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Efficient key pathway mining - Combining networks and OMICS data

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Abstract:

Systems biology has emerged over the last decade. Driven by the advances in sophisticated measurement technology the research community generated huge molecular biology data sets. This comprises rather static data on the interplay of biological entities, for instance protein-protein interaction network data, as well as quite dynamic data collected for studying the behavior of individual cells or tissues in accordance to changing environmental conditions, such as DNA microarrays, RNA sequencing or genome-wide methylation assays. Here we bring the two different data types together for unraveling the molecular basis of complex diseases, such as cancer.

Therefor, we developed KeyPathwayMiner. Given a biological network modeled as graph and a set of expression studies, KeyPathwayMiner efficiently finds and visualizes connected sub-networks where most components are expressed in most cases. It identifies all maximal connected sub-networks where all nodes but K exceptions are expressed in all experimental studies but at least L exceptions. I will briefly introduce a set of exact and heuristic algorithms that tackle this NP-hard combinatorial optimization problem.

I will demonstrate the power of KeyPathwayMiner by comparing it to similar approaches with gene expression data previously used to study Huntington's disease. In addition, we demonstrate its flexibility and applicability to non-array data by analyzing genome-scale DNA methylation profiles from colorectal tumor cancer patients. KeyPathwayMiner is available as Java library, as a Cytoscape plugin and online at http://keypathwayminer.mpi-inf.mpg.de

project web site: `http://keypathwayminer.mpi-inf.mpg.de`

[1] Alcaraz NM, Friedrich T, Koetzing T, Krohmer A, Mueller J, Pauling J, Baumbach J (2012) *Efficient key pathway mining - Combining networks and OMICS data*. Integr Biol. 2012 (in press). DOI: 10.1039/C2IB00133K.

[2] Alcaraz NM, Kucuk H, Weile J, Wipat A, Baumbach J (2011) *KeyPathwayMiner - Detecting case-specific biological pathways by using expression data*. Int Math. 2011, 7:4, 299-313.

[3] Baumbach J, Friedrich T, Koetzing T, Kromer A, Mueller J, Pauling J (2012) *Efficient algorithms for extracting biological key pathways with global constraints*. Proceedings of the Genetic and Evolutionary Computation Conference, GECCO 2012, accepted.