

A159 · Visualize Scverse Data Structures and 3D Tissue Maps in Vitessce

Presenter: Mark Keller — Harvard Medical School

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Vitessce (<https://vitessce.io>) is an open-source, web-based framework designed for interactive visualization and exploration of multi-modal and spatially-resolved single-cell data. Its modular architecture supports diverse data types—including transcriptomic, proteomic, genome-mapped, and imaging modalities—and is compatible with 2D and 3D tissue maps and high-resolution microscopy images. This enables researchers to contextualize molecular information within spatial structures at cellular and subcellular resolution. Its coordinated multiple views enable flexible and intuitive visual analysis across different types of single-cell and spatially-resolved assays. Vitessce is optimized for integration with computational pipelines and external data repositories, and it operates without the need for specialized server-side infrastructure. It loads data from cloud object storage systems, including from Scverse (<https://scverse.org>) data structures such as AnnData and SpatialData, making it cost-effective to deploy interactive visualizations. We have recently developed functionality for visual comparisons of single-cell datasets in case-versus-control style, supporting both exploratory and confirmatory workflows. This allows researchers to interrogate individual biomarkers or combinations of biomarkers between conditions such as organ, anatomical structure, sex, disease state, or age group. By enabling interactive and comparative analysis, Vitessce empowers researchers to generate and refine biological hypotheses, facilitating deeper insights into cellular organization, disease mechanisms, and potentially therapeutic targets.

Visualize Scverse Data Structures and 3D Tissue Maps in Vitessce

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