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Single-cell analysis. Simplified.

User-friendly single-cell multiomic analysis tools from Partek™ Flow™ software enable deeper biological insights

Single-cell techniques, including RNA-Seq, ATAC-Seq, and CITE-Seq, provide a high-resolution view of cell-to-cell variation, revealing the extensive cellular heterogeneity underlying complex biological systems. Partek Flow software offers an easy-to-use bioinformatics platform for analyzing and visualizing single-cell data, empowering researchers of all skill levels to maximize insights from multiomic studies.

Point-and-click analysis
Analyze data easily with an intuitive, context-sensitive interface

Advanced visualization tools
Create informative, publication-ready visualizations with just a few clicks

Powerful statistics
Access industry-standard statistical algorithms for results you can trust

Customizable workflows
Build custom analysis pipelines visually and share with collaborators

## Supported **single-cell applications**

- Single-cell RNA-Seq
- Single-nucleus RNA-Seq
- CITE-Seq
- ECCITE-Seq
- TotalSeq
- REAP-Seq
- Feature barcoding
- Antibody capture sequencing
- Flow cytometry and mass cytometry
- V(D)J sequencing
- Spatial omics
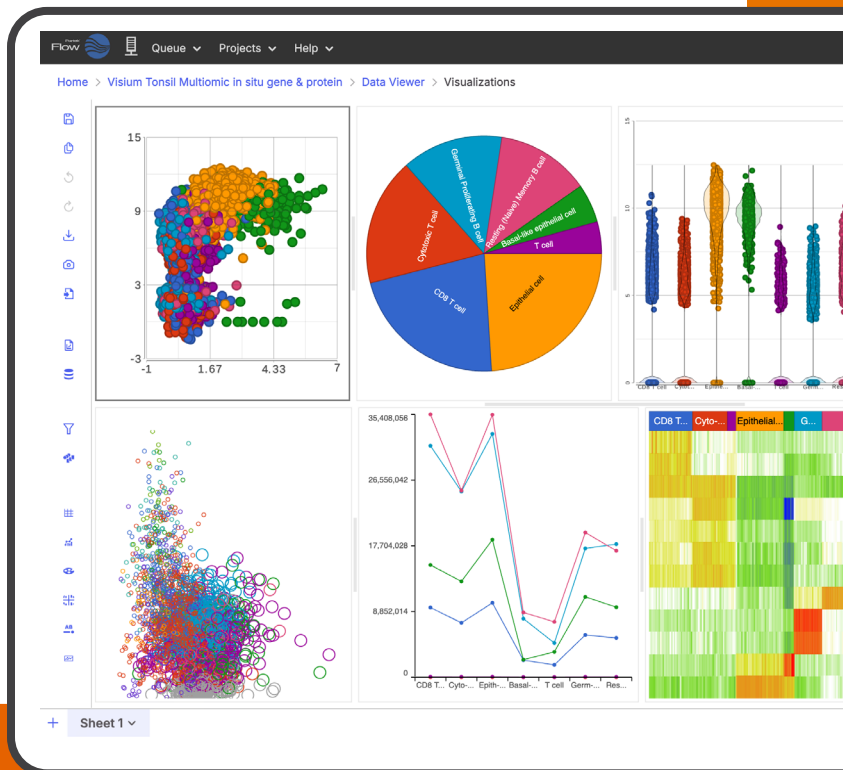
Powerful analysis and visualization tools

Whether investigating patterns in gene expression or regulation, building cell-type atlases for tissues and organs, tracing cell lineages, identifying biomarkers to track response to drug treatment, or exploring T or B cell clonotypes, Partek Flow software has the tools you need to analyze and visualize your single-cell multiomics data easily.
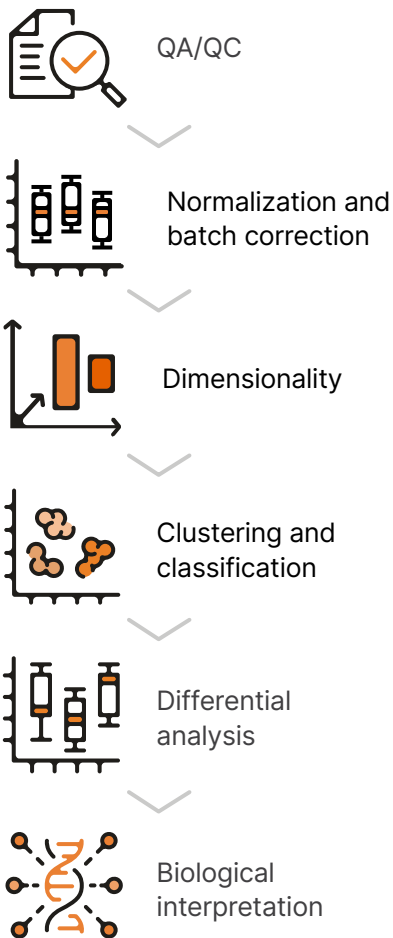

mRNA t-SNE and Clustering
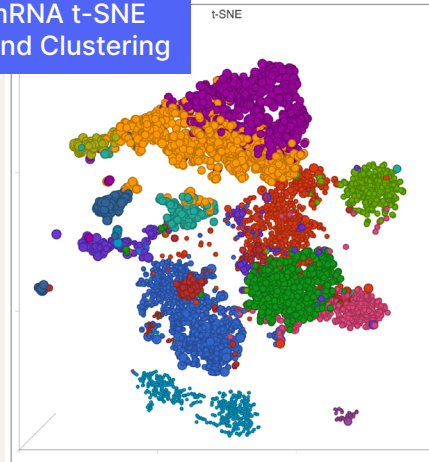
Protein Scatter plots
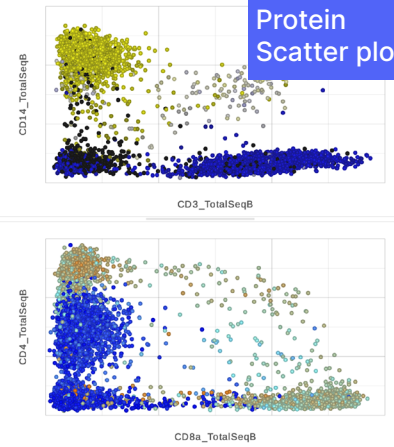
View, select, and classify cell types by combining single-cell RNA-Seq and TotalSeq protein data.

Steps in the **single-cell analysis workflow**

QA/QC

Normalization and batch correction

Dimensionality

Clustering and classification

Differential analysis

Biological interpretation

## Data to **biological insights in a single solution**

- Start the single-cell analysis pipeline with data files (eg, count matrix or Seurat objects) generated using any major single-cell analysis platform

- Assess data quality and remove low-quality barcodes to obtain filtered barcodes

- Normalize data and remove batch effects

- Classify cell types manually or using automated approaches, including the Garnett algorithm

- Create and import custom gene lists for analysis

- Cluster cell types, discover cell subpopulations, and assess differential gene and protein expression

- Visualize data multiple ways with t-SNE, UMAP, PCA, heat maps, volcano plots, bubble maps, KEGG pathways, *in situ* expression images, and more

- Integrate gene and protein expression data from multiomics experiments and correlate feature types

# Multiple ways to **explore single-cell data**

Transform single-cell data into interactive figures and maximize biological insights from your multiomics studies. The data viewer in Partek Flow software makes visualizing cell types and differential expression fast and easy.
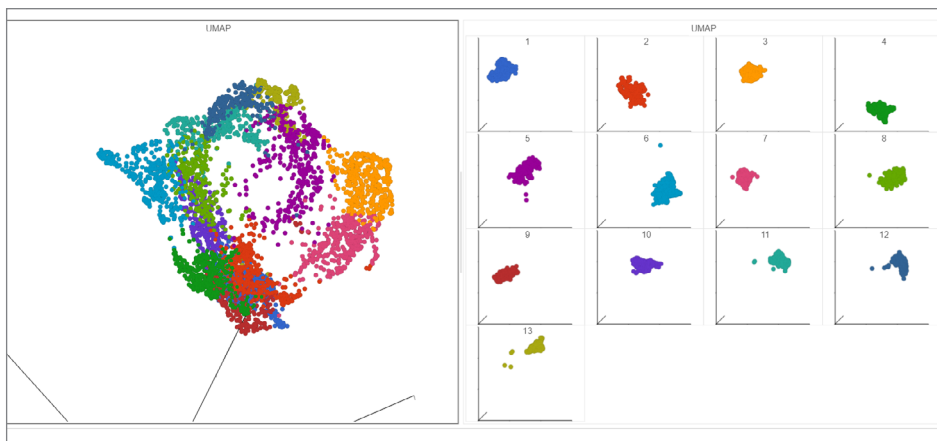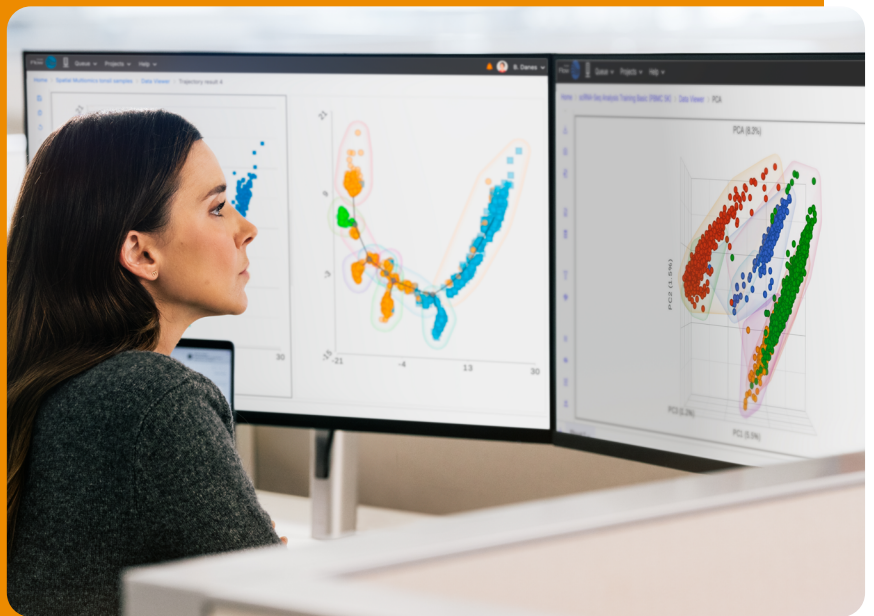

Split TotalSeq scatter plots into multipanel charts to focus on one cluster at a time for a high-resolution look into protein expression in individual cells.
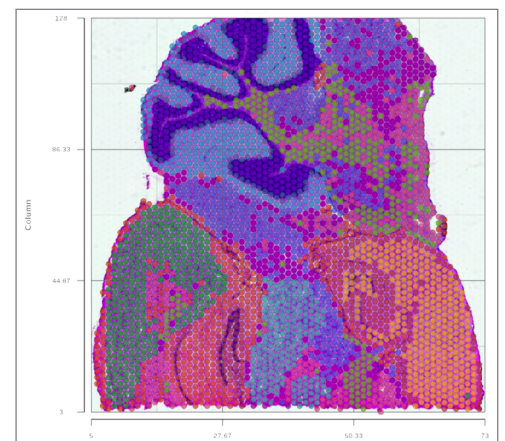

Overlay single-cell RNA-Seq data on histological images to visualize spatial transcriptomics.
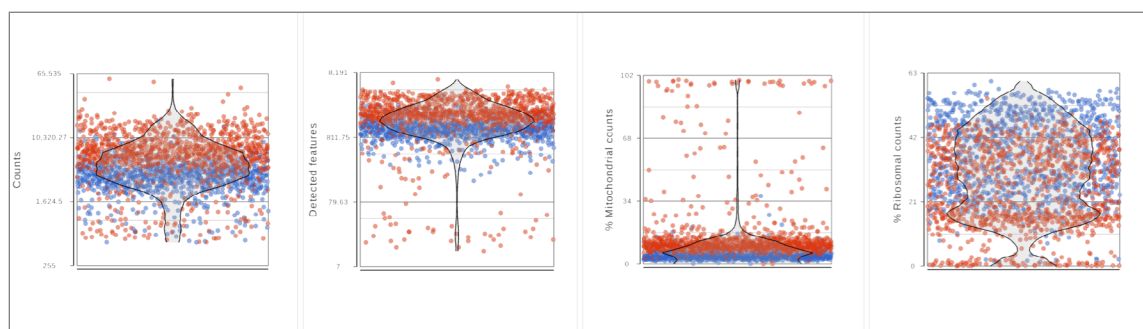
Perform quality control on single-cell data using interactive UMI counts, detected genes, and fraction of mitochondrial and ribosomal counts to filter barcodes.
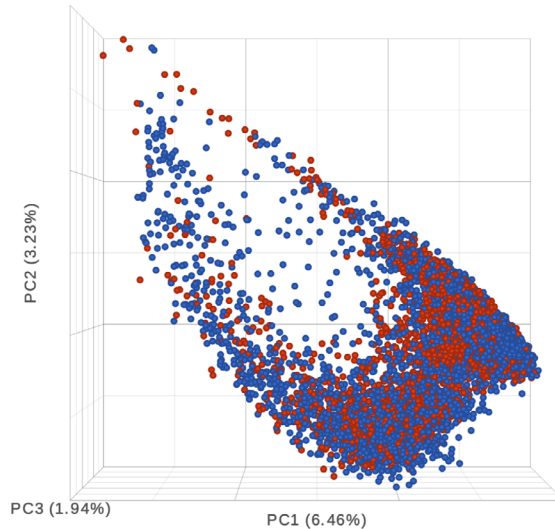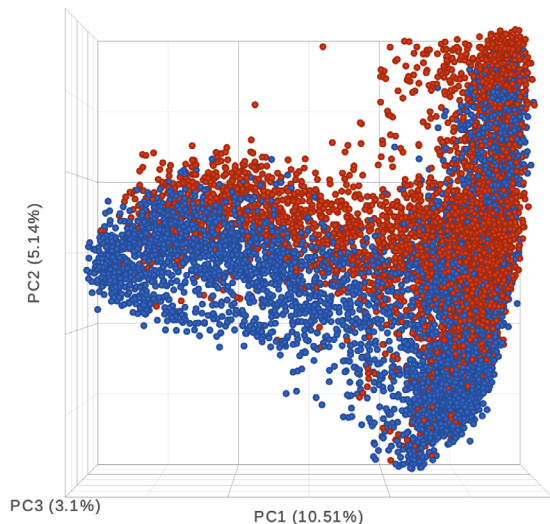
Remove noise and discover biological variation with batch correction methods such as the general linear model, Seurat3 integration, and Harmony. Shown here is a PCA (left) before and (right) after batch correction colored by sample.
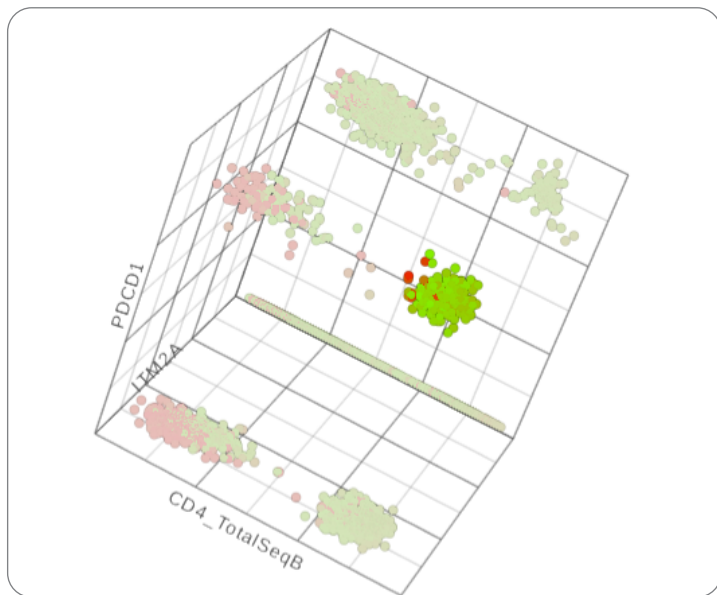
Integrate single-cell RNA-Seq and protein expression data into a single chart.

Learn more

Partek Flow software

Request a free 14-day trial

Abbreviations: ATAC-Seq, assay for transposase-accessible chromatin with sequencing; CITE-Seq, cellular indexing of transcriptomes and epitopes by sequencing; ECCITE-Seq, expanded CRISPR-compatible cellular indexing of transcriptomes and epitopes by sequencing; KEGG, Kyoto encyclopedia of genes and genomes; PCA, principal component analysis; QA, quality assurance; QC, quality control; REAP-Seq, RNA expression and protein sequencing; REST API, representational state transfer application programming interface; RNA-Seq, RNA sequencing; t-SNE, t-distributed stochastic neighbor embedding; UMAP, uniform manifold approximation and projection for dimension reduction; UMI, unique molecular identifier

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