

Pathview: an R/Bioconductor package for pathway-based data integration and visualization

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Project: <http://pathview.r-forge.r-project.org/>

BioC release (doc, code) <http://bioconductor.org/packages/release/bioc/html/pathview.html>

License: GPL (>=3.0)

Pathview is a novel tool set that maps, integrates and renders a large variety of biological data on pathways, and produces interpretable graphs with publication quality [1].

Pathview generates both native KEGG view and Graphviz view for pathways. KEGG view keeps all the pathway meta-data, including reaction and signaling contexts important for human reading and interpretation. Graphviz view provides better control of node and edge attributes, better view of pathway topology and analysis statistics.

Pathview provides strong support for data integration. It works with: 1) essentially all types of biological data mappable to pathways, 2) over 10 types of gene or protein IDs, and 20 types of compound or metabolite IDs, 3) pathways for over 2000 species as well as KEGG Orthology, 4) various data attributes and formats, i.e. continuous/discrete data, matrices/vectors, single/multiple samples or time-series etc.

Pathview is open source, fully automated and error-resistant. Although built as a stand-alone program, Pathview may seamlessly integrate with pathway and functional analysis tools for large-scale and fully automated analysis pipelines.

Pathview has been published with Bioinformatics [1], and ranked as a most-read among ALL Bioinformatics papers in 5 consecutive months (June-October, 2013). The software has been widely adopted by scientists worldwide and has downloaded over 6500 times within 12 months: <http://bioconductor.org/packages/stats/bioc/pathview.html>. In fact, it is a most used Bioconductor package released in 2013. Pathview has received hundreds of user inquiries or recommendations through emails, major mail-lists and bioinformatics forums, such as Bioconductor help list, seqanswers.com and biostars.org etc. All impact statistics available upon request.

1. Luo W, Brouwer C: **Pathview: an R/Bioconductor package for pathway-based data integration and visualization**. *Bioinformatics* 2013, **29**(14):1830-1831.