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.

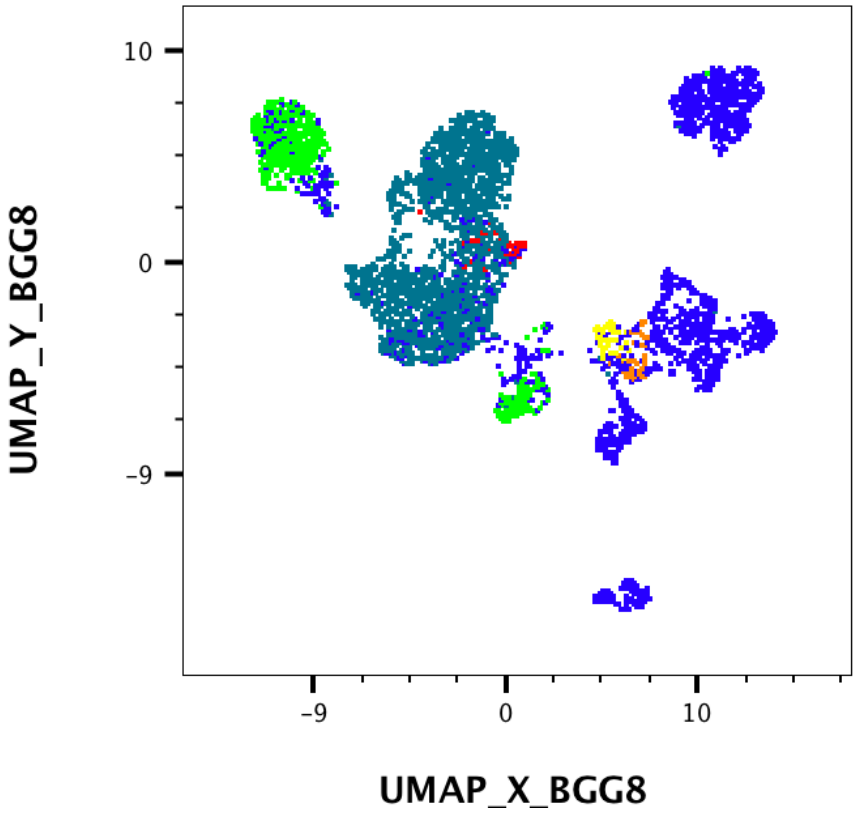
Note: The FlowJo, LLC UMAP plugin does not currently run on Windows - it is a Mac only plugin. This is due to unknown problems in the Python dependencies on Windows. Windows compatible version coming soon.

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