

Pathwave

About PathWave

PathWave enables the identification of disease specific regulation patterns by combining gene expression data and network topology. PathWave is preferable to classical enrichment tests as it offers a much higher sensitivity for detecting such functionally related regulation patterns. Additionally, it is more precise to a permutation based enrichment method (Schramm et al 2010).

CITING PATHWAVE: please cite Piro et al (2014) for PathWave version 2.1, Schramm et al (2010) for PathWave version 1.0, and both papers (Schramm et al 2010; Piro et al 2014) for PathWave in general.

Downloads

PathWave version 2.1 (Piro et al. 2014):

The R package does already include all necessary data for BiGG/Human recon 1 (H. sapiens) and KEGG (H. sapiens, M. musculus, D. melanogaster, C. elegans, D. rerio, E. coli)

- [R package PathWave v2.1.3 \(Linux\)](#)
- [R package PathWave v2.1.3 \(Windows\)](#)
- [PathWave v2.1 - User Manual](#)
- [PathWave v2.1 - Usage Example \(Quick Guide\)](#)

Additional software for PathWave version 2.1:

The following software is needed only to preprocess further pathway data sets from KEGG (KGML) or BiGG (SBML), not for applying PathWave to already available, preprocessed pathway data. Note: GridArranger is also included as external code in the PathWave 2.1 R package. We provide it here as an independent package because it may be useful for other purposes.

- [GridArranger v1.0](#) - used to arrange pathways into compact 2D lattice grids (see Schramm et al 2010; Oswald et al., 2012; Piro et al 2014).
- [GridArranger v1.0 README](#) - basic information on installation and usage.
- [ABACUS v2.4-alpha](#) - required by GridArranger; this package is provided with kind permission of the original authors at the University of Cologne, Germany, because newer versions of ABACUS (available at the [ABACUS webiste](#)) are not compatible with GridArranger.

PathWave version 1.0 (Schramm et al. 2010):

- [Short manual](#)
- [Executable R file usePathWave.R](#)
- [R package PathWave v1.0 \(Linux\)](#)
- [R package PathWave v1.0 \(Windows\)](#)
- [PathWaveFilesFeb04_2009 \(Linux\)](#)
- [PathWaveFilesFeb04_2009 \(Windows\)](#)
- [Optimized grids for human \(.RData file\)](#)

Publications

[Network topology-based detection of differential gene regulation and regulatory switches in cell metabolism and signaling](#)

BMC Systems Biology8:56, 2014.

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[PathWave: Discovering patterns of differentially regulated enzymes in metabolic pathways](#)

Bioinformatics26(9):1225-1231, 2010.

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[Exact solution of the 2-dimensional grid arrangement problem](#)

Discrete Optimization9:189-199, 2012.

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