

Working with substrate information in **opm**

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Abstract

here some abstrac-text. This is the tutorial of **opm** in the version of September 8, 2013.

Keywords: Bootstrap, Cell Lines, **grofit**, Growth Curves, **lattice**, Metadata, Microbiology, Respiration Kinetics, Splines, YAML, JSON, CSV.

1. Introduction

After comparative analyses of Phenotype Microarray data, users might be interested in mapping the data on pathway maps for biological interpretation of higher-level systemic functions. KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies. Pathway Mapping KEGG PATHWAY mapping is the process to map molecular datasets, especially large-scale datasets in genomics, transcriptomics, proteomics, and metabolomics, to the KEGG pathway maps for biological interpretation of higher-level systemic functions.

2. Acknowledgements

See the acknowledgements section in the main **opm** vignette.

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