

Introduction

ProHits-viz is a suite of web tools designed principally to aid visualizing protein-protein interaction data although it can be used for any data set composed of conditions and readouts. The goal of this project is to make datasets of any size accesible through interactive visualization and a variety of analysis and display options.

The navigation menu at left can be used to find the help you need. If you have a question not covered by this guide, feel free to contact us at contact@prohits-viz.org (<mailto:contact@prohits-viz.org?Subject=ProHits-viz%20help>)

File format

ProHits-viz requires tabular input files in either tab-delimited or csv format. At a minimum, the file must contain four columns specifying the bait/condition, prey/readout, abundance measure (spectral count, intensity, etc) and a confidence metric (e.g. FDR). Explicity support is provided for files output from SAINT and CRAPome/Reprint. If you are the maintainer of another tool and would like us to support your ouput, please let us know. Datasets from unsupported tools can still be used provided they meet the tabular format criteria mentioned above, however, you will have to specifiy the columns to use as they cannot be automatically recognized.

Sample files

For detailed information on tools that generate compatible input for ProHits-viz, see the references and links below:

Publications

- [SAINT](http://www.ncbi.nlm.nih.gov/pubmed/21131968)
- [SAINTexpress](http://www.ncbi.nlm.nih.gov/pubmed/24513533)
- [SAINT-MS1](http://www.ncbi.nlm.nih.gov/pubmed/22352807)
- [ProHits](http://www.ncbi.nlm.nih.gov/pubmed/20944583)
- [ProHits Protocol](http://www.ncbi.nlm.nih.gov/pubmed/22948730)
- [ProHits 4.0](http://www.ncbi.nlm.nih.gov/pubmed/27132685)
- [CRAPome](http://www.ncbi.nlm.nih.gov/pubmed/23921808)

Sites

- [SAINT](http://saint-apms.sourceforge.net/Main.html)
- [ProHits](http://prohitsms.com)
- [CRAPome](http://www.crapome.org)
- [GalaxyP](https://usegalaxy.org/)

Tools

Dotplot

After the data has been processed, the user will be prompted to download a dotplot-results.zip file that contains the results in three subfolders. By default the unzipped parent folder will be named "results" but this name can be modified as desired. The subfolders are:

1. **SVGs:** This folder contains the dot plot and heat map images, as well as a legend. The output bait vs bait and prey vs prey images are the clustered distance matrices visualized as heat maps. In contrast to similar images generated by our correlation tool, baits (or preys) in these images have not been subjected to correlation analysis prior to clustering. Instead, the metric used is the distance metric calculated from the clustering option specified above. These files can be opened and edited in Adobe Illustrator or a similar program.
2. **PDFs:** This contains the same images as in the SVG folder but in PDF format.
3. **InteractiveFiles:** Contains plain text files formatted for our interactive viewer found at ProHits-viz that allows navigation and analysis of images. These files should be loaded directly into that tool without modification. Their extension is "-interactive.txt".
4. **CytoscapeFiles:** This folder contains plain text files for importing to Cytoscape. The file "bait-prey-cytoscape.txt" contains only bait-prey pairs that have passed the primary filter, with the abundance equal to its post-transformation value (after control subtraction, normalization, etc.). This allows users to import only desired bait-prey pairs into Cytoscape with an abundance value suitable for edge-weighting that has been processed according to the user's need. Two additional files are also present in this folder that contain all bait-bait and prey-prey pairs from the distance matrices with an additional column containing the distance metric itself that can be used for filtering which pairs will be displayed in Cytoscape. These files are generated so that users can view bait-bait and prey-prey information in a network format as an alternative the heat map format we provide here.
5. **OtherFiles:** This folder contains bait-bait and prey-prey dendrograms and will contain additional files generated by the nested clustering option, if selected. Finally, the "results" folder will also contain a log file that contains information on the input parameters that were selected for the user's future reference (e.g. to assist with writing the Methods section for a manuscript).