Overview of Pathview software package

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Pathview is a novel tool set we developed that maps, integrates and renders a large variety of biological data on molecular and genetic pathways, and produces interpretable graphs with publication quality [1] (Figure 1A). Pathview has 3 important features:

Dual output styles: KEGG view for easy interpretation and Graphviz view for better graphical control.
Strong data integration capacity. It works with: 1) all data mappable to pathways, 2) 30 of molecular ID types (genes/protein, compound/metabolite), 3) 3000 species, 4) various data attributes and formats.
Simple and powerful. Pathview is fully automated and error-resistant, seamlessly integrates with a wide range of pathway and gene set (enrichment) analysis tools.

Pathview has generated global impact within a short time. It was 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 used by scientists worldwide and ranks top 5% among all Bioconductor packages with over 1100 downloads each months (Figure 1B). It has been adopted by numerous courses in academia and products/services in industry. Hundreds of user inquiries or recommendations were made through emails and bioinformatics forums. For more information about Pathview and its impact please check the following links.

Software package: http://bioconductor.org/packages/release/bioc/html/Pathview.html
A short overview talk at ISMB 2014: http://www.youtube.com/watch?v=sne_Nb9au20
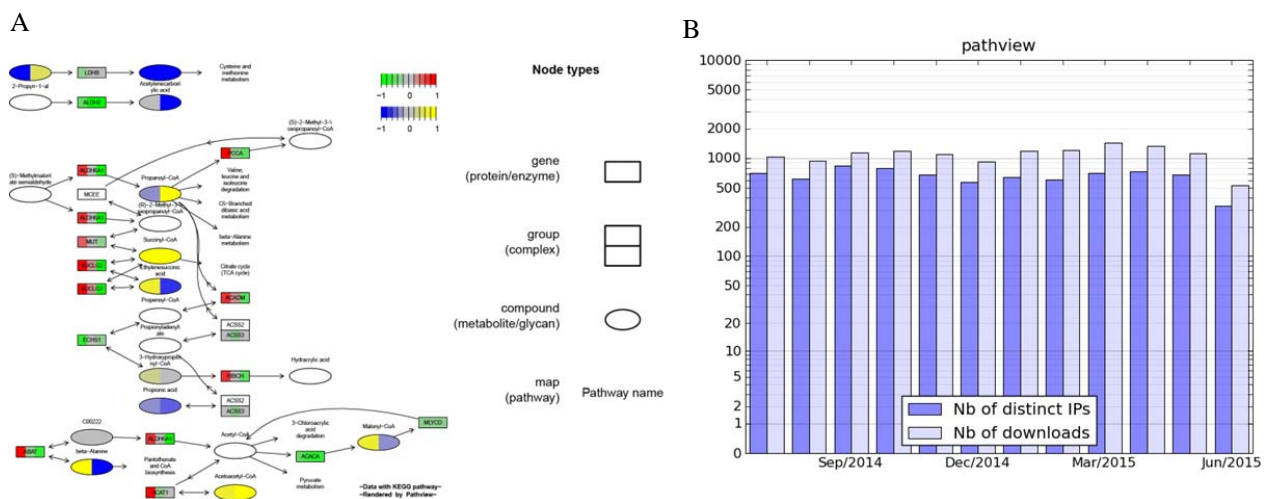

Figure 1. Overview of Pathview software package: A) A representative pathway graph with multiple samples and multiple types of data integrated. B) The official download statistics (06/15/2015) from Bioconductor project: http://bioconductor.org/packages/stats/bioc/pathview.html.

References

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