

Unravelling complexities of multiomics using Illumina Partek™ Flow™

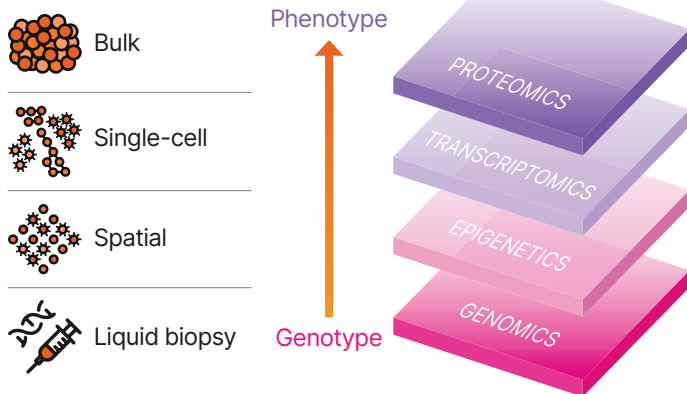
Are you a researcher seeking to leverage the power of multiomics data *without the steep learning curve* of bioinformatics?

Discover our revolutionary multiomics data analysis software, designed with you in mind. With intuitive interfaces and powerful analytical tools, you can unlock comprehensive biological insights effortlessly.



“Whatever your skill level you can perform very powerful statistical analysis and create these beautiful and interactive visualizations all by simply pointing and clicking”
 – Alex Rutkovsky, Field Application Scientist, Illumina

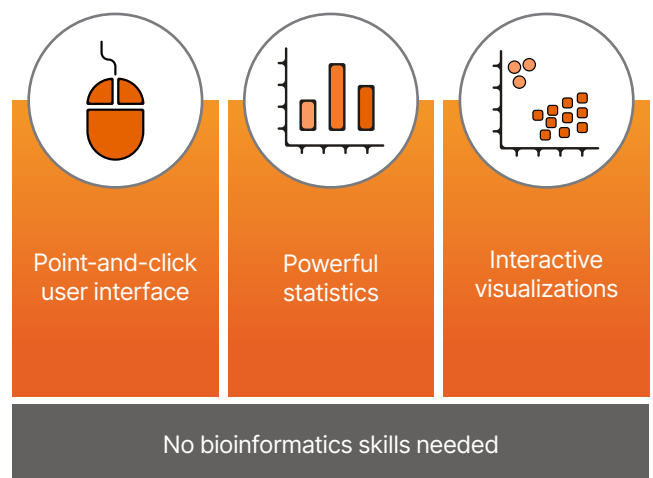
Resolution



Partek Flow is a comprehensive start-to-finish bioinformatics data analysis solution for next-generation sequencing applications. Across a wide range of data and application types, it provides a *user-friendly experience*, allowing all researchers to analyse data and take on their analysis journey at their *own pace and skill level*.

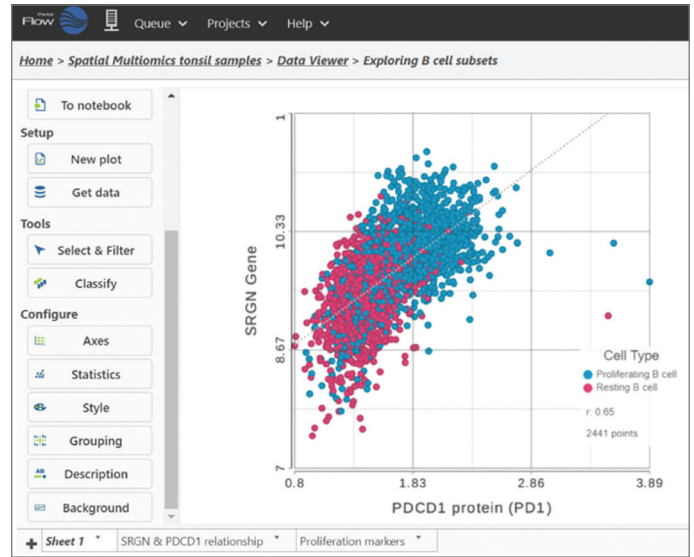
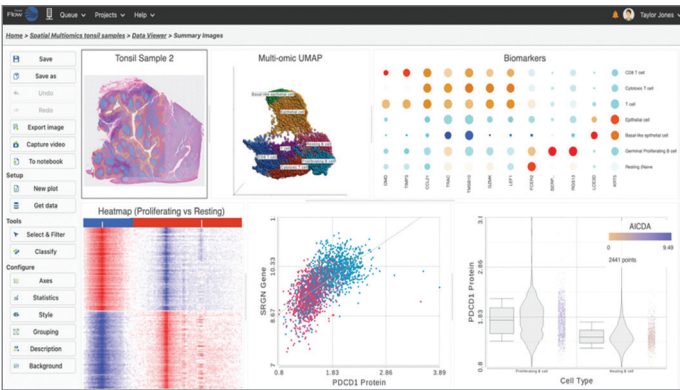
Rigorous statistics tools support advanced comparisons and can be used to assess relationships between different omic layers. Moreover, plots can be configured in your preferred style to generate publication-ready figures.

Multiomics involves profiling two or more omes, ideally from the same sample, often in the same experiment to maximise discovery through a data-driven and untargeted approach. Among the many benefits, using a multiomics approach enables researchers to derive maximal information from precious samples, avoiding missed information from complex systems.



- QA/QC
- Normalization
- Dimension reduction
- Unsupervised clustering
- Automatic cell classification
- Batch removal
- Differential analysis
- Cell type abundance analysis
- Trajectory analysis
- Biological interpretation

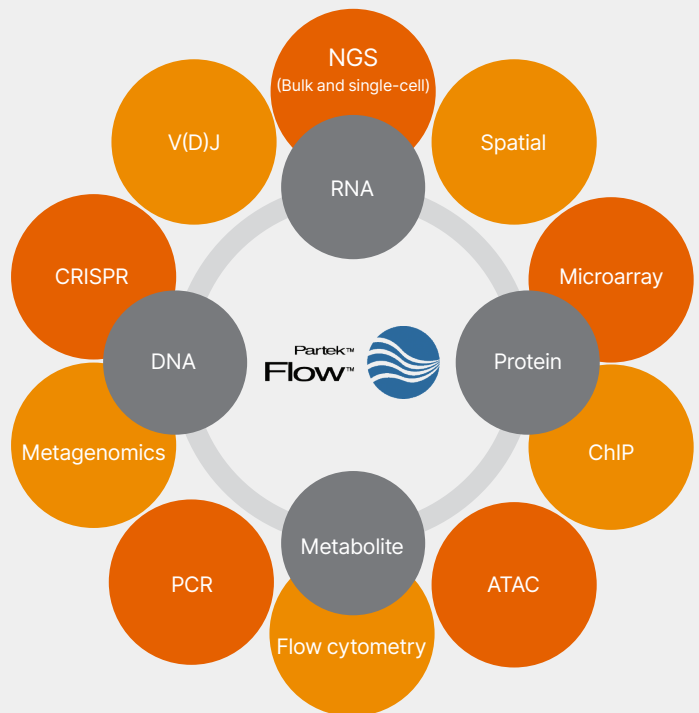
In one of the use cases, we showcase how Partek Flow can be utilized in an integrated spatial multiomics study using transcriptomics and proteomics data to identify cell populations and key markers for B cell differentiation. The flexible pipeline lets you choose filtering options, like fold change, for differential gene expression, convert data into plots and configure the plots the way you want them for your publication.



Shown above, Proliferative B cells express higher PD1 protein and correlation analysis with a differentially expressed gene list show a positive correlation with SRGN gene expression in proliferating B cells (blue) compared to resting cells (red).

The pipeline is platform agnostic and as such, compatible with platforms from different suppliers. A wide range of data types are supported, i.e., individual or bulk multiomics and multimodal, as well as sequencing and microarray.

Partek Flow enables you to explore from genotype to phenotype and the layers in between. Feel free to watch the recording of our webinar that has been summarized in this article.



[Click here to access the webinar: 'Illumina Partek Flow: unravelling complexities of multiomics'](#)

To explore the future of data analysis today, get in touch for a free demo with our specialist team.

After the demo, a limited-time trial offer will allow hands-on manipulation of your data sets. Scan the QR code, fill in our contact request form, and we'll be in touch to set up a demo.

