# TTD Caltech. Multiplexed, transcriptome-wide detection of mRNAs: technology development

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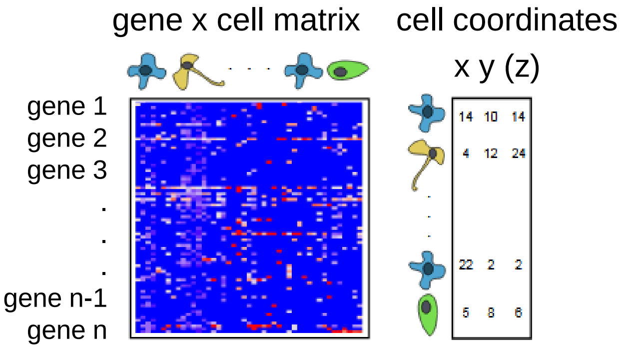
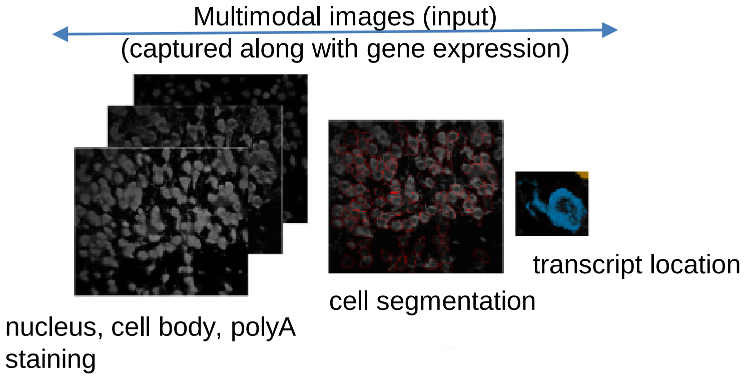
# Computational spatial transcriptomic pipeline, Giotto

- With development of advanced spatial technologies, there’s an increasing need for biologists to examine the data generated by these technologies in a spatial context.
- Giotto is a customized pipeline for spatial mRNA data analysis.

**Giotto Analyzer**

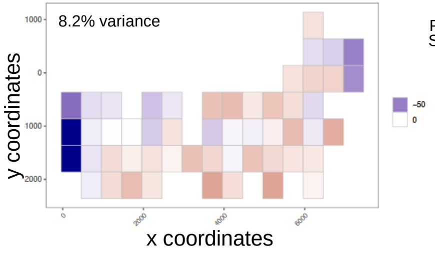


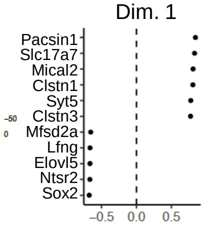
**Giotto Viewer**

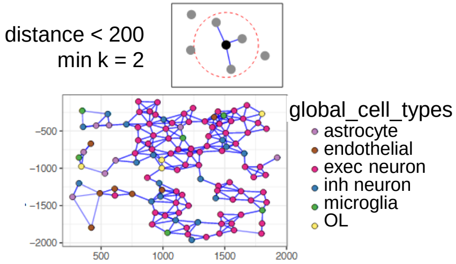


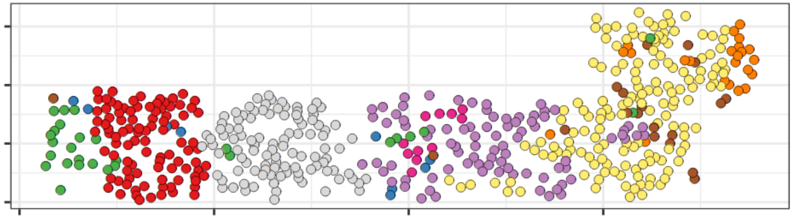
# Giotto analyzer supports a range of analyses

- Clustering (dim. reduction, Louvain, Leiden)
- Detection of spatial genes and patterns

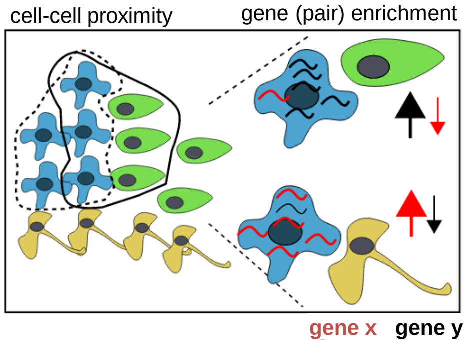


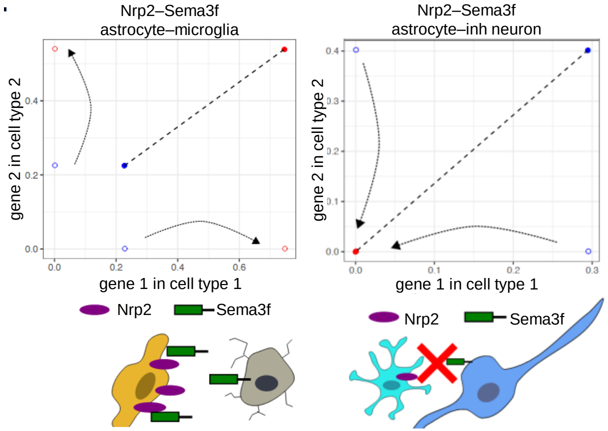






- Cell-cell interaction analysis





# Giotto viewer can overlay cell segmentation, staining, annotation, transcript information

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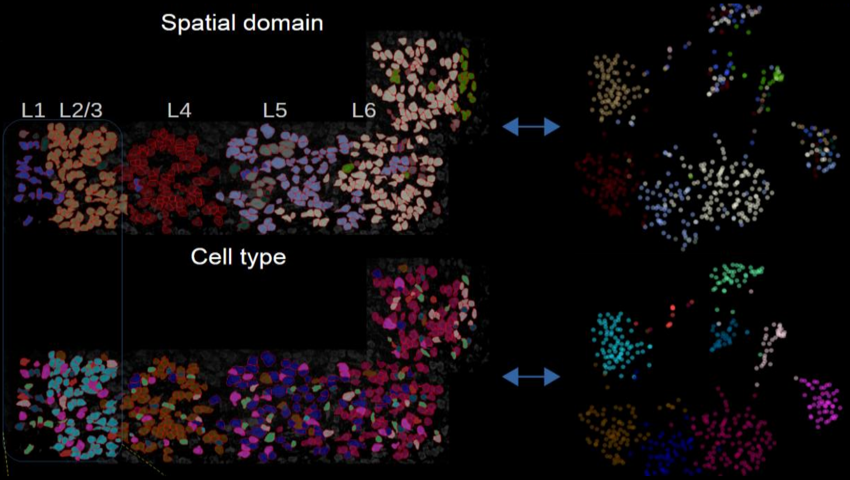

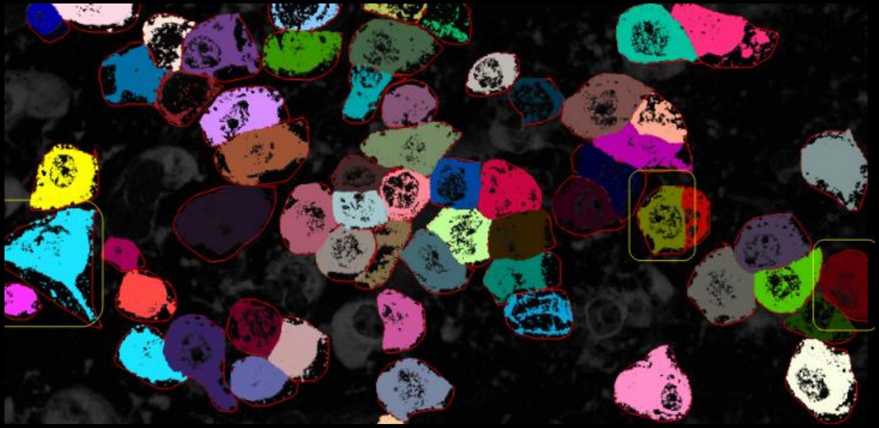

# Future extensions of Giotto

- Extend to datasets of other spatial technologies (Slide-seq, STARmap, HDST, etc)

- Extend to 3-dimensional spatial transcriptomic datasets

- Improve pipeline efficiency and scalability to large datasets

# Collaborations within HuBMAP

- Touched base with Nils Gehlenborg (HMS) on:
  - Connection of Giotto analysis pipeline with their visualization pipeline
  - Sharing of seqFISH+ spatial expression data with his group
- Communicated with Katy Borner (Indiana U.):
  - Sharing of seqFISH+ spatial expression data
  - Performed a demonstration to her group and got useful feedback
- Shared seqFISH+ data with other members of HuBMAP (CMU)