

CABIN 2.1 Release Notes

Features

- R-squared/correlation values in the Scatter Plot Matrix Viewer
- Create sub-network from all or selected points in the Weighted-Combined Evidence Viewer, Matrix/Table Viewer, and Network Viewer
- Option to assign an edge attribute as the edge identifier when importing networks individually
- Delete all imported networks in CABIN
- Find/search functionality extended to allow finding multiple proteins (comma separated)

Changes

- Ability to choose default weight and missing value when importing all networks
- Preferences menu added
- Users must accept the Sample Data Release Policy before loading sample data into CABIN
- Users have the option to choose networks when loading sample data or importing all networks from Cytoscape
- CABIN is cleared when it is closed

Bug Fixes

- “Ignore” missing values (---) preserved when saving interactions to file
- When changing the missing value to “Ignore”, values are now correctly updated in the Matrix/Table viewer
- All CABIN related windows close when CABIN closes

CABIN 2.0 Release Notes

Features

- Filtering option in Scatter Plot Matrix Viewer
- Interaction selection in detailed scatter plots in Scatter Plot Matrix Viewer
- Right-click option to create a subnetwork from selected interactions in Weighted-Combined Evidence Viewer, Matrix/Table Viewer, and Cytoscape View
- Interaction dialog for user to enter/choose a numerical confidence value when string values are found for edge values in a network. Default values of 1.0, 0.75, 0.5, and 0.0 are provided.
- Weighted Combined column added in Matrix/Table Viewer
- “Select All” checkbox added in Scatter Plot Evidence-Network Selection panel

Changes

- Default missing value set to “Zero” (0).
- Default weight of an imported network set to 1.
- Count column for the total number of duplicates for each duplicate interaction in the duplicate interaction dialog when importing networks

- Progress bar offers more user feedback on progress of importing networks
- Progress bar added for updating and deleting networks
- CABIN layout changed to show all views
- Matrix/Table Viewer panning disabled

Bug Fixes

- Update the total number of interactions in the status bar when a network is deleted
- Rollback to previous set of networks when a network fails to import

CABIN 1.0 Release Notes

Changes

- Check for duplicate interactions and prompt for selecting the value to keep while importing a network
- Regular expression based Search/Find tool to search for a protein of interest with Help on constructing regular expressions
- Information about number of selected, filtered and total interactions imported within CABIN
- Clicking on Scatter plot opens in bigger window with legend of color coding of points based on density

Bug Fixes

- When importing networks with string or empty "Interaction Type" in the SIF file, default value of 1.0 is assigned

CABIN BETA Release Notes

Multiple Coordinated Views

- Scatter Plot Matrix View - matrix of scatter plots of chosen evidence-networks
 - Color gradient used to indicate density of points
- Weighted Combined Evidence View - scatter plot of the interactions with confidences based on the weighted sum of all its evidences
- Matrix View –heat map representation of the data values for all the evidence sources in a tabular format with an overview panel
 - Sortable – ascending or descending
 - Continuous and discontinuous selection of rows using the SHIFT and CTRL keys
 - Filter option
- Cytoscape View – shows the selected evidence-network in a node-edge format
 - Spring embedded layout

Saving interactions to a file

Right-click options to save all interactions or selected interactions to a file the Weighted Combined Evidence View, Matrix View, and Cytoscape View

Filtering

- Filter interactions in an evidence-network according to their confidence values
- Specify the relation between each filter – AND or OR
- Show formulated filter query
- Limited to one filter for each evidence-network

Importing Networks

- Import all Cytoscape networks into CABIN
- Import Cytoscape networks individually into CABIN
- Load sample networks

Delete Networks

Find Interactions

- Search for one protein involved in the interaction
- Search for both proteins involved in the interaction
- Interactions matching the search are highlighted in all views

***Get Evidence from Prolinks**

- Retrieve data from the Prolinks database and automatically create networks in Cytoscape for each evidence type selected

Help / User Guide

** Only available in the PNNL internal version*