

# INTEGRATIVE MODELS OF AGING CORE



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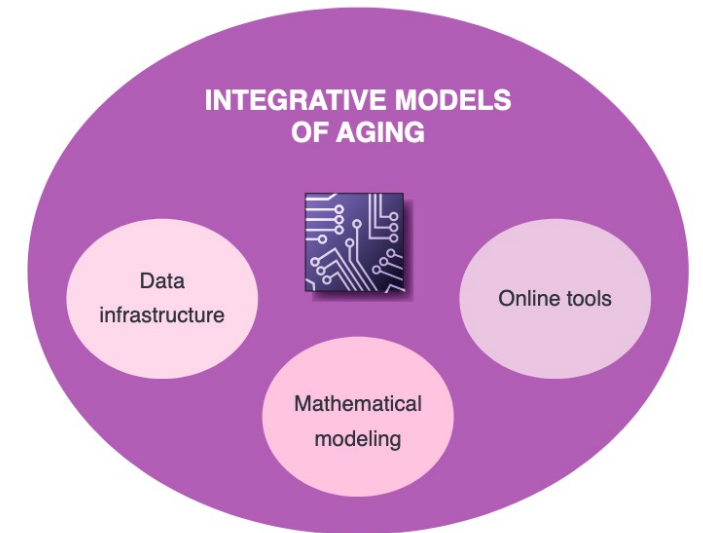


SAN DIEGO NATHAN SHOCK CENTER  
**2022 WORKSHOP**

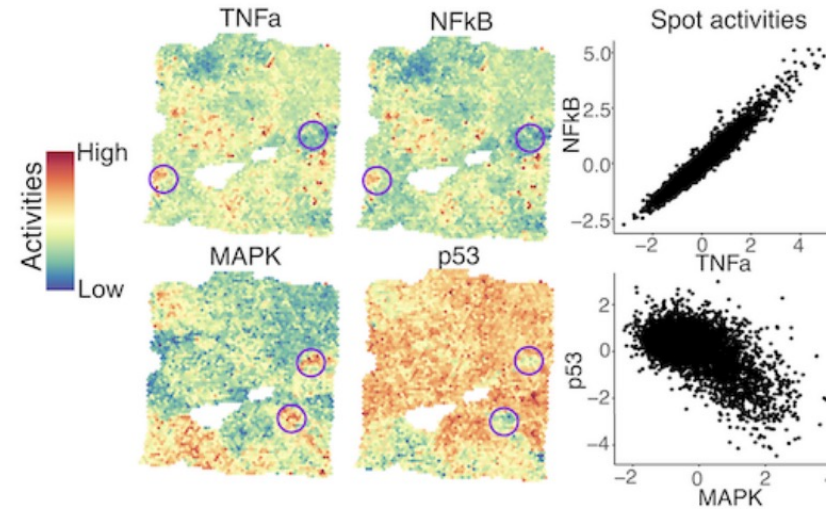


## Services offered

- Brainstorming / Project Design
  - Assay selection, replicates, controls, timelines
- Data storage and curation
  - Redundant storage, data sharing, submission to online repositories
- Quality control
- Standard and customized analyses
  - Ask us about our pipelines and tools, or we can help implement new ones
- Data integration
  - Mathematical modeling, machine learning, hyperbolic embedding
- Access to analyses through online tools
  - Interactive data visualization and tool development
- Training
  - Workshops, 1-on-1, online materials



- Use network-based analysis and ligand-receptor biology to predict signaling between groups of cells
  - CellChat
  - COMUNET
  - NATMI
  - SingleCellSignalR
  - CCIx
- Spatial Transcriptomics
  - MISTv



### Cellular communication analysis

Identification of signaling roles for cells using network centrality analysis

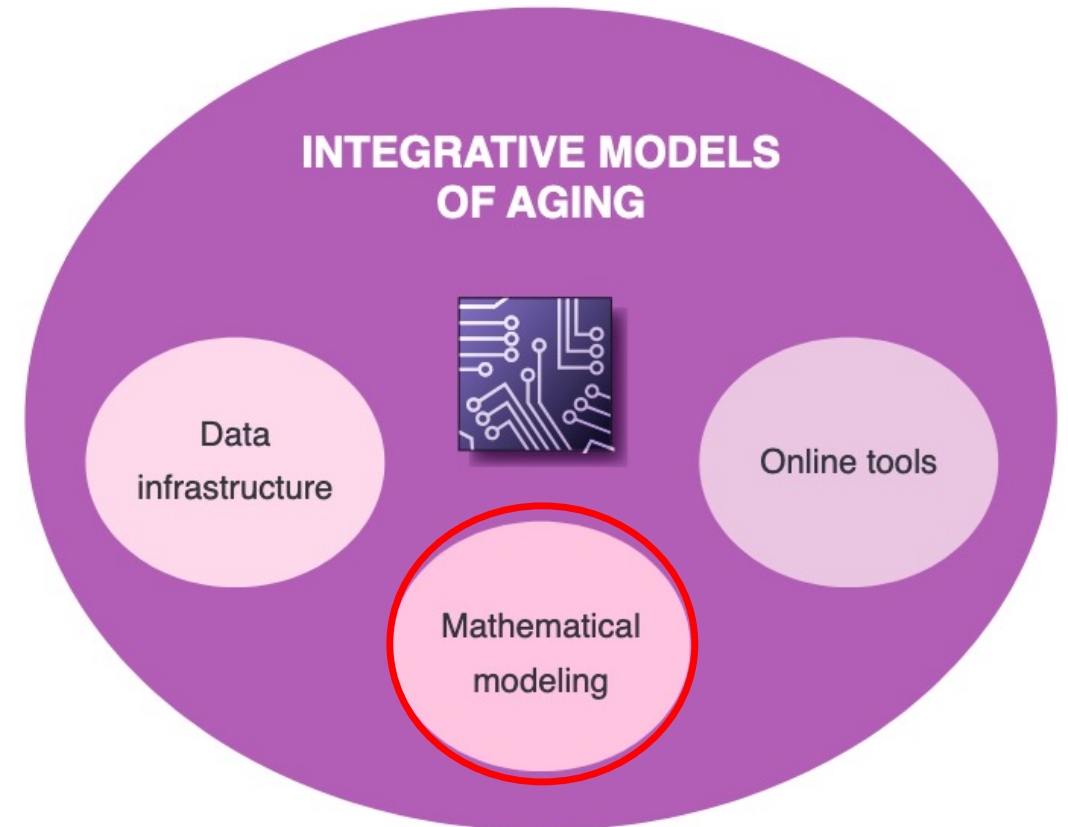
Discovery of dominant cell communication patterns

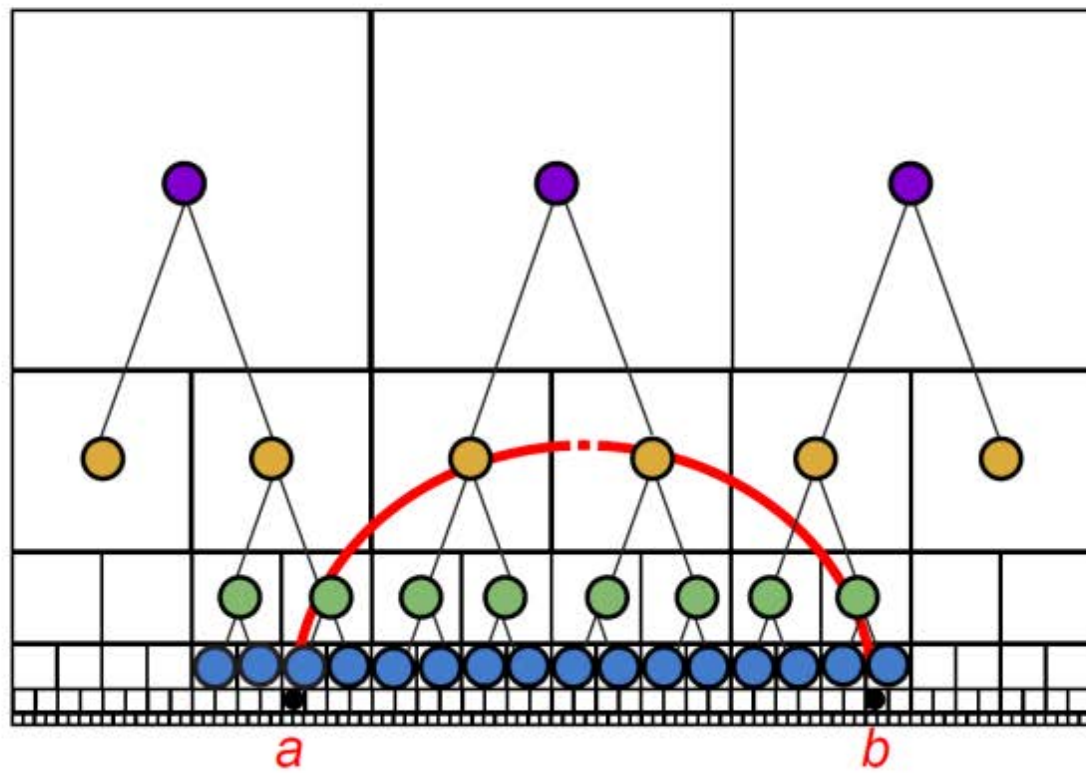
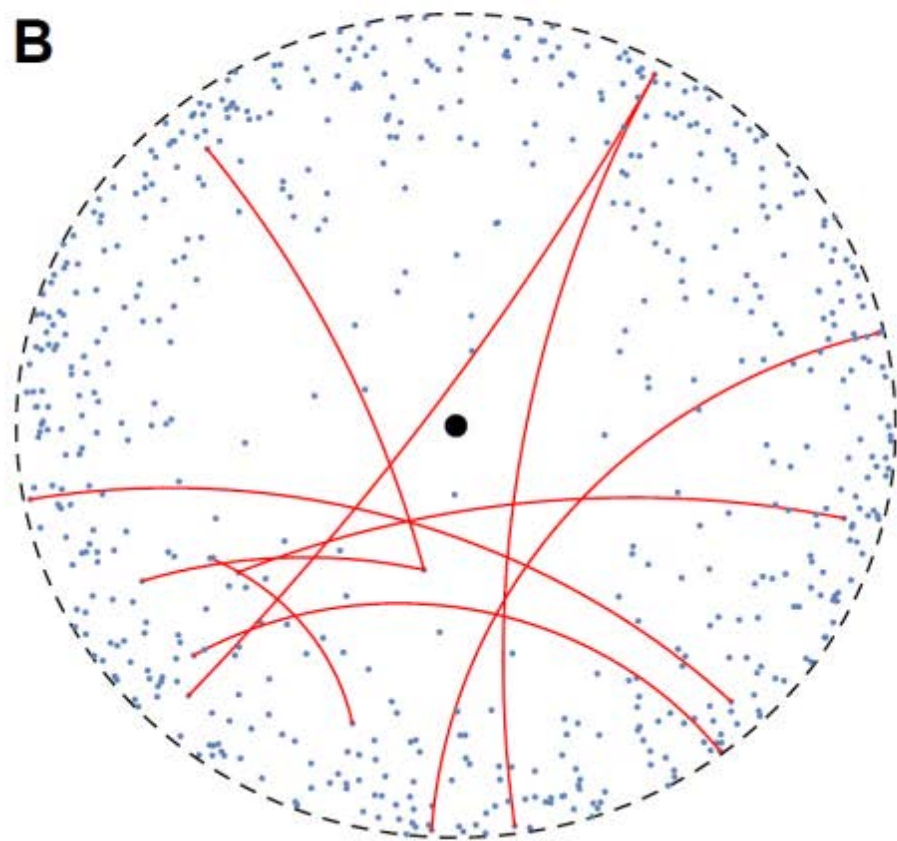
Classification of signaling pathways Topological and functional similarity

Identification of shared and context-specific signaling across distinct conditions

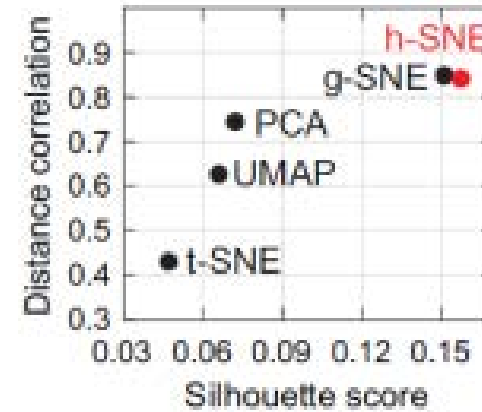
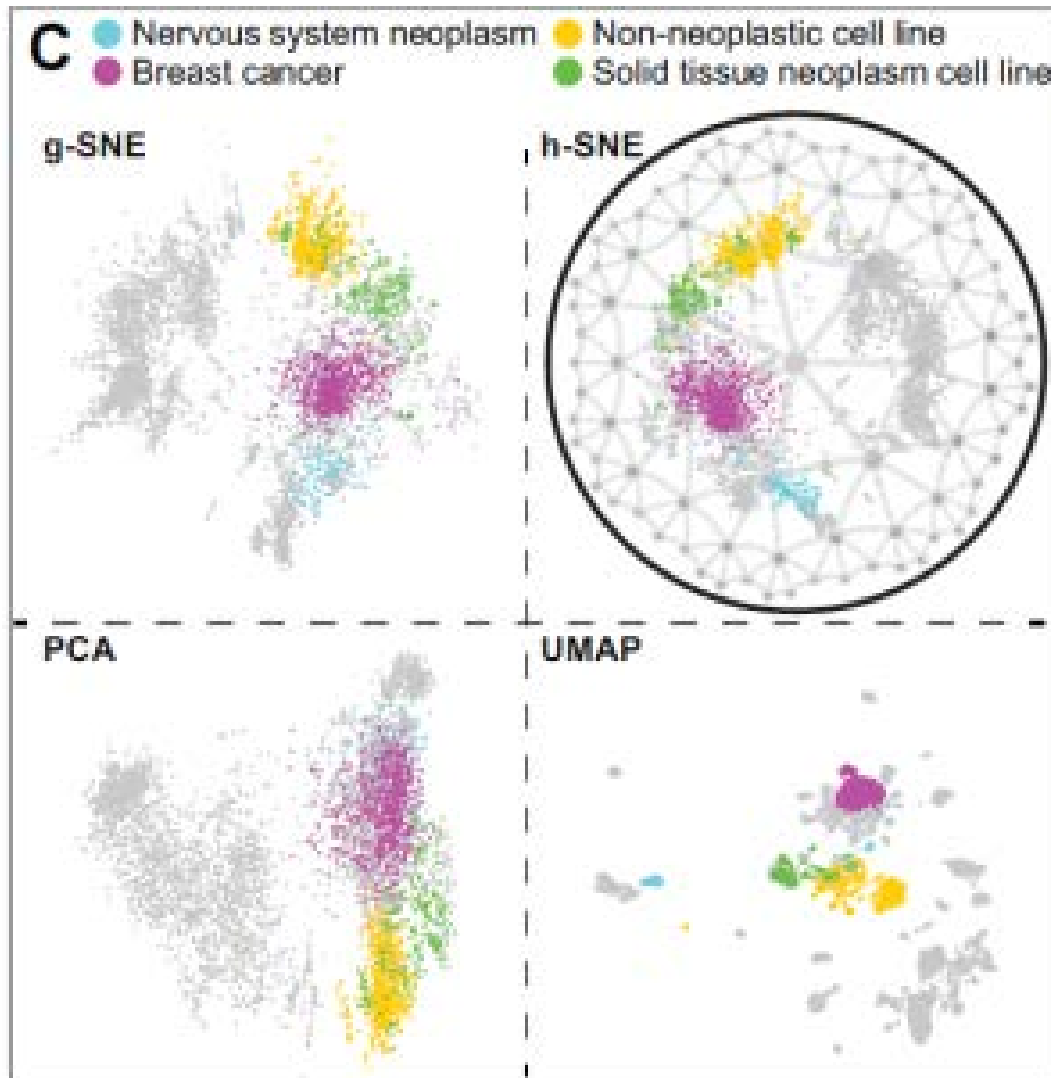
- **Describing hierarchical data**

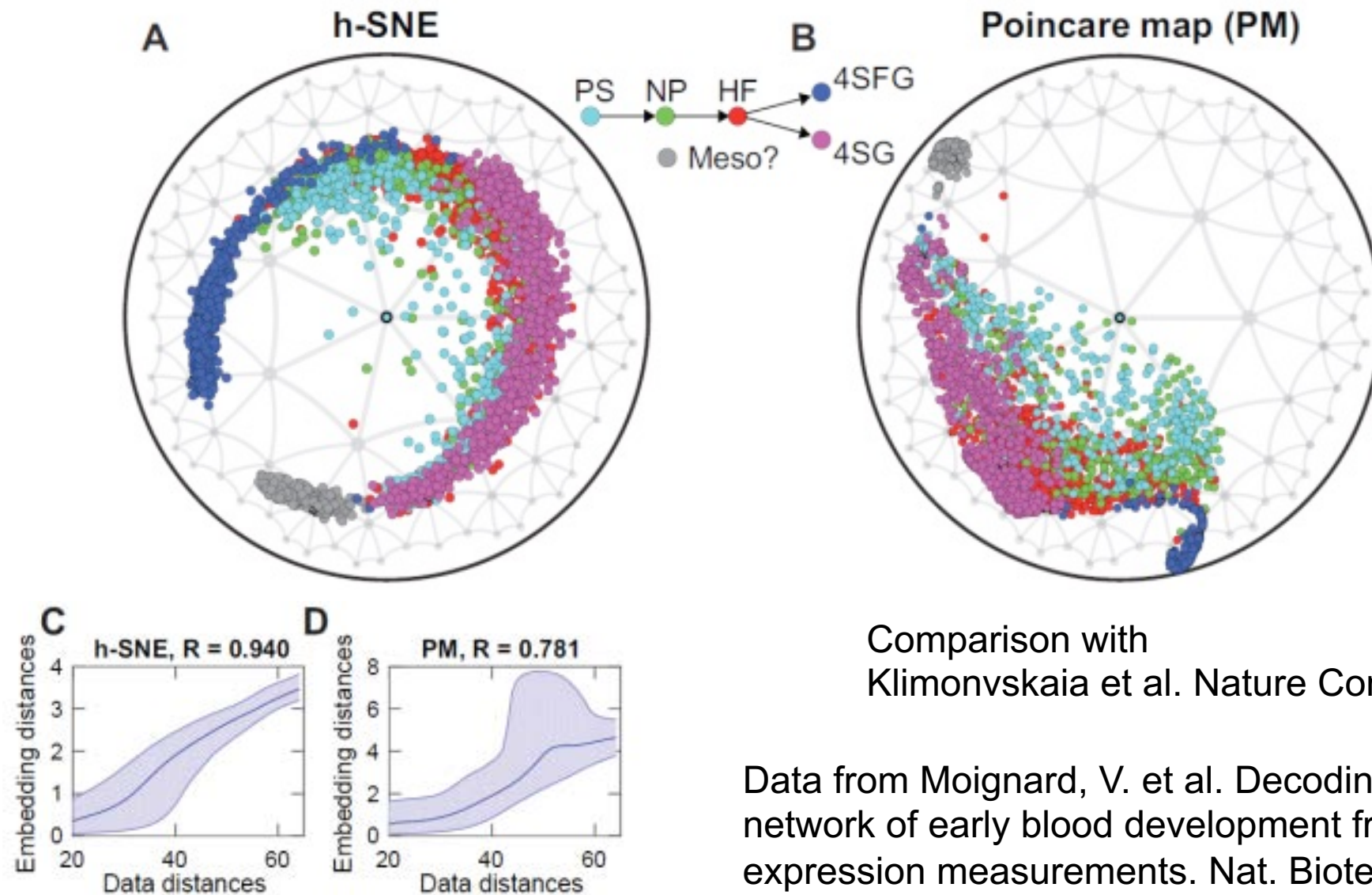
- **Identifying driver nodes & causal interactions in networks**
- **Visualization methods for hierarchical data**
- **Custom methods for “batch correction”**



**A****B**

# HYPERBOLIC GEOMETRY IN GENE EXPRESSION DATA





Comparison with  
Klimonvskaja et al. Nature Communications 2020

Data from Moignard, V. et al. Decoding the regulatory network of early blood development from single-cell gene expression measurements. Nat. Biotechnol.33, 269 (2015)

## Summary of current methods for analyzing hierarchical data

- **Visualization methods (t-SNE, UMAP, PCA, **hyperbolic SNE, hyperbolic MDS**).**
- **Methods for geometry detection, dimensionality reductions**
- **Methods for identifying driver nodes**



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COLLABORATION SPOTLIGHT

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*HETEROGENEITY OF EPIGENETIC  
LANDSCAPE AT SINGLE CELL LEVEL.*



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