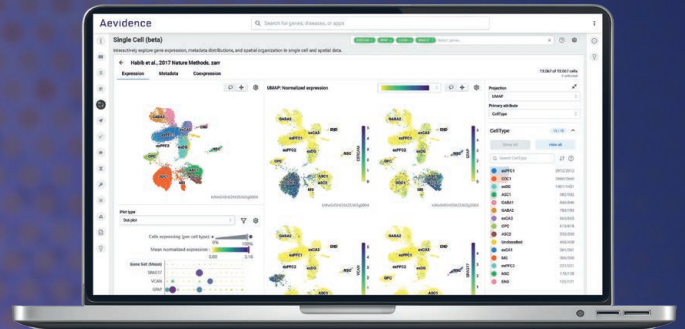


# Enable Single Cell Analysis

The High-Performance Hub for  
Interactive Transcriptomics



→ You want to Navigate Complex Cellular Landscapes and Molecular Signatures in Seconds?

## Experience Single Cell App

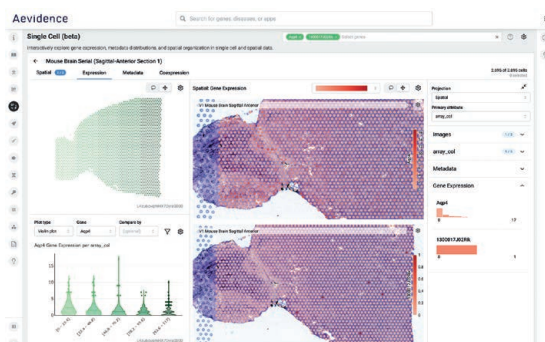
High-performance, interactive environment designed for exploring complex transcriptomic data, spatial data, and high-dimensional cellular maps.

## Integrated Evidence

Combines overarching projections and tissue slides with gene-specific facets to reveal molecular profiling across thousands of cells.

## Seamless Orchestration

Within visynPlatform, Single Cell uses cloud-native streaming (Zarr on S3) and data layers like Lamin to provide serverless access to million-cell datasets, enabling high-speed, integrative visualomics directly in your browser.



## Discovery Workflows



**Cell Type Mapping:** Identifying clusters by searching for markers and visualizing expression across UMAP or spatial projections.



**Subpopulation Triage:** Using lasso tools to isolate cell clusters and instantly analyze their metadata or gene signatures.



**Batch Effect Validation:** Normalizing data by donor or condition to distinguish true biological signals from technical artifacts.



**Gene relationships:** Calculating gene co-expression percentages to pinpoint the exact cell types driving specific molecular interactions.



**Population Refinement:** Cleaning up complex datasets by toggling off irrelevant groups to isolate rare cell types or specific biological signals.

# Strategic Capabilities

## Interactive Lasso & Sync

Use the lasso tool to select high-expression clusters and instantly update all views. This real-time synchronization across UMAPs and spatial coordinates allows for fluid subpopulation isolation and metadata observation.

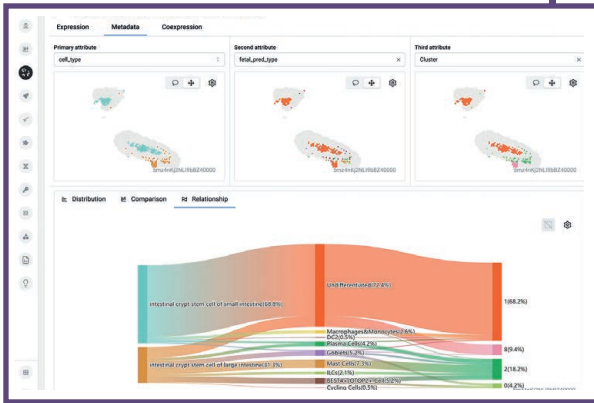
## Relational Metadata Mapping

Utilize Sankey diagrams and multi-attribute faceting to visualize cellular hierarchies. Seamlessly sync selections between tabs to instantly highlight physical boundaries and explore complex metadata overlaps.

Ready to unlock cellular heterogeneity?



# Part of Aevidence



# Precision Analysis Modules

**Spatial Tab** Map cellular identity to tissue architecture by rendering cells onto high-resolution morphological images. Sort and select tissue sections based on cell-type abundance or gene signatures.

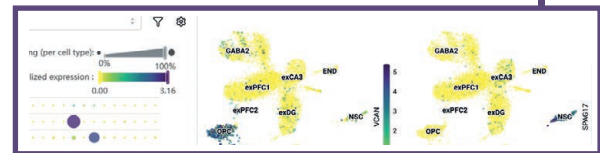
**Differential Expression** Isolate drivers of biological variation. Compare cell types or conditions (e.g., Tumor vs. Healthy or Drug vs. Vehicle) to uncover the statistical signatures defining cellular identity and experimental impact.

**Co-expression** Analyze pairwise gene behavior. Calculate co-expression percentages and identify specific cell-type drivers through a dedicated matrix and scatter plot validation.



**Metadata Tab** Quantify population shifts across study groups. Use frequency charts and Sankey diagrams to map cellular relationships and pinpoint biological drivers of abundance across samples.

**Expression Tab** Correlate gene expression with tissue slides or UMAPs. Leverage Dot Plots for frequency, Heatmaps for marker identification, and Distribution Plots to distinguish uniform expression from sub-population drivers.



Contact us

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