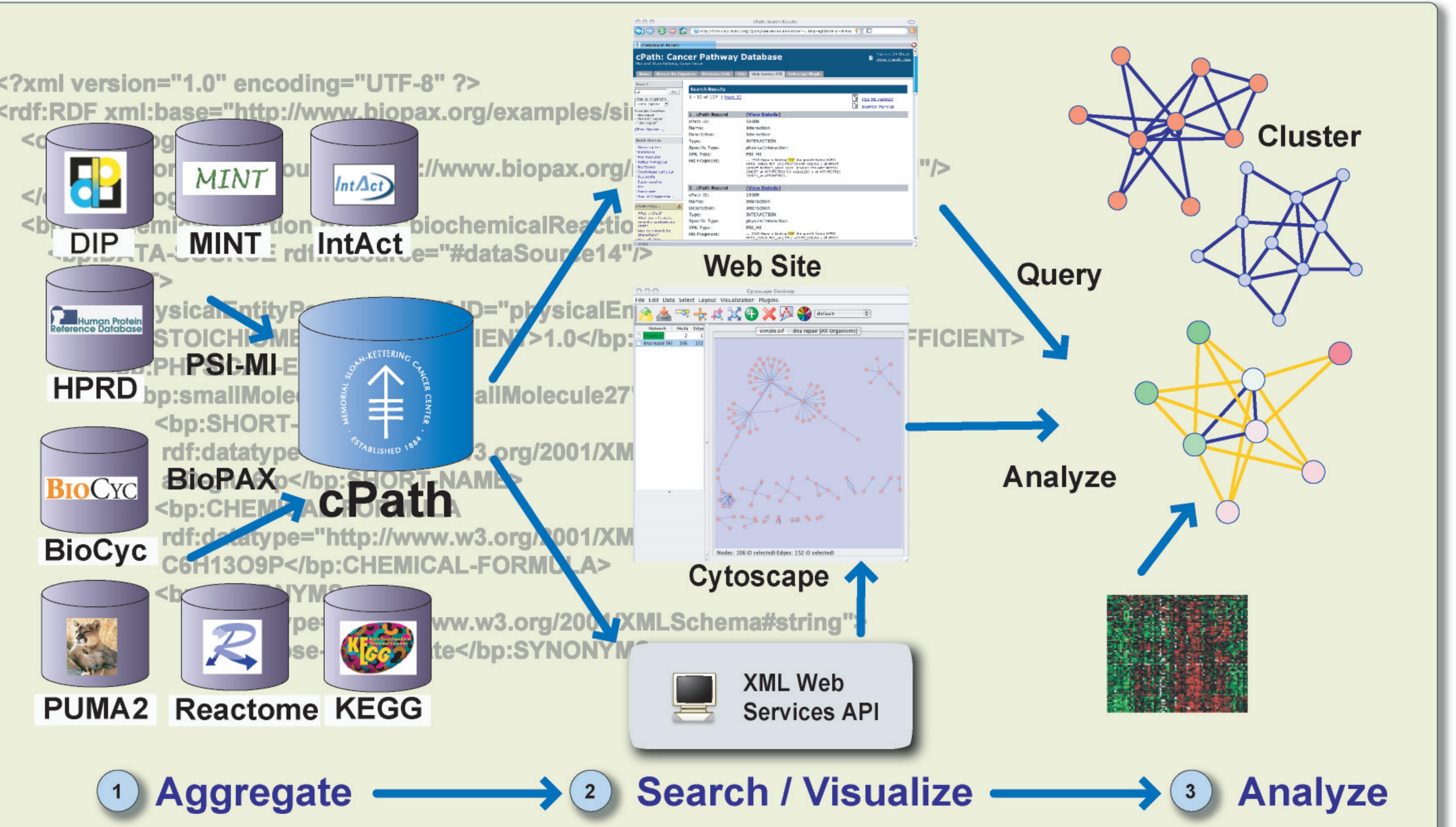


cPath: Pathway Database Software for Systems Biology

Ethan Cerami, Gary D. Bader, Benjamin Gross, Chris Sander

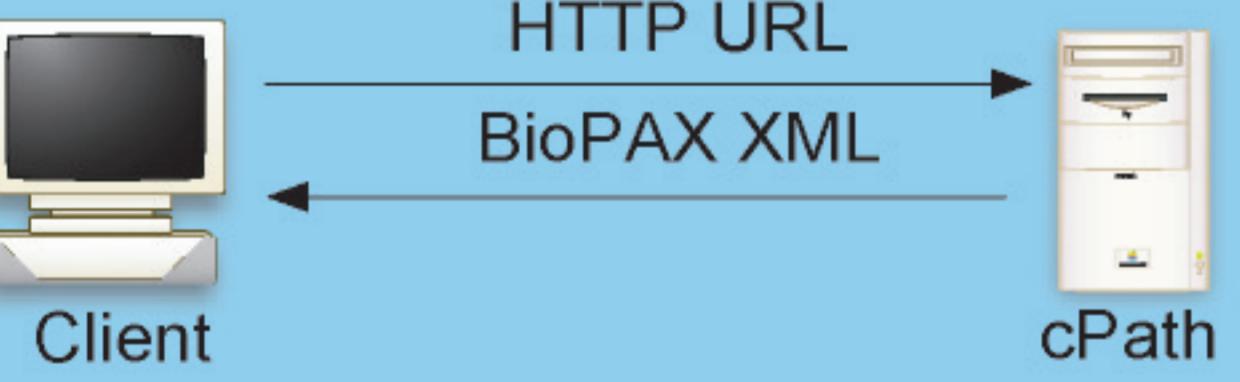
I. Introduction

- Freely available, open source pathway database software built to support systems biology research.
- Import pipeline capable of aggregating pathway and interaction data sets from multiple sources, including: MINT, IntAct, HPRD, DIP, BioCyc, KEGG, PUMA2 and Reactome.
- Import/Export support for the Proteomics Standards Initiative Molecular Interaction (PSI-MI) and the Biological Pathways Exchange (BioPAX) XML formats.
- Data visualization and analysis via Cytoscape.
- Simple HTTP URL based XML web service.
- Complete software is freely available for local install. Easy to install and administer.
- Activity Center Plugin provides for analysis of transcription profile data in the context of biological pathways.
- Partly funded by the U.S. National Cancer Institute, via the Cancer Biomedical Informatics Grid (caBIG), and aims to meet "silver-level" requirements for software interoperability and data exchange.



III. cPath XML Web Services API

All cPath data is available via a HTTP-Based XML Web Services API.



Requests to the cPath Web Service are formed by specifying URL parameters. Parameters are as follows:

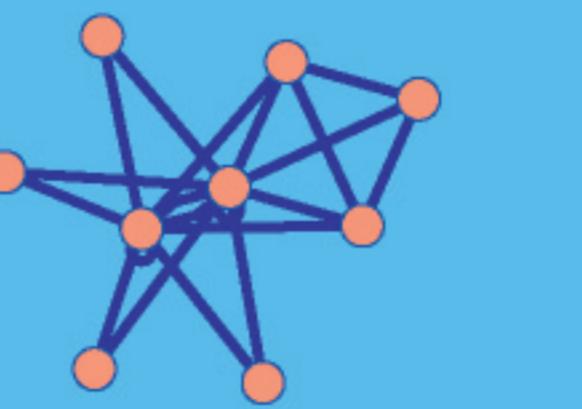
- q:** query parameter, e.g. "5824".
- format:** format of returned results. Current valid formats are: "biopax".
- version:** version of the web service protocol. The only supported version is currently "1.0".
- cmd:** indicates the command to execute. Current valid commands are defined as follows:

Command	Description
help	Requests the help page.
get_top_level_pathway_list	Returns a summary of all "top-level" pathways in the database. The response is a BioPAX XML document. Retrieves the complete contents of the specified record. The response is a BioPAX XML document.

Example Query:
The following requests a summary of all top-level pathways in the database:
http://www.cbio.mskcc.org/cpath/webservice.do?version=1.0&cmd=get_top_level_pathway_list&format=biopax

IV. cPath Cytoscape Plugins

About the Cytoscape cPath Plugin:



The cPath Plugin enables Cytoscape users to query, retrieve and visualize interactions from the cPath database.

About the Cytoscape BioPAX Path Plugin:

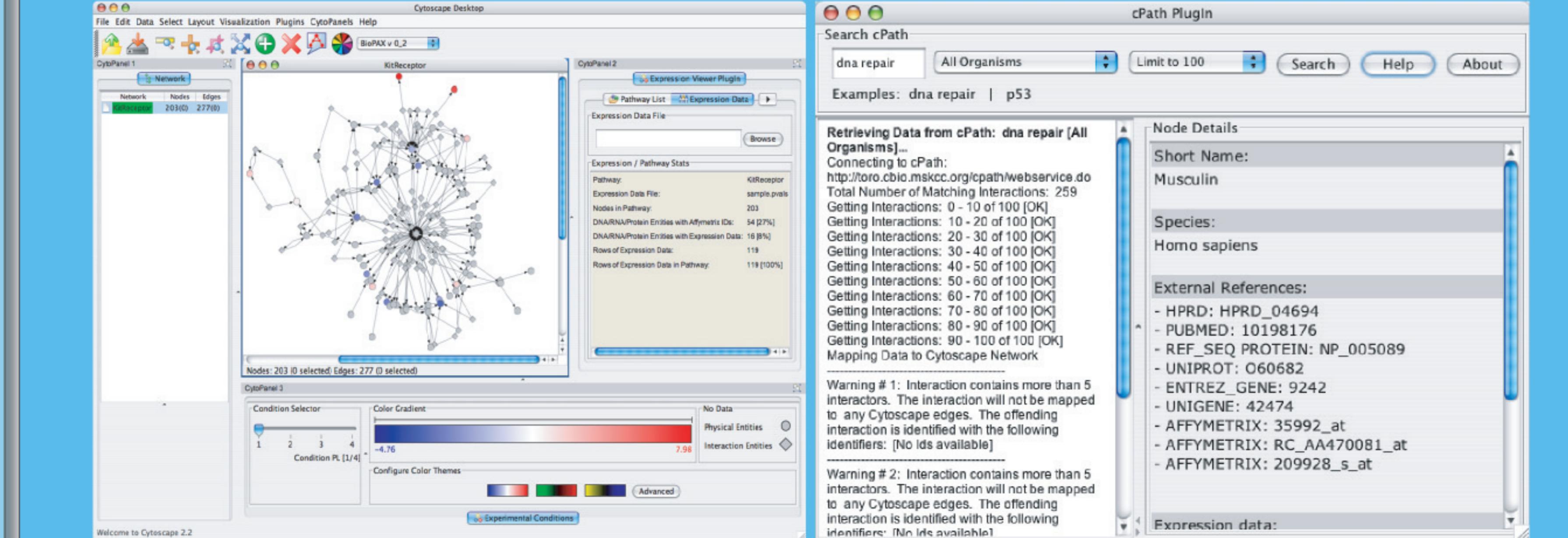
The BioPAX Plugin enables Cytoscape users to retrieve and visualize BioPAX files from the web or a local file system.

About the Cytoscape Expression Viewer Path Plugin:

With the aid of the BioPAX Plugin, the Expression Viewer Plugin enables Cytoscape users to visualize expression data in the context of biological pathways.

About Cytoscape:

Cytoscape is an open source bioinformatics software platform for visualizing molecular interaction networks and integrating these interactions with gene expression profiles and other state data.



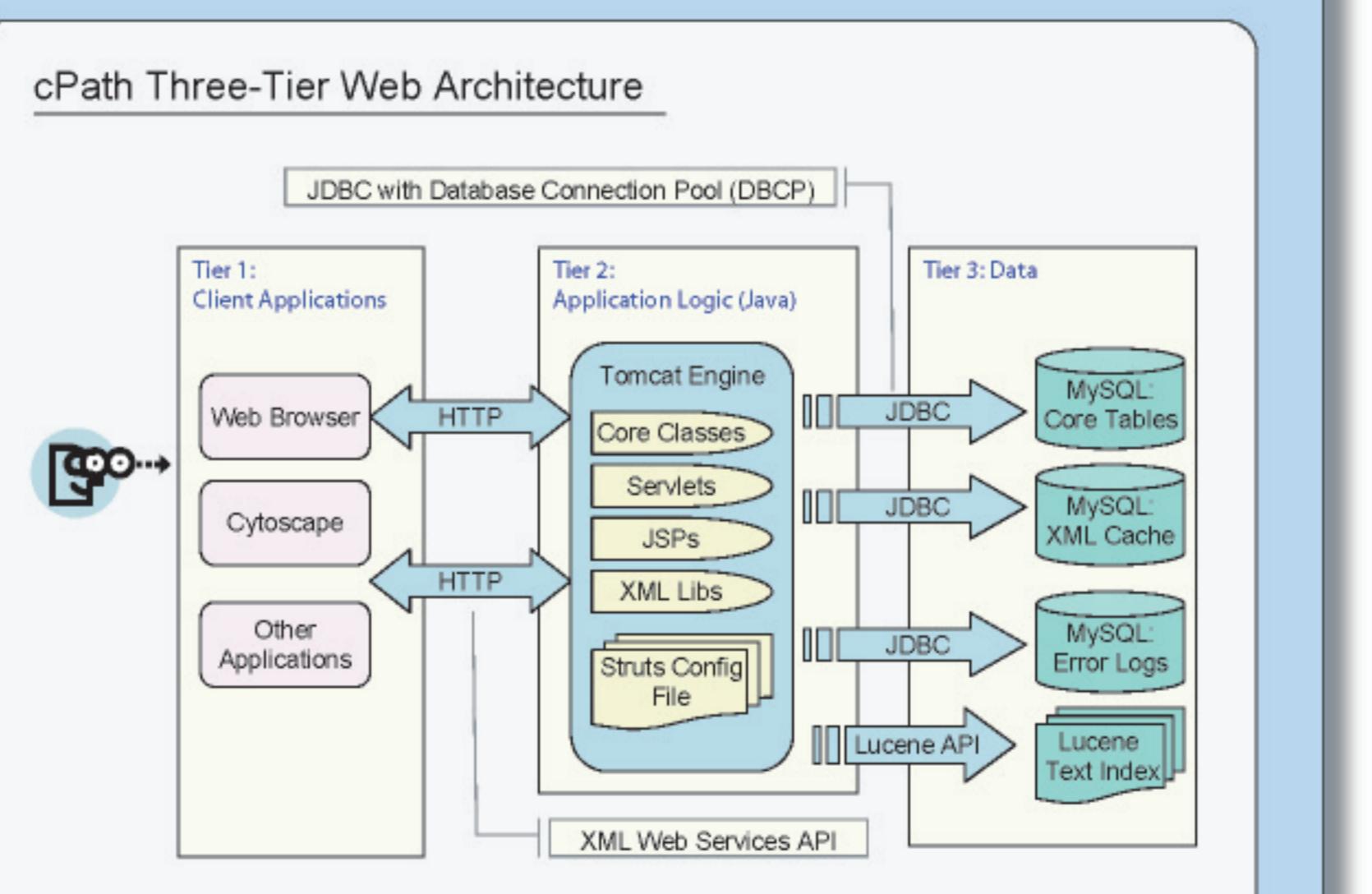
V. Technical Architecture

Three-Tier Web Architecture

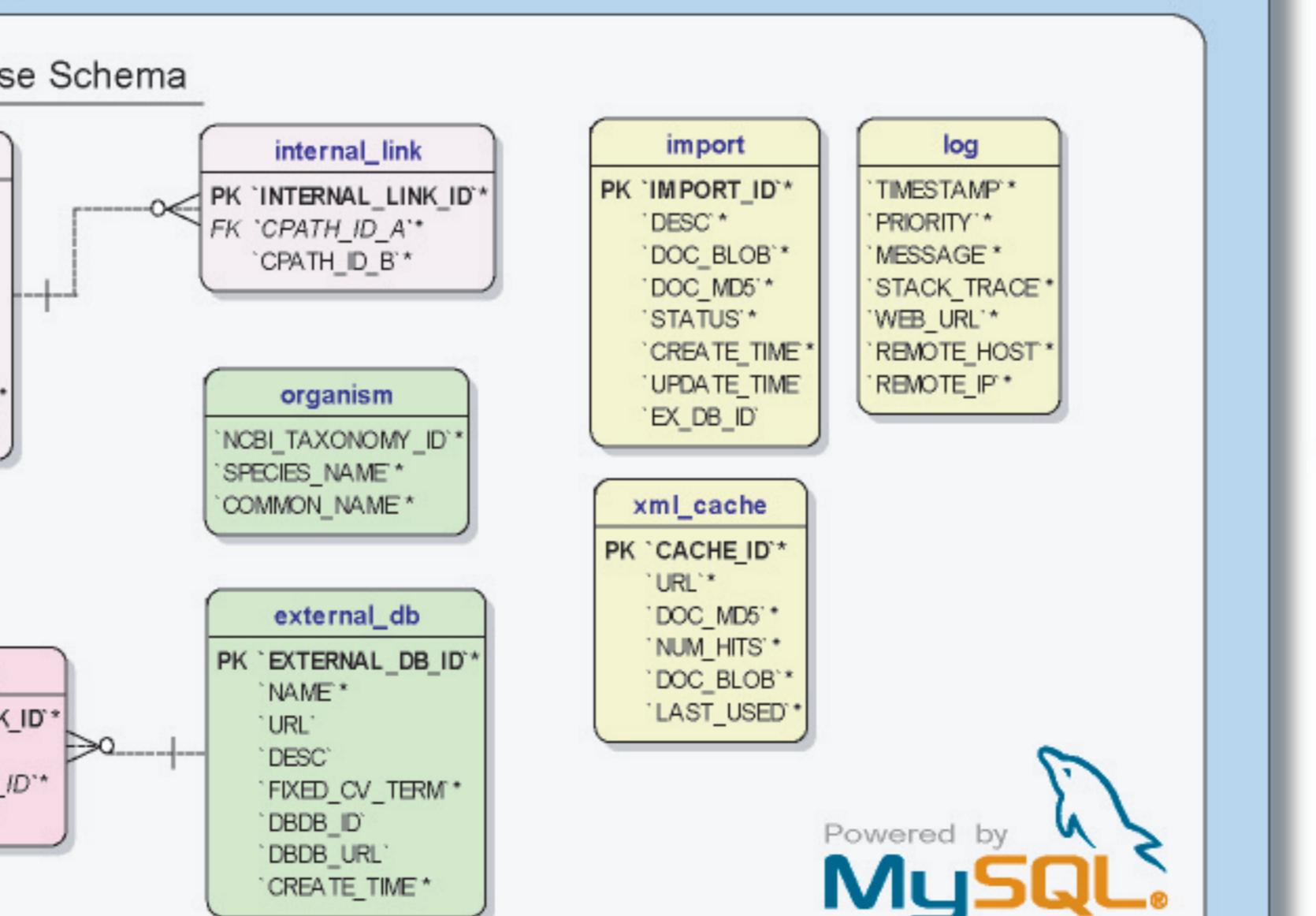
cPath is a database driven web site that uses a traditional three-tier architecture.

Tier 1: consists of web browsers, Cytoscape, and other third-party applications which retrieve data via the cPath XML Web Services API.

Tier 2: consists of Java code running on the open source Jakarta Tomcat Server. This layer consists of core Java classes, Java Servlets, Java Server Pages (JSPs), custom JSP Tags, and various XML libraries.



Tier 3: consists of a MySQL relational database and a text index created and maintained by Jakarta Lucene. The MySQL database stores XML document fragments, internal identifiers and external references.



Testing Practices

The cPath development team makes extensive use of the open source JUnit test framework and the AntEater functional-test framework.

VI. Get Involved

Get Involved

http://www.cbio.mskcc.org/dev_site/cpath/

cPath is an open source project licensed under the LGPL.

If you are an open source developer interested in contributing to a high quality software development project to support a cancer pathway database, please let us know.

A community development site is available for interested open source developers. The site is maintained with the Apache Maven project management system and is automatically updated nightly. Tech documentation, including architecture guides, javadoc, issue tracking, source cross-referencing and many other features are available through this site. A nightly snapshot of the CVS repository can be downloaded from this site as well.

Mailing List

cpath@googlegroups.com - user chat and help requests

Acknowledgements

cPath is partly funded by the U.S. National Cancer Institute, and is part of the Cancer Biomedical Informatics Grid (caBIG).

cPath includes software developed by the Apache Software Foundation.

