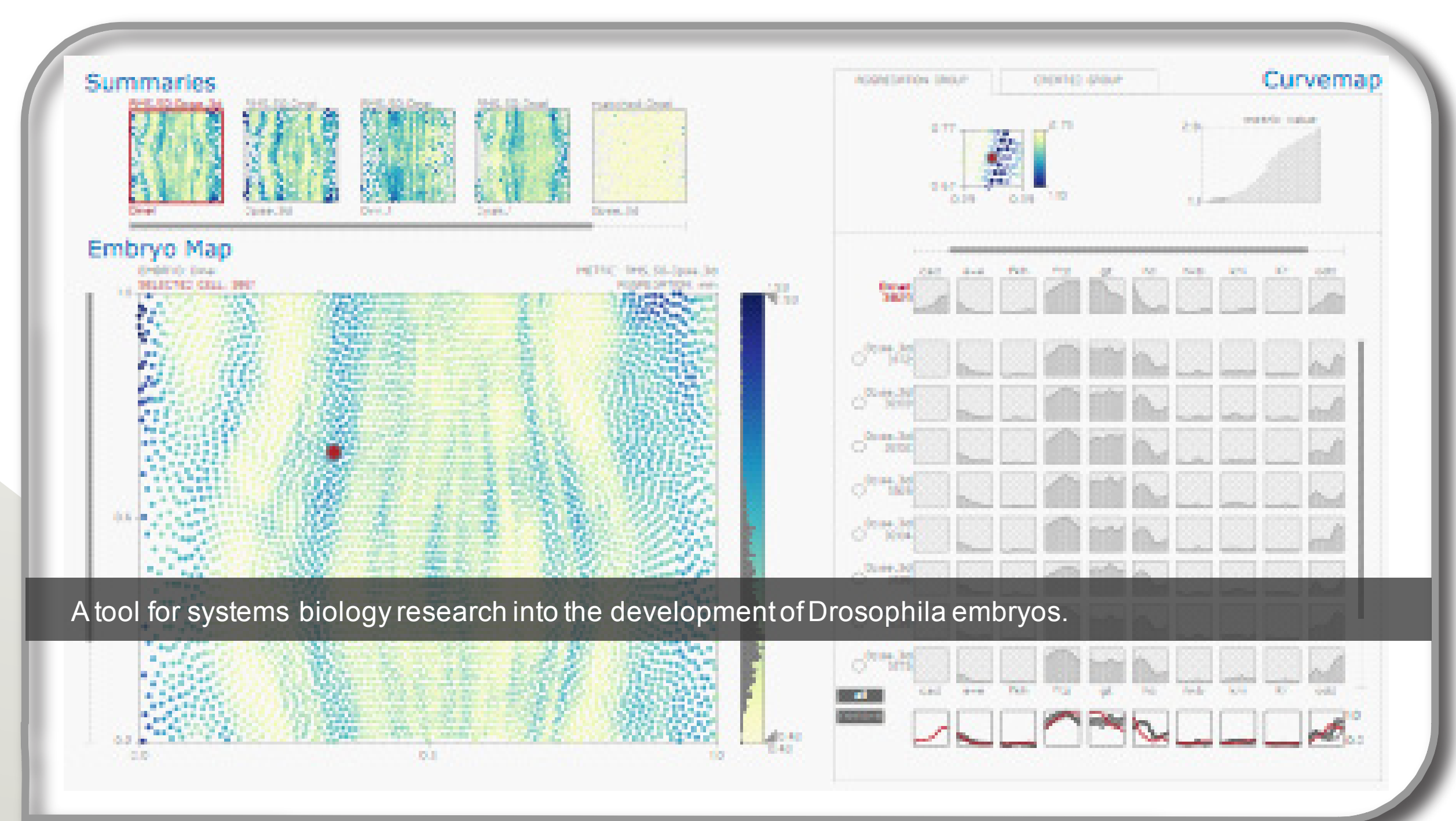## Visualizing Biological Data

DATA VIS LAB

Computational tools are essential for deriving meaning from the deluge of data that we are faced with today. To facilitate an understanding of the complex relationships embedded in this data, visualization research leverages the power of the human perceptual and cognitive systems, encoding meaning through images and enabling exploration through human-computer interactions. In my research I design visualization systems that support exploratory, complex data analysis tasks for scientific research. These systems allow scientists to validate their computational models, to understand their underlying data in detail, and to develop new hypotheses and insights. Currently I am working with biologists who are analyzing large amounts of heterogeneous data from high-throughput sequencing technologies
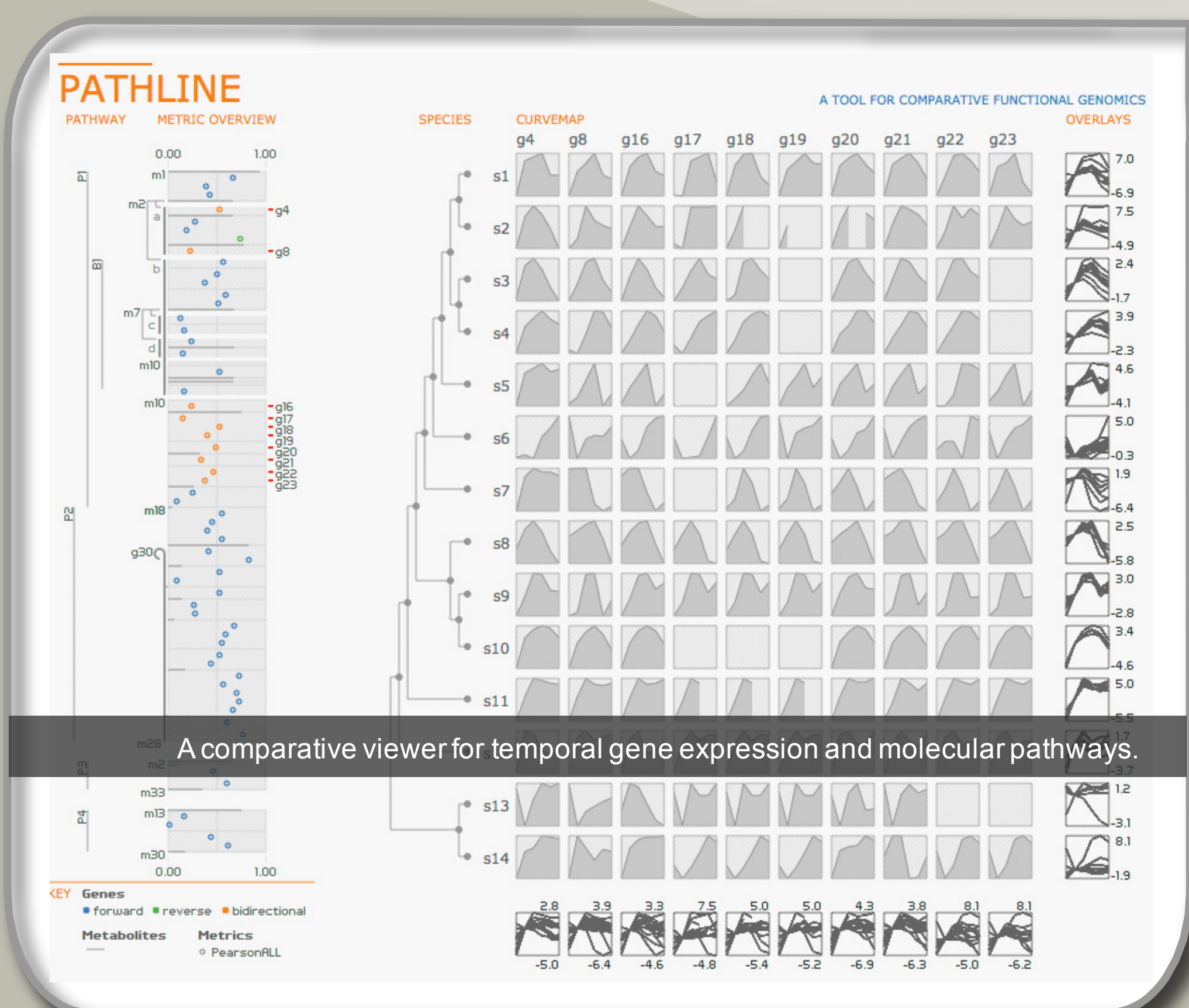
Collaborations:

Comparing Gene Expression in Drosophila Embryos: Angela DePace, Department of System Biology, Harvard Medical School

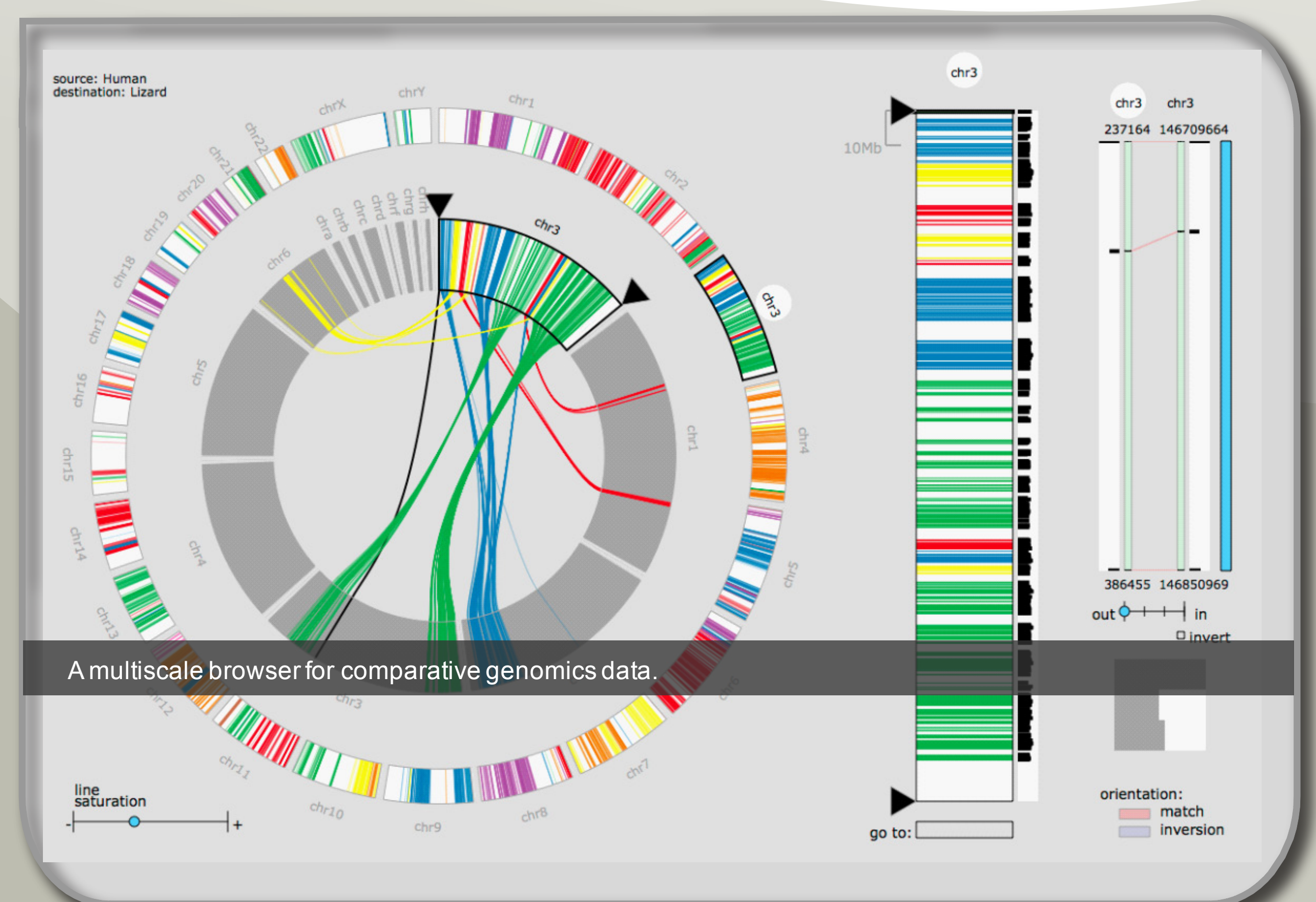Finding Patterns in ChIP-Seq Data: Bang Wong, Broad Institute of MIT and Harvard

Usability in Next-Gen Sequencing Pipelines: Nicola Camp, Division of Genetic Epidemiology, University of Utah School of Medicine

A tool for systems biology research into the development of Drosophila embryos.

MulteeSum www.multeesum.org

A comparative viewer for temporal gene expression and molecular pathways.

Pathline www.pathline.org

A multiscale browser for comparative genomics data.

MizBee www.mizbee.org

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