

# “How To PaCMAP”

## Introduction

The PaCMAP algorithm has been developed and implemented as a Python package by Yingfan Wang, Haiyang Huang, Cynthia Rudin, out of Duke University, and Yaron Shaposhink out of University of Rochester (1).

PaCMAP (Pairwise Controlled Manifold Approximation) is a dimensionality reduction method that can be used for visualizing your high dimensional data in fewer dimensions. The advantage of PaCMAP over other dimensionality reduction algorithms, is that it is capable of more robustly maintaining both global and local structures between populations within a data matrix. Earlier dimensionality reduction algorithms focus on local structure or global structure, but not both.

PaCMAP has three main stages, it first emphasizes global structure, then gradually eases its global structure optimization and starts optimization of the local structure. In the final stage, it is just refining the local structure. PaCMAP optimizes the low dimensional space using three kinds of points: neighbor pairs, mid-near pair, and further pairs. This method uses the mid-near pairs to first capture global structure and then refine the local structure.

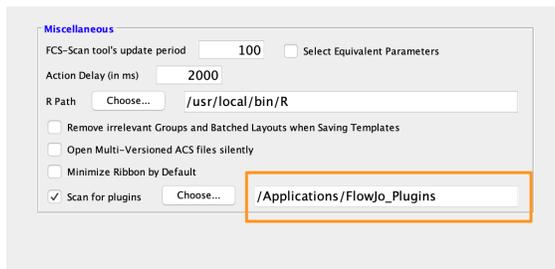
This implementation of the plugin will initialize the calculation with PCA for further speed improvements.

## Usage

As a Python based plugin, the “PaCMAP.jar” file is all you need to allow the plugin to run automatically without the need to install external dependencies on Windows 10 and modern Mac OS’.

To run the plugin:

1. Place the “PaCMAP.jar” file into your plugins folder.
2. Point FlowJo or SeqGeq to your plugins folder (also in the Diagnostics preferences):



3. Restart FlowJo or SeqGeq.
4. Within the workspace samples area, select the population of interest (for embedding).
5. Within the Workspace tab of the workspace, select the Plugins option, and choose “PaCMAP”:

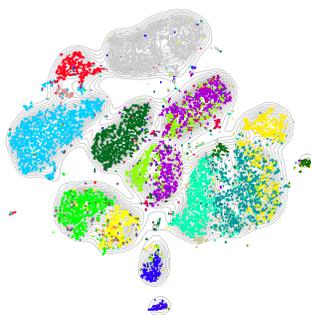
- This will launch a plugin dialog, all Comp- prefixed parameters will be selected initially, and default settings applied. Choose any subset of parameters that you want to be considered for dimensionality reduction and adjust settings as desired.



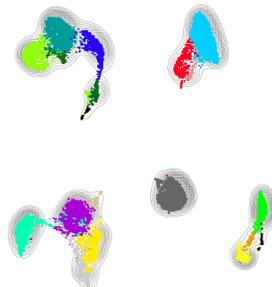
**Notes**

- \* **Parameters:** All Comp- prefixed parameters will be selected initially. Choose any subset of parameters that you want to be considered for dimensionality reduction.
- \* **Nearest Neighbors:** The number of nearest neighbors according to the Euclidean distance. These points will be strongly attracted to one another.
- \* **Mid-Near Ratio:** The number of mid-near pairs to compute. These points will be weakly attracted.
- \* **Further pairs (FP):** The number of non-neighbors to compute. These points will be repulsed.
- \* **Number of Components:** The number of dimensions to return.

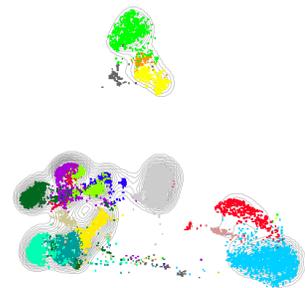
By running the tool, a new set of PaCMAP parameters should be generated as a CSV file within the plugin derivatives folder, and that information will be merged into the current workspace, automatically.



PCA Guided tSNE



PaCMAP\_1\_0Z9H



TriMap\_X\_B2IM

### Leave us your feedback

Please write to [flowjo@bd.com](mailto:flowjo@bd.com) with any questions!

### References

1. Yingfan Wang, Haiyang Huang, Cynthia Rudin, and Yaron Shaposhnik. “Understanding How Dimension Reduction Tools Work: An Empirical Approach to Deciphering t-SNE, UMAP, TriMap, and PaCMAP for Data Visualization” *Journal of Machine Learning Research*. 22(201):1-73, 2021. <http://jmlr.org/papers/v22/20-1061.html>