Introduction to Partek® Flow®

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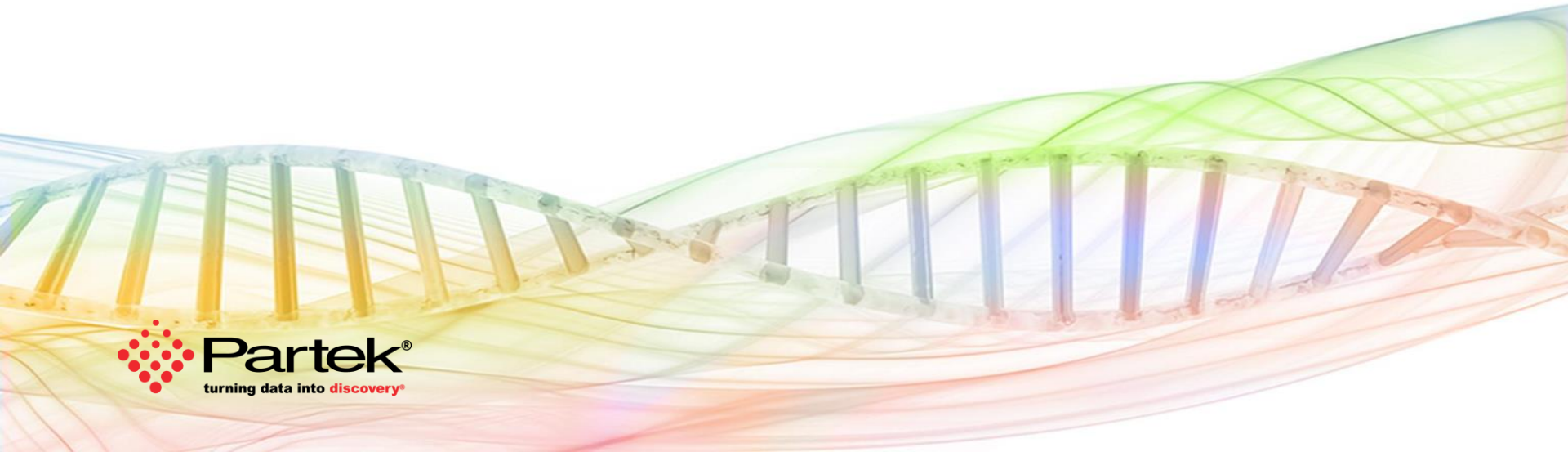
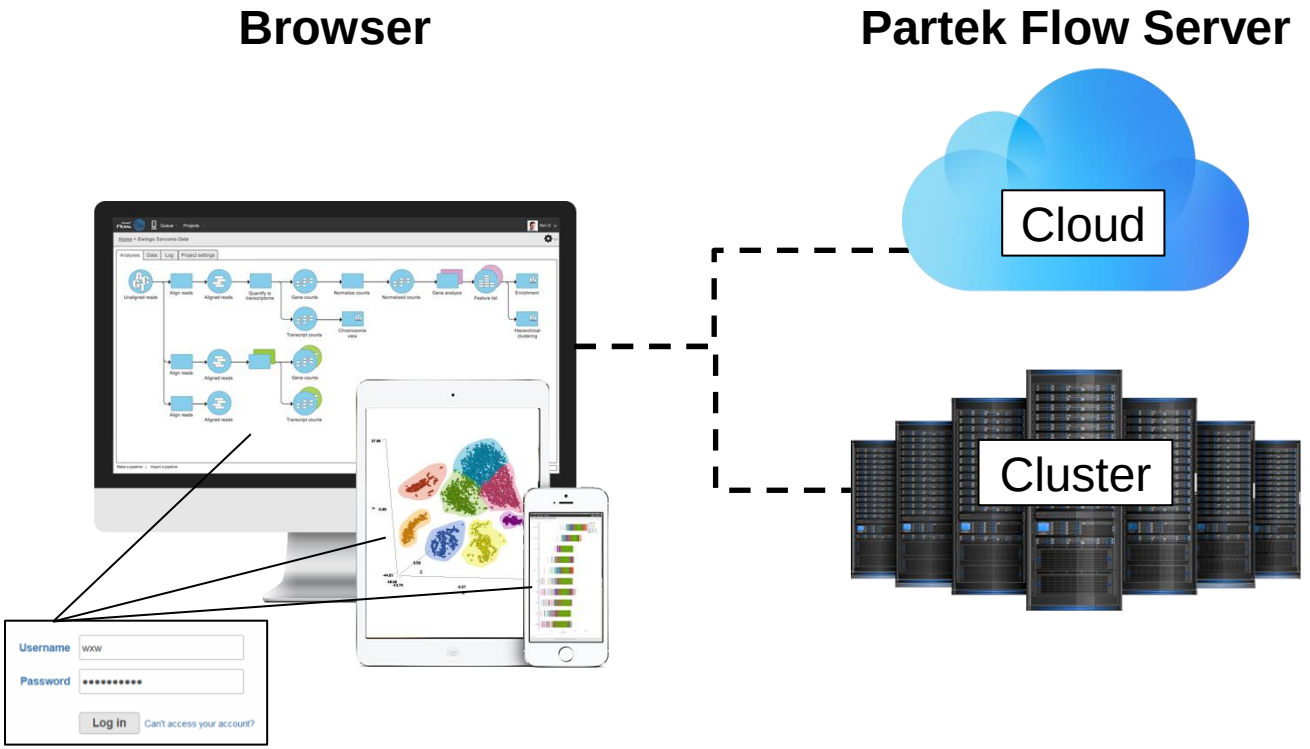
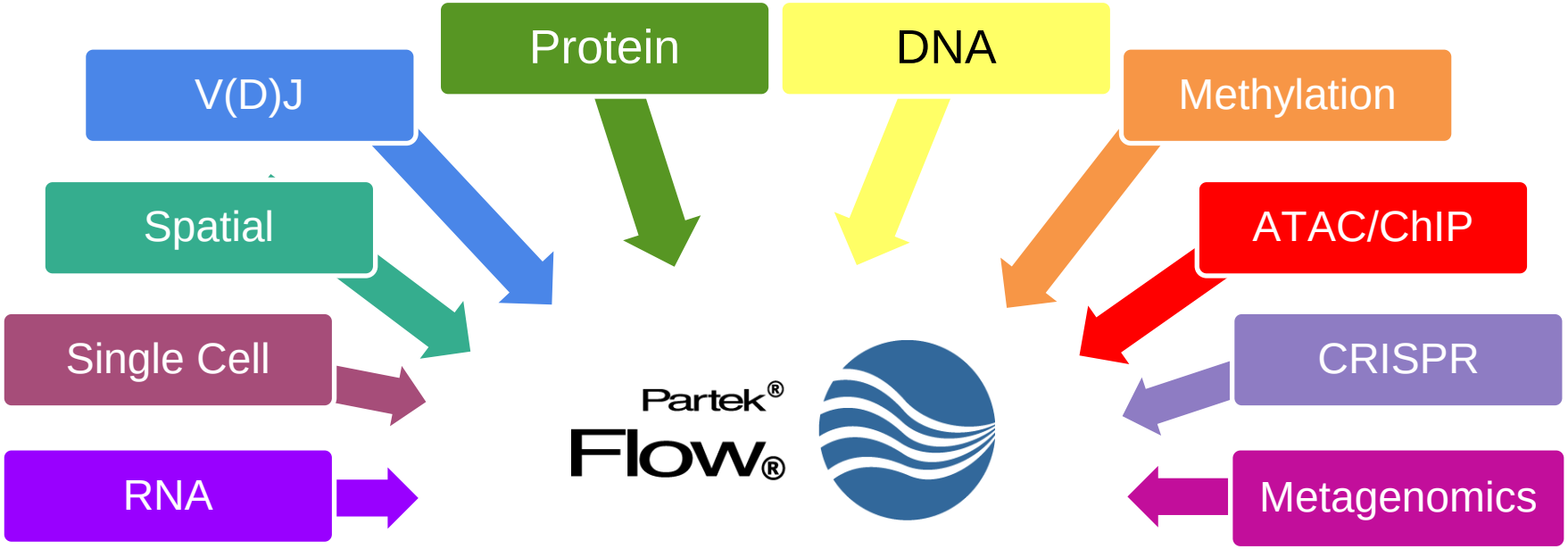


Partek Flow – Browser Based

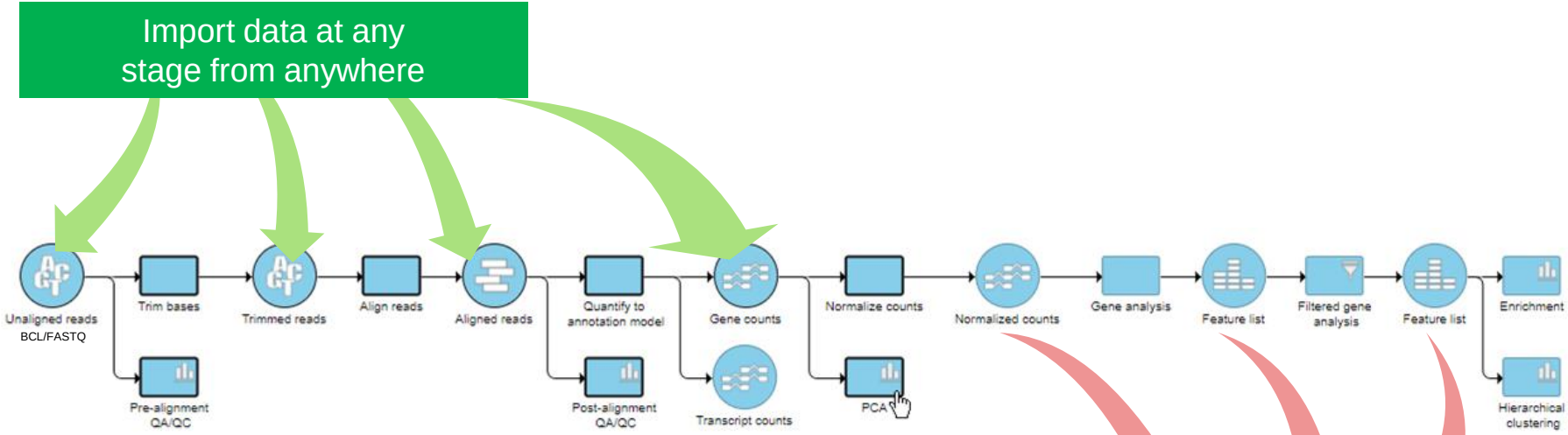


Bulk and Single Cell Sequencing Technologies



\+ **More**

Import & Export Data at Any Stage



.bcl
.fastq
.cel
.bam
.vcf/bcf

.txt/csv
.h5
Seurat obj
More…

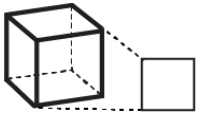
Export data at any point in industry standard formats

Partek®

Comprehensive and Robust Statistics Tools

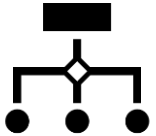
QA/QC

Normalization



Dimension Reduction

Unsupervised Clustering



Automatic Cell Classification

Batch Removal

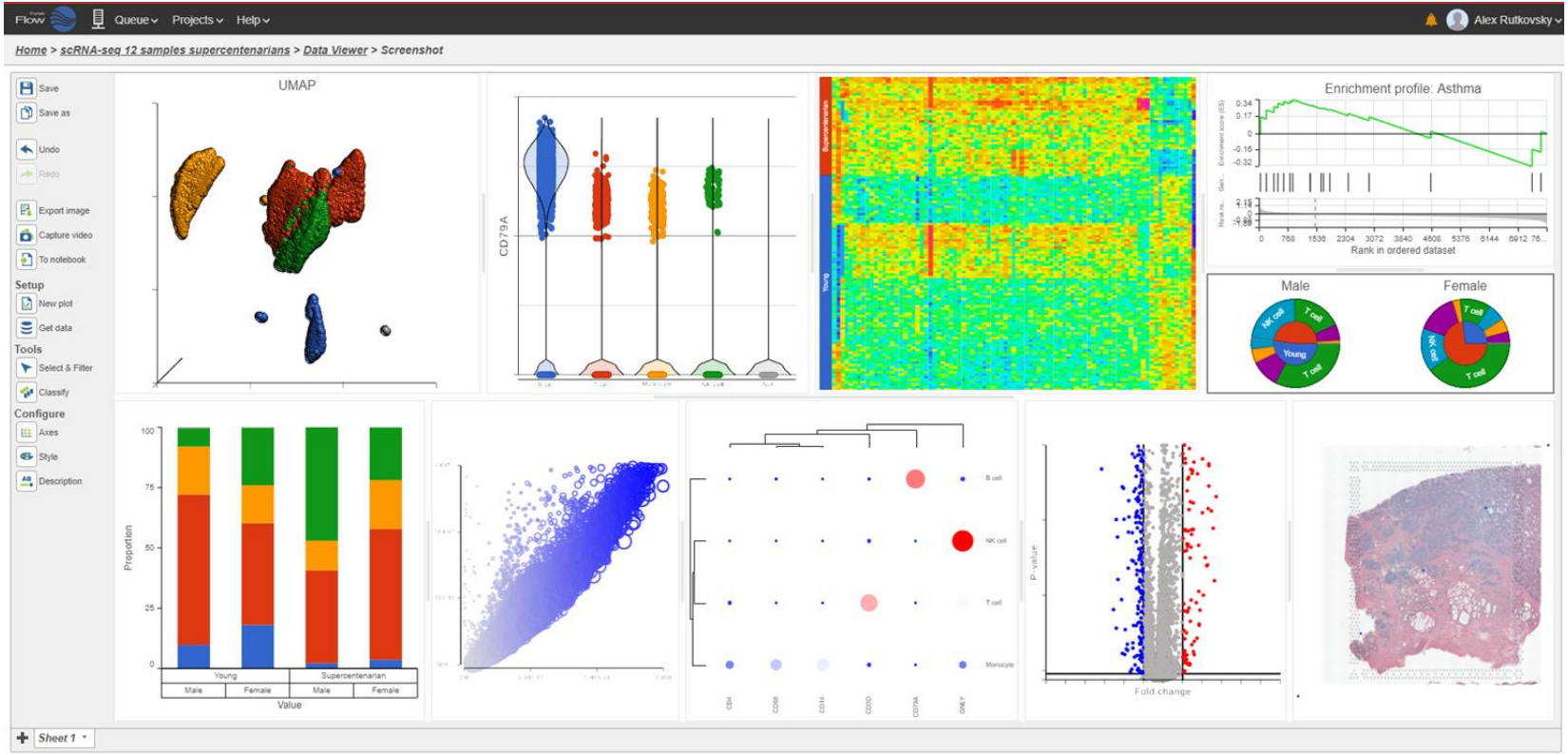
Differential Analysis

Cell Type Abundance Analysis

Trajectory Analysis

Biological Interpretation

Interactive and Publication Quality Visualizations



.png .pdf .svg

Partek®

Audit Trail

Tracks what was done, by who, & when

UMAP

Task UMAP Xiaowen Wang 9 Nov 2022, 09:43 PM CST 00:00:08 197.66 KB

Option	Value
Quantification file	pca.mat.matrix, pca.oids, pca.col.matrix, pca.ids, clustered.row.annotation
Local neighborhood size	15
Minimal distance	0.1
Distance metric	Euclidean
Number of iterations	0
Random generator seed	0
Initialize output values	Random
Number of principal components	10
Split by sample	No

All selected values are the defaults.

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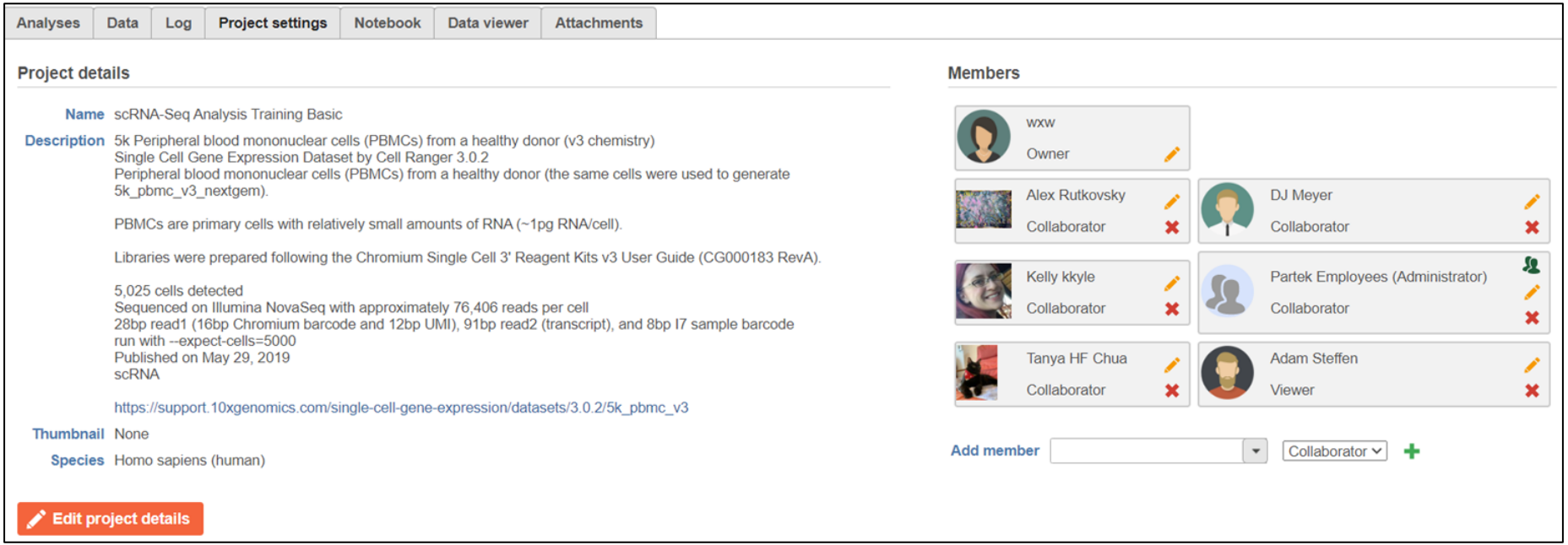
Collaborate and Share



Access Partek Flow at NIH

Access through NIH Library: All NIH Researchers:
https://www.nihlibrary.nih.gov/resources/tools/partek-flow

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Access through NCI: NCI Researchers:
https://www.nihlibrary.nih.gov/resources/tools/partek-flow

Get Help

Discovery Services

Worldwide Technical Support

Educational Resources

User guides, tutorials, and videos

Try Out The Software For Free:

www.partek.com/free-trial/

Live Demo