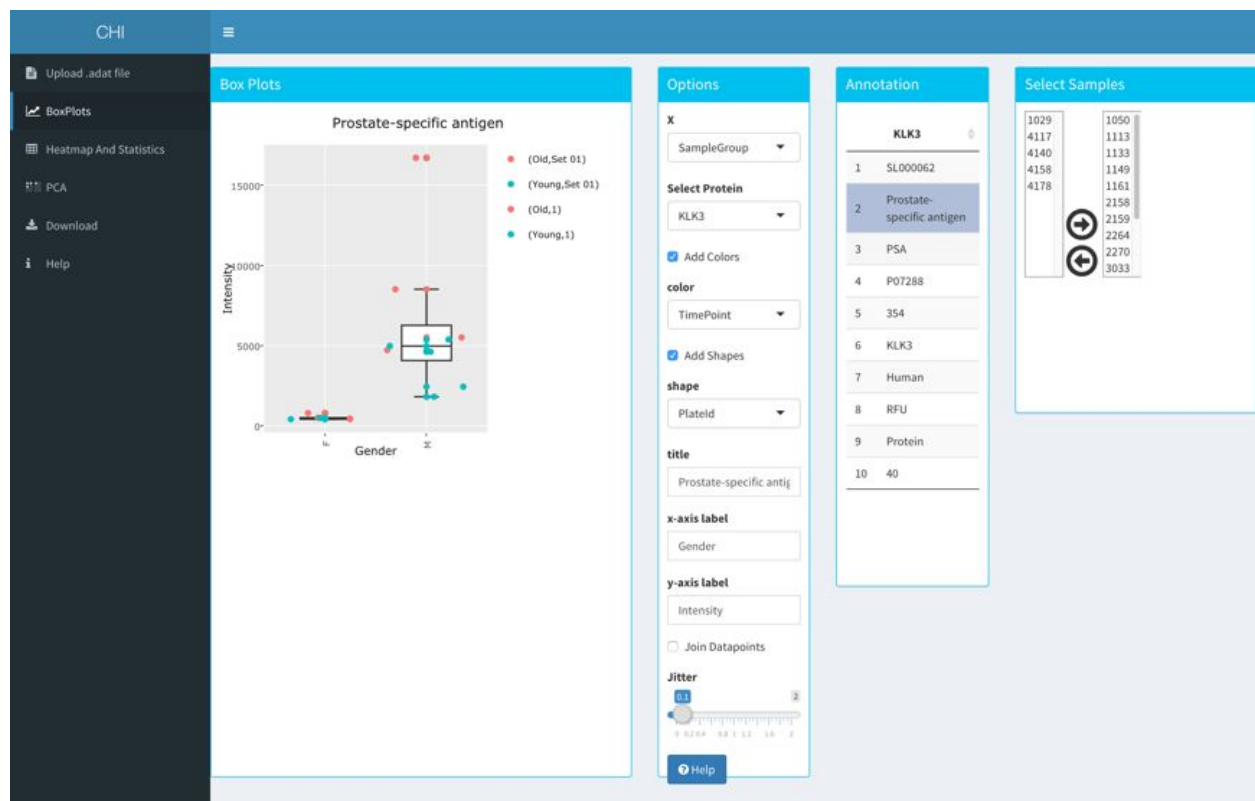


How to generate Box Plots

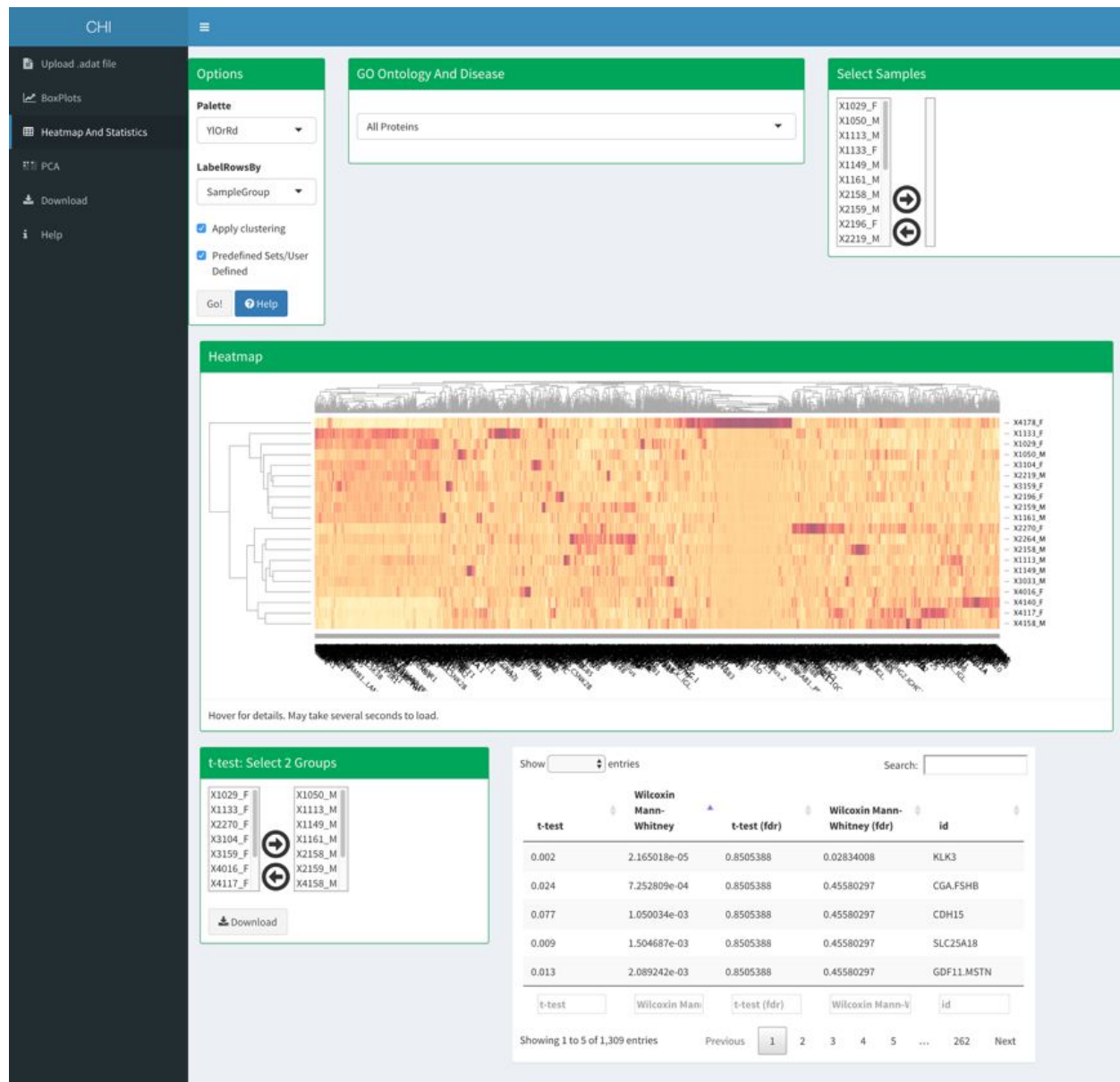


The “BoxPlots” tab page contains four boxes in a row-based layout. The first box going from left to right) labeled “Box Plots” allows the user to display interactive plots for selected protein as shown on above.

1. Click on the “BoxPlots” tab page
2. Select different variables to be plotted on X (categories) eg: SampleGroup
3. Select different proteins to be plotted on Y Axis eg: KLK3
4. Shapes and colors can be added to the plots to represent samples by clicking on the check boxes.
5. To add a main title or axis labels to the plot, enter text in the corresponding text box.
6. The “Annotation” displays a table that contains proteins annotation from the ADAT file such as: Somald, TargetFullName, Target, UniProt, EntrezGeneID, EntrezGeneSymbol, Organism, Units, Type and Dilution.
7. “Select Samples” allows filtering of individual samples by using a dueling select box: once activated, samples in the left box will be immediately removed from the plot.

8. Plots can be downloaded by clicking on the top left hand side of the interactive box plot.

How to generate Heat Maps



The 'Heatmap And Statistics' tab shows five boxes appears: “Options”, “GO Ontology And Disease” or “Select Proteins”, “Select Samples”, “Heatmap” and “t-test: Select 2 Groups”.

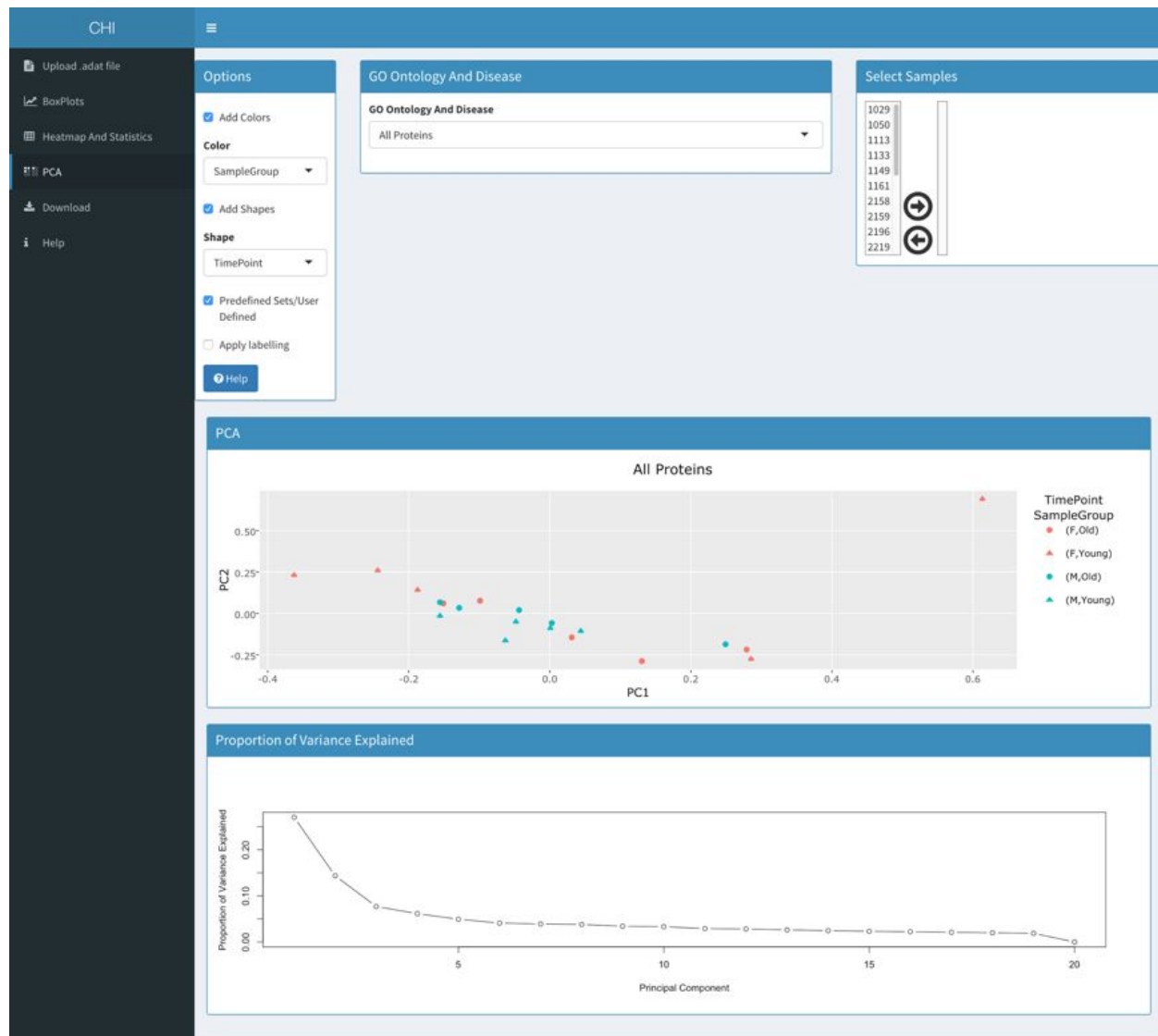
1. Click on the “Heatmap And Statistics” tab page
2. Select protein sets based on GO process or Disease ID or generate a user defined set or show all proteins available.
3. The box entitled “Options” allows you to modify various options for the heatmap plot. Drop down boxes are available to change the heatmap color gradients and labels while check boxes allow the user to toggle whether to cluster or not the heatmap’s rows and columns.
4. Clicking on the “Go” button generates a new heatmap plot.
5. The third box labeled “Select Samples” allows you to filter samples.
6. The interactive heatmap allows you to get the row/column/value under the mouse cursor and zoom in by dragging a rectangle over the heatmap.

Currently, the heatmap plot has to be downloaded manually by using your favorite webpage screenshot.

How to run t-test and Mann-Whitney Statistics

1. The fifth box labelled “t-test: Select 2 Groups” allows the user to select two groups of samples and will automatically execute a t-test and Mann Whitney test comparing these groups. The output of raw and FDR corrected p-values is displayed as an interactive data table that can be searched, filtered, and sorted as required.
2. To run an analysis in the heatmap panel for a subset of the available samples, you need to first filter for your samples of interest on the top right, and then on the bottom left in the t-test panel split them into the two groups of 3.

How to generate PCA plots



The “PCA” tab allows users to run Principal Component Analysis which has become a standard procedure for looking at population substructure to identify co-founders such as batch effects, and to identify relatedness in cohorts between observations.

1. Click on the “PCA” tab page
2. Select protein sets based on GO process or Disease ID or generate a user defined set or show all proteins available.
3. The box entitled “Options” allows you to modify various options for the PCA plot.

Check boxes are available to change the sample color and sample shapes and add sample labels.

4. The third box labeled "Select Samples" allows you to filter samples.