

Experience Meets Innovation

Management and Analysis in the
Cytobank Platform



Intellectual Property

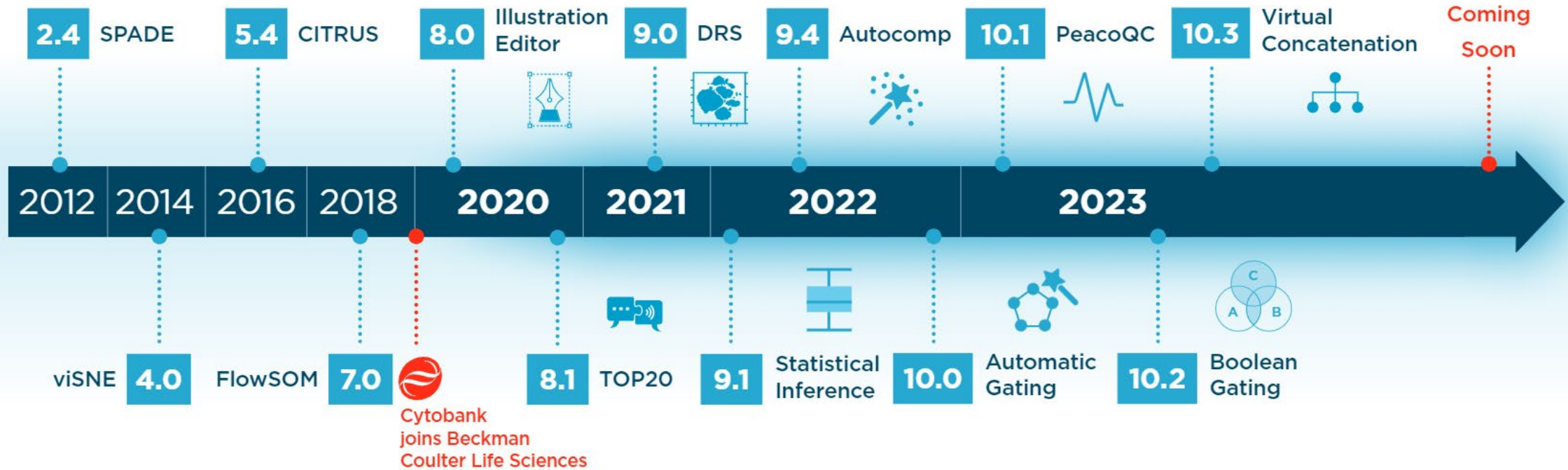
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The Cytobank platform: algorithms and more



Cytobank | Timeline of Releases



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 2023: GBL-EN-100746-v3

Security- first approach for your data



- Cytobank cloud uses current security technology and practices to protect your data
- Transmission security utilizes HTTPS, SSH, SSL, and TLS
- Data are backed up daily, stored at secondary centers and encrypted using AES256
- Cytobank Enterprise is aligned with ISO 27001 and FISMA, and other key policies
- Audited by and actively used by leading global pharma and biotech
- Each Cytobank Enterprise is a virtual private subnet with Single Sign-On capability
- Automated, continuous security scans of codebase and web infrastructure are routinely run with Cybric
- Clinical (human) specimens are safe to store in Cytobank but need to be de-identified



Do you have so many files to analyze that your desktop software crashes?



The Cytobank platform offers fast analysis, structured data management and easy collaboration.

Does repetitive manual gating take up too much of your time?



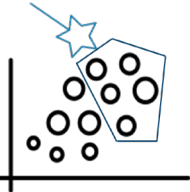
Automate your gating strategy exactly how you want to define cellular subsets.

Do you want to use no-code machine learning for discovery?



Access fully tested and integrated dimensionality reduction, clustering and biomarker identification algorithms.


Algorithms and statistical tools for a complete workflow



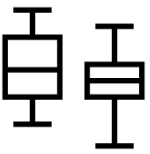
Automatic gating option



viSNE, tSNE-CUDA, UMAP, opt-SNE
for Dimensionality Reduction

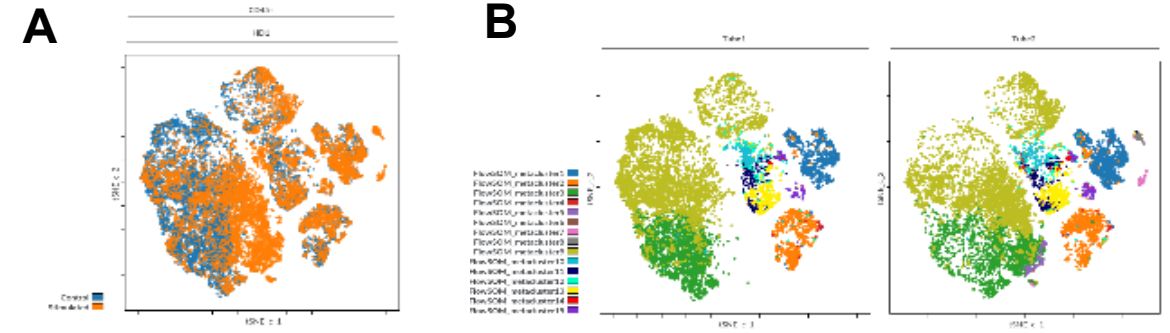


FlowSOM and SPADE
for unsupervised clustering

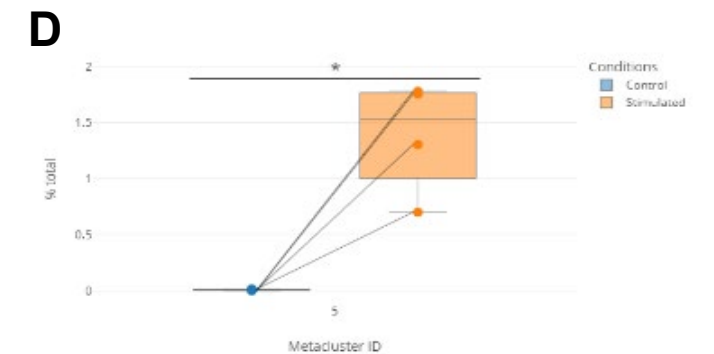
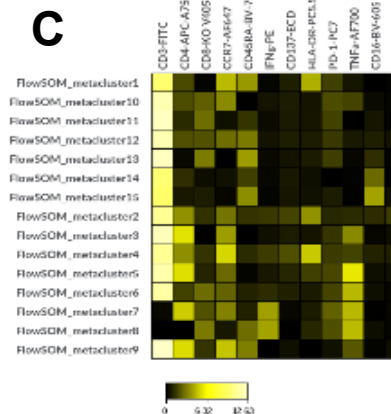


Summary charts and statistical tests
(Student's t-test, Mann-Whitney, Kruskal-Wallis, ANOVA...)

ooo **MORE TO COME!**

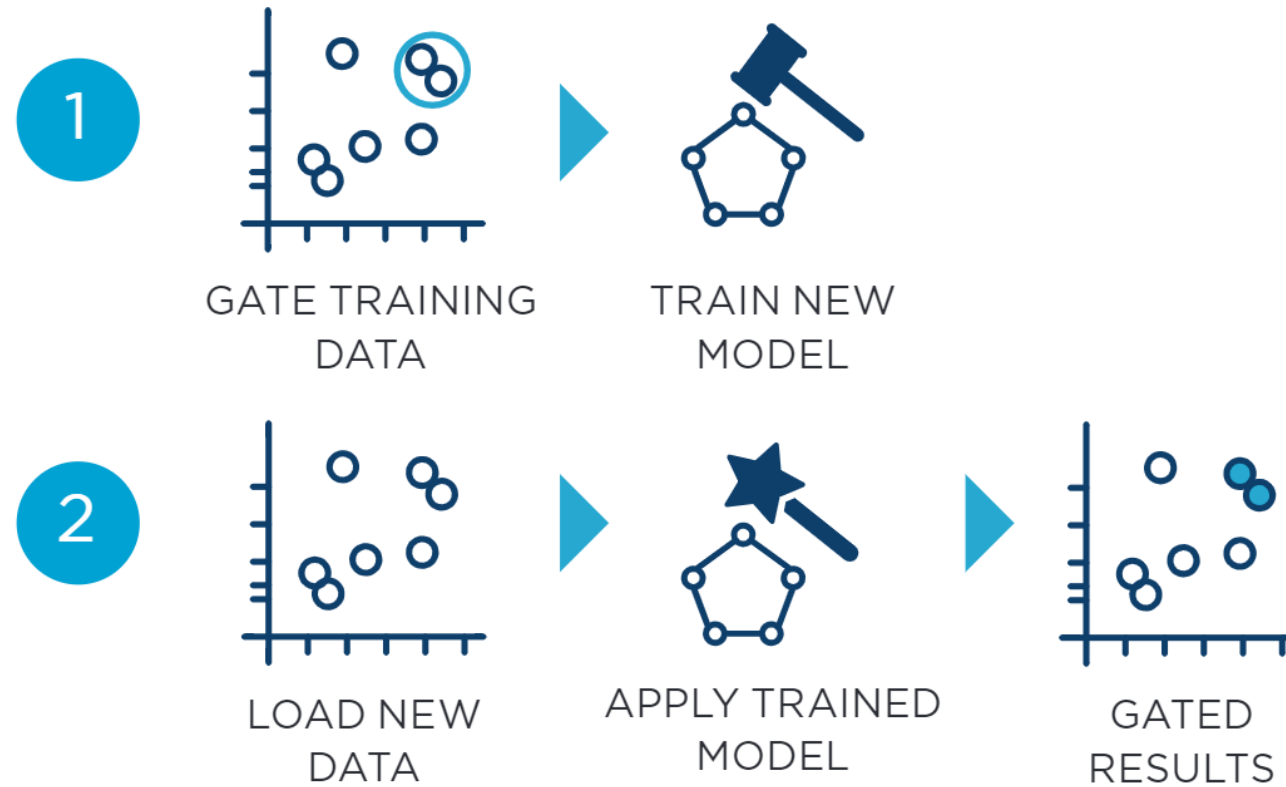


Overlay of conditions (A) or FlowSOM metaclusters (B) on dimensionality reduction maps

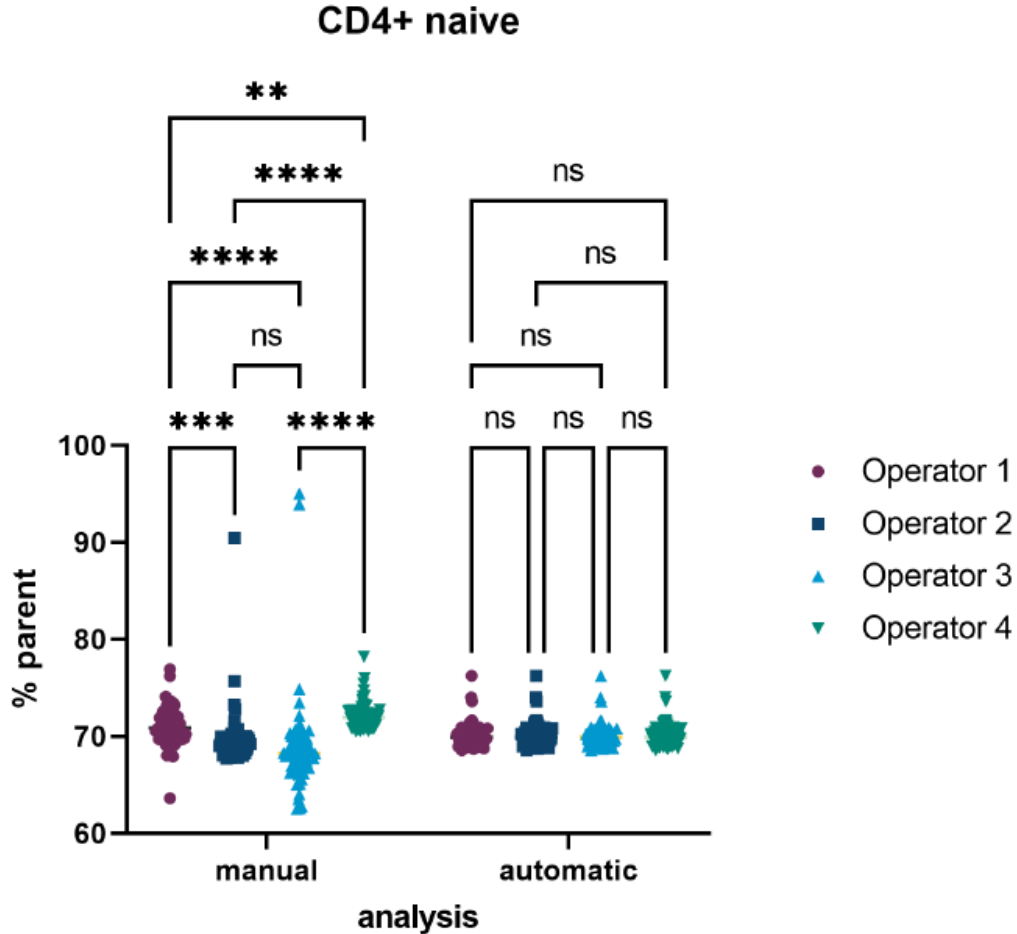


C. Metacluster heatmap for median expression of several markers. D. Boxplot showing % of cells in metacluster 5 in control and stimulated samples. Statistical significance assessed with paired Student's T test.

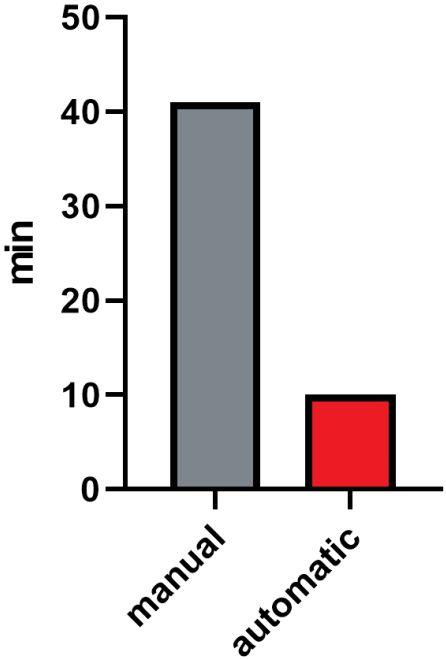
Automatic gating workflow



Cytobank Automatic gating reduces inter-operator differences and speeds up time to results

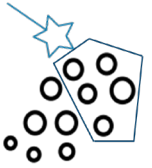


72 files, 7 gates

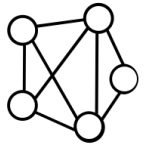


Time required for training and application of automatic model is 75% shorter compared to manual gating of the full dataset for population identification in 72 files with 7 gates.

Algorithms and statistical tools for a complete workflow



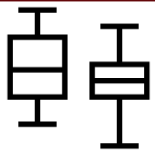
Automatic gating option



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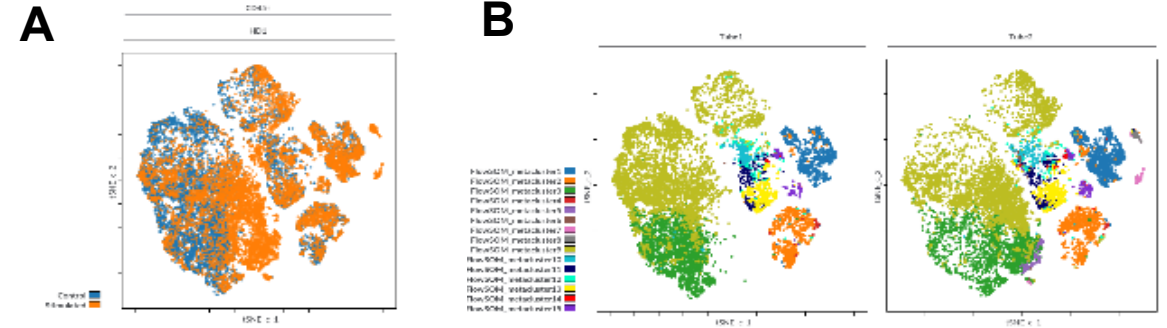


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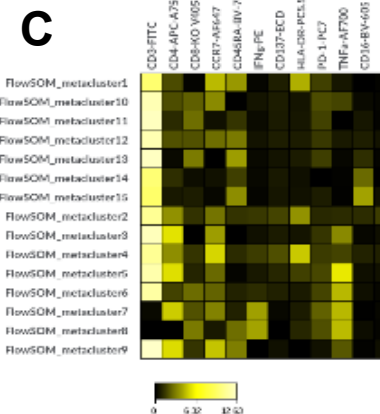


Summary charts and statistical tests
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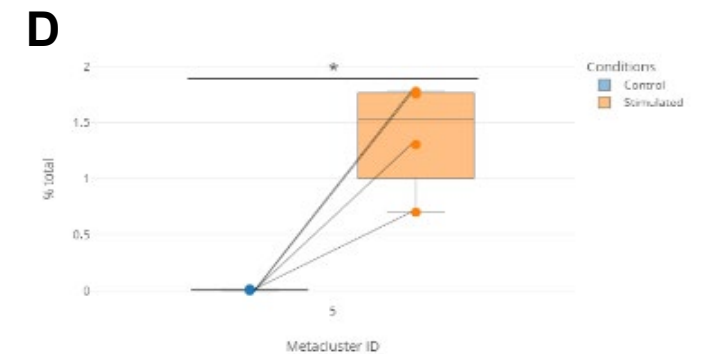
ooo MORE TO COME!



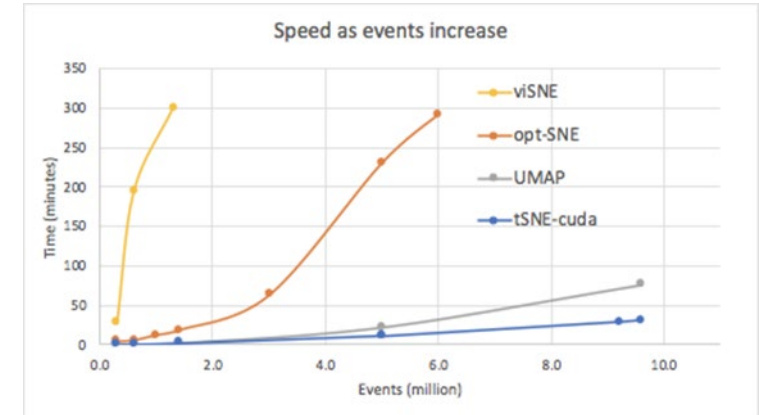
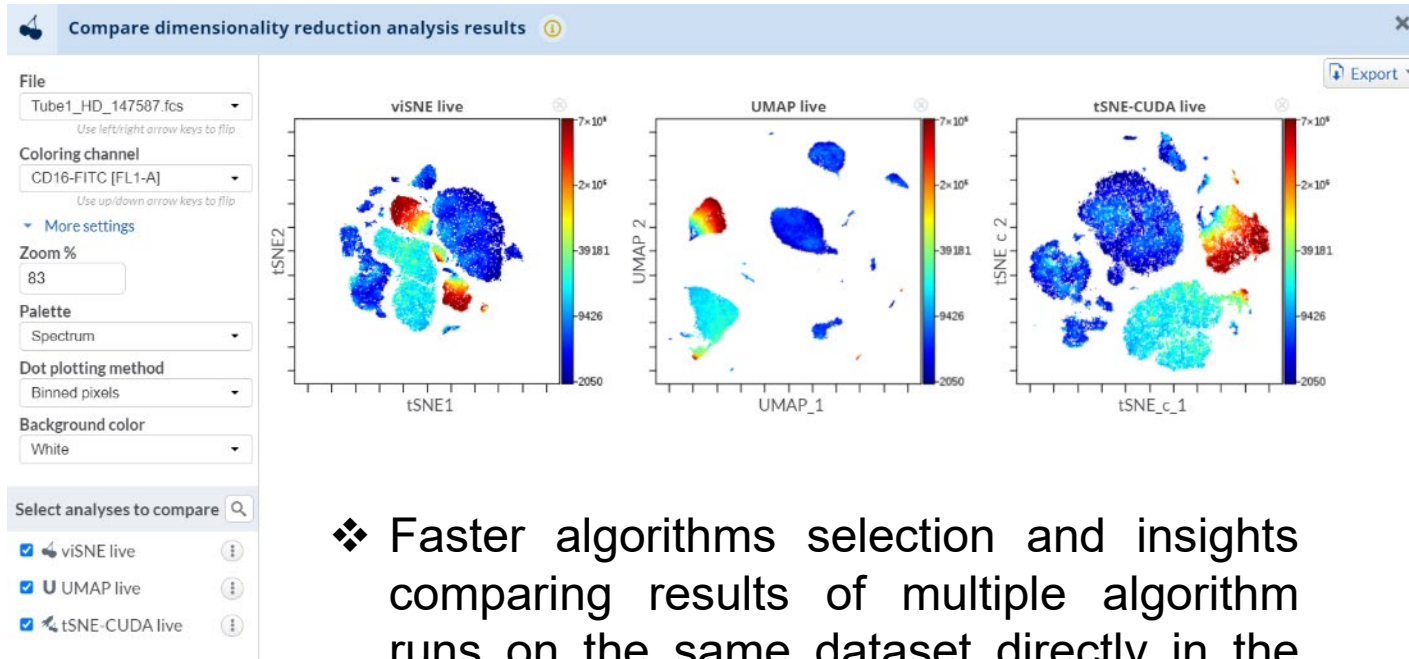
Overlay of conditions (A) or FlowSOM metaclusters (B) on dimensionality reduction maps



C. Metacluster heatmap for median expression of several markers. D. Boxplot showing % of cells in metacluster 5 in control and stimulated samples. Statistical significance assessed with paired Student's T test.



Time matters: visualize your results, faster.



❖ Faster algorithms selection and insights comparing results of multiple algorithm runs on the same dataset directly in the analysis setup page

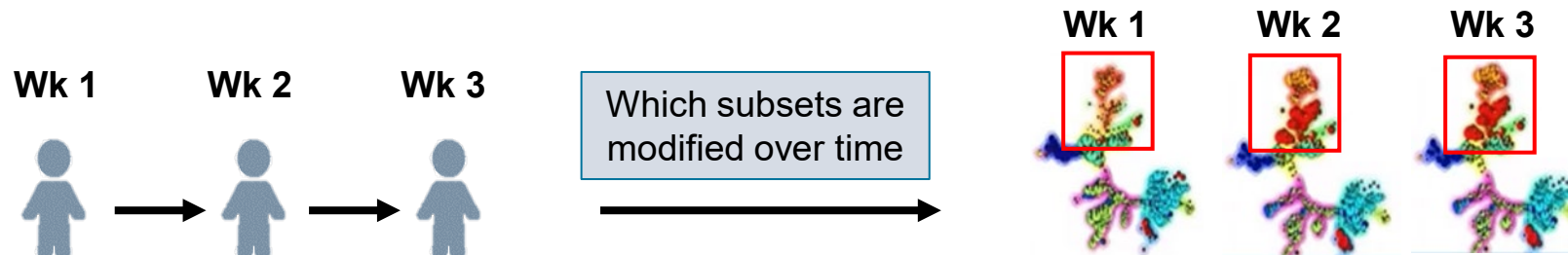
❖ tSNE-CUDA and GPU-UMAP implementations use the parallel processing power of the graphic processing unit (GPU) to boost computational performance. They can handle up to 10M events per run in the Cytobank platform

Unsupervised Clustering: SPADE or FlowSOM

Use case study #2

- ✓ I want to remove subjectivity when phenotyping cells.
- ✓ I need to directly compare cell subsets from a new sample to a previous analysis (longitudinal study).

Persistent SOM Enables Comparison of Samples



SPADE: Peng Qiu, Erin F. Simonds, Sean C. Bendall, Kenneth D. Gibbs, Robert V. Bruggner, Michael D. Linderman, Karen Sachs, Garry P. Nolan, Sylvia K. Plevritis. (2011). Phenotypically determined self-organization of flow cytometry data with spanning-tree progression analysis of density normalized events. *Nature Biotechnology*.

FlowSOM: Van Gassen S, Callebaut B, Saeys Y (2019). FlowSOM: Using self-organizing maps for visualization and interpretation of cytometry data.

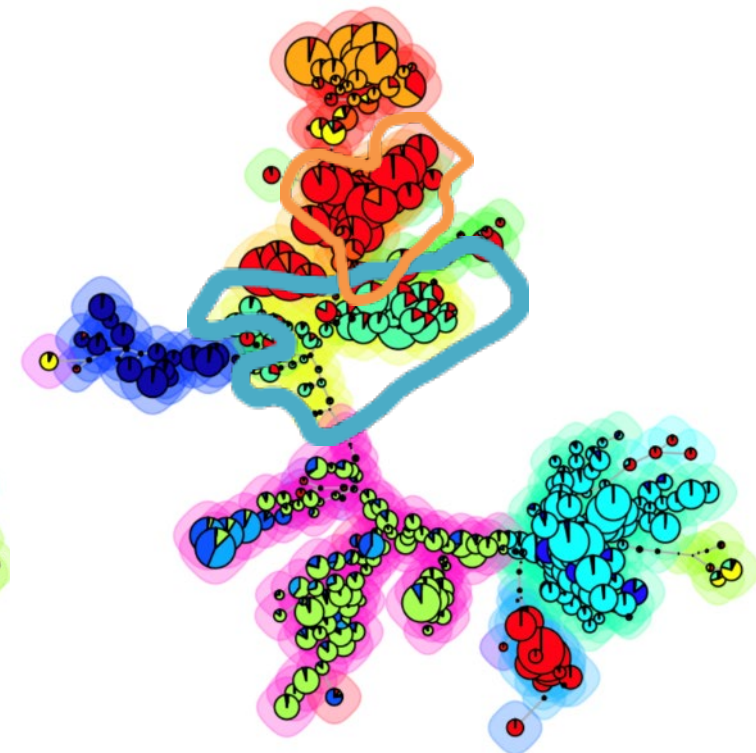
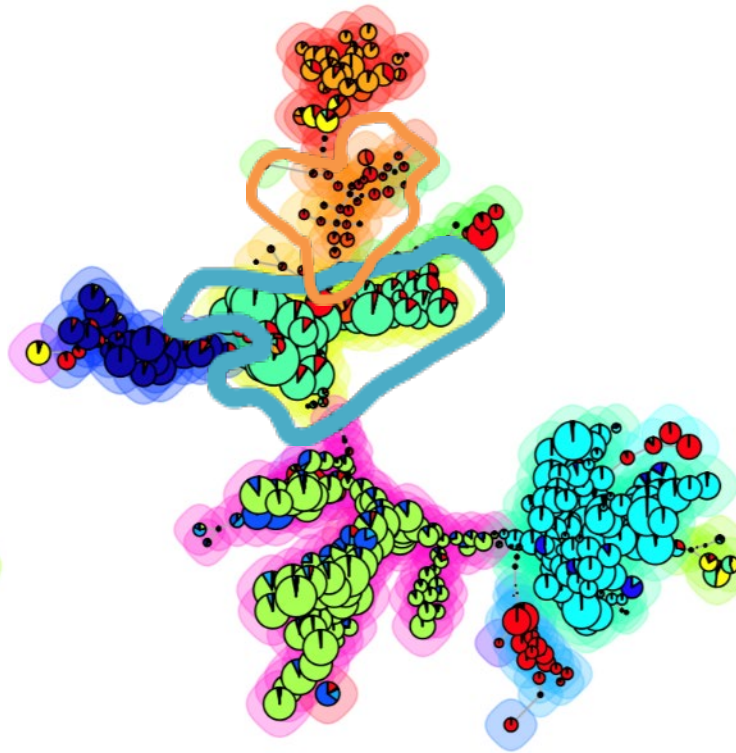
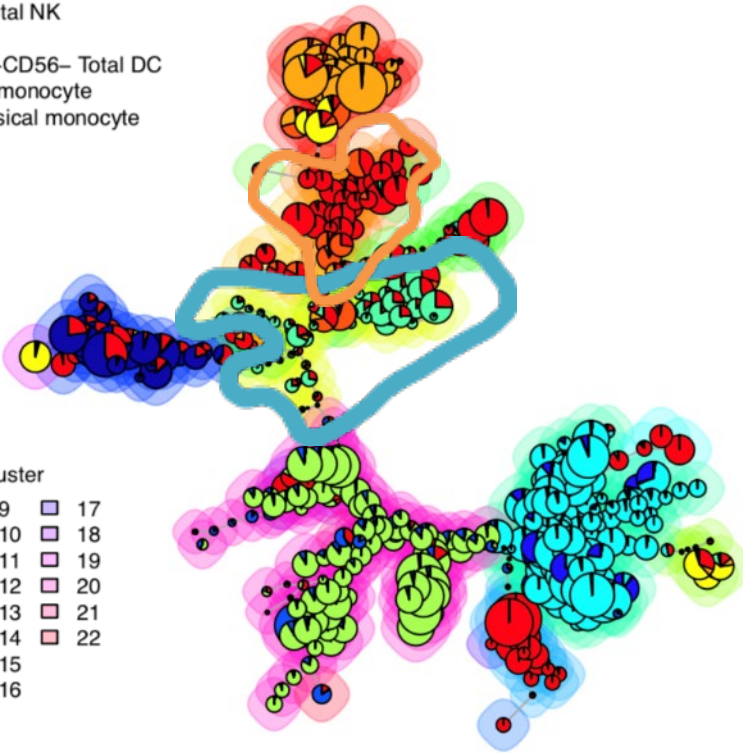
FlowSOM Results: Visual Comparison of Cluster Abundance and Composition with MSTs

- CD14+ monocyte
- CD19+
- CD25+CD127- Treg
- CD3+
- CD3+CD56+ NKT
- CD4+
- CD56+ Total NK
- CD8+
- HLA-DR+CD56- Total DC
- Classical monocyte
- Non-classical monocyte
- Live

Sample 1

Sample 2

Sample 3



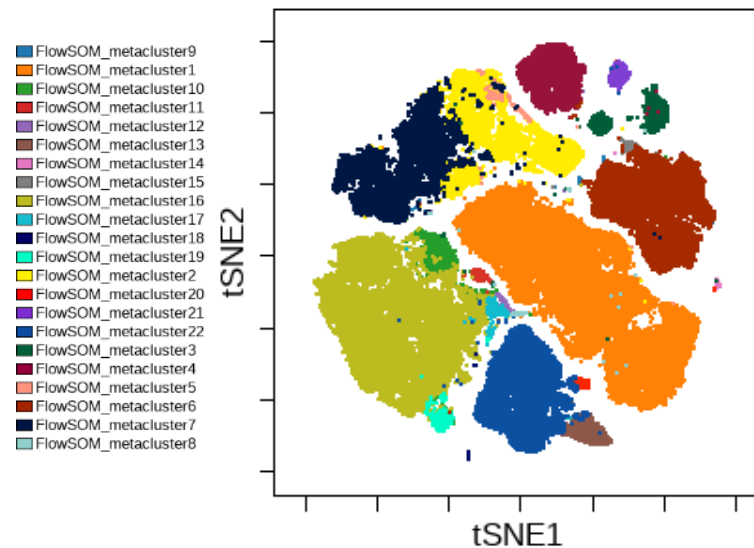
- Metacluster
- | | | |
|-----|------|------|
| ■ 1 | ■ 9 | ■ 17 |
| ■ 2 | ■ 10 | ■ 18 |
| ■ 3 | ■ 11 | ■ 19 |
| ■ 4 | ■ 12 | ■ 20 |
| ■ 5 | ■ 13 | ■ 21 |
| ■ 6 | ■ 14 | ■ 22 |
| ■ 7 | ■ 15 | |
| ■ 8 | ■ 16 | |

Downloaded CSV files provide quantitative abundance and marker expression for each cluster and metacluster

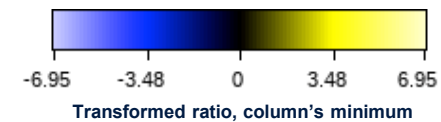
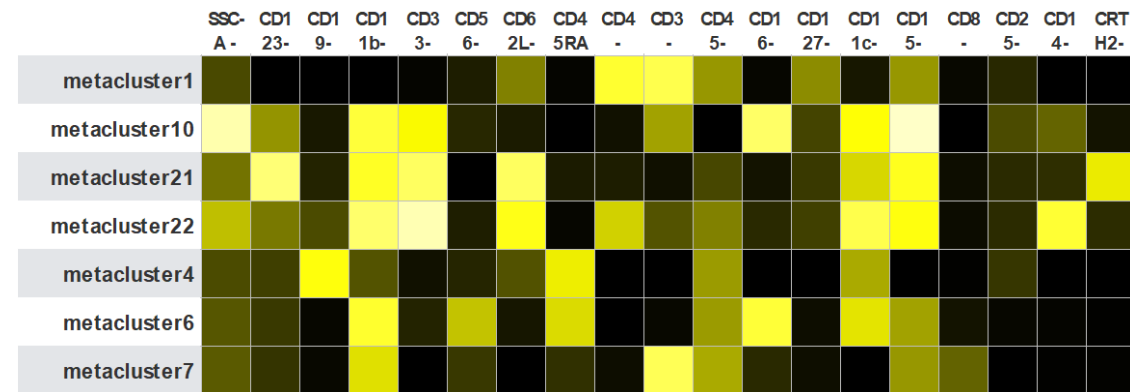
Analysis Pipeline: FlowSOM on viSNE

FlowSOM ran on viSNE experiment, 22 metaclusters,
Clustering channels for FlowSOM is the same as the channels used for viSNE

FlowSOM metaclusters overlaid on viSNE map



FlowSOM metaclusters heatmap

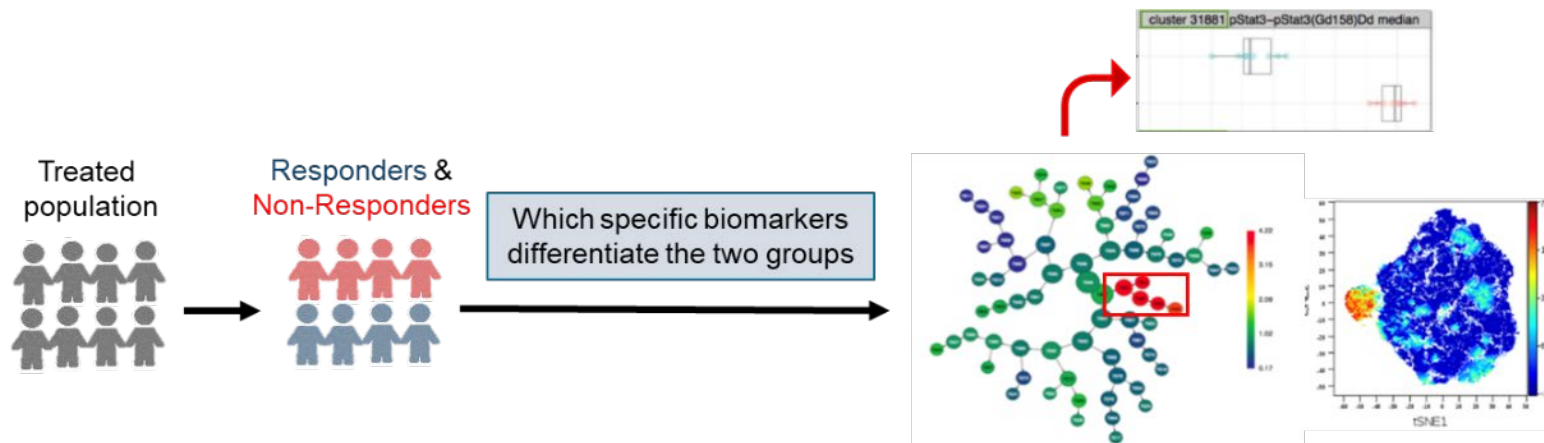


Automatically Identify Predictive Biomarkers: CITRUS

Use case study #3

- ✓ I have different conditions that I want to compare statistically.
- ✓ I'm looking for a tool to identify new biomarkers.

CITRUS: Cluster Identification, Characterization and Regression

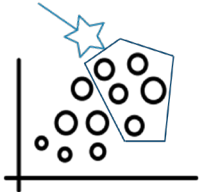


Data-driven approach to identifying stratifying subpopulations in multi-dimensional cytometry data

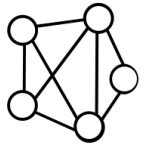
- automated
- objective
- scalable
- sensitive

Robert V. Bruggner, Bernd Bodenmiller, David L. Dill, Robert J. Tibshirani, and Garry P. Nolan. (2014). Automated identification of stratifying signatures in cellular subpopulations. PNAS. <https://doi.org/10.1073/pnas.1408792111>

Algorithms and statistical tools for a complete workflow



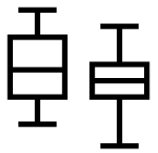
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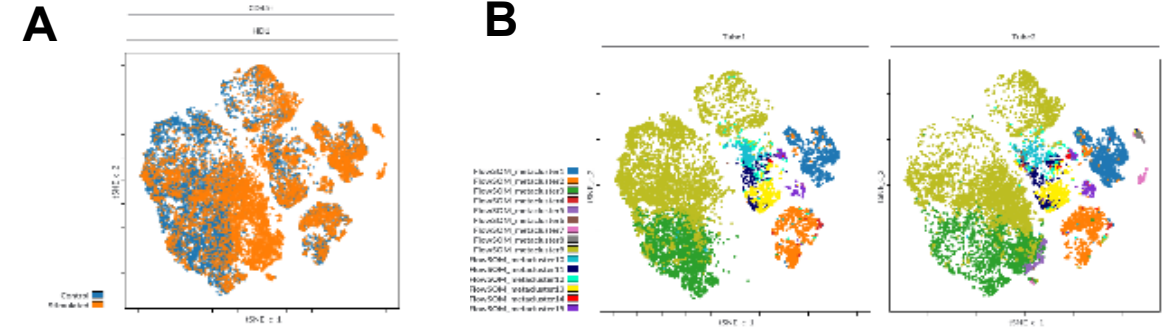


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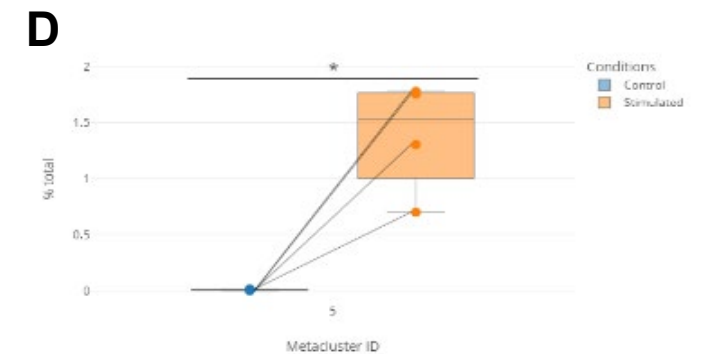
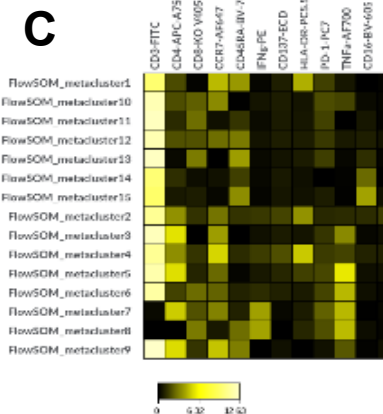


Summary charts and statistical tests
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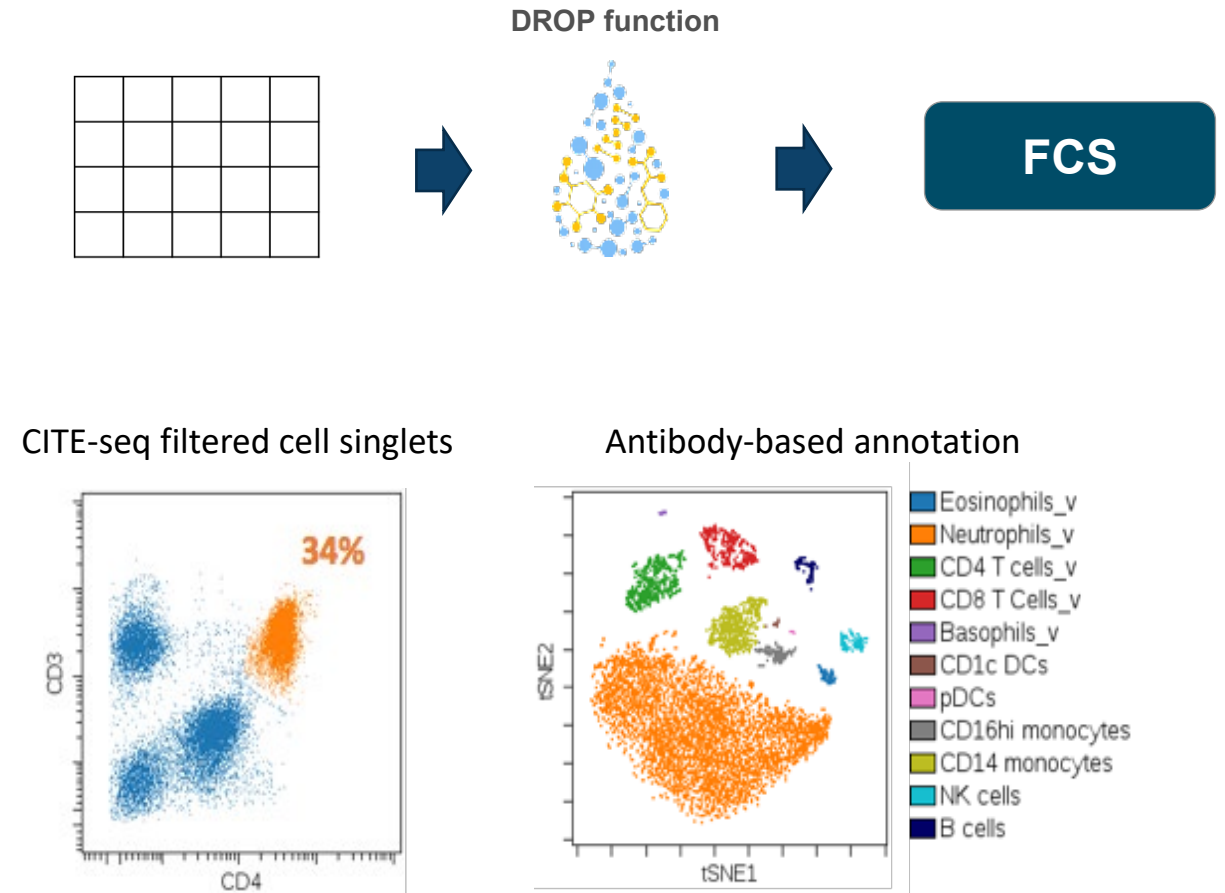
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DROP: analyze other data types in the Cytobank platform

- DROP allows you to convert tabular data into FCS format
- Leverage machine learning tools to other single-cell data types besides mass & flow cytometry (e.g., CITEseq, genomic, RNA-seq, imaging data)
- DROP can work also with bulk data:
 - Sequencing
 - Nanostring
 - Luminex

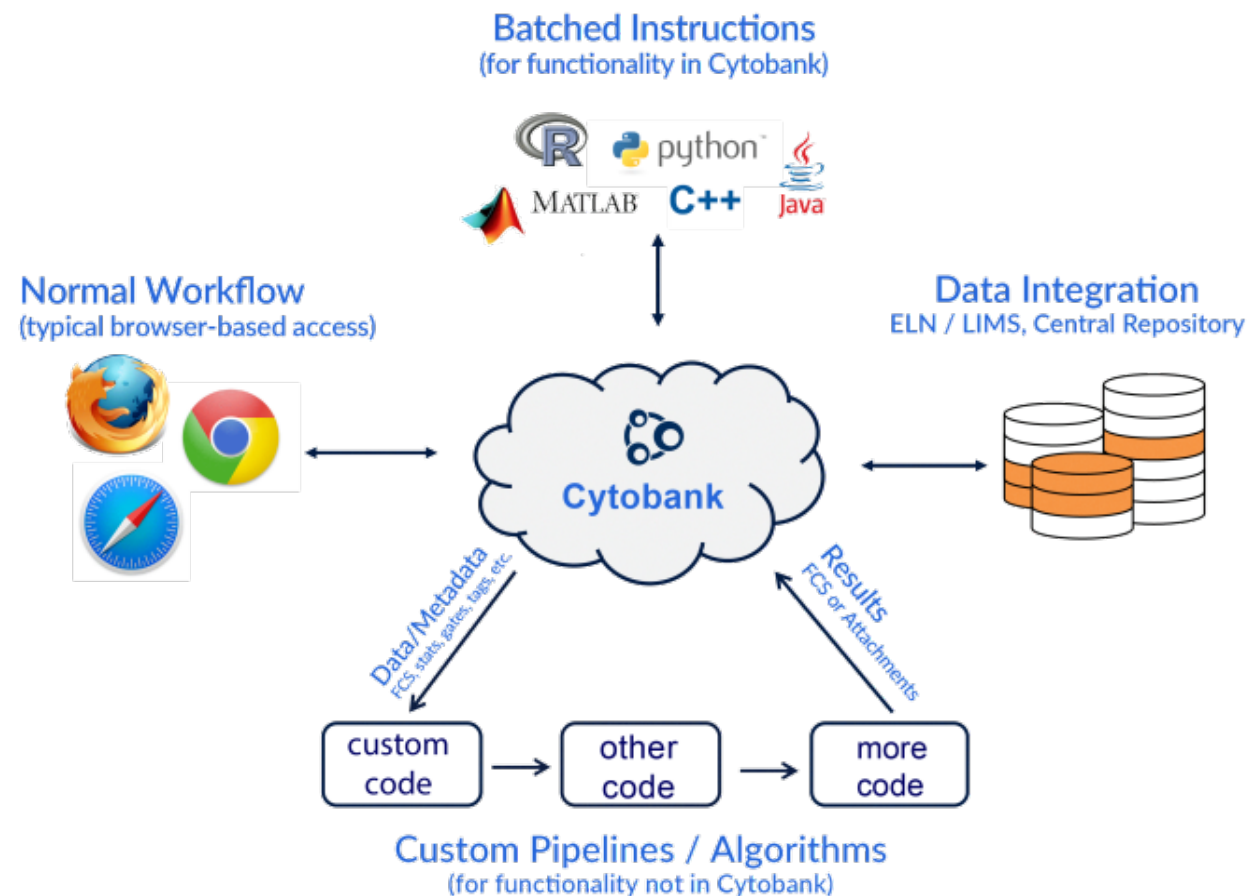


Data provided by Dr. Adeeb Rahman

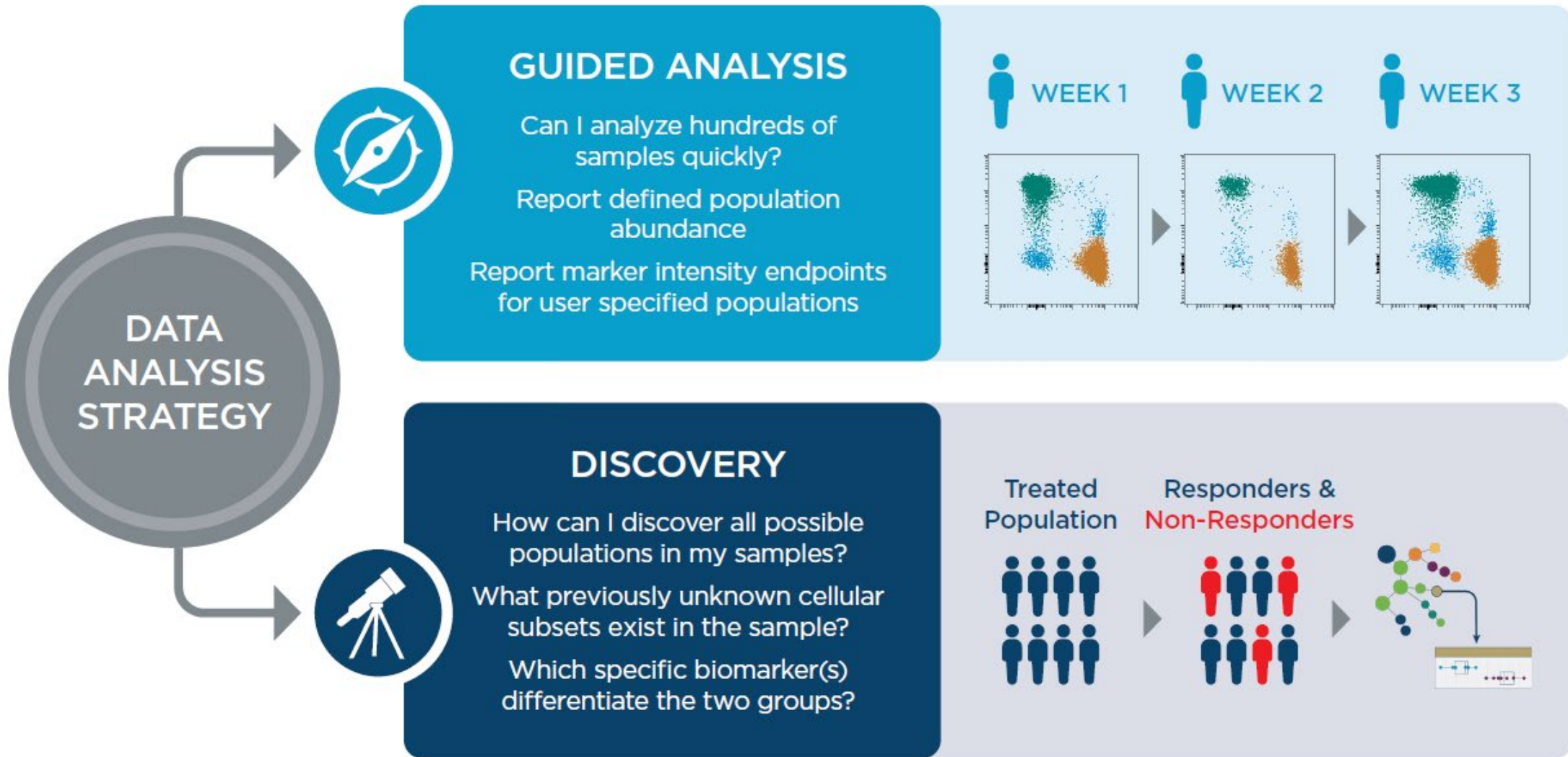
Customizable Workflow: Application Programming Interface (API)

Why coding?

- Extend functionalities: improve upon your existing analysis pipeline
- Reduces errors/improves reproducibility by standardizing analysis
- Speeds up workflow: enhance efficiency and cost by decreasing time from data acquisition to analysis
- Frees up time for other meaningful tasks



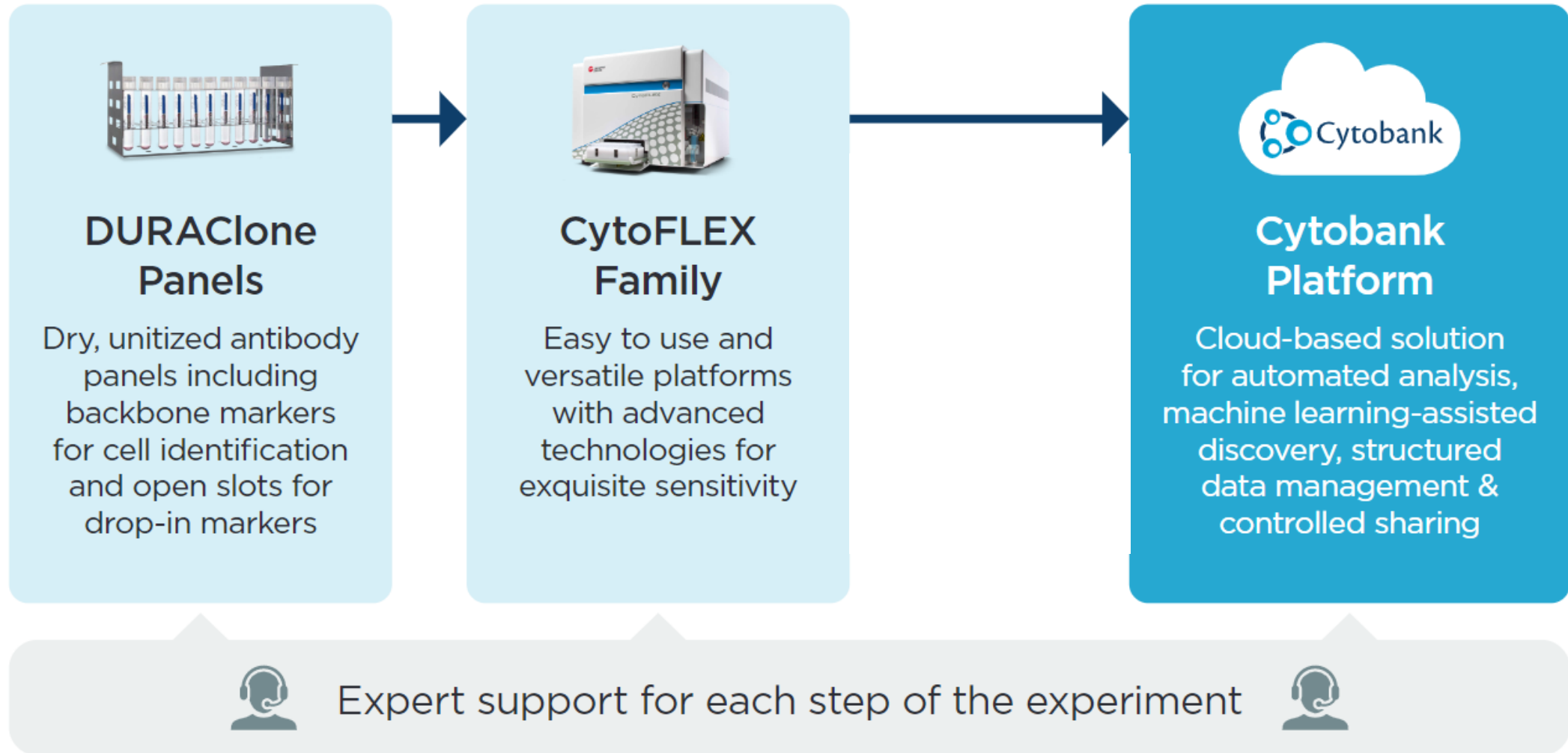
Fit for purpose tools covering guided and discovery settings



Cytobank support: centered on our customers



End-to-end solution for consistent research insights



Take home message



- ✓ Unbiased data analysis with ML- assisted tools with no coding required
- ✓ Instrument agnostic
- ✓ Suitable for different data types with DROP functionality
- ✓ Increased reproducibility with Automatic gating option
- ✓ Improved collaboration and data sharing thanks to the cloud architecture
- ✓ Automated workflows through the API
- ✓ Security- by- design approach to protect the data

Learn more



SUBSCRIBE FOR A 30- DAY FREE TRIAL

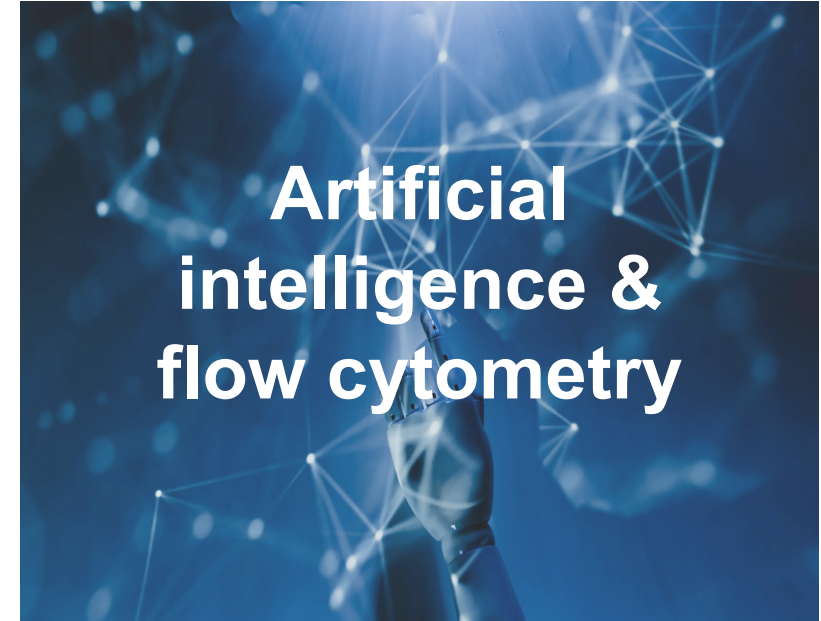


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Don't let data analysis stop your research



**STEP INTO
THE FUTURE
OF DATA ANALYSIS**



**Artificial
intelligence &
flow cytometry**