

# HyperFinder

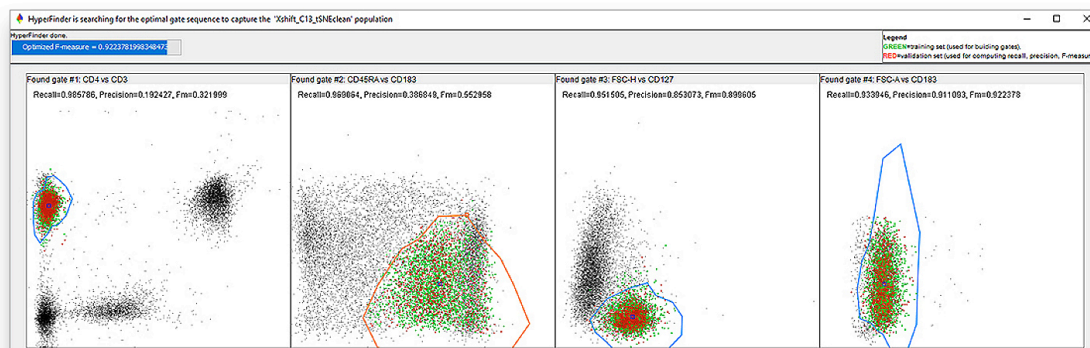
A workflow to sort high-dimensional populations with FlowJo™ Software and BD FACSDiva™ Software

You've found one or more interesting high-parameter populations by clustering, but now how do you isolate them for downstream functional studies? Computationally defined populations present a unique challenge because cell sorters require a 2-D gating hierarchy, but the right gating strategy is not always obvious.

## About HyperFinder

With HyperFinder, you will automatically find the optimal gating strategy to isolate your population of interest. Then, with the Export to BD FACSDiva functionality, this gating strategy can be used on your BD FACSAria™ or BD FACSsymphony™ S6 Cell Sorter.

HyperFinder is an intuitive and easy-to-use novel algorithm for gating sequence prediction for any population of interest. HyperFinder is easy-to-use as a FlowJo™ Software plugin with a simple user interface that does not require any programming knowledge. It can easily be downloaded from [flowjo.com](http://flowjo.com) and added to your FlowJo™ Software functionalities.



HyperFinder returns a gating strategy for the targeted population. The training set is in green (used for building gates) and the validation set is in red (used for computing recall and precision, the F-measure)

## Why use HyperFinder for computational population discovery analysis?

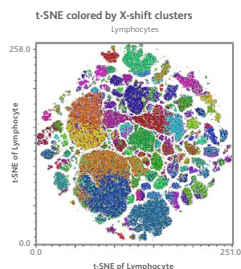
The HyperFinder workflow bridges the gap from multidimensional analysis to sorted samples. It enables sorting cells based on three use cases:

- Clustered, or otherwise computationally defined populations
- Populations whose gating hierarchy is too complex
- Cells where some markers are not suitable for sorting

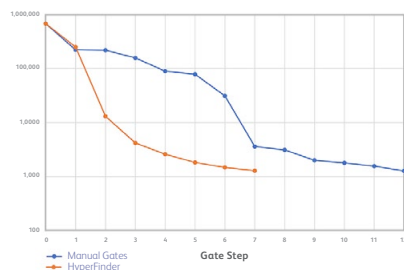


# HyperFinder supports computational population discovery and sorting for multiomics analysis in just a few steps:

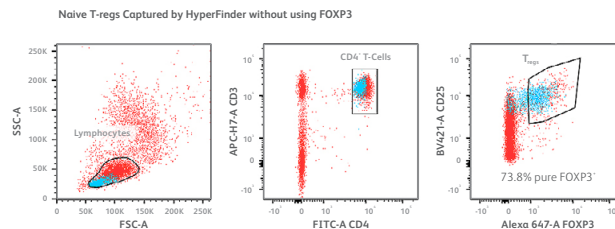
- Splits the data into training and validation sets
- Finds a set of gates that optimally capture a clustered population
- Creates a gating strategy that utilizes a specific subset of markers



Clustered populations captured by the HyperFinder algorithm



Comparing cells remaining after each gating step



Blue events are HyperFinder derived Tregs over-layed with manual gating (red)

## Key features

- Algorithmically creates a gating strategy for any population defined using a combination of clustering, gating and dimensionality reduction
- Shortens the gating strategy to a specified number of gates by removing redundant gates
- Optimizes gate boundaries globally (stochastically optimize boundaries)
- User-friendly UI
- Integrates with the sorting workflow and BD FACSDiva™ Software
- An easy next step after using other FlowJo™ Software plugins, like dimensionality reduction tools such as X-shift, Phenograph, FlowSOM, visualization tools such as tSNE, UMAP or Tri-Map or other tools like Cluster

## The result

Utilizing the HyperFinder workflow will allow you to continue your experiment by isolating the populations you care about for your downstream assays. Enabling these experiments can help you move your discovery forward as you learn about the functional or genomic aspects of your cells of interest.

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