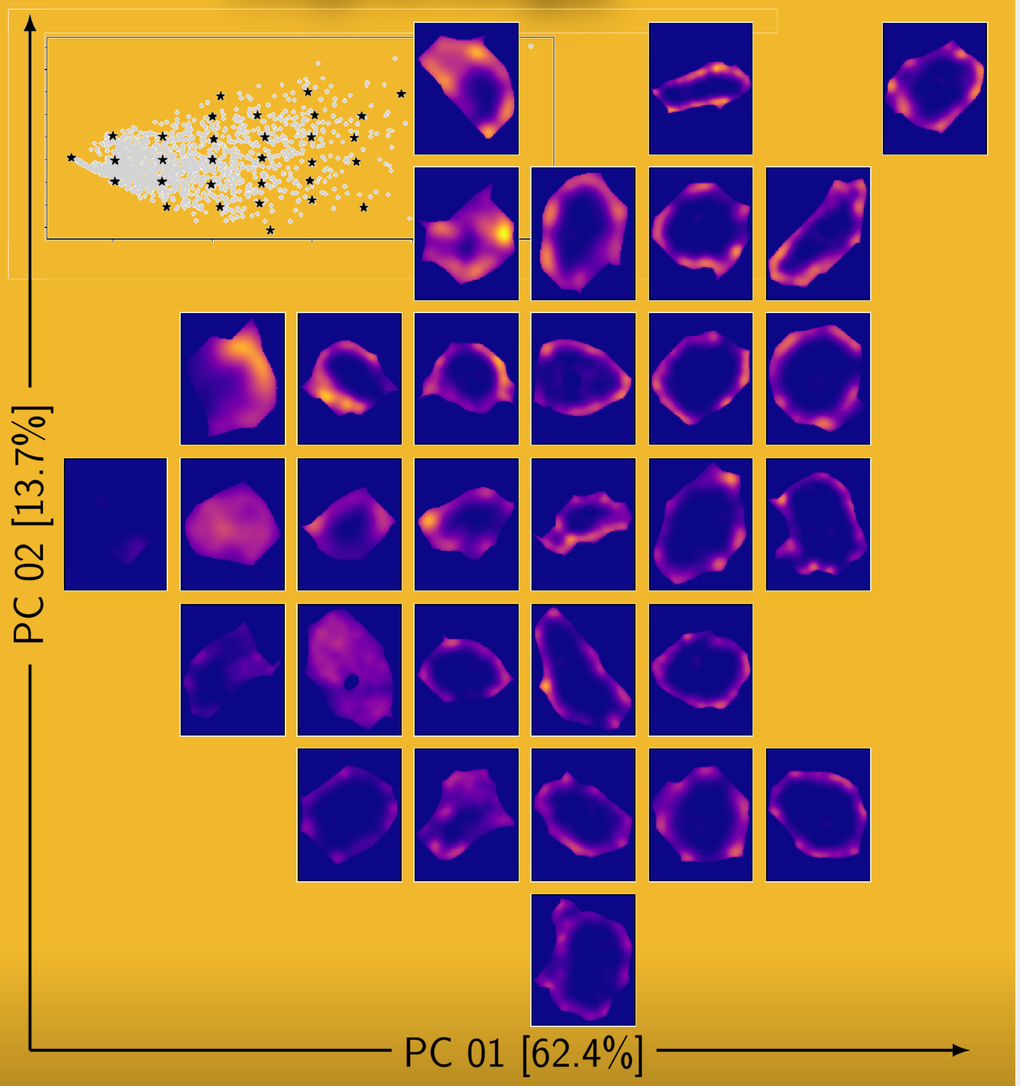
Model **sub-cellular** transcript **patterns** with **topology**



↓More details↓
bit.ly/mcarto

Topological Data Analysis to characterize transcriptomic spatial distributions

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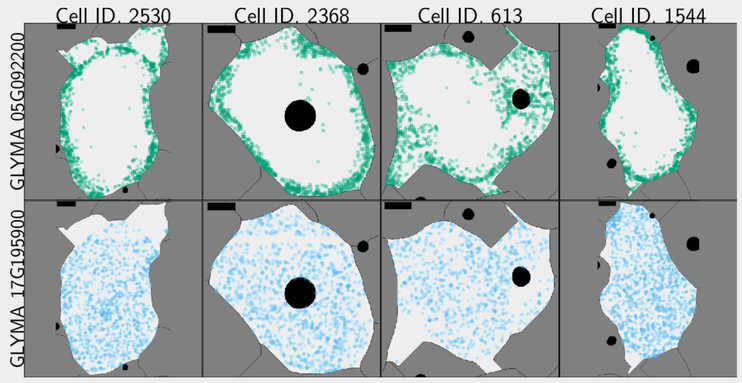
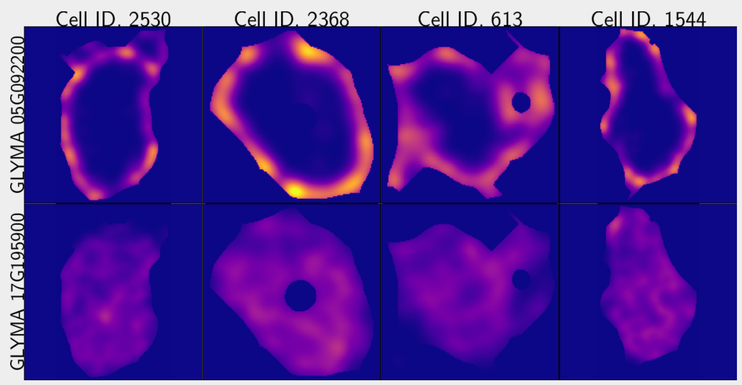
Molecular Cartography™

- Soybean nodule 10µm thick cross-sections.
- (X,Y,Z) coordinates for 3.7M+ cytosolic transcripts.
- 97 genes (including 10 bacterial ones).
- 2938 cells → 918 infected ones.

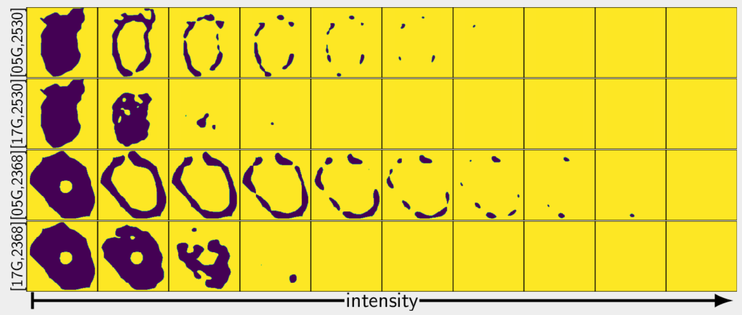
TDA: A **framework** that can **compare** all kinds of spatial distributions and **patterns** regardless of **different** cell sizes, shapes, orientations, and transcript number.



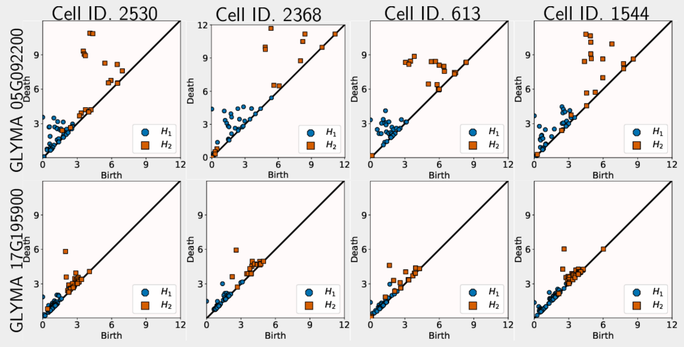
Kernel Density Estimation (KDE)



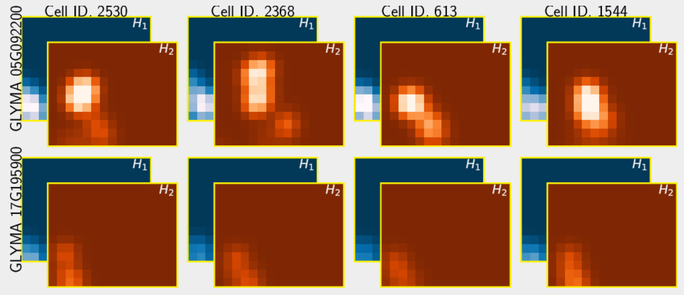
Sub-level set persistence



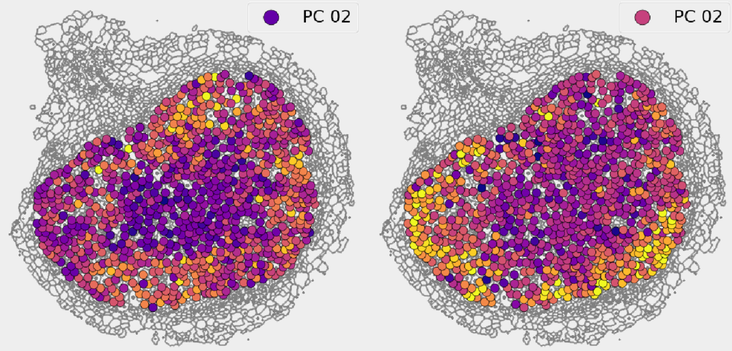
Persistence diagrams (H1 and H2)

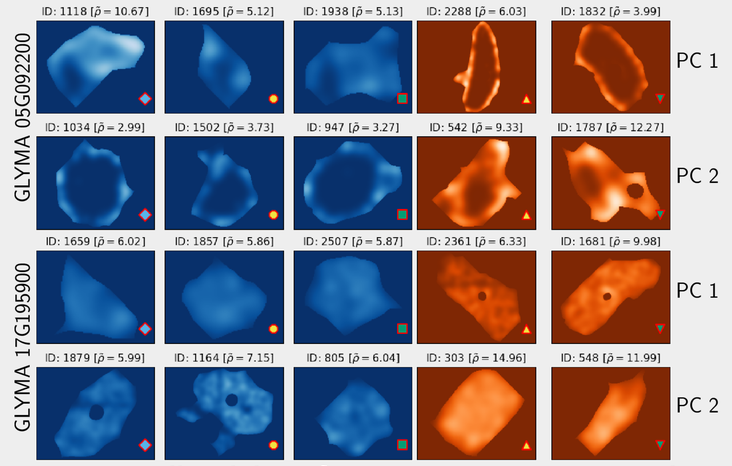


Persistence Images



Relate back to the nodule





- **Senescent** cells exhibit a **distinct** transcriptomic spatial **pattern** compared to the rest of population.
- Loss of mRNA **localization** may be a lesser known **contributor** to cell senescence.

Acknowledgements

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