

# PathwayAccess: CellDesigner plugins for pathway databases

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## ABSTRACT

**Summary:** CellDesigner provides a user-friendly interface for graphical biochemical pathway description. Many pathway databases are not directly exportable to CellDesigner models. PathwayAccess is an extensible suite of CellDesigner plugins, which connect CellDesigner directly to pathway databases using respective Java application programming interfaces. The process is streamlined for creating new PathwayAccess plugins for specific pathway databases. Three PathwayAccess plugins, MetNetAccess, BioCycAccess and ReactomeAccess, directly connect CellDesigner to the pathway databases MetNetDB, BioCyc and Reactome. PathwayAccess plugins enable CellDesigner users to expose pathway data to analytical CellDesigner functions, curate their pathway databases and visually integrate pathway data from different databases using standard Systems Biology Markup Language and Systems Biology Graphical Notation.

**Availability:** Implemented in Java, PathwayAccess plugins run with CellDesigner version 4.0.1 and were tested on Ubuntu Linux, Windows XP and 7, and MacOSX. Source code, binaries, documentation and video walkthroughs are freely available at <http://vrac.iastate.edu/~jlv>

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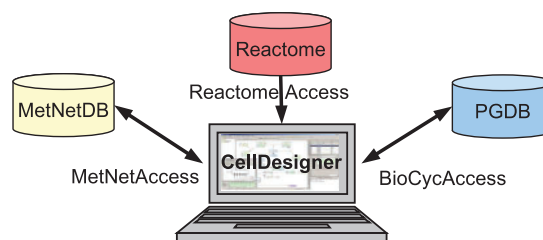
**Supplementary information:** Supplementary data are available at [Bioinformatics](http://bioinformatics.oxfordjournals.org/) online.

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## 1 INTRODUCTION

CellDesigner (Funahashi *et al.*, 2008) is a tool for graphically building biochemical pathway models, which integrate model representation by Systems Biology Markup Language (SBML; Hucka *et al.*, 2003) with graphical representation by Systems Biology Graphical Notation (SBGN; Moodie *et al.*, 2009). There exist many databases providing application programming interface (API) libraries enabling programmatic queries. These API libraries include many biologically meaningful objects, which carry out intuitive functions. For example, a pathway object can report the set of reaction objects it contains, a protein complex object can report the monomer objects that construct it and a metabolite object might report its SMILES and InChi codes. The problem is that a Pathway object in one API is not the same as a Pathway object in the API of a different database. The same biological concept is represented using independently developed in-silico representations, preventing any single application from communicating and integrating across databases.

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**Fig. 1.** Dataflow for PathwayAccess plugins. PathwayAccess plugins use respective APIs to communicate with different pathway databases and integrate data in CellDesigner. As indicated by arrows, depending on functionality supported by the datasource, dataflow is uni- or bi-directional.

## 2 FUNCTIONALITY

PathwayAccess plugins directly interact with pathway databases so that the user can download one or more pathways to a CellDesigner model and upload (or commit) a CellDesigner model to a database. Figure 1 shows a dataflow diagram for typical use of the PathwayAccess plugins.

The PathwayAccess plugin framework confers three major benefits, depending on whether individual database APIs support data retrieval and modification. First, the plugins make pathways stored in remote databases available to the powerful modeling and simulation functionality already provided by CellDesigner. Second, SBGN implemented by CellDesigner provides a standard representation for biologists to curate pathway databases; the user can create a pathway model and commit it to the database of his choice. A user can also download a pathway model from a database, edit it and commit it back to the database, either replacing the original pathway or creating a different version. Third, CellDesigner can be effective in visually comparing and integrating pathway data from one or many different databases; metabolic networks can be downloaded directly into CellDesigner and integrated into custom super-pathways. CellDesigner can export pathways *into files* for loading into other software such as Cytoscape (Shannon *et al.*, 2003), where SBGN is an ancillary feature to network analysis functions.

Since CellDesigner and most datasources' user interfaces provide good automatic layouts, layouts are left to the datasources and CellDesigner independently.

### 2.1 Pathway integration across databases

When PathwayAccess plugins download pathways, they are integrated with the growing model in memory. CellDesigner is suited to support integration because it uses the XML-based SBML data model not only for file storage, but also for objects in memory—ideal for representing annotations integrated from different sources.

Among other annotations, PathwayAccess stores synonyms this way, enabling it to match integrated objects in the same subcellular compartment that may be named differently across databases. To prevent duplicate reactions in integrated pathways, a reaction hashing algorithm calculates a unique integer for every combination of reaction substrates, products and catalysts (see Supplementary Material). Each PathwayAccess plugin has a unique, but editable highlight color, which can be used to color the model objects downloaded using that plugin. Objects from multiple databases are colored by mixing the colors of the plugins that downloaded them.

## 2.2 Creating new PathwayAccess plugins

The PathwayAccess framework includes a core library plus one or more independent plugins. A plugin developer can easily create a new CellDesigner plugin that communicates with any pathway database providing a Java API. Simply create a new CellDesigner plugin object using the PathwayAccess library and define a set of simple database query operations, depending on whether the plugin will support download and/or saving a model to the database. To create a PathwayAccess plugin that downloads a pathway, define 18 simple functions such as to get the synonyms of an object (pathway, metabolite, gene, etc). To design a commit feature, define nine simple functions such as add substrates to a reaction in the database. With these simple operations defined for communicating with a database, PathwayAccess handles all interaction both with CellDesigner and the database, similarly to Cytoscape's Data Integration Request For Comments (Killcoyne *et al.*, 2009), and provides a way to enrich objects beyond the annotation used for integration.

## 2.3 Examples

Three PathwayAccess plugins, MetNetAccess, BioCycAccess and ReactomeAccess were created. In addition to representing biological objects differently, each uses a different communication protocol: SQL, Sockets and Web Services, respectively.

**2.3.1 BioCycAccess: download and commit to a Pathway Genome Database** BioCyc databases are individually deployed for specific organisms and purposes (<http://www.biocyc.org>; Karp *et al.*, 2005). BioCycAccess uses JavaCycO, our new library wrapped around the JavaCyc API (Krummenacker *et al.*, 2005; Mueller *et al.*, 2005), running in client mode to connect to a BioCyc Pathway Genome Database that is running JavaCycO in server mode. It supports both downloading and committing pathways.

**2.3.2 ReactomeAccess: download from Reactome** Reactome is a large repository for pathways (Matthews *et al.*, 2009). ReactomeAccess supports downloading pathways from Reactome directly into CellDesigner models via an API wrapped around Reactome's web services.

**2.3.3 MetNetAccess: download and commit to MetNet** MetNetAccess provides CellDesigner access to the pathway database MetNetDB using MetNetAPI (Sucaet *et al.*, 2010), which is wrapped around SQL queries. It supports both downloading and committing pathways. MetNetDB is an integrated pathway database

that currently includes *Arabidopsis thaliana*, yeast, soybean and the grapevine. MetNetAccess has been used to curate many pathways for different organisms in MetNetDB (Wurtele *et al.*, 2007). MetNet allows public downloading of data, but only registered curators may modify data in MetNetDB.

## 3 IMPACT

The PathwayAccess suite of CellDesigner plugins is a powerful tool for researchers who work with metabolic pathway data and wish to take advantage of graphical and computational CellDesigner features. By directly accessing and publishing to pathway databases, decentralized pathway integration and comparison is made possible over simply saving and loading SBML files. Although three PathwayAccess plugins have been released, the practical scope of the PathwayAccess library is as wide as the number of databases to which CellDesigner can connect because communication requires a Java API. MetNetAccess, BioCycAccess, ReactomeAccess and future PathwayAccess plugins enable CellDesigner users to expose pathway data to analytical CellDesigner functions as well as visually integrate and curate pathway data from different databases using standard SBGN—something that has been previously prevented by disparate *in silico* representations of biological objects.

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## REFERENCES

- Funahashi, A. *et al.* (2008) Celldesigner 3.5: a versatile modeling tool for biochemical networks. *Proc. IEEE*, **96**, 1254–1265.
- Hucka, M. *et al.* (2003) The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models. *Bioinformatics*, **9**, 524–531.
- Karp, P.D. *et al.* (2005) Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. *Nucleic Acids Res.*, **19**, 6083–6089.
- Killcoyne, S. *et al.* (2009) Cytoscape Data Integration RFC. Request for comments, Cytoscape. Available at <http://cytoscape.wodaklab.org/wiki/DataIntegration> (last accessed date July 28, 2010).
- Krummenacker, M. *et al.* (2005) Querying and computing with BioCyc databases. *Bioinformatics*, **21**, 3452–3455.
- Matthews, L. *et al.* (2009) Reactome knowledgebase of biological pathways and processes. *Nucleic Acids Res.*, **37**, D619–D622.
- Moodie, S. *et al.* (2009) Systems biology graphical notation: process description language level 1. Available from Nature Precedings <<http://dx.doi.org/10.1038/npre.2009.3721.1>>.
- Mueller, L. *et al.* (2005) The SOL genomics network: a comparative resource for Solanaceae biology and beyond. *Plant Physiol.*, **138**, 1310–1317.
- Shannon, P. *et al.* (2003) Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome Res.*, **13**, 2498–2504.
- Sucaet, Y. *et al.* (2010) MetNetAPI. Available at <http://metnet3.vrac.iastate.edu/api> (last accessed date July 28, 2010).
- Wurtele, E.S. *et al.* (2007) MetNet: Systems Biology Software for Arabidopsis. *Concepts in Plant Metabolomics*, Springer, pp. 145–158.