What is SeqGeq?

SeqGeq™ [seek-geek] v1.5+ is a desktop bioinformatics platform for the analysis of single cell RNA sequencing data. Import and analyze any gene expression data or list of genes and share your entire analysis with a single zip file (GeqZip analysis). Explore, visualize, and shape your next-gen sequencing data with interactive graphs that are designed to help you focus on the insights that matter most.

Getting Started

SeqGeq runs on a standard laptop or desktop computer, and is available for Mac OS and PC.

Download the current installer at:

flowjo.com/solutions/seqgeq/downloads

After you download and install the application, launch SeqGeq. Sign in with the FlowJo Portal sign-in dialog so you can analyze your data anywhere. To create a free account, click **Create a FlowJo Portal Account**. You can also create a FlowJo Portal account at cloud.flowjo.com. You then use your FlowJo Portal ID to sign in to SeqGeq.

If you don't have an active SeqGeq license, click **Free Trial** to activate a free trial license from your FlowJo Portal account.

Adding Data

Gene expression data in almost any format can be added using the **Add Samples** button in the Navigate toolbar, or by dragging files into the SeqGeq workspace. We've included some demo datasets in the Data folder automatically included in of your install of SeqGeq.

To add data from your BaseSpace account, click the **Add from BaseSpace** button to launch the import window connected directly to BaseSpace.
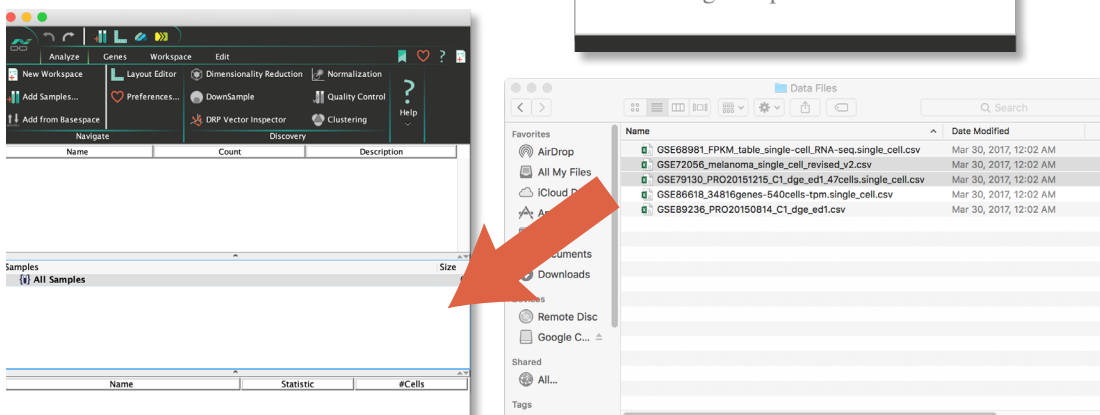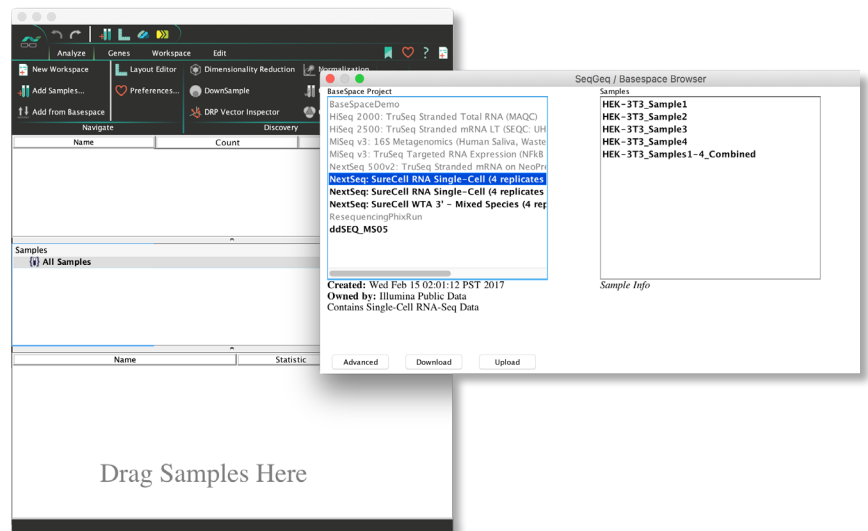
Dimensionality Reduction

To calculate PCA, LDA, or tSNE, click **Dimensionality Reduction** in the Discovery Band, select the genes and samples to be included, and click **Run**. Upon completion, results will be automatically displayed in a graph window.
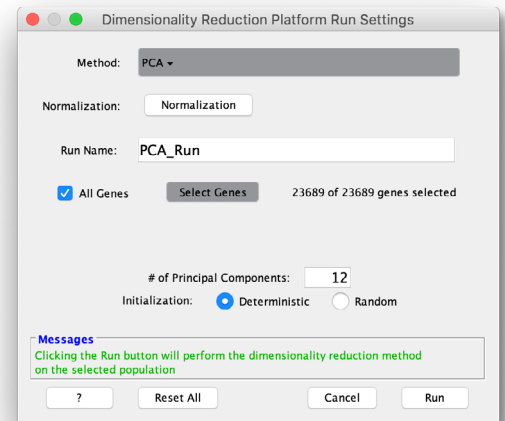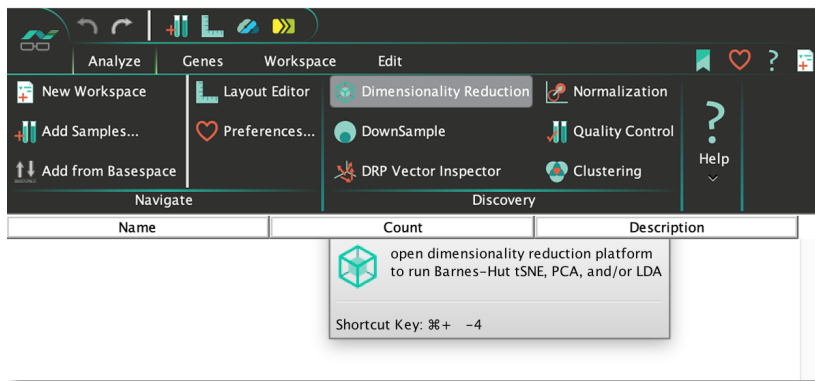

The Graph Window: Cell view and selecting populations

The **Graph Window** can be used to display any parameters in your dataset, such as genes, tSNE axes, or principal components. A variety of displays are available under options, and 3rd parameters can be mapped over the display with the color axis.


To select sub-populations of cells, use the gating tools at the top of the window. This adds the selected populations as groups under the active sample in the workspace.
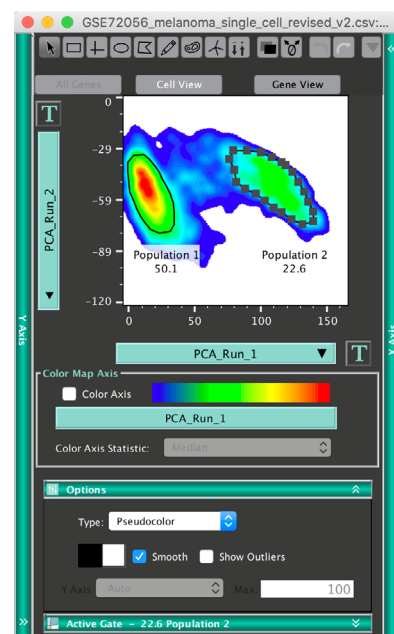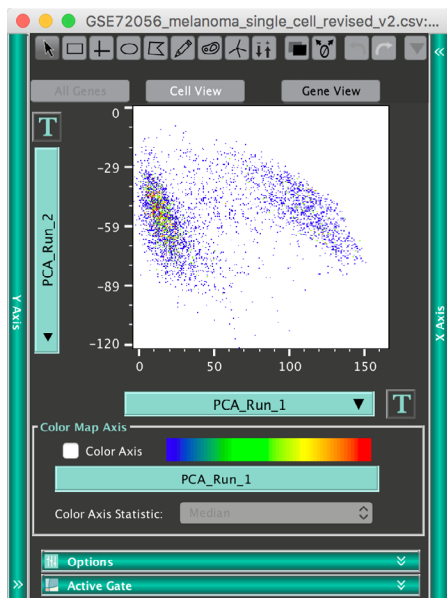
# The Graph Window: Gene view and differential expression

By default, the Graph Window shows **Cell View**, where each point represents a single cell in your sample, and these cells are plotted based on the parameters selected. Changing the mode to **Gene View** plots each gene as a point, and the relative expression of that gene in the two populations selected determines its position on the graph.

Selecting genes using the gating tools in Gene View adds an analytic gene set to the gene sets pane of the workspace. To perform differential expression analysis from a Gene View plot, calculate corrected p-Value and Fold-Change statistics in a volcano plot.
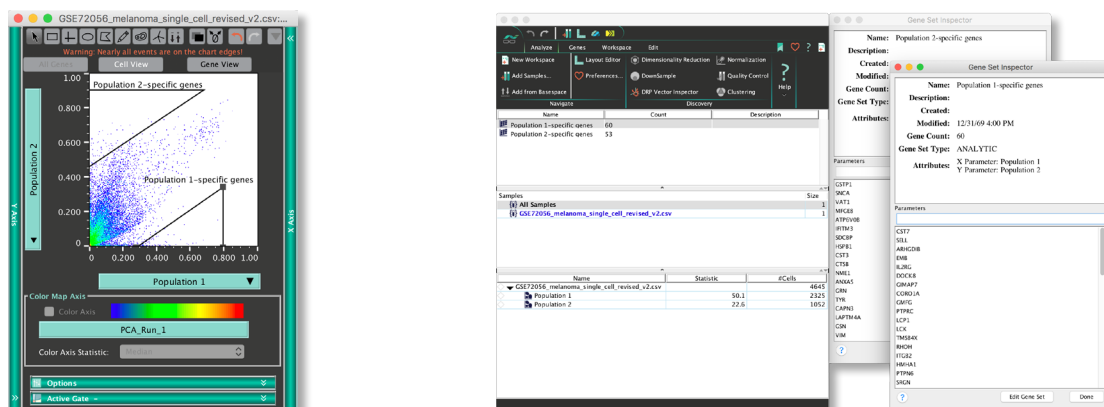

Visualizing Gene Sets and Importing Pathways

In addition to analytic gene sets, which are generated from your data, static gene sets can be generated and organized or imported as .csv files via the Genes tab of the Workspace. Gene sets can reflect diverse biological pathways or processes, and can be visualized, for example using dimensionality reduction.
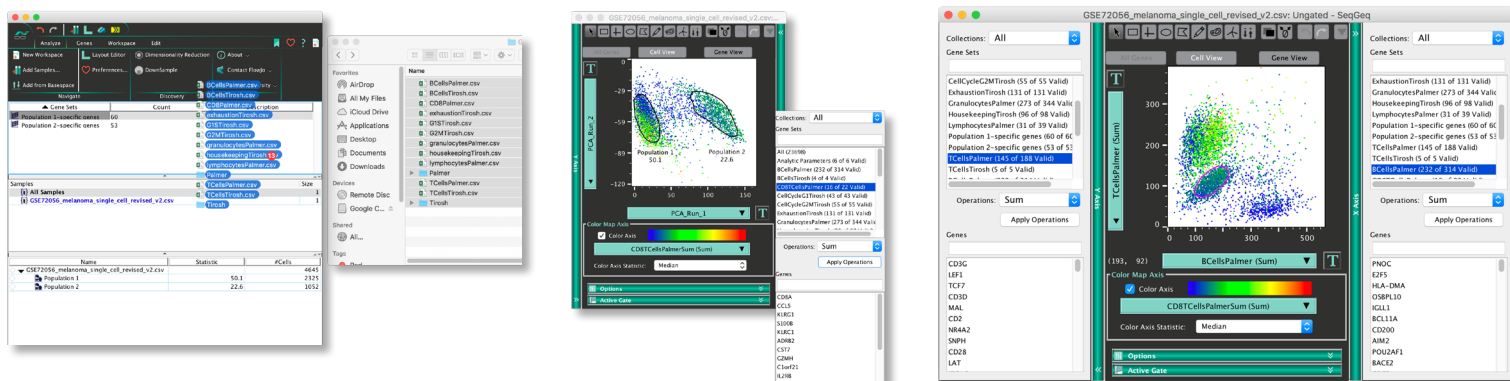
Creating Layouts

The **Layout Editor** allows you to generate publication-ready graphics and figures. To add figures, drag samples from the workspace into the editor. Figures update in real time when they are updated in the workspace. Batch reports allow you to repeat an analysis for many samples at once. These reports are fully customizable, allowing you to rearrange and annotate figures and even to import your own graphics.
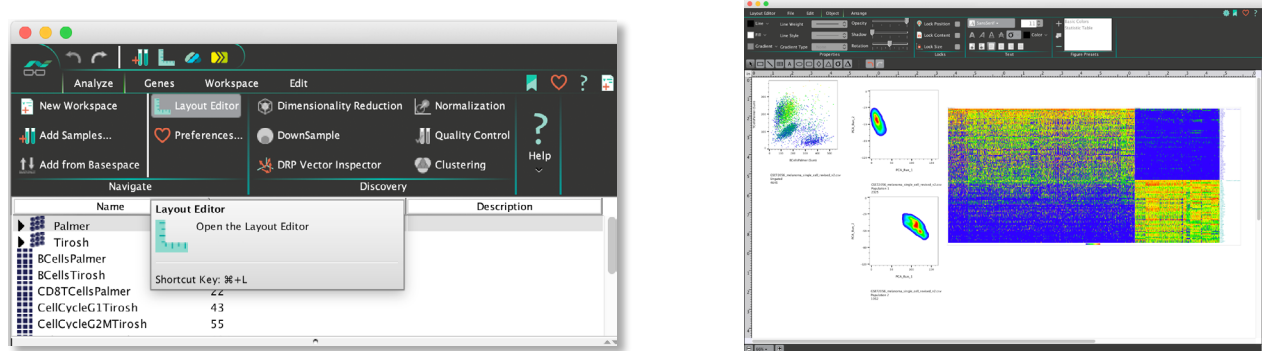
SEQGEQ

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The customer support team can be reached between 7:30 am and 4:00 pm PST*
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