

# **Quantitative Phosphoproteomics-based molecular network description for high-resolution kinase-substrate interactome analysis**

## **Supplemental information**

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## **1. Overview**

Post translational modification (PTM)-dependent cellular signaling is known to play a diverse role in regulating multiple cellular processes such as proliferation, differentiation and apoptosis. PTM mapper (PTMapper) is a Cytoscape plugin for PTM-dependent protein interaction network analysis. Users can add the information on PTM sites and their upstream regulators to protein-protein interaction (PPI) networks using PTMapper. This document shows how to use PTMapper for construction of the phosphorylation site-oriented networks in Cytoscape based on quantitative phosphoproteome data. Furthermore, it introduces extraction of significantly regulated sub-networks from PTMapper-based high-resolution PPI networks using jActiveModules.

PTMapper is available in Cytoscape version 3.0 and later.

## **2. Example data**

As the example data to construct phosphorylation site-oriented networks, we provided

the following four files generated from our previous phosphoproteome data (Kozuka-Hata *et al.*, 2012).

Download these files from <https://www.github.com/y-narushima/PTMapper>.

1. The file named “ppi\_network\_SIF.txt” contains the information on the proteins (Uniprot ID) and their interactions regarding the phosphoproteome data based on the PPI public database, Pathway Commons (Cerami *et al.*, 2011). This file is used to construct PPI networks.

2. The file named “phosphosite\_kinase\_data.txt” contains the information on the substrates (Uniprot ID), phosphorylation sites and their upstream kinases (Uniprot ID) regarding the phosphoproteome data, which is used to create PTM site-oriented networks via PTMapper. The detailed information on kinase-phosphorylation site relationships is based on the integrated dataset generated from four public phosphorylation site-related databases; PhosphoSitePlus (Hornbeck *et al.*, 2012), Phospho.ELM (Dinkel *et al.*, 2011), PhosphoNetworks (Hu *et al.*, 2014) and UniprotKB (Magrane *et al.*, 2011).

3. The file named “all\_phosphosite\_data.txt” contains the information on the phosphorylated proteins (Uniprot ID) and their PTM sites regarding the phosphoproteome data, which is used to add the nodes for all quantified phosphorylation sites via PTMapper.

4. The file named “quantification\_data.txt” contains the information on the phosphorylated proteins and their PTM sites (Uniprot ID, description) along with quantification data (log2[ratio], significance A) based on the phosphoproteome data, which is used to extract significantly regulated sub-networks.

### 3. Usage

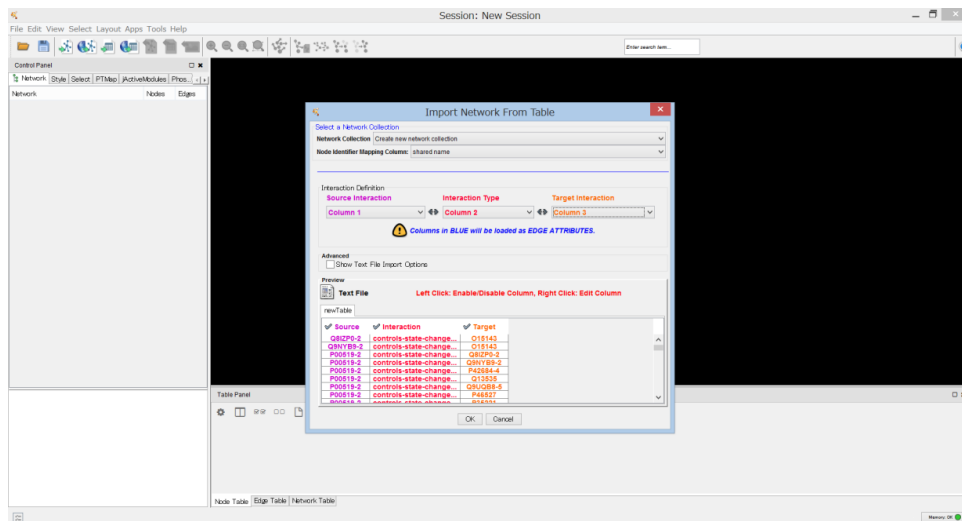
#### 3.1 Installation of PTMapper

1. Download the PTMapper Jar file from Github (<https://www.github.com/y-narushima/PTMapper/>).

2. Start Cytoscape and install the PTMapper via “Apps” -> “App Manager”. Select “Install from File” and browse for the jar file.

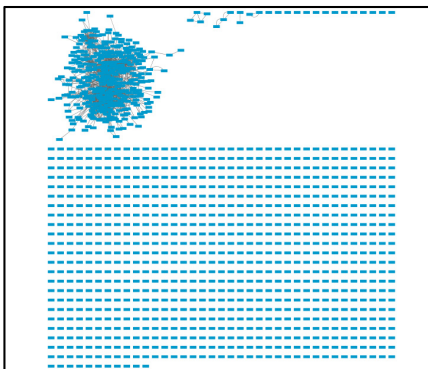
### 3.2 Import protein-protein interaction network

1. Import interaction data file via “File” -> “Import” -> “Network” -> “File...”. Choose “ppi\_network\_SIF.txt”.
2. Choose “Column 1” (Source), “Column 2” (Interaction) and “Column 3” (Target) for “Source Interaction”, “Interaction Type” and “Target Interaction”, respectively.
3. Click “OK”.




4. Click “Apply Preferred Layout”  to visualize the entire PPI networks.

Using the example data, the PPI network consisted of 1,276 nodes will be shown.



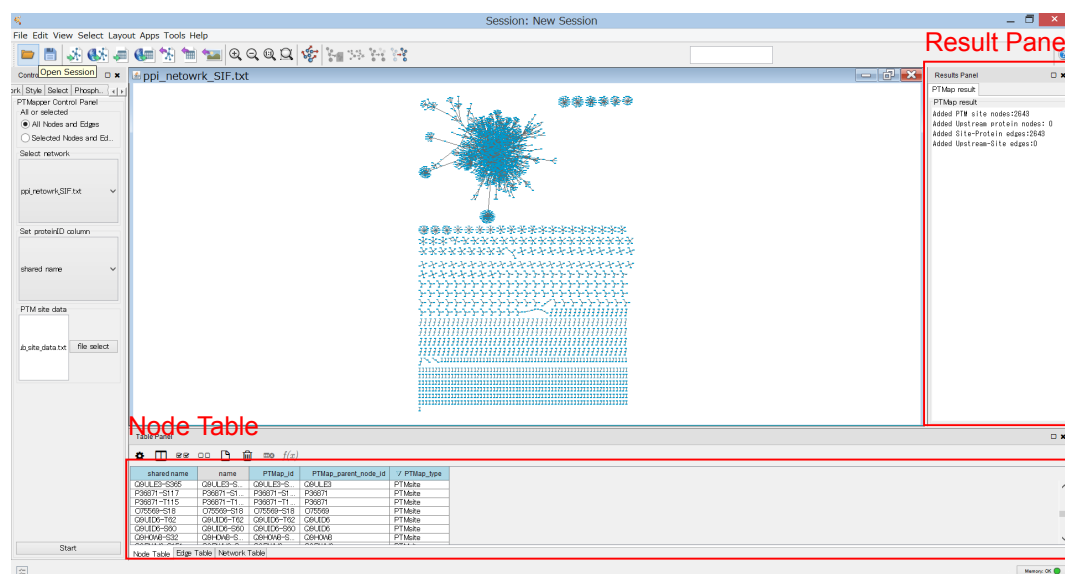
### 3.3 Import kinase-specific phosphorylation site information via PTMapper

1. Select the “PTMapper” tab in the Control Panel.
  2. Select “All nodes and edges” in the “Select or Not” section.
  3. Select “ppi\_network\_SIF.txt” in the “Select network” section.
  4. Select “shared name” in the “Set proteinID column” section.
  5. Click “file select” in the “PTM site data” section and choose data file containing kinase-specific phosphorylation information (“phosphosite\_kinase\_data.txt”).
  6. Click “Start” at the bottom in the “PTMapper” panel.
- \* Repeat the above steps (\*) using the phosphorylation site data (“all\_phosphosite\_data.txt”). PTMapper enables us to add the nodes for phosphorylation sites to the target networks, optionally.

8. Click “Apply preferred layout”  to visualize the entire PTM site-oriented networks.

PTM site nodes, PTM regulator nodes and their relationships will be added to the network. In the “Node Table”, “PTMap\_id”, “PTMap\_parent\_node\_id” and “PTMap\_type” (PTMsite, UpstRegulator and default) will be added. The number of nodes and edges added through PTMapper will be shown in the Result Panel.

Using the example data, the phosphorylation site-oriented network consisted of 4,171 nodes will be shown.



The screenshot displays the PTMapper software interface. The Control Panel on the left shows settings for PTMapper, including selecting all nodes and edges, using the ppi\_network\_SIF.txt network, and setting the proteinID column to shared name. The PTM site data section shows a file select button. The Network View in the center displays a complex network graph. The Node Table at the bottom shows a list of nodes and their relationships. The Result Panel on the right shows the PTMap result, including the number of added PTM site nodes (2543) and edges (1348).

shared name	name	PTMap_id	PTMap_parent_node_id	PTMap_type
OSULES-5365	OSULES-5	OSULES-5	OSULES-5	PTMsite
P9871-5117	P9871-51	P9871-51	P9871-51	PTMsite
P9871-1115	P9871-11	P9871-11	P9871-11	PTMsite
OR959-518	OR959-518	OR959-518	OR959-518	PTMsite
OSULES-702	OSULES-702	OSULES-702	OSULES-702	PTMsite
OSULES-590	OSULES-590	OSULES-590	OSULES-590	PTMsite
OSULES-590	OSULES-590	OSULES-590	OSULES-590	PTMsite
OSULES-590	OSULES-590	OSULES-590	OSULES-590	PTMsite

### Added columns

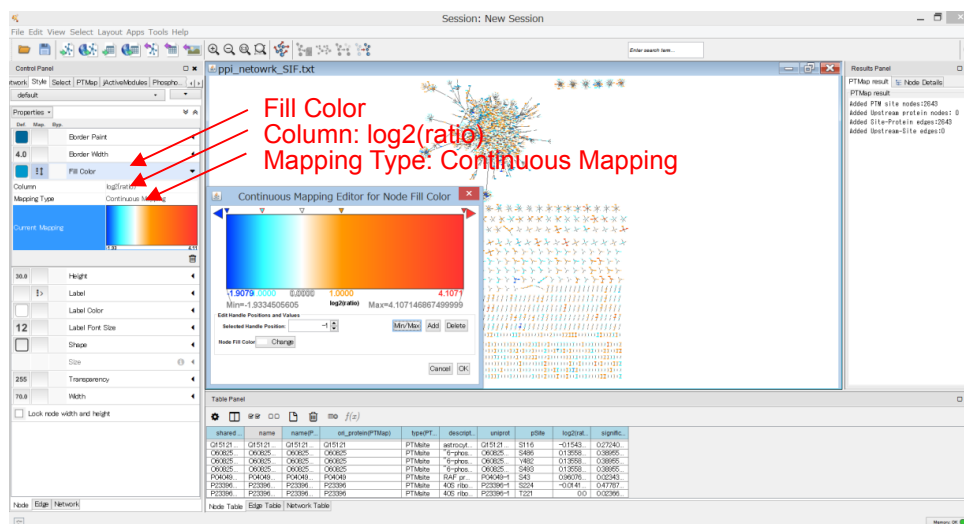
shared name	name	PTMMap_id	PTMMap_parent_node_id	PTMMap_type	description	uniprot_id	pSite	log2(ratio)	significance_A
Q14486-2-S117	Q14486-2-S117	Q14486-2-S117	Q14486-2	PTMSite	RNA-binding protein 39 isoform...	Q14486-2	S117	0.039196324	0.466510813
Q14486-2-Y95	Q14486-2-Y95	Q14486-2-Y95	Q14486-2	PTMSite	RNA-binding protein 39 isoform...	Q14486-2	Y95	-0.117237675	0.322777127
Q14486-2-S136	Q14486-2-S136	Q14486-2-S136	Q14486-2	PTMSite	RNA-binding protein 39 isoform...	Q14486-2	S136	-0.06983669	0.408637279
Q8NEV1-S648	Q8NEV1-S648	Q8NEV1-S648	Q8NEV1	PTMSite	neuron navigator 1 isoform 1 [...]	Q8NEV1-1	S648	0.149608344	0.378477297
Q8NEV1-S377	Q8NEV1-S377	Q8NEV1-S377	Q8NEV1	PTMSite	neuron navigator 1 isoform 1 [...]	Q8NEV1-1	S377	0.19088462	0.34647044
Q8NEV1-S142	Q8NEV1-S142	Q8NEV1-S142	Q8NEV1	PTMSite	neuron navigator 1 isoform 1 [...]	Q8NEV1-1	S142	0.199490411	0.338624457
Q8NEV1-S90	Q8NEV1-S90	Q8NEV1-S90	Q8NEV1	PTMSite	neuron navigator 1 isoform 1 [...]	Q8NEV1-1	S90	-0.109562738	0.342262018

### 3.4 Annotation with the quantification data on proteins/PTM sites.

1. Import quantification data file via “File” -> “Import” -> “Table” -> “File...”.
2. Choose “quantification\_data.txt”.
3. In the “Import Columns From Table” window, keep default setting and click “OK”.

In the “Node Table”, “description”, “uniprot\_id”, “pSite”, “log2(ratio)” and “significance\_A” will be added.

4. Select the “Style” tab in the Control Panel.
5. Select “Fill Color” and then choose the column “log2(ratio)”.
6. Select “Continuous Mapping” as mapping type and set the node color as shown below.

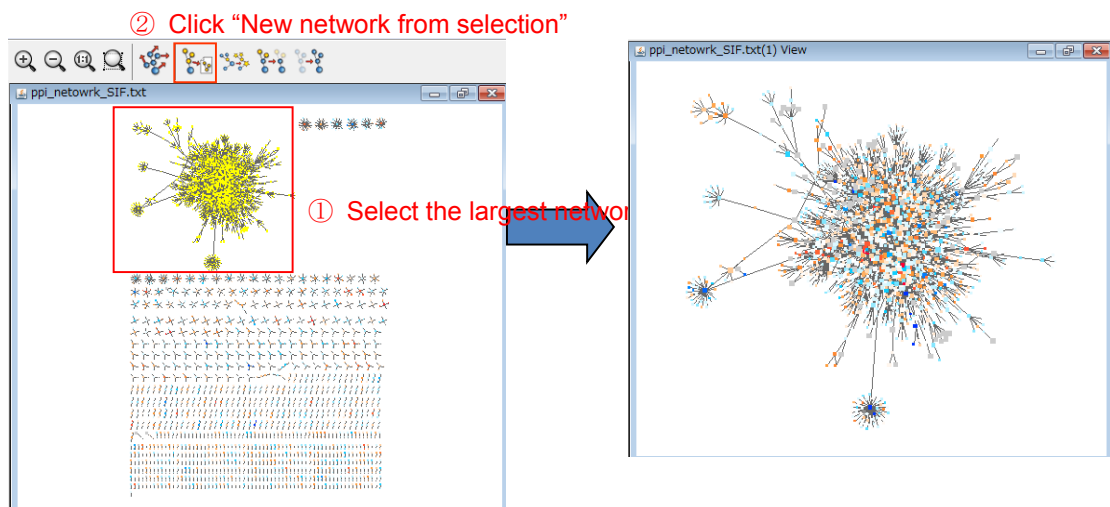
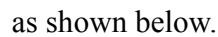


### 3.5 Extraction of sub-networks

After the annotation of the nodes with the significance values, you can extract regulated sub-networks using the other Cytoscape application “jActiveModules” (Ideker *et al.*,

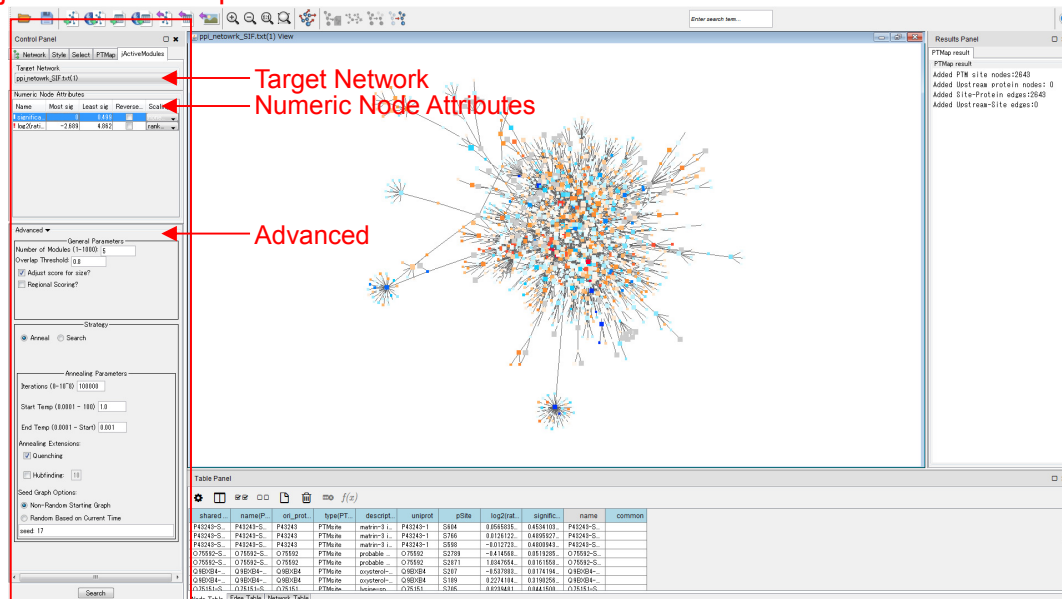
2002), which can identify the highest scoring sub-network by simulated annealing algorithm.

1. Select the largest network (1,581 nodes) and click “New Network From Selection”



2. Select the “jActiveModules” tab in Control Panel.

## jActiveModules panel



3. Set the below parameters in the “jActiveModules” panel.

Target Network: ppi\_network\_SIF.txt(1)

Numeric Node Attributes: significance\_A

Advanced:

Number of Modules: 5

Overlap Threshold: 0.8

Adjust score for size?: on

Regional Scoring: off

Strategy: Anneal

Iterations: 100000

Start Temp: 1.0

End Temp: 0.001

Annealing Extensions: Quenching

Seed Graph Options: Non-random Starting Graph (seed: 17)

4. Click the “Search” button.

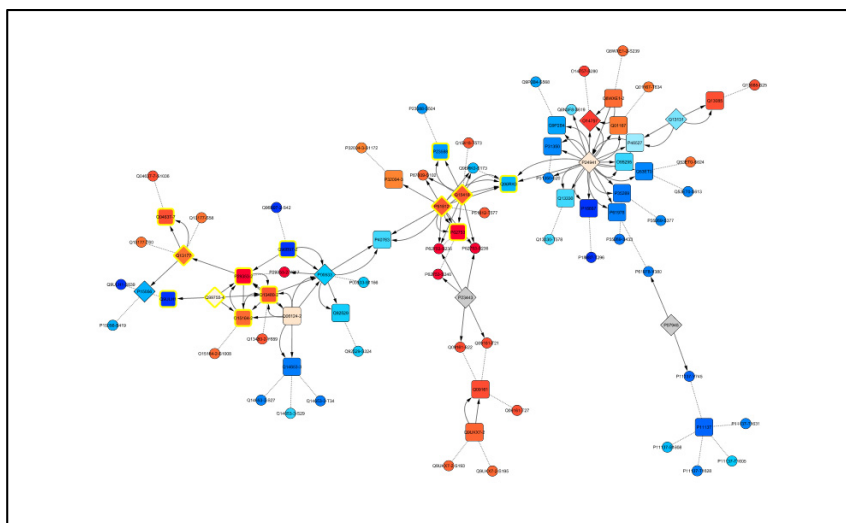
5. Select the “Network” tab in the Control panel

6. Select “Module\_0\_1” in the “Network” panel.

7. Select the “Style” tab in the Control panel.

8. Change the style from “jActiveModules Module Style” to “default” at the top of the Style panel.

The significantly regulated sub-networks will be visualized as indicated below.



## 4. References

- Cerami,E.G. *et al.* (2011) Pathway Commons, a web resource for biological pathway data. *Nucleic Acids Res.*, **39**, D685–D690.
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