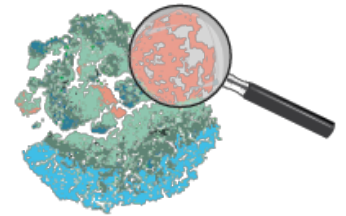


ClusterExplorer

Reduce complexity and save time to insights with ClusterExplorer, which allows you to summarize high-dimensional results quickly and easily in one visual dashboard.

About ClusterExplorer

This tool illustrates a profile of relative intensity values across parameters in flow cytometry data and enables you to translate complex experiment results into visual science. It creates summary plots from clustering algorithms (e.g., FlowSOM, Phenograph or X-shift) and illustrates those populations on dimension-reduced space (e.g., tSNE, UMAP), line plots and heat maps.



Visually explore your experimental details with interactive dashboards

Summarize data

- Populations from clustering algorithms (e.g., Phenograph) are presented on a line trace plot; each cluster is a different color.
- Clusters are back-mapped onto UMAP, tSNE or other dimension-reduced space or conventional 2-D plots.
- Filter populations of interest with interactive Boolean gates

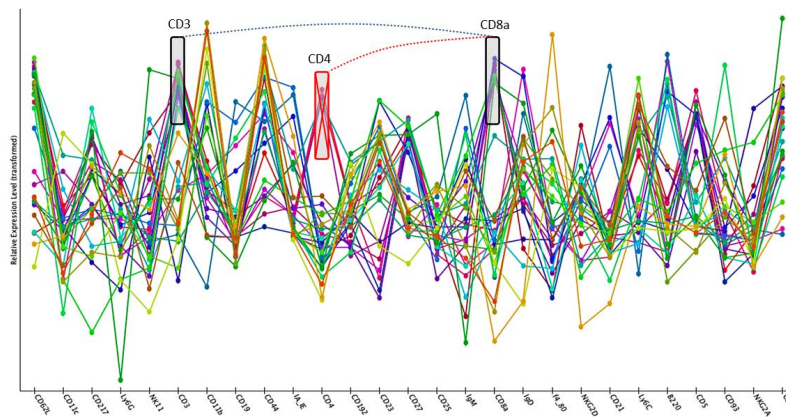


Figure 1A. In this line trace plot image, CD3+CD8+ T cells are selected using three gates placed on lineage markers within the line trace plot window.

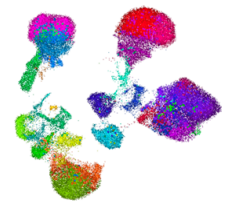


Figure 1B. Prior to gating, all populations are rendered onto the 2-D plot as a UMAP.

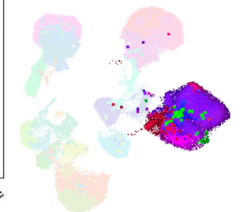


Figure 1C. After gating, the isolated clusters are back-mapped onto a 2-D plot (UMAP here) in full color, while unselected clusters are toned down.

Determine trends with heatmaps

Include experimental variables in the heatmap table to identify how clusters vary in expression levels.



Figure 2. Cluster 14 is absent in blood, bone marrow and lymph node but abundant in spleen. Clusters 23 and 24 are abundant in bone marrow but absent from other compartments.

Easy to control dashboard



Adjust cluster hierarchy, compare clustering algorithms mathematically, add Boolean logic, iterate through populations and add more 2-D plots for further exploration easily through the dashboard.

Reduce complexity and rapidly identify and compare populations

Quickly find rare and abundant populations with cluster bar charts.

- Use in combination with the line trace plot or heat map to explore the population's phenotype.

Easily scrutinize highly similar populations and merge similar clusters when warranted.

- Boolean filters, back-gating and 2-D plots allow you to compare expression of markers to help you evaluate whether two or more clusters may be the same phenotype.

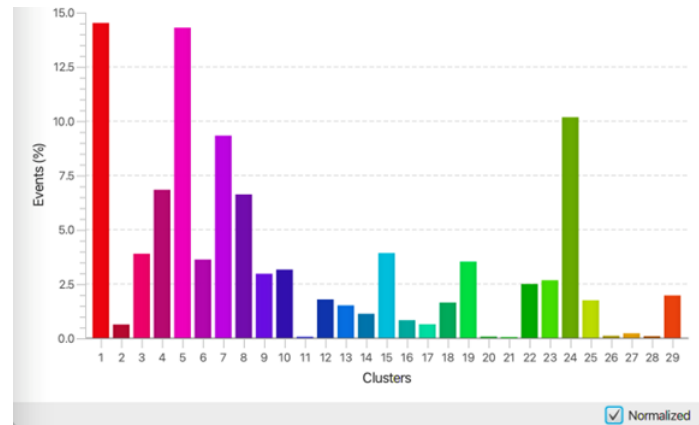


Figure 3. Clusters 11, 20, 21, 26, 27 and 28 make up less than 0.5% of the cells combined.

Mathematically compare clustering algorithms and commonalities

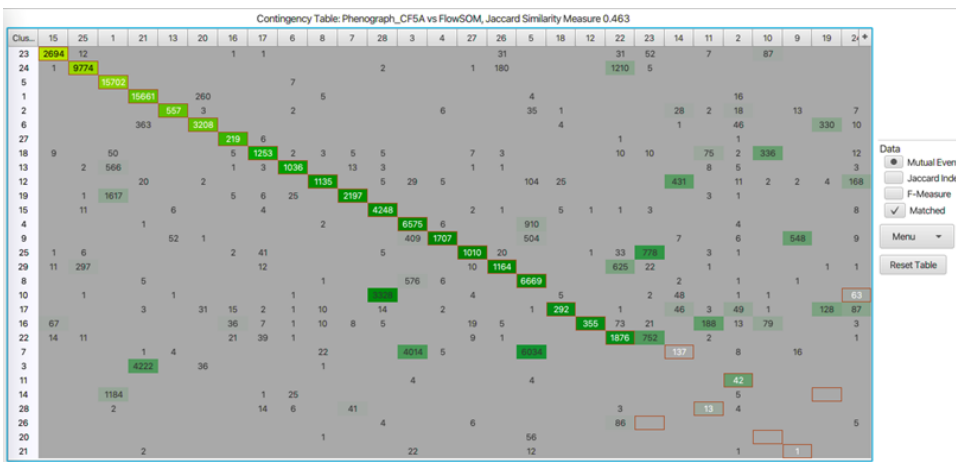


Figure 4. This contingency table shows that Cluster 23 from Phenograph is most similar to Cluster 15 from FlowSOM, sharing 2,694 cells in common.

Utilize intuitive tools for image adjustment and figure creation

- Easily visualize rare cells or diminish the impact of outliers with the feature to scale the dot size with the resolution adjuster.

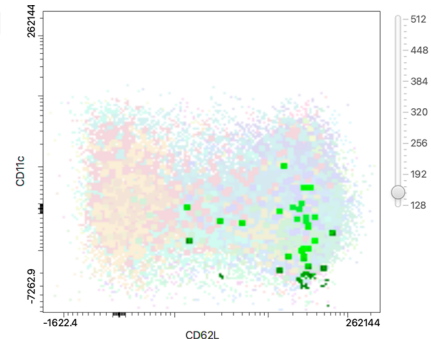


Figure 5. The resolution adjuster makes it easy to see rare cells or the impact of outliers.

Get started with ClusterExplorer today!

Learn more at <https://www.flowjo.com/learn/flowjo-university>

Download ClusterExplorer at: <https://www.flowjo.com/exchange/#/plugin/profile?id=30>

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