

KEGG pathway support in Cytoscape and data mapping by custom graphics

KGMLReader project web site: <http://code.google.com/p/kgmlreader>

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Abstract

KEGG is the most comprehensive pathway database and these maps are used extensively in life science research. In this poster, new features have been incorporated. However, in Cytoscape, we supported KEGG pathway (Figure1). So we supported KGML (eXtensible Markup Language) import plugin name "KGML Reader". This plugin automatically supports to read all metabolic logic. In this poster we introduce the new features and the future plan of this plugin.



Figure1: network using old KEGG importer



Figure2: network using KGML

Features

KEGG pathway import using KGML

KGML reader supports all metabolic pathways (Figure2) which include KEGG new pathway called global metabolism map. This global map is useful to compare the entire metabolism in different organism (Figure3-5) or conditions such as dynamic changes of gene expression in a time-series microarray experiment (Figure6).

Custom pathway search user interface

Manual change of KEGG pathway is troublesome. So we will add a KEGG

specimen search and selection tool here.

Filtering items

• KEGG category

• KEGG module

• KEGG pathway

• KEGG reaction

• KEGG metabolite

• KEGG enzyme

• KEGG protein

• KEGG nucleic acid

• KEGG compound

• KEGG location

• KEGG disease

• KEGG pathway

• KEGG reaction

• KEGG metabolite

• KEGG enzyme

• KEGG protein

• KEGG nucleic acid

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