PATIKA*web*: A Web Service for Querying, Visualizing, and Analyzing a Graph Based Pathway Database

web.patika.org

C. Aksay, F. Arik, E. Ataer, A. Ayaz, O. Babur §, E. Belviranli, A. Cetintas, R. Colak, G. Cozen, E. Demir §, A. Dilek, U. Dogrusoz §, †, E. Z. Erson, E. Giral, E. Kaya, H. Kucuk, A. S. Tekin, H. Yildirim

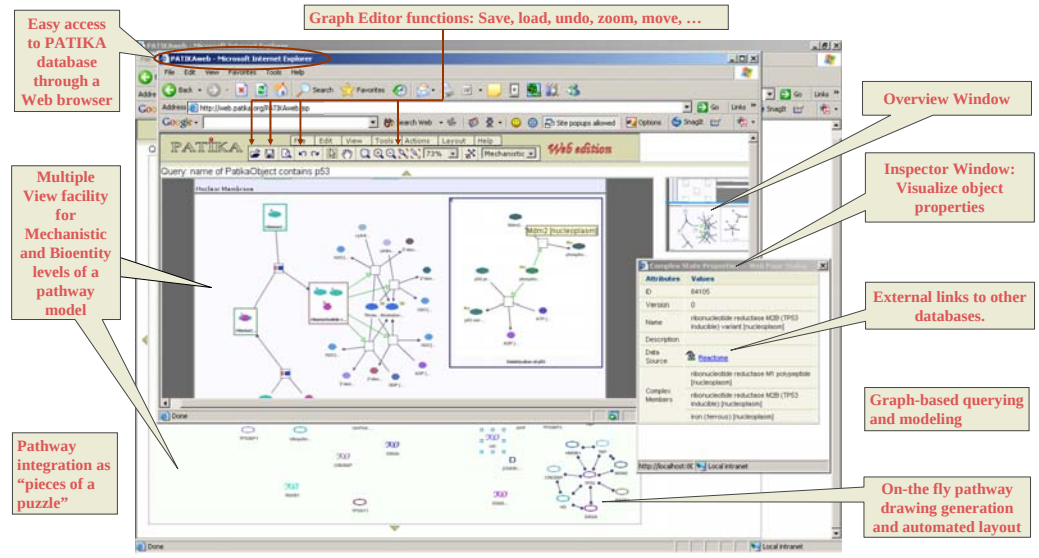
Center for Bioinformatics and Computer Engineering Department, Bilkent University, Ankara 06800, Turkey

§ Presenting authors † Corresponding author

The **PATIKA Project** aims to develop methods and software tools for effective analysis of complex biological data at a functional level. **PATIKA*pro*** (currently in development) and **PATIKA*web*** are tools that have been developed within this project.

PATIKA*web* is a Web service for retrieving and analyzing biological pathways in PATIKA database. The service provides user-friendly and easy access to:

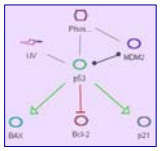
- dynamic pathway visualization,
- extensive querying interface providing advanced graph-theoretic queries,
- pathway data in PATIKA database, which currently contains data integrated from popular public pathway databases like Reactome, UniProt, and Entrez Gene,
- pathway data exporting facility to various standard exchange formats like BioPAX and SBML.



Ontology

We define an intuitive, comprehensive, uncomplicated representation of cellular networks.

Basics

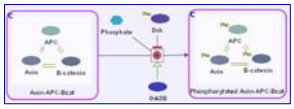


Bioentities: actors of the cellular events; genetic (e.g., DNAs, proteins), chemical (e.g., ions), or physical (e.g., heat).

Bioentity Interactions: high level, imprecise relations: protein-protein interaction, transcriptional regulation or generic.

States: different forms of Bioentities via chemical modification (acetylated protein), localization (cytoplasmic ion), aberration (mutant gene), homomerization (dimers), etc.

Transitions: changes that states undergo.

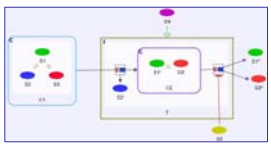


Interactions: relations of states with transitions such as substrate, product, activator and inhibitor.

Molecular Complexes: Non-covalently bound clusters of molecules behaving as a single state.

Cellular compartments: part of the model.

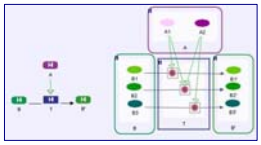
Incomplete Information



Since the data on cellular processes is incomplete, different levels of information may be available for certain events. On the left, it is unknown whether *S4* activates either of two transitions.

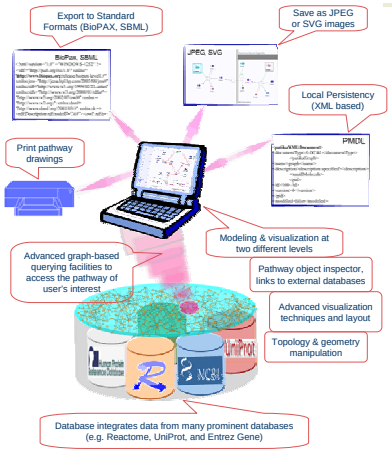
Homologies

B is transformed into B' by activation of A. In the actual case there are two A homologs, three B homologs and three B' homologs.

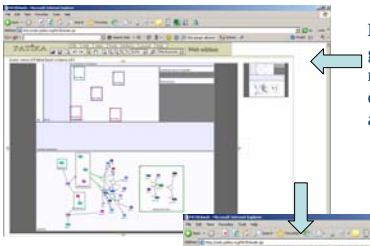


Software

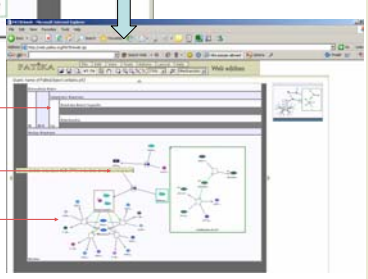
Overview



Advanced Topology & Geometry Manipulation



Before topology and geometry manipulation operations have been applied.



After

- Cell model manipulation by separator relocation operation
- Collapsing a node
- Applying automated layout
- Node deletion

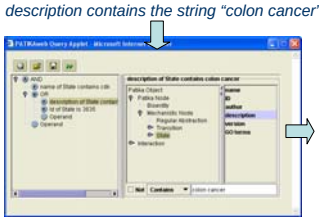
Querying

Extensive querying facilities using

- SQL-like queries;
- An array of graph-theoretic queries such as *feedback loops*, *positive / negative paths*, *common targets and regulators*, or *interesting subgraphs based on user's genes of interest*.

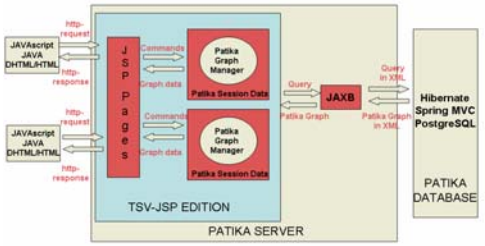
Simple example:

Find all states whose name contains "cdk" among all whose description contains the string "colon cancer" or whose ID is "3835"



Results displayed graphically as shown in the above screen-shot after a layout, either separately or after being merged into the current model.

Client-Server Architecture



Database

- Data from **Entrez Gene**, **UniProt**, **PubChem**, **GO**, and **Reactome**.
- Focuses only on human pathway data, and currently contains several thousands of states of many different biological entities and a few thousands of reactions; and more to come: **BIND**, **IntAct**, and **HPRD**.

Previous Contributors

Many people have previously worked on the project, to whom we'd like to thank, including G. Nisanci, G. Gulesir, A. Gursoy, R. Cetin-Atalay, M. Ozturk, S.F. Akgul, B. Caskurlu, E.D. Ozkan, C. Gerede, A. Kocatas, E. Karakoc, O. Kurt, Z. Madak, E. Sahin, E. Senel, S. Onay, B. Ozmen, A. Civril, O. Sakarya, C. Bilgin, and O. Gerdaneri.