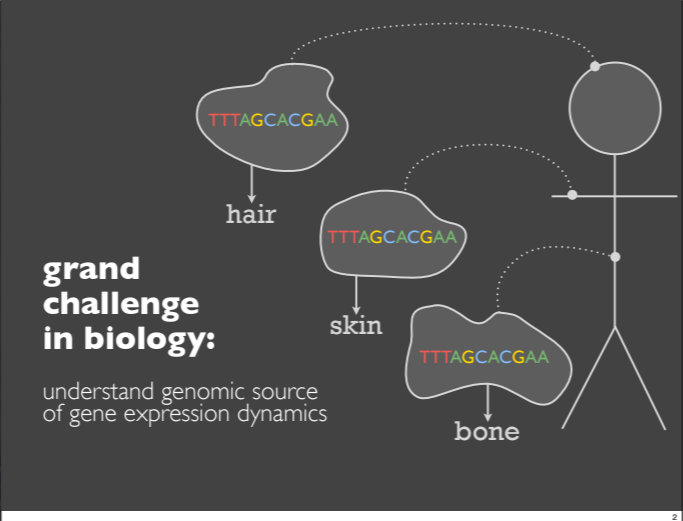


MulteeSum

A Tool for Comparative Spatial and Temporal Gene Expression Data

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² University of British Columbia
³ Harvard Medical School



collaborators: DePace lab at Harvard Medical School

model species: fruit fly

scientific goal: link changes in the regulatory part of the genome to species variation

requires: characterize differences in gene expression patterns between species

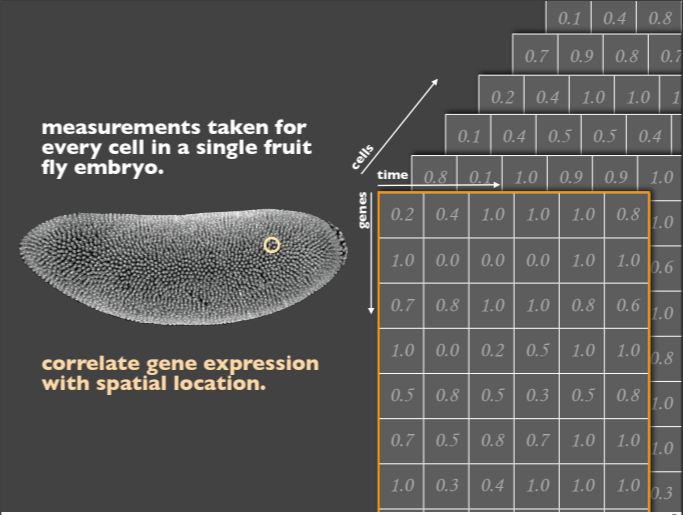
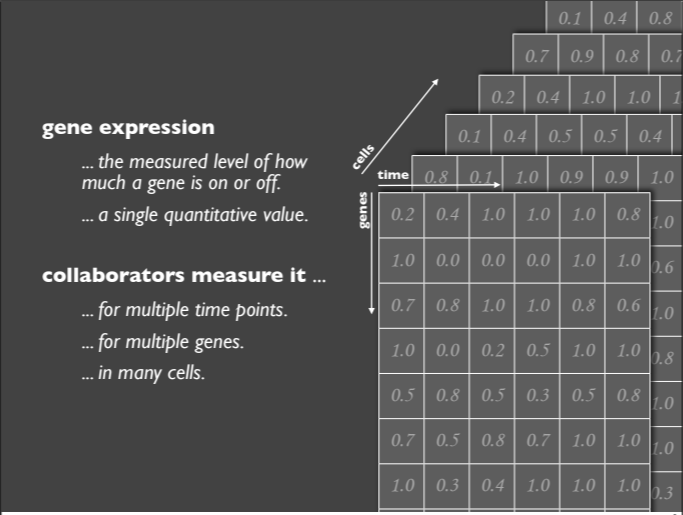
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process

- two year collaboration
- two early prototype systems
- feedback from six biologists
informal interviews, emails
one day a week in biology lab
- tool deployed
currently used several times a week

data & tool & tasks

summaries & groups
 encodings & interaction
 conclusions



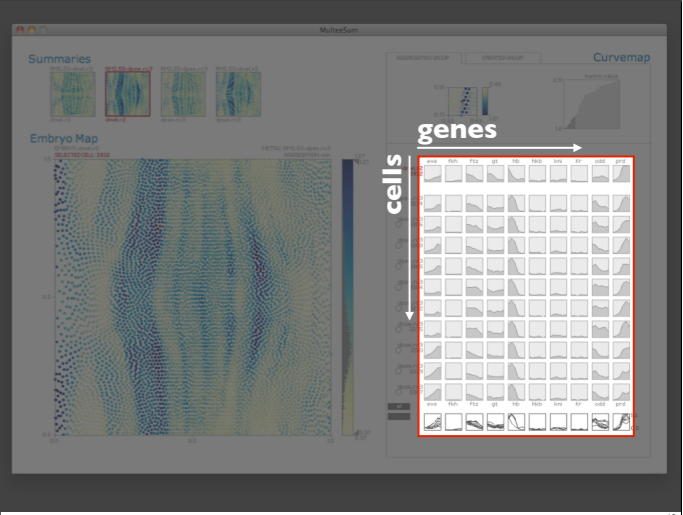
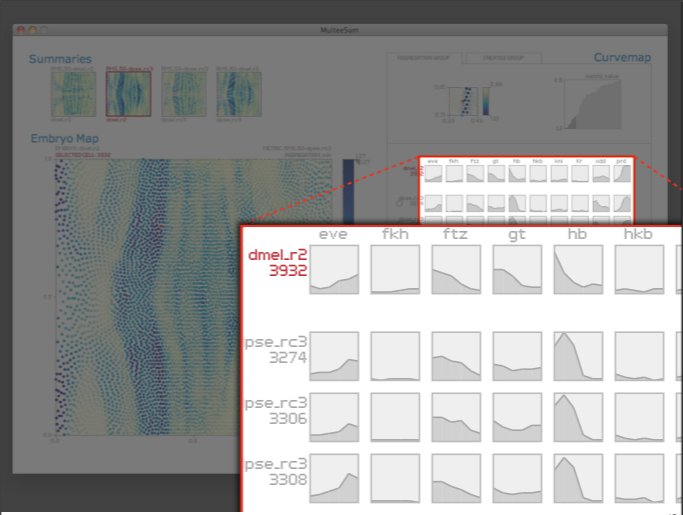
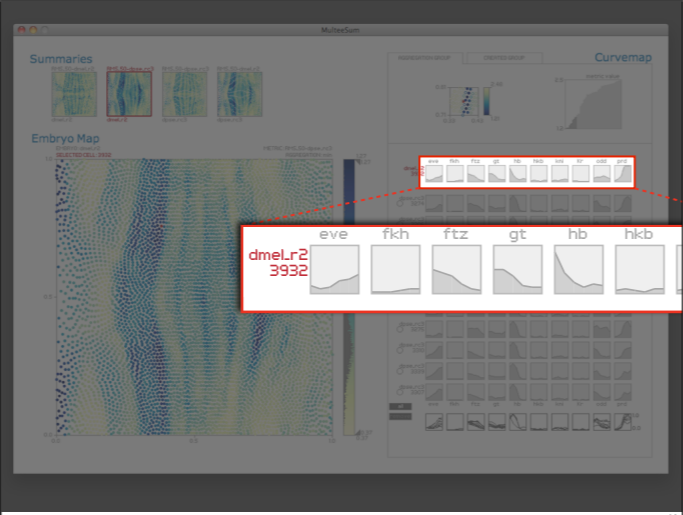
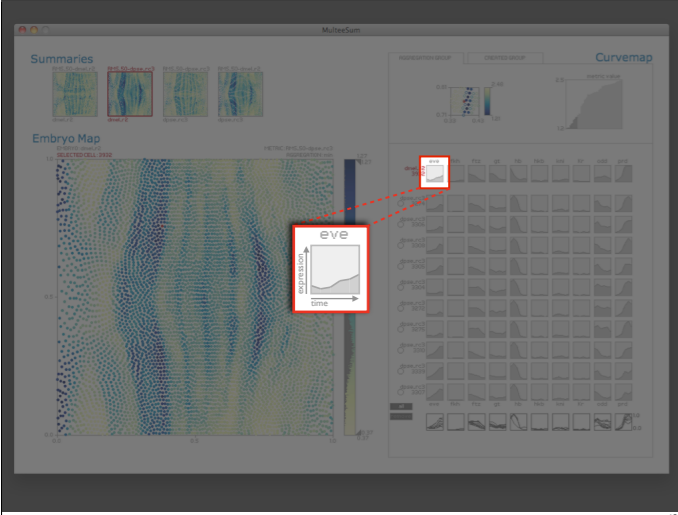
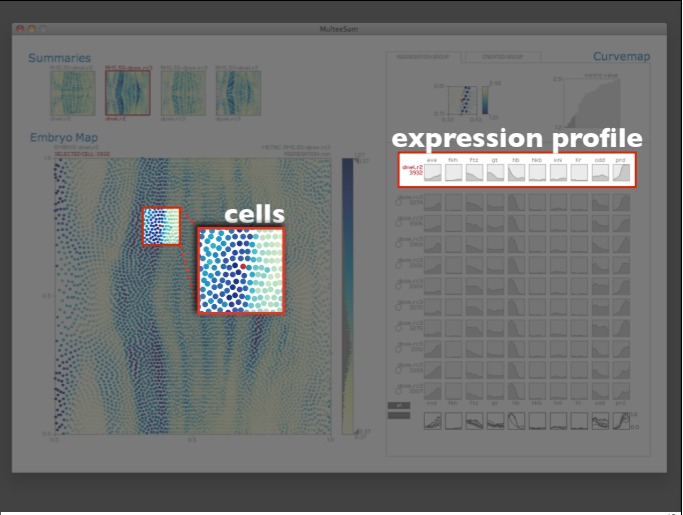
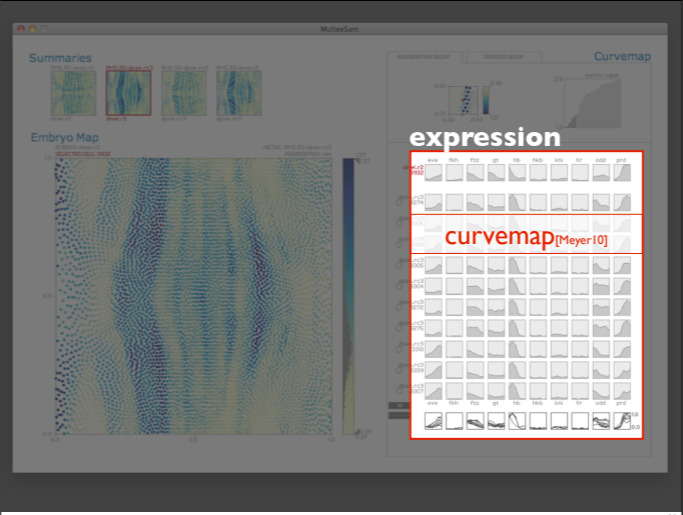
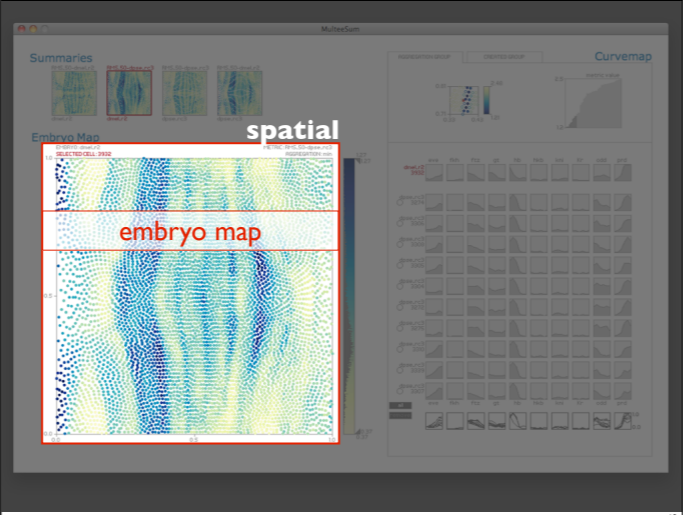
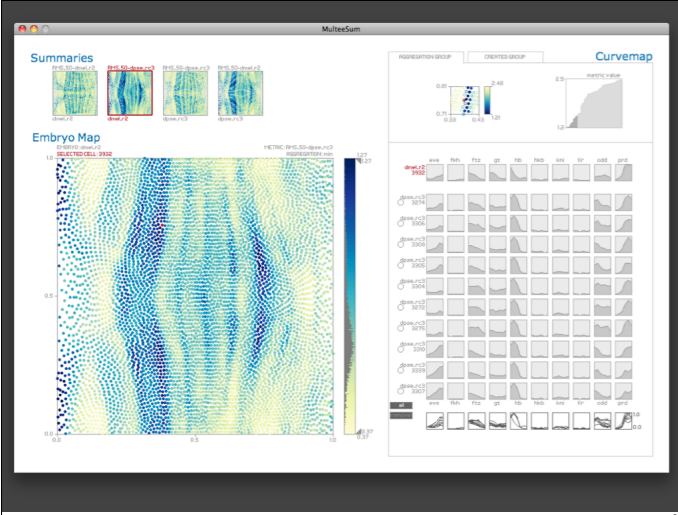
virtual embryo

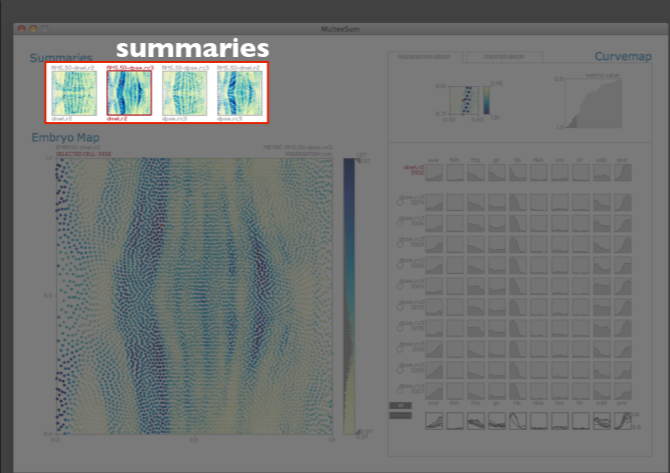
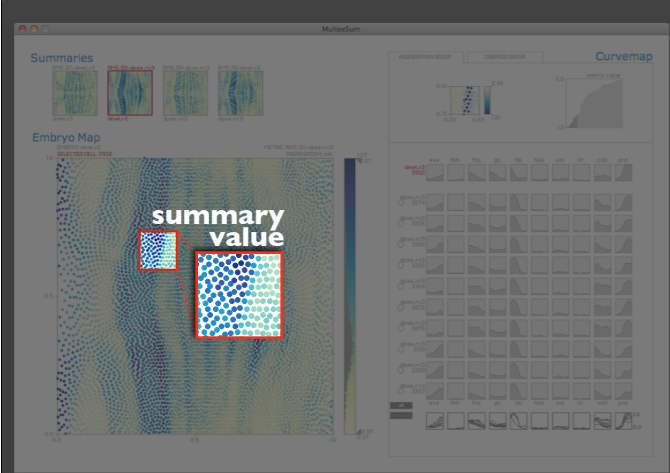
several thousand cells [5,000 ± 1,000]

each cell has:

- expression profile** [6 time points × 50 genes]
- spatial position** [3D and 2D coordinates]

12 related species
 one complete
 three preliminary





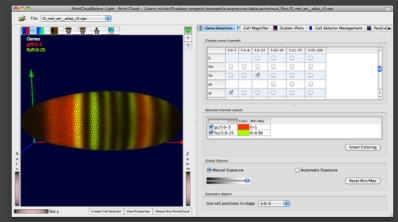
Characterize differences in gene expression patterns between species.

differences related to:
spatial position
gene expression profiles
complex combination

challenging to characterize manually

support mechanisms:
summaries, groups

previous work



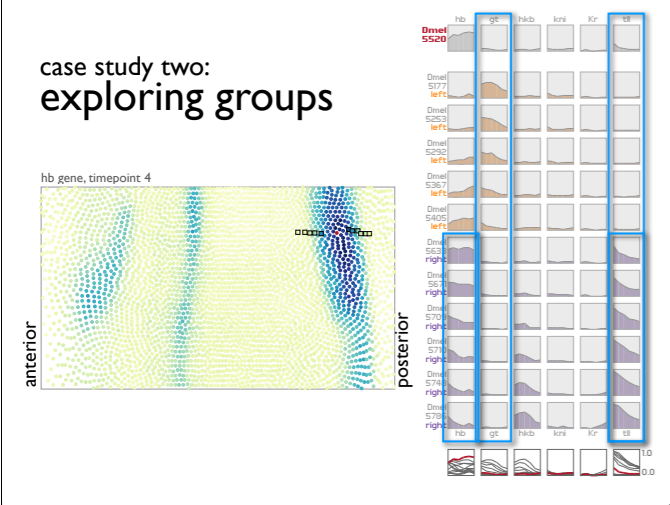
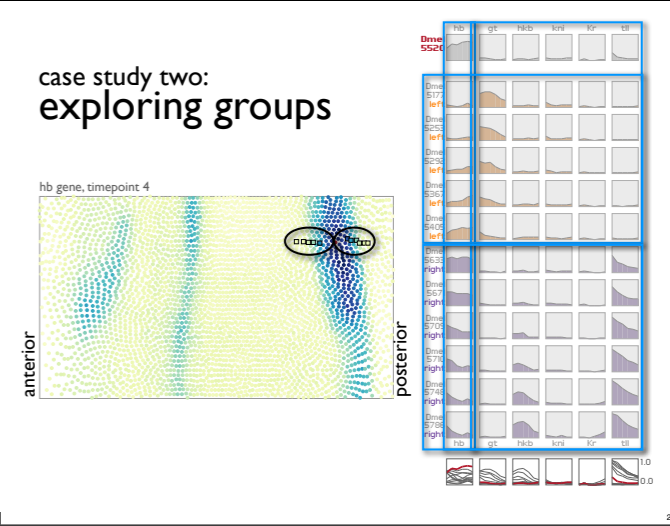
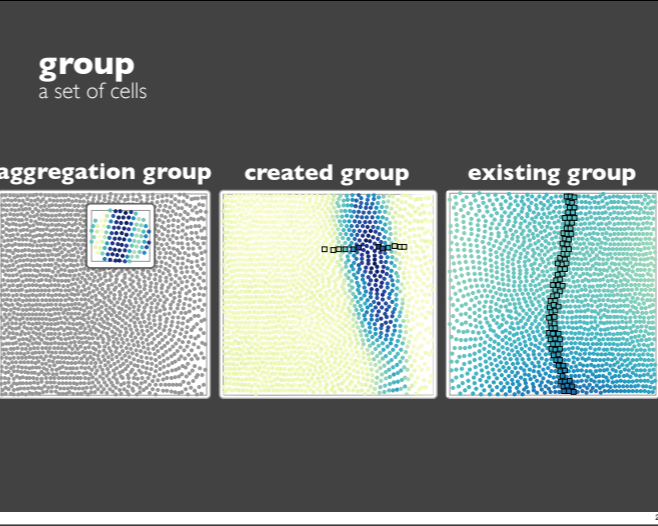
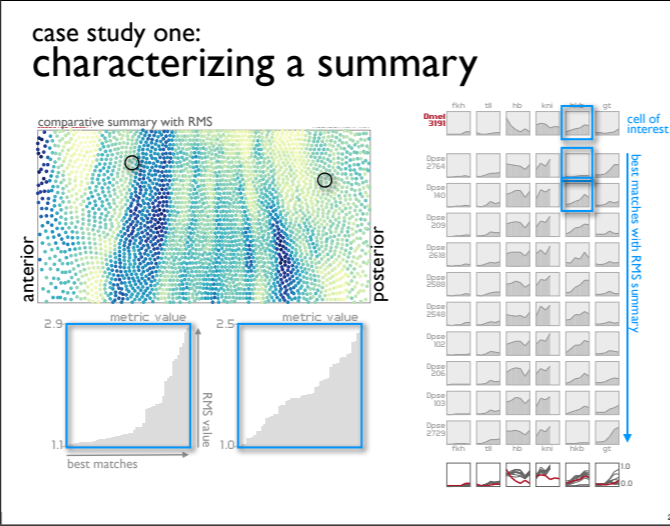
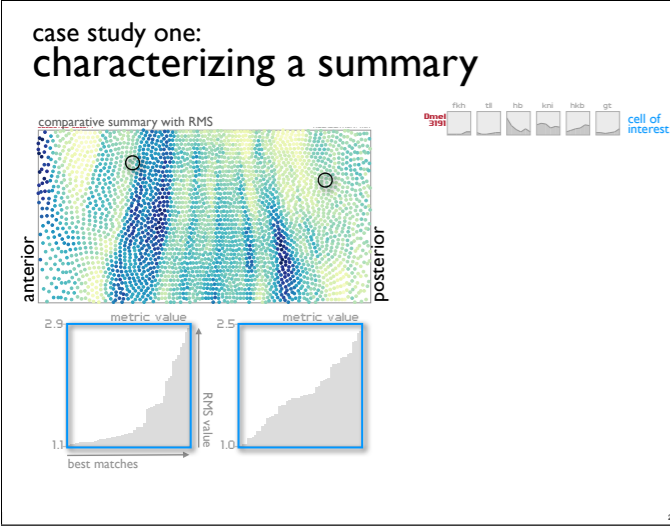
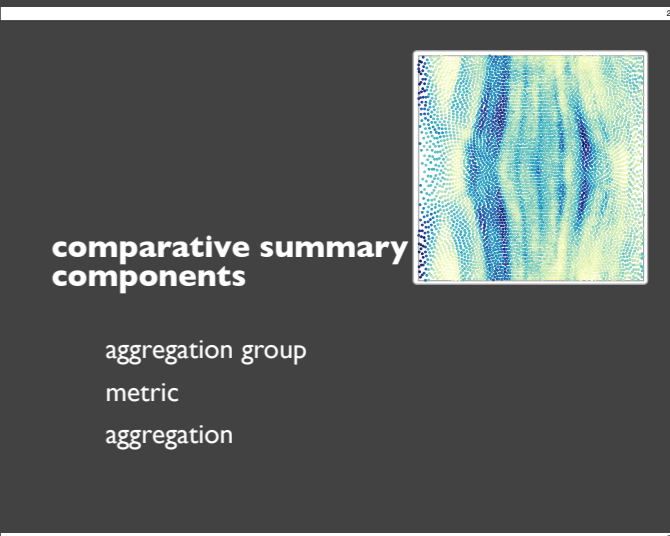
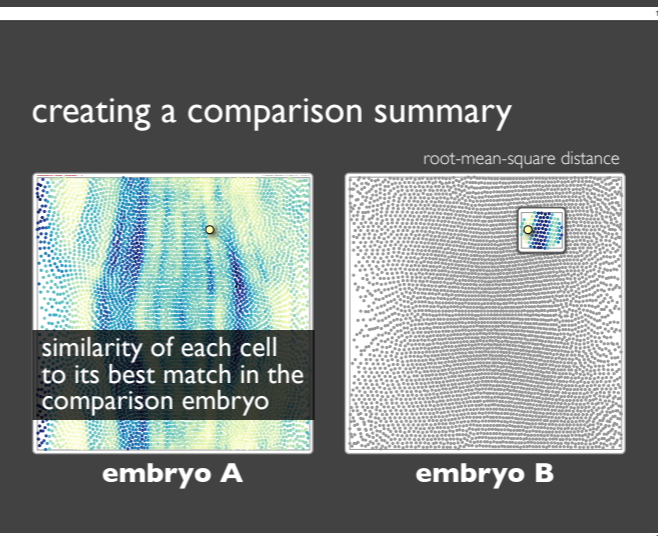
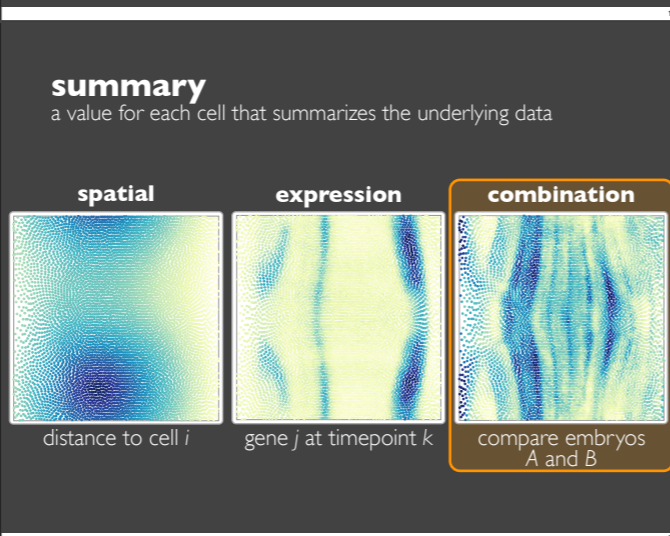
PointCloudXplore
 [Rübel06][Weber09][Rübel10]

selection: multiple genes ≠ single gene
 single time point ≠ multiple time points

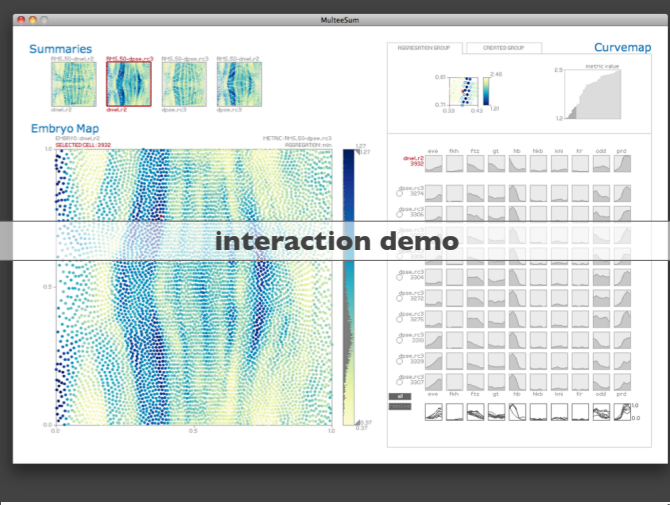
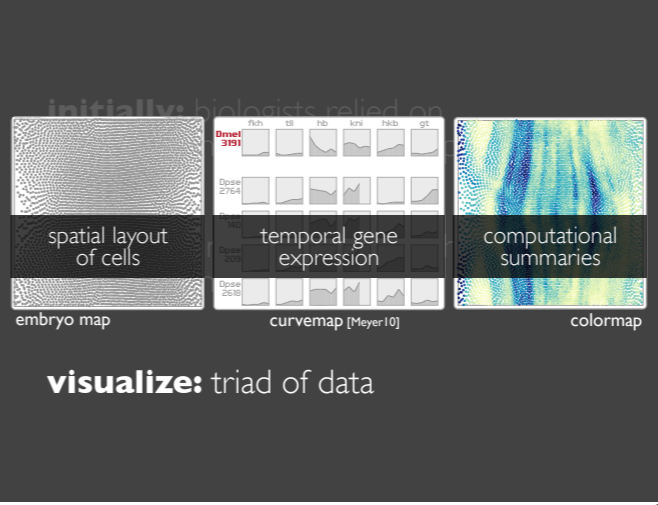
encodes: a few genes for all of the cells
 all the genes for a few cells

supports: a single virtual embryo
 multiple virtual embryos

data & tool & tasks
 summaries & groups
 encodings & interaction
 conclusions



data & tool & tasks
 summaries & groups
 encodings & interaction
 conclusions



data & tool & tasks

summaries & groups

encodings & interaction

conclusions

contributions

MulteeSum

spatial and temporal gene expression data from multiple species

workflow

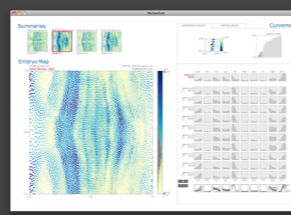
visualization supports upstream computation via summaries

validation

case studies, deployment

Cellular resolution comparison of gene expression in *Drosophila* reveals coordinated shifts in the segmentation network.

DePace et al, in preparation.



future work

design is broadly applicable

consider: scalability of curvemap

consider: mapping of other spatial data to 2D

continuing to support collaborators

additional features in MulteeSum

new summary designs

multeesum.org
questions?

acknowledgements

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Charless Fowlkes

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