

# Introduction to Partek® Flow®

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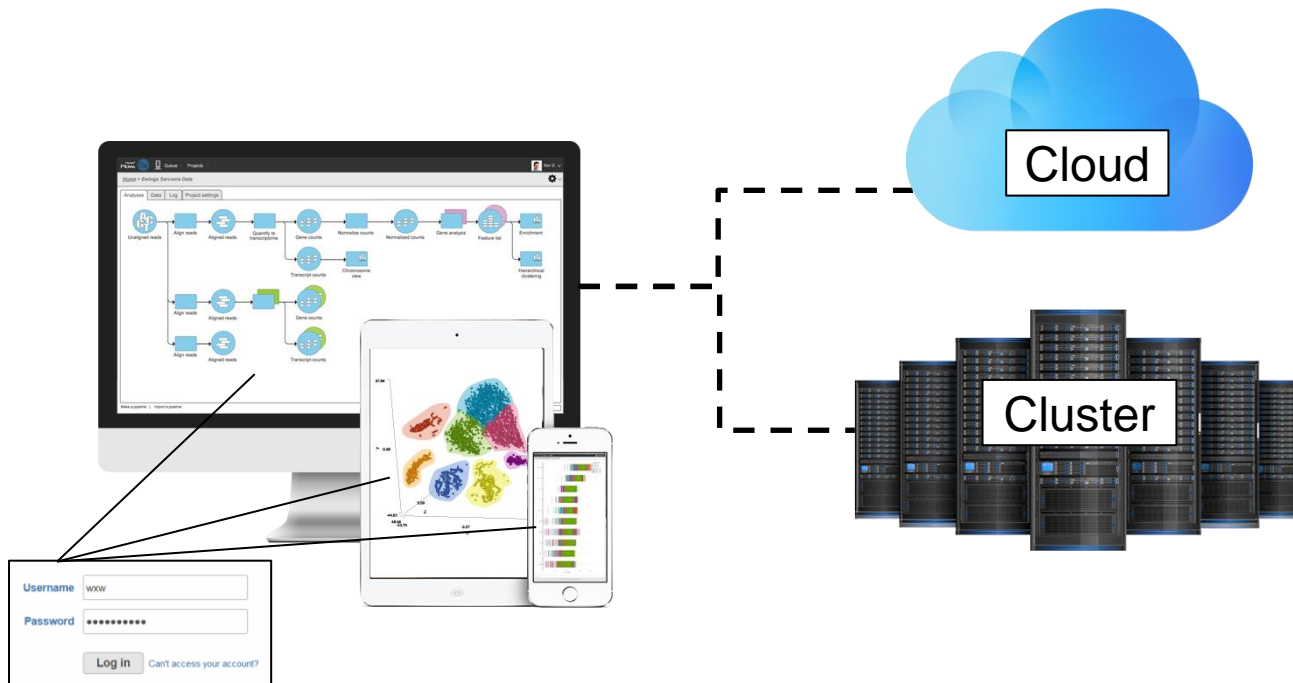
**Alex Rutkovsky, MS PhD**  
*Field Application Scientist*  
*Partek Incorporated*



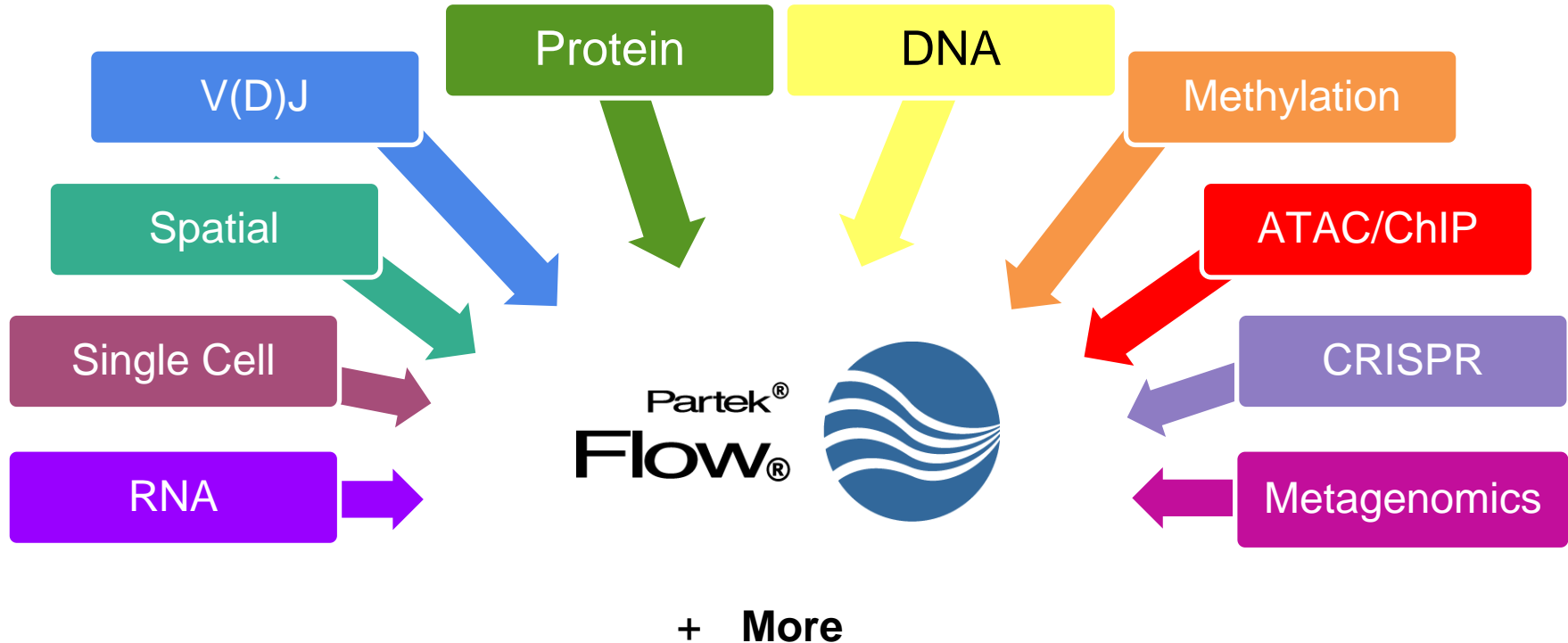
# Partek Flow – Browser Based

## Browser

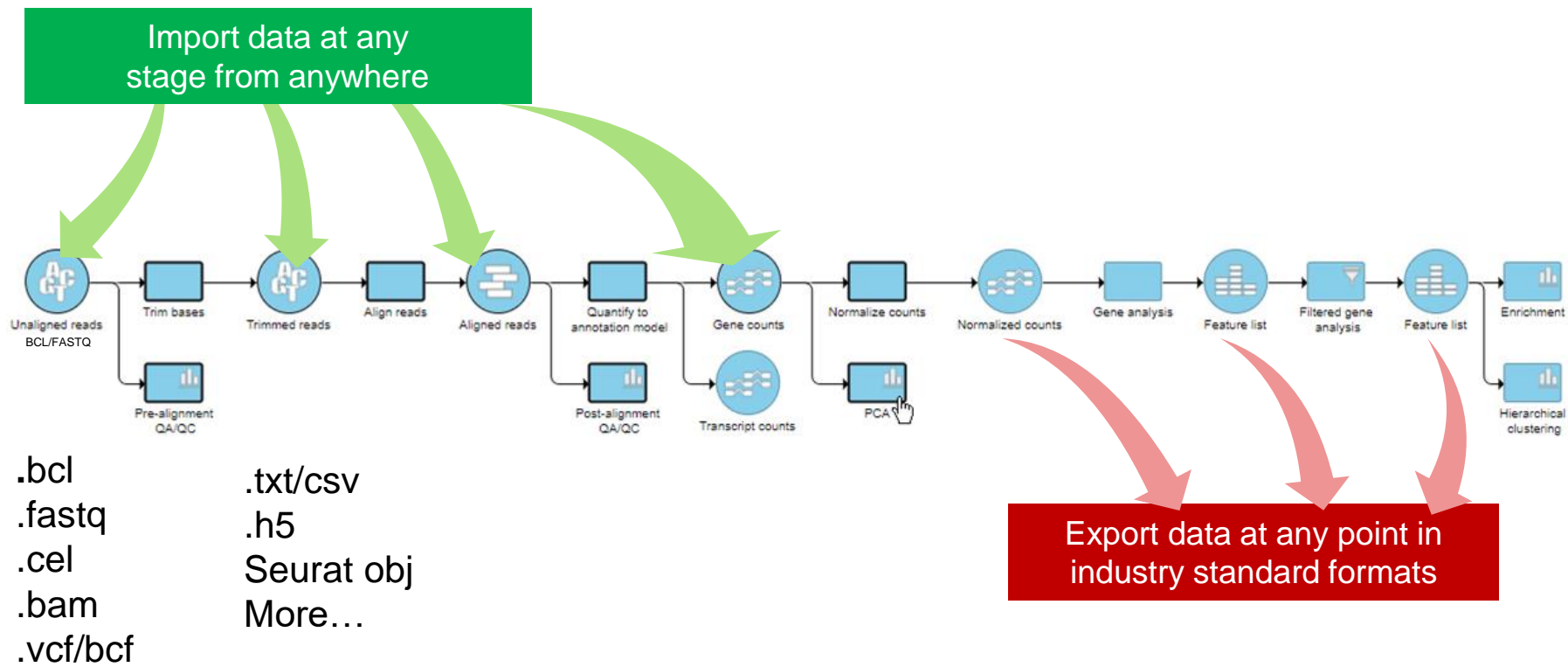
## Partek Flow Server



# Bulk and Single Cell Sequencing Technologies



# Import & Export Data at Any Stage



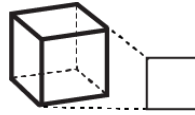
# Comprehensive and Robust Statistics Tools



QA/QC



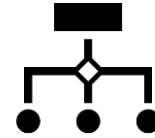
Normalization



Dimension  
Reduction



Unsupervised  
Clustering



Automatic Cell  
Classification



Batch  
Removal



Differential  
Analysis



Cell Type  
Abundance  
Analysis

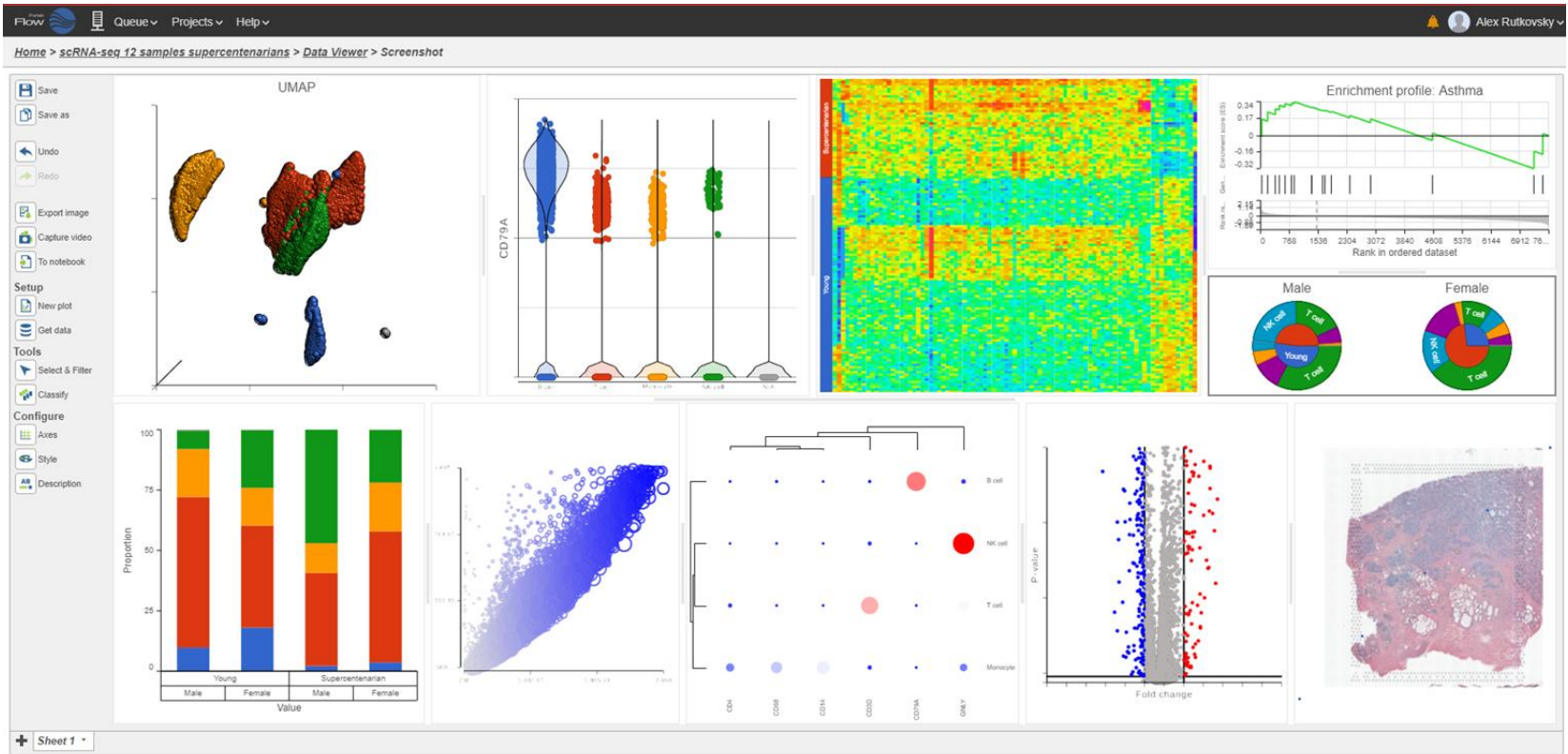


Trajectory  
Analysis



Biological  
Interpretation

# Interactive and Publication Quality Visualizations



.png .pdf .svg

Home > demo > Data summary report (174739)

- Sample data**  
 Xiaowen Wang 9 Nov 2022, 09:32 PM CST 14.62 MB  
[Show/hide details](#)
- Filter counts**  
**Task Filter counts** Xiaowen Wang 9 Nov 2022, 09:33 PM CST 00:00:10 14.03 MB  
[Show/hide details](#)
- Filter features**  
**Task Filter features** Xiaowen Wang 9 Nov 2022, 09:33 PM CST 00:00:14 6.54 MB  
[Show/hide details](#)
- Normalize counts**  
**Task Normalization** Xiaowen Wang 9 Nov 2022, 09:33 PM CST 00:00:06 21.10 MB  
[Show/hide details](#)
- PCA**  
**Task PCA** Xiaowen Wang 9 Nov 2022, 09:34 PM CST 00:00:04 1.66 MB  
[Show/hide details](#)
- Graph-based clustering**  
**Task Graph-based clustering** Xiaowen Wang 9 Nov 2022, 09:34 PM CST 00:00:05 280.78 KB  
[Show/hide details](#)
- UMAP**  
**Task UMAP** Xiaowen Wang 9 Nov 2022, 09:43 PM CST 00:00:08 197.66 KB  
[Show/hide details](#)

# Audit Trail

Tracks what was done, by who, & when

**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.

# Collaborate and Share

Analyses Data Log **Project settings** Notebook Data viewer Attachments

## Project details

**Name** scRNA-Seq Analysis Training Basic

**Description** 5k Peripheral blood mononuclear cells (PBMCs) from a healthy donor (v3 chemistry) Single Cell Gene Expression Dataset by Cell Ranger 3.0.2  
Peripheral blood mononuclear cells (PBMCs) from a healthy donor (the same cells were used to generate 5k\_pbmc\_v3\_nextgem).

PBMCs are primary cells with relatively small amounts of RNA (~1pg RNA/cell).


Libraries were prepared following the Chromium Single Cell 3' Reagent Kits v3 User Guide (CG000183 RevA).

5,025 cells detected  
Sequenced on Illumina NovaSeq with approximately 76,406 reads per cell  
28bp read1 (16bp Chromium barcode and 12bp UMI), 91bp read2 (transcript), and 8bp I7 sample barcode  
run with --expect-cells=5000  
Published on May 29, 2019  
scRNA






















[https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.2/5k\\_pbmc\\_v3](https://support.10xgenomics.com/single-cell-gene-expression/datasets/3.0.2/5k_pbmc_v3)




**Thumbnail** None

**Species** Homo sapiens (human)

 **Edit project details**

## Members

 wwx Owner 	
 Alex Rutkovsky Collaborator  	 DJ Meyer Collaborator  
 Kelly kyle Collaborator  	 Partek Employees (Administrator) Collaborator   
 Tanya HF Chua Collaborator  	 Adam Steffen Viewer  

**Add member**   Collaborator  



# 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/](http://www.partek.com/free-trial/)

# Live Demo

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