

A167 · Interactive Guided Annotation for Single-Cell and Spatial Multi-Omics Visualization in Vitessce

Presenter: Ryan P. Seaman — Harvard Medical School

Authors: Ryan P. Seaman, Mark S. Keller, Nils Gehlenborg

Session: Day 1 · Thu Oct 1, 2026 · 2:15–4:15 PM

Communicating findings from a spatial or single-cell dataset typically requires moving from the tool used for exploration into separate software for presentation. We present an annotation and storytelling system built directly into Vitessce (<https://vitessce.io>), the open-source framework for single-cell and spatial multi-omics visualization, so that curated interpretation can live alongside the data itself.

A story is built from multiple frames, and each frame can define or modify the state of every visualization panel (“view”) on screen. For example, a frame may specify which regions of interest are visible in each view, which channels or markers are visible, or how cell types are colored. Any frame can also hold annotations drawn on top of the data, such as text, arrows, rectangles, ellipses, or polygons. These annotations are currently supported in views that display data on a 2D coordinate system (embedding scatterplot and spatial & imaging views), with plans to generalize these annotations to all view types in the future. Readers step through story frames in sequence, like slides that stay fully interactive.

What makes a story more than a slideshow is synchronization across panels. A single frame can choreograph several views at once, spotlighting a cell population in a tissue image while pointing to that same population in a UMAP scatterplot beside it. Stories can be embedded in the visualization configuration file or linked from a separate file, so a narrative can be shared, versioned, and hosted on its own.

By making annotation and storytelling native to a general-purpose visualization framework, this work enables interactive scientific narratives to be authored, shared, and reproduced entirely within the environment where the data already lives.

Interactive Guided Annotation for Single-Cell and Spatial Multi-Omics Visualization in Vitessece

R. Seaman^{1*}, M. Keller¹, N. Gehlenborg¹

¹Harvard Medical School, Department of Biomedical Informatics, 10 Shattuck St, Boston, MA, USA

* Presenting Author; ryan_seaman@hms.harvard.edu

Communicating findings from a spatial or single-cell dataset typically requires moving from the tool used for exploration into separate software for presentation. We present an annotation and storytelling system built directly into Vitessece (<https://vitessece.io>), the open-source framework for single-cell and spatial multi-omics visualization, so that curated interpretation can live alongside the data itself.

A story is built from multiple frames, and each frame can define or modify the state of every visualization panel (“view”) on screen. For example, a frame may specify which regions of interest are visible in each view, which channels or markers are visible, or how cell types are colored. Any frame can also hold annotations drawn on top of the data, such as text, arrows, rectangles, ellipses, or polygons. These annotations are currently supported in views that display data on a 2D coordinate system (embedding scatterplot and spatial & imaging views), with plans to generalize these annotations to all view types in the future. Readers step through story frames in sequence, like slides that stay fully interactive.

What makes a story more than a slideshow is synchronization across panels. A single frame can choreograph several views at once, spotlighting a cell population in a tissue image while pointing to that same population in a UMAP scatterplot beside it. Stories can be embedded in the visualization configuration file or linked from a separate file, so a narrative can be shared, versioned, and hosted on its own.

By making annotation and storytelling native to a general-purpose visualization framework, this work enables interactive scientific narratives to be authored, shared, and reproduced entirely within the environment where the data already lives.

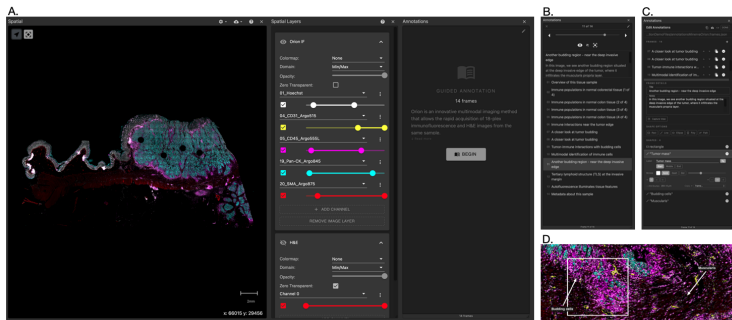


Figure 1. Interface overview on example dataset. (A) Full application view. (B) Frame playback view. (C) Authoring interface. (D) Rendered annotations on spatial view.