Pathway Projector: Web-Based Zoomable Pathway Browser Using KEGG Atlas and Google Maps API

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Biochemical pathways provide an essential context for understanding comprehensive experimental data and the systematic workings of a cell. Therefore, the availability of online pathway browsers will facilitate post-genomic research, just as genome browsers have contributed to genomics. Many pathway maps have been provided online as part of public pathway databases. Most of these maps, however, function as the gateway interface to a specific database, and the comprehensiveness of their represented entities, data mapping capabilities, and user interfaces are not always sufficient for generic usage. To this end, here we present a web-based pathway browser named Pathway Projector. Pathway Projector provides integrated pathway maps that are based upon the KEGG Atlas, with the addition of nodes for genes and enzymes, and is implemented as a scalable, zoomable map utilizing the Google Maps API. Users can search pathway-related data using keywords, molecular weights, nucleotide sequences, and amino acid sequences, or as possible routes between compounds. In addition, experimental data from transcriptomic, proteomic, and metabolomic analyses can be readily mapped.

Pathway Projector's pathway maps were based on the KEGG Atlas map, for the familiarity of its layout and for the availability of various analysis tools. However, because the KEGG Atlas only represents metabolite nodes, we added all gene and enzyme nodes semi-automatically on the reference pathway map. As a result, our pathway map contains 1572 metabolite nodes and 1813 enzyme nodes. In the organism specific pathway maps, the number of gene nodes are 1365 in *Escherichia coli*, and 2883 in human, for example. The software was implemented using AJAX (Asynchronous JavaScript + XML) programming paradigm and the main interface framework was built with Ext JS 2.0 library. For the representation of the global pathway map, we adopted zoomable user interface (ZUI) using Google Maps API through G-language Genome Analysis Environment. Detailed information of each node in pathway map is shown in an information window upon clicking. These windows include the common name, identifier, structural formula or chemical equation, and links to external databases. Organism specific pathway maps are currently available for 843 species.

Pathway Projector has four types of search functionalities, including those by keywords and identifiers, by molecular mass, by possible routes between two metabolites using PathComp, and by sequence similarity using BLAST. The results are listed in a search result panel and are also visually highlighted by red markers onto the respective components on the pathway map. The pathway mapping tool can change parameters for size, color, and labels of edges and nodes, and subsequently creates an overlay image. When values for time-series or multiple conditions are specified for nodes, graphs generated by the Google Chart API are displayed on the nodes. Quikmaps was utilized to implement manual annotation and editing capabilities.

The understanding of omics layers is important for systems biology, and biochemical pathways supply a necessity context for this purpose. Since pathways do not exist independently, but are rather interconnected *in vivo*, the observation of an integrated map is desirable, especially for the mapping of comprehensive experimental data. Pathway Projector has an intuitive interface by utilizing Google Maps and Ext JS and KEGG pathway maps. Moreover, capabilities of this software such as searching, editing, annotation, mapping and links to various databases, will be a useful gateway for pathway analysis.

Web server of Pathway Projector is freely available for academic users at http://www.g-language.org/PathwayProjector/.

Reference:

1. Kono N, Arakawa K, Ogawa R, Kido N, Oshita K, Ikegami K, Tamaki S, Tomita M, "Pathway Projector: Webbased Zoomable Pathway Browser using KEGG Atlas and Google Maps API", PLoS One, 2009, 4(11):e7710.

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