How-to-UMAP

Uniform Manifold Approximation and Projection (UMAP) is a machine learning algorithm used for dimensionality reduction to visualize high parameter datasets in a two dimensional space. (1)

The UMAP plugin will run with both FlowJo and SeqGeq bioinformatics data analysis platforms.

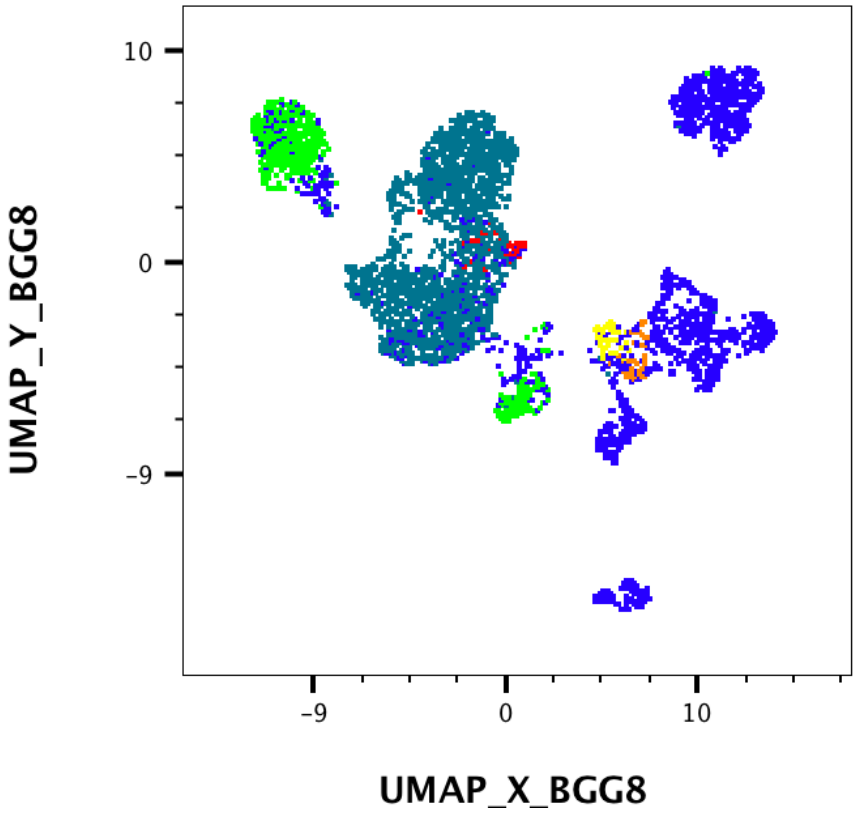
Note: The UMAP plugin for FlowJo requires some extra steps to instal on Windows, and requires a 64bit OS. This is due to complications in the Python dependencies which must be installed manually there. See the documentation associated with this plugin for detailed instructions on how to get Python installed on a Windows system for more details.

Install

Simply place the UMAP jar file into your SeqGeq plugins folder, point the Diagnostics section of SeqGeq's preferences to that folder, and restart SeqGeq to access the plugin.

Running

Select your population of interest, find the UMAP plugin from the Plugins section of the Workspace tab in SeqGeq's workspace, and select the parameters on which you'd like to run the algorithm. Once the calculation is completed, check the list of parameters within your population for "UMAP_X", and "UMAP_Y":



References:

1. McInnes, Healy,. UMAP: Uniform Manifold Approximation and Projection for Dimension Reduction. Feb, 2018. arXiv:1802.03426