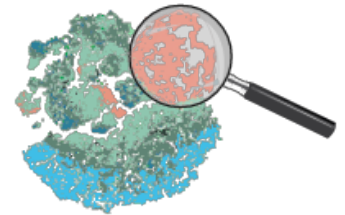


# ClusterExplorer

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 XShift) 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

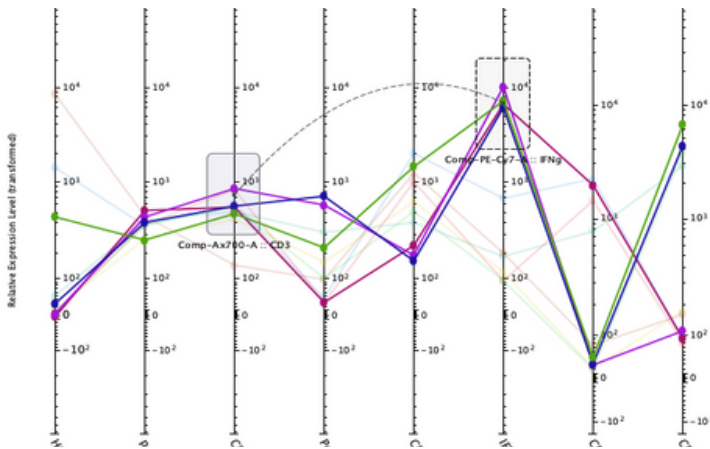


Figure 1A. In this line trace plot image, CD3+CD8+ T cells are selected using three gates placed on lineage markers within the line trace plot window.

- Visualize populations on a line trace plot; each cluster is a different color.
- Visualize cluster or non-cluster populations
- Populations are plotted in dimension-reduced space or conventional 2-D plots.
- Filter populations of interest with interactive Boolean gates



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

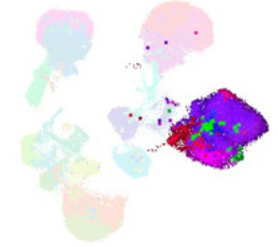


Figure 1C. After gating, the selected clusters are highlighted on a 2-D plot (UMAP here) in full color, while unselected clusters are toned down.

## Determine trends with heat maps

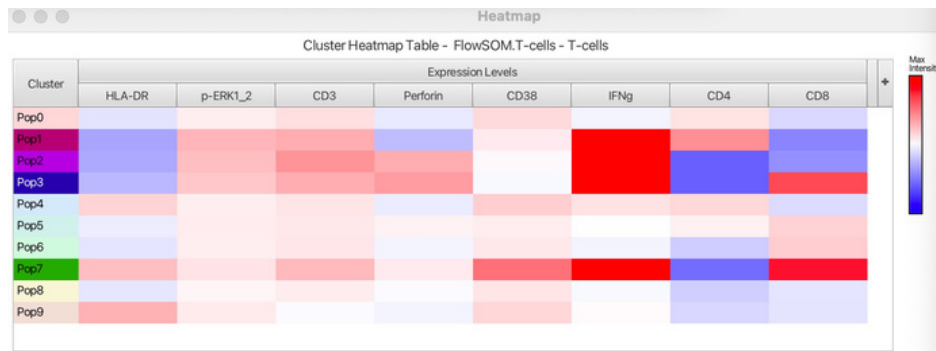


Figure 2. Heatmap of clustering results, synchronized to all other displays. The large heatmap windows and scroll bars enable visualization of large sets of clustering results.

- Include experimental variables in the heatmap table to identify how clusters vary in expression levels
- Re-order populations and parameters in the heatmap via drag and drop.
- In the heatmap view, population names are now colored using the same color used throughout the other views to identify each cluster.



## 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 heatmap 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.
- Merge clusters and add newly merged populations to the workspace as populations for further exploration.

### 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.

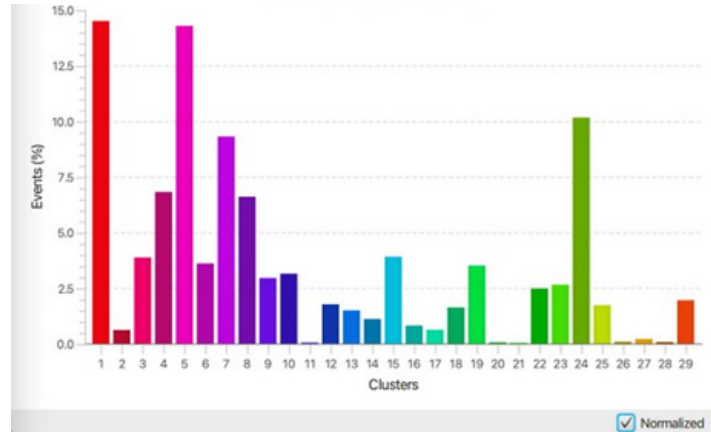


Figure 3. Clusters 11, 20, 21, 26, 27 and 28 make up less than 0.5% of the cells combined.

### 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.

### 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.

Get started with ClusterExplorer today!

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

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

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