

Supporting information

A network module for the Perseus software for computational proteomics facilitates proteome interaction graph analysis

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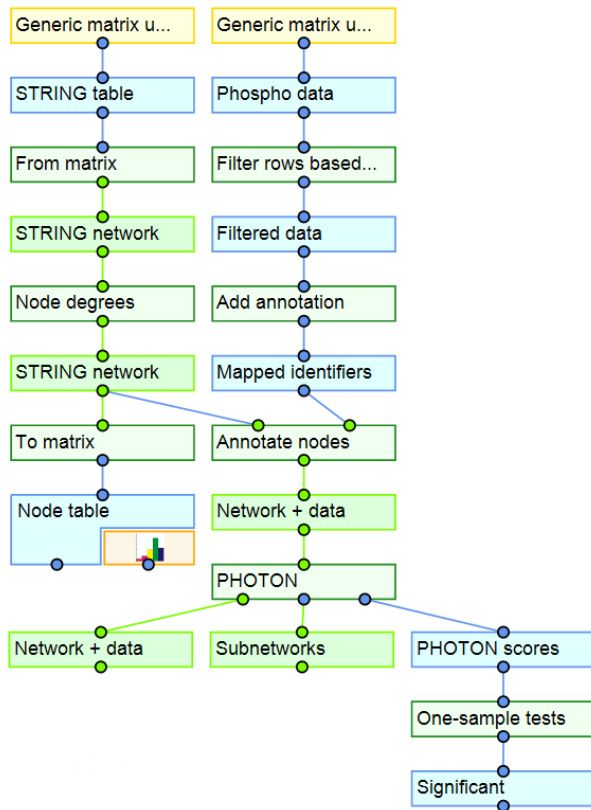


Figure S1. Graphical workflow combining matrix and network activities. Matrix (blue) and network collection (bright green) data types are analyzed side-by-side. Different activities (light green) analyze, process, and transform a number of both matrix, and network collection data.

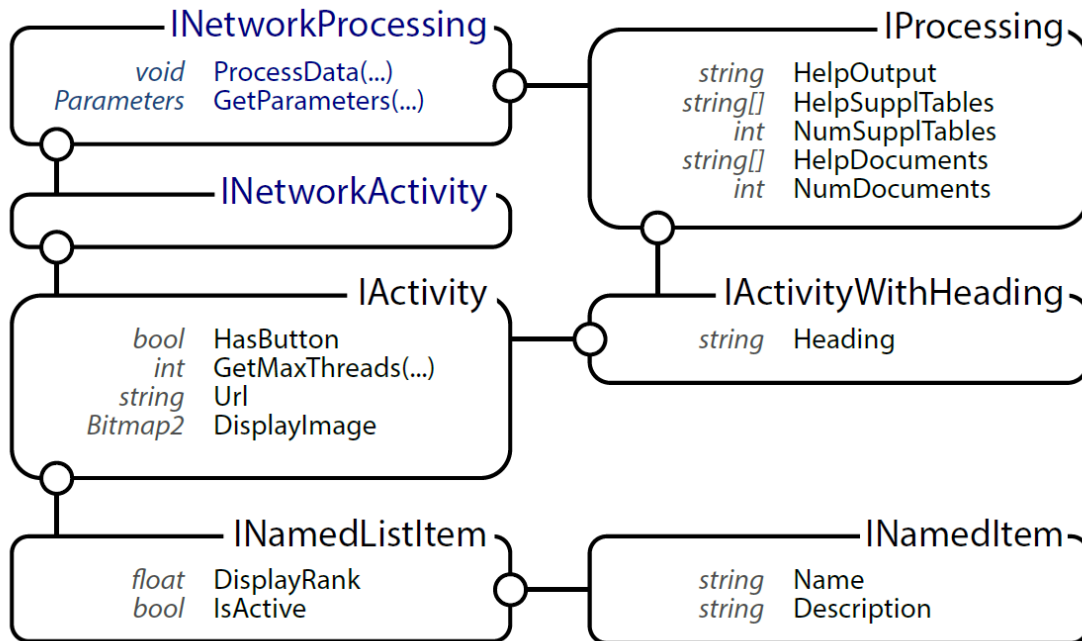


Figure S2. Organization of the new Perseus plugin API for networks. The network API is implemented in a number of C# interfaces. Network specific interfaces (blue) extend more generic interfaces (black) which underlie all plugins in Perseus. Additional interfaces, including e.g. `INetworkFromMatrix` and `INetworkExport`, are organized similarly. The the Perseus plugin API can be inspected by reading the source code and developers can directly consume the .DLL for plugin development.

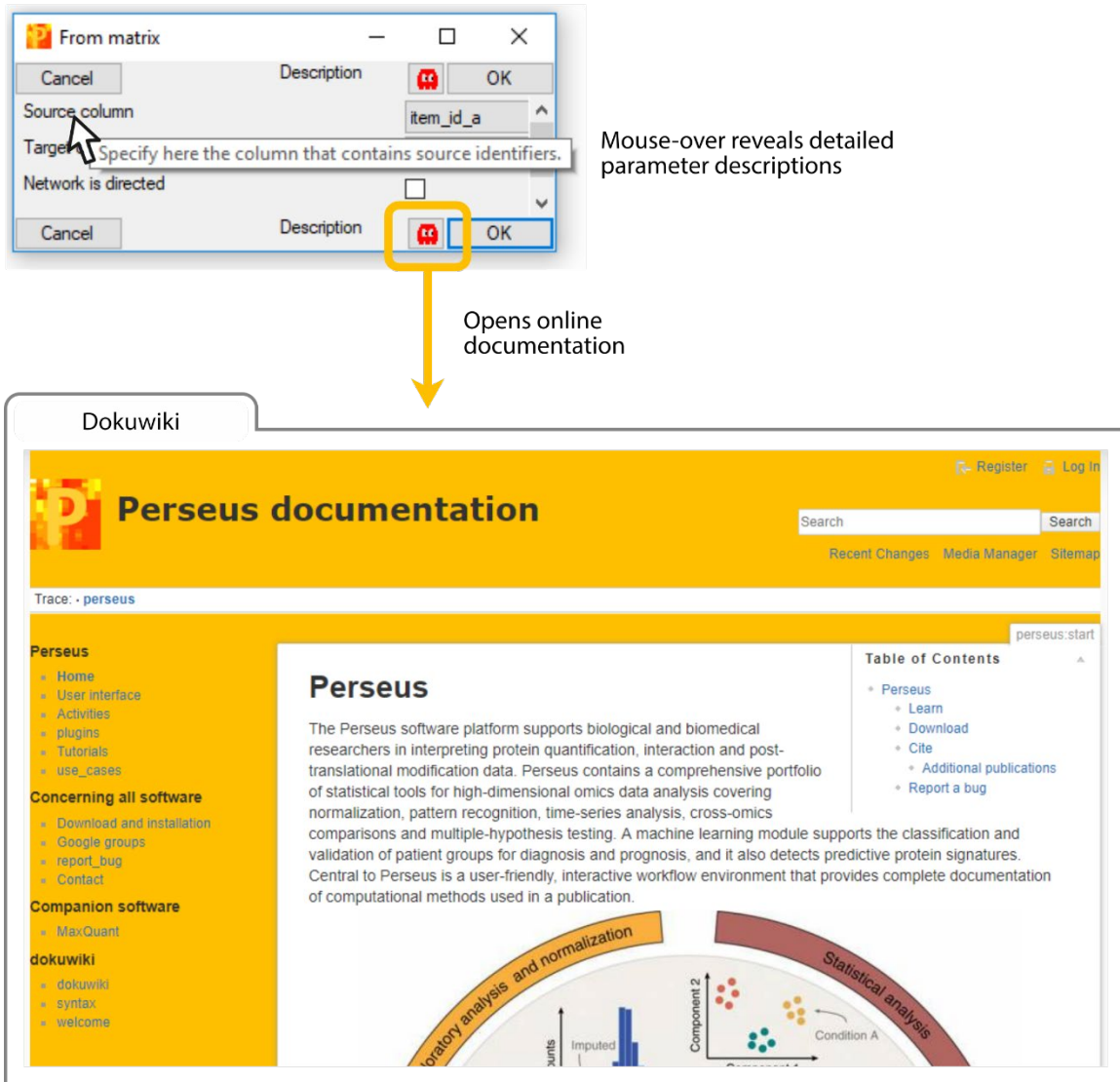


Figure S3. Context-specific documentation. Performing most analyses requires the selection of adequate parameters using the graphical user interface. Mouse-overs reveal additional details for each parameter. Clicking the red ghost icon opens the online documentation of Perseus which contains a more detailed description of the selected activity as well as general information and help.

Table S1. AP-MS pull-down screen.

Large scale interaction dataset with label-free quantification¹. The data set was reduced to the baits Eed, Ring1b, and Bap1. Pull-downs were measured in two cell lines ESC and NPC. Data was pre-processed according to Experimental Section.

Table S2. Phosphoproteomics of EGF stimulation.

Phosphoproteomic SLIAC dataset of MCF7 cells after EGF stimulation². Data was pre-processed according to Experimental Section.

Table S3. Clinical proteomics dataset.

Breast cancer proteomics dataset with label-free quantification and clinical annotations³. Data was pre-processed according to Experimental Section.

1. Kloet, S. L. *et al.* The dynamic interactome and genomic targets of Polycomb complexes during stem-cell differentiation. *Nat. Struct. Mol. Biol.* **23**, 682–690 (2016).
2. Jan Daniel Rudolph, Marjo de Graauw, Bob van de Water, Tamar Geiger & Roded Sharan. Elucidation of Signaling Pathways from Large-Scale Phosphoproteomic Data Using Protein Interaction Networks. *Cell Syst.* **3**, 585–593 (2016).
3. Yanovich, G. *et al.* Clinical Proteomics of Breast Cancer Reveals a Novel Layer of Breast Cancer Classification. *Cancer Res.* (2018).