From SNPs to pathways: Integration of functional effect of sequence variations on models of cell signalling pathways

Anna Bauer-Mehren, Laura I Furlong[§], Michael Rautschka, Ferran Sanz

Research Unit on Biomedical Informatics (GRIB), IMIM-Hospital del Mar, Universitat Pompeu Fabra. C/Dr. Aiguader, 88, 08003. Barcelona, Spain

[§]Corresponding author

Guide to map SNP data onto biological networks

A: Import networks	2
B: Import node attributes	<u>3</u>
<u>C: Import visual style</u>	4

A: Import networks

A.1: Import network from file

- 1. File->Import->Network (multiple file types)...
- 2. Select network file
 - a. EGFR_signaling.owl (BioPAX format)
 - b. ErbB_signaling.xml (SBML format)

[UniProt id attribute does not exist, for mapping SNP data onto this

pathway, please import first the UniProt_mapping_ErbB_signaling.attr as

described in **B**]

- c. any other pathway
- 3. Import
- 4. Optional: Change network layout

A.2: Import network from webservice

Please check:

http://www.cytoscape.org/cgi-bin/moin.cgi/Cytoscape_User_Manual/ImportingNetworksFromWebServices

B: Import node attributes

1. Make sure that there exists a node attribute containing the UniProt identifier

[if you have imported ErbB_signaling.xml, you need to import

UniProt_mapping_ErbB_signaling.attr first]

- 2. File->Import->Attribute from Table (Text/MS Excel)...
- 3. Select attribute file (see supplementary material)
 - a. Mutagenesis data only (mutagenesis.attr)
 - b. Polymorphism data only (polymorphism.attr)
 - c. Combination of both (mutPoly.attr)
- 4. Enable options
 - a. In the "Advanced" section: Show Mapping Options
 - b. In the "Advanced" section: Show Text File Import Options
 - c. In the "Text File Import Options" section: Transfer first line as attribute names
- In the "Advanced" section: Select Key Column in Annotation File: Select as Primary Key "uniProtId"
- 6. Select as Key Attribute for Network the attribute that contains the UniProt id
- 7. Import
- 8. Enable the attributes of interest (for detailed description see Table 2) in the node attribute browser in the data panel

C: Import visual style

- 1. Make sure one of the attribute files is imported
- 2. File->Import->Vizmap Property File...
- 3. Select visual style of interest (see supplementary material)
 - a. mutPoly_BioPAX.props for pathways in BioPAX format
 - b. mutPoly_SBML.props for pathways in SBML format
- 4. Select the appropriate visual style in the VizMapper