



SOFTWARE TOOL ARTICLE

cy3sabiork: A Cytoscape app for visualizing kinetic data from SABIO-RK [version 1; referees: 2 approved with reservations]

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Abstract

Kinetic data of biochemical reactions are essential for the creation of kinetic models of biochemical networks. One of the main resources of such information is SABIO-RK, a curated database for kinetic data of biochemical reactions and their related information. Despite the importance for computational modelling there has been no simple solution to visualize the kinetic data from SABIO-RK.

In this work, I present cy3sabiork, an app for querying and visualization of kinetic data from SABIO-RK in Cytoscape. The kinetic information is accessible via a combination of graph structure and annotations of nodes, with provided information consisting of: (I) reaction details, enzyme and organism; (II) kinetic law, formula, parameters; (III) experimental conditions; (IV) publication; (V) additional annotations. cy3sabiork creates an intuitive visualization of kinetic entries in form of a species-reaction-kinetics graph, which reflects the reaction-centered approach of SABIO-RK. Kinetic entries can be imported in SBML format from either the SABIO-RK web interface or via web service queries. The app allows for easy comparison of kinetic data, visual inspection of the elements involved in the kinetic record and simple access to the annotation information of the kinetic record.

I applied cy3sabiork in the computational modelling of galactose metabolism in the human liver.



This article is included in the [Cytoscape apps](#) channel.

Open Peer Review

Referee Status: ? ?

Invited Referees		
	1	2
version 1	?	?
published 18 Jul 2016	report	report

- 1 **Barry Demchak**, University of California, San Diego USA
- 2 **Ali Salehzadeh-Yazdi**, University of Rostock Germany

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Introduction

One of the main challenges for the modeling of biochemical systems is the availability of reliable information on the individual reaction steps and their kinetics from the literature. This information includes kinetic parameters with their rate equations as well as detailed descriptions of how these were determined¹.

SABIO-RK (<http://sabio.h-its.org/>) is a manually curated database for kinetic data storing comprehensive information about biochemical reactions and their kinetic properties, with data manually extracted from the literature and directly submitted from lab experiments^{1,2}. Available information comprises kinetic parameters with their corresponding rate equations, kinetic law and parameter types and experimental conditions under which the kinetic data were determined. In addition, information about the biochemical reactions and pathways including their reaction participants, cellular location and the catalyzing enzyme are recorded².

The information in SABIO-RK is structured in datasets, so called database entries, which can be accessed either through the web-based user interface (<http://sabiork.h-its.org/newSearch/index>) or via web services (<http://sabiork.h-its.org/sabioRestWebServices>). Both interfaces support the export of the data in the Systems Biology Markup Language (SBML), a free and open interchange format for computer models of biological processes³.

Database entries are annotated with controlled ontologies and vocabularies based on Minimum Information Required for the Annotation of Models (MIRIAM⁴), e.g. reaction participants (e.g. small chemical compounds and proteins), as well as kinetic rate laws, and parameters. The annotation information is encoded in the form of RDF-based MIRIAM annotations, and additional XML based SABIO-RK specific annotations, e.g. for experimental conditions. These annotations integrate the kinetic information with external resources like ChEBI (<https://www.ebi.ac.uk/chebi/>)⁵, UniProtKB (<http://www.uniprot.org/>)⁶, PubMed (<http://www.ncbi.nlm.nih.gov/pubmed/>), or KEGG (<http://www.kegg.jp/>)⁷.

Despite the importance of kinetic information for computational modelling there has been no simple solution to visualize the database entries from SABIO-RK, and provide access to the structure of the kinetic entries and the information encoded in the annotations.

In this work, we present cy3sabiork, an app for the visualization of kinetic data from SABIO-RK for Cytoscape, an open source software platform for network visualization⁸. cy3sabiork creates an intuitive visualization of kinetic entries in the form of a species-reaction-kinetics graph extended with kinetic information, which reflects the reaction-centered approach of SABIO-RK. Hereby, the kinetic information is accessible via a combination of graph structure and annotations of nodes, with provided information consisting of: (I) reaction details, enzyme and organism; (II) kinetic law, formula, parameters; (III) experimental conditions; (IV) publication; (V) additional annotations. cy3sabiork allows for easy comparison of kinetic data, visual inspection of the elements

involved in the kinetic record and simple access to the annotation information of the kinetic record.

Methods

Implementation

cy3sabiork was written in Java as an OSGi bundle for Cytoscape 3 using the app infrastructure. The bundle activator adds the cy3sabiork Action to the Cytoscape icon bar, which provides access to the JavaFX based cy3sabiork dialog. The cy3sabiork GUI is a combination of web based components handled in a WebView and classical GUI components. The combination of Swing and JavaFX is implemented based on a JFXPanel with JavaFX GUI updates in Platform.runLater, Swing GUI updates via SwingUtilities.invokeLater. The JavaFX approach allows for the integration of rich Web-based content using HTML/JavaScript/CSS with Cytoscape. The GUI was created utilizing FXML based GUI definitions created in JavaFX Scene Builder, a JavaFX tool which allows to quickly design JavaFX application user interfaces by dragging UI components into a content view area. FXML code for the UI layout is created by the tool which was styled using CSS. The downside of the JavaFX-Swing hybrid approach are additional complexity in handling Events and EventListeners in different threads, some issues with Windows Management and Focus Handling, and full support of JavaFX in old felix OSGi containers.

SABIO-RK entries are retrieved via the web services using the RESTful API. SBML from the web service calls or the web interface export is imported using a Cytoscape Task created by the LoadNetworkFileTaskFactory. CyNetworks and CyNetworkViews for the imported kinetic entries are created by a CyNetworkReader registered for SBML files provided by cy3sbml⁹. During the app development the SBML CyNetworkReader was extended to support the SABIO-RK specific annotations and data. RDF based annotations are read with JSBML^{10,11} and hyperlinks to the respective resources are created by parsing the resources.

By implementing cy3sabiork as a desktop app, in comparison to a solely web-based solution with Cytoscape.js, tight integration with cy3sbml was possible, thereby providing rich functionality for the kinetic entries in SBML, like for instance access to the annotation information or the raw SBML files of the kinetic entries.

Operation

An overview over the typical cy3sabiork workflow is depicted in [Figure 1](#). The main steps of operation are searching entries in SABIO-RK, loading entries in cy3sabiork, and visual exploration of results:

Searching kinetic entries. Kinetic entries can either be searched via the web services available from the cy3sabiork panel or directly in the SABIO-RK web interface available at <http://sabiork.h-its.org/newSearch/index>.

The web interface enables the search for reactions and their kinetics by either a free text search or an advanced search, which supports the creation of complex queries by specifying reactions

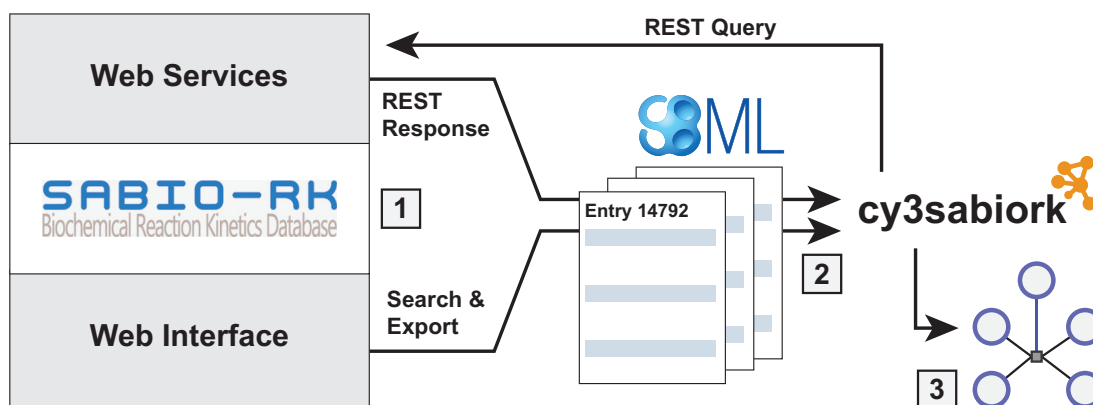


Figure 1. cy3sabiork workflow. The main steps of operation are: (1) Searching entries in SABIO-RK: Kinetic entries are retrieved from SABIO-RK via calls to the RESTful web services or via searching the web interface and exporting selected entries as SBML; (2) Loading entries in cy3sabiork: The exchange format between SABIO-RK and cy3sabiork is SBML; (3) Visual exploration of results. The kinetic graphs for the imported entries are generated providing simple access to kinetic information and annotations. An example query with resulting SABIO-RK information and subsequent visualization is shown in Figure 2.

by their participants (substrates, products, inhibitors, activators etc.) or identifiers (KEGG or SABIO-RK reaction identifiers and KEGG, SABIO-RK, ChEBI or PubChem compound identifiers), pathways, enzymes, UniProt identifiers, organisms (NCBI taxonomy¹²), tissues or cellular locations (BRENDA tissue ontology (BTO)¹³), kinetic parameters, environmental conditions or literature sources^{1,2}. After finalizing the search the selected kinetic entries are exported as SBML.

The web interface supports the same query options, which can be added in the REST query GUI, but allows a direct import of the SBML without the requirement for search in the web interface and export and subsequent import of the SBML.

Example queries are depicted in Figure 2 and Figure 4 with resulting SBML available as Supplementary File S1 and Supplementary File S2.

Loading kinetic entries. The SBML exported from web interface searches is imported as in Cytoscape using cy3sbml⁹ (File → Import → Network → File). For queries to the web services the response SBML is imported automatically without the need for additional file operations.

Visual exploration. The final step is the exploration of the kinetic entries in the species-reaction-modifier and the kinetic graph (e.g. in Figure 2 and Figure 4). The information from a wide range of resources and databases is integrated with the graph

visualization of the kinetic records accessible as hyperlinks from the cy3sbml panel. Examples are the access to the source publication on PubMed from which the kinetic information was retrieved, the UniProtKB protein for which the kinetic information was measured, KEGG and ChEBI information for species involved in the reaction, or links back to the SABIO-RK database entry and reaction.

Use cases

We applied cy3sabiork for kinetic parameter search and model construction of a kinetic model of galactose metabolism of the human liver (<https://github.com/matthiaskoenig/multiscale-galactose>) within the Virtual Liver Network (VLN) and Systems Medicine of the Liver (LiSyM) projects. A crucial step in building kinetic models of metabolism is the collection of kinetic information from the literature for the parameterization of the biochemical reactions. The search and visual exploration with cy3sabiork provides easy-access to a high-quality starting set of kinetic parameters and corpus of relevant publications for the processes of interest. Hereby, subsequent literature search and retrieval of referenced publications is simplified.

A representative SABIO-RK query for galactokinase (EC:2.7.1.6, UniProtKB:P51570), the first step of hepatic galactose metabolism is depicted in Figure 2 retrieving the SABIO-RK kinetic record 14792. A more complex query used for parameter search is depicted in Figure 3 and Figure 4 retrieving all kinetic records available for human galactose metabolism.

A SABIO-RK Entry 14792

General information				
Organism	Homo sapiens			
Tissue	-			
EC Class	2.7.1.6			
SABIO reaction id	1354			
Variant	wildtype His-tagged			
Recombinant	expressed in Escherichia coli HMS174(DE3)			
Experiment Type	in vitro			
Pathways	Amino sugar and nucleotide sugar metabolism Galactose metabolism			
Event Description	-			
Substrates				
name	location			
D-Galactose	cytosol			
ATP	cytosol			
Products				
name	location			
ADP	cytosol			
alpha-D-Galactose 1-phosphate	cytosol			
Modifiers				
name	location	effect	comment	protein complex
galactokinase(Enzyme)	cytosol	Modifier-Catalyst	-	P51570
Enzyme (protein data)				
UniProtKB_AC	name	mol. weight (kDa)		deviation (kDa)
subunit	P51570	-		-
complex	-	-		-

Kinetic Law							
type	Michaelis-Menten						
formula	$(E \cdot kcat \cdot A)/(Km+A)$						
annotation	SBO:0000029						
Parameter							
name	type	species	start val.	end val.	deviat.	unit	comment
E	concentration	Enzyme	32.0	67.0	-	nM	-
A	concentration	ATP	0.0	80.0	-	µM	-
kcat	kcat	-	8.7	-	5	s ⁻¹ (-1)	-
kcat_Km	kcat/Km	ATP	260000.0	-	0.4E5	M ⁻¹ (-1)*s ⁻¹ (-1)	-
Km	Km	ATP	34.0	-	4	µM	-
Experimental conditions							
start value	end value		unit				
pH	8.0		-				
temperature	37.0		°C				
buffer	20 mM Hepes, 150 mM NaCl, 5 mM MgCl2, 1 mM KCl, 10% (v/v) glycerol, 1 mM NADH, 1 mM dithiothreitol, 400 µM phosphoenolpyruvate, 7.5 U pyruvate kinase, 10 U lactate dehydrogenase						
comment	-						
Reference							
title	author	year	journal	volume	pages	PubMed	
Functional analysis of disease-causing mutations in human galactokinase	Timson DJ, Reece RJ	2003	Eur J Biochem	270	1767-74	12694189	

Reaction details, enzyme, organism

Kinetic law, formula, parameters

Experimental conditions

Source

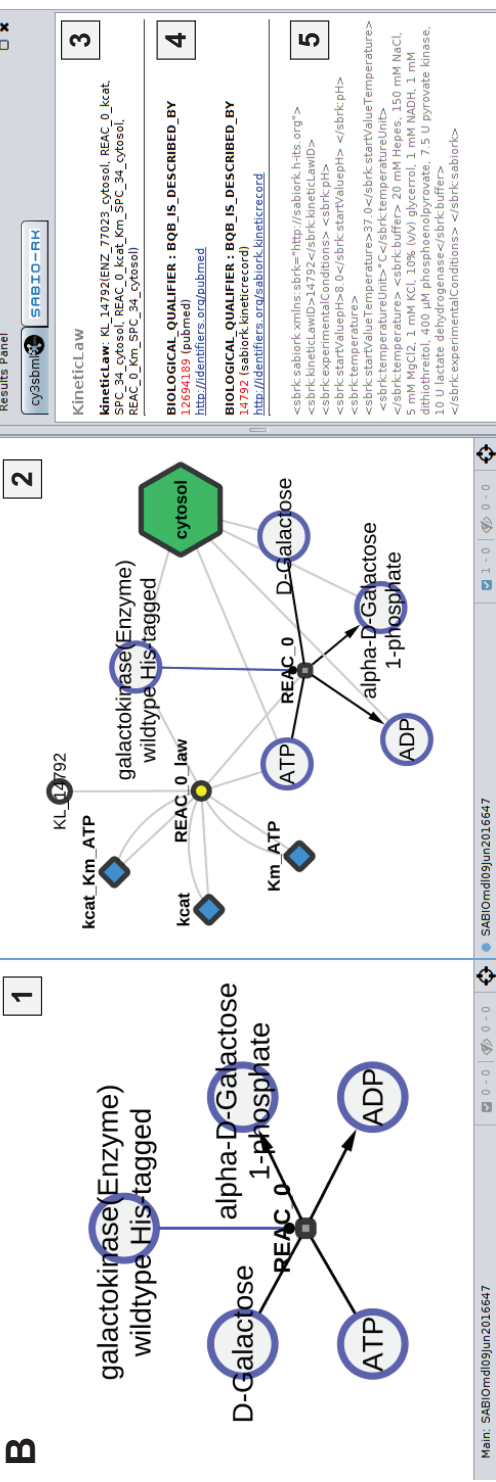


Figure 2. Overview of kinetic information and visualization for a single SABIO-RK entry. The kinetic entry 14792 for galactokinase (EC:2.7.1.6, UniProtKB:P51570) was retrieved via the web service query <http://sabiork.h-its.org/sabioreactWebServices/kineticLaws/14792> (status 10-06-2016, SBML of query in [Supplementary File S1](#)). (A) Overview of kinetic information for SABIO-RK entry (http://sabiork.h-its.org/kineticLawEntry.jsp?viewData=true&kinlawid=14792) with color coding according to 1. (B) cy3sabiork information for entry 14792: (1) Resulting species-reaction-modifier graph. The galactokinase enzyme catalyzes the conversion of D-Galactose + ATP → α-D-Galactose 1-phosphate + ADP (see also Substrates, Products and Modifiers in A); (2) Kinetic graph with additional nodes for kinetic law, parameters and localization; (3) Selecting nodes in the graphs provides access to the annotation information and links to databases. In the example the kinetic law information is displayed in the Results Panel. (4) MIRIAM annotations with respective links to databases are available via the Results Panel; (5) Additional SABIO-RK annotations in XML for the experimental conditions are displayed in this section.



Query Builder Kinetic Law Entries

Keyword **Search Term**

Organism

KeGGID

KeGGReactionID

KineticMechanismType

Organism

Organization

OtherModifier

ParameterType

Pathway

REST Query

searchKineticLaws/sbml?q=Pathway:"galactose metabolism" AND Organism:"homo sapiens"

Status 200
Time 16390 [ms]

SABIO-RK Entries (88)

#	Id	Organism	Tissue	Reaction
31	14785	9606	-	galactokinase(Enzyme) wildtyp...
30	14786	9606	-	galactokinase(Enzyme) mutant...
32	14787	9606	-	galactokinase(Enzyme) mutant...
33	14788	9606	-	galactokinase(Enzyme) mutant...
35	14789	9606	-	galactokinase(Enzyme) mutant...

```
[13:09:06 INFO] Load information for Kinetic Law <14785>
[13:09:06 INFO] Load information for Kinetic Law <14785>
[13:08:18 INFO] SABIO-RK returned status <200> after 16390 [ms]
[13:08:01 INFO] ... waiting for SABIO-RK response ...
[13:08:01 INFO] GET <searchKineticLaws/sbml?q=Pathway:"galactose
metabolism" AND Organism:"homo sapiens">
[13:08:01 INFO] <88> Kinetic Law Entries for query in SABIO-RK.
[13:08:01 INFO] GET COUNT
<searchKineticLaws/sbml?q=Pathway:"galactose metabolism" AND
```

Kinetic data for SABIO Kinetic law id 14785

General information			
Organism	Homo sapiens		
Tissue	-		
EC Class	2.7.1.6		
SABIO reaction id	1354		
Variant	wildtype His-tagged		
Recombinant	expressed in Escherichia coli HMS174(DE3)		
Experiment Type	in vitro		
Pathways	Amino sugar and nucleotide sugar metabolism Galactose metabolism		
Event Description	-		
Substrates			
name	location	comment	
D-Galactose	cytosol ↗	-	
ATP	cytosol ↗	-	
Products			
name	location	comment	
ADP	cytosol ↗	-	
alpha-D-Galactose 1-phosphate	cytosol ↗	-	
Modifiers			
name	location	effect	comment
galactokinase(Enzyme)	cytosol ↗	Modifier-Catalyst	PS1570 ↗
Enzyme (protein data)			
UniProtKB AC	name	mol. weight (kDa)	deviation (kDa)
subunit	PS1570	-	-
complex	-	-	-
Kinetic Law			
type	formula		
Michaelis-Menten	$(E \cdot kcat \cdot A) / (Km + A)$ ↗		
Parameter			
name	type	species	start val.
E	concentration ↗	Enzyme	32.0
A	concentration ↗	D-Galactose	0.0
kcat	kcat ↗	-	8.7
kcat_Km	kcat/Km ↗	D-Galactose	8900.0
Km	Km ↗	D-Galactose	970.0
Experimental conditions			
start value		end value	
pH	8.0	-	
temperature	37.0	-	
buffer	20 mM Hepes, 150 mM NaCl, 5 mM MgCl2, 1 mM KCl, 10% (v/v) glycerol, 1 mM NADH, 1 mM dithiothreitol, 400 μM phosphoenolpyruvate, 7.5 U pyruvate kinase, 10 U lactate dehydrogenase		
comment	-		
Reference			
title	author	year	journal
Functional analysis of disease-causing mutations in human galactokinase	Timson DJ, Reece RJ	2003	Biochem
		1767-	74
		12694189	↗

Figure 3 cy3sabiork GUI for web service queries. For human galactose metabolism 88 entries are available (status 28-06-2016, SBML of query in Supplementary File S2). For the selected Entry 14785 detailed information is provided on the right side.

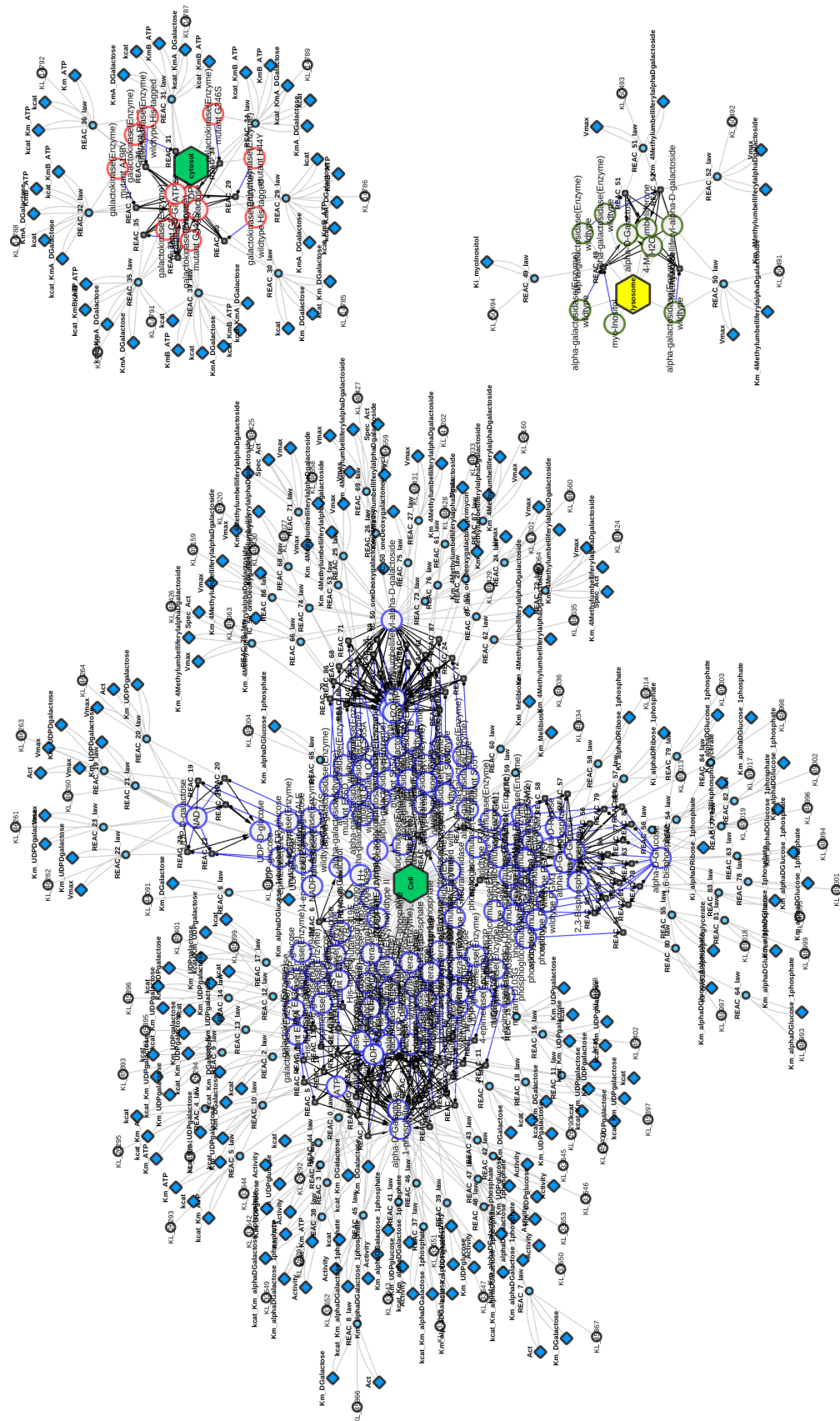


Figure 4. Kinetic graph for human galactose metabolism. Graph of SABIO-RK kinetic information available for human galactose metabolism consisting of 88 entries (status 28-06-2016, SBML of query in [Supplementary File S2](#)). The kinetic graph consists of three clusters, separated based on the reported localization of the catalyzing enzyme. The lysosomal entries are non-canonical reactions in the galactose metabolism.

During model building publications with kinetic information not yet available in SABIO-RK were included in the database by the SABIO-RK curation service.

Conclusion

cy3sabiork is a Cytoscape app for visualizing kinetic data from SABIO-RK providing the means for visual analysis of kinetic entries from SABIO-RK within their reaction context. Herby, the integration of kinetic parameters with computational models is supported. The availability of direct links to annotated resources from within the network context of the kinetic records provides important information for the knowledge integration with computational models.

Software availability

Software available from: <http://apps.cytoscape.org/apps/cy3sabiork>

Latest source code: <https://github.com/matthiascoenig/cy3sabiork>

Archive source code as at the time of publication: <http://dx.doi.org/10.5281/zenodo.5742814>

License: GNU General Public License, version 3 (GPL-3.0): <https://opensource.org/licenses/GPL-3.0>

Supplementary material

Supplementary File S1: Kinetic entry 14792.

SBML for query <http://sabiork.h-its.org/sabioRestWebServices/kineticLaws/14792>

Supplementary File S2: Kinetic entries for human galactose metabolism.

SBML for query: <http://sabiork.h-its.org/sabioRestWebServices/searchKineticLaws/sbml?q=Pathway:%22galactose%20metabolism%22%20AND%20Organism:%22homo%20sapiens%22>

Author contributions

MK developed the app and wrote the manuscript. All authors were involved in the revision of the draft manuscript and have agreed to the final content.

Competing interests

No competing interests were disclosed.

Grant information

This work was supported by the Federal Ministry of Education and Research (BMBF, Germany) within the research network Systems Medicine of the Liver (LiSyM, grant number 031L0054) and the Virtual Liver Network (VLN, grant number 0315741).

The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Acknowledgments

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[Data Source](#)

Open Peer Review

Current Referee Status:



Version 1

Referee Report 12 September 2016

doi:10.5256/f1000research.9914.r16239



Ali Salehzadeh-Yazdi

Department of Systems Biology and Bioinformatics, University of Rostock, Rostock, Germany

- The current study is a Cytoscape app which visualized kinetic data from SABIO-RK. The article and results are of interest, but overall the article will be largely improved if the novelty and aims of the app are clearer.
- The abstract should be more focused and make shorter.
- The introduction should be more concise and informative of previous works. A paragraph explaining that different approaches have been described the visualization of the kinetic data based on in platform. (and explain the highlights of each method).
- The Figures are not in a high-quality resolution and figure 4 is not informative. The author just showed the main three clusters of human galactose metabolism. I suggest illustrating the method clearer (specially the operation).

Competing Interests: No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Referee Report 04 August 2016

doi:10.5256/f1000research.9914.r15057



Barry Demchak

Department of Medicine, University of California, San Diego, La Jolla, CA, USA

This paper describes the cy3sabiork Cytoscape app, which enables users to query the SABIO-RK kinetics database from within Cytoscape and then formats the results as a Cytoscape network. It also allows a Cytoscape user to import an SBML file generated by the SABIO-RK web site via browser-based interactive use.

The paper is generally well structured and worded. My comments mainly address affordances that allow

the paper to deliver more value via wording changes, formatting improvements, and the addition of critical additional information. These comments address small points that add up to real value to new readers and readers only semi-fluent with SABIO-RK.

The abstract is difficult to read because it lacks white space between paragraphs. Additionally, adding back in some missing articles (e.g., "the" and "and") would improve flow.

"cy3sabiork" is a hard name to read ... readability can be improved with a phonetic pronunciation (... would this be si-three-sab-york ??)

The operation of cy3sabiork isn't clear from the paper. The web interface is described, but it would be helpful to have a tutorial describing step-by-step operation and giving a tour of the result of each step. This would be helpful both in this paper and on the App Store web site.

The Introduction proposes a visualization, but it's unclear what the visualization shows or why it was chosen. For someone trying to understand more about the value of this app, a short explanation would be valuable.

The Implementation section is detailed and sufficient. It would be very worthwhile adding text that claims this app as the first to render its UI using JavaFX, and discussing the pros and cons of this approach from both the developer and user perspective.

In the Operation section, it should be made clear that when the web interface generates SBML, it is written to a file that the user must then manually import into Cytoscape. Making this more apparent in the "After finalizing the search ..." sentence would be helpful, and avoiding the nominative case in the "Loading kinetic entries" section would make clear that the user is doing the work. Similar clarification in Figure 1 would be helpful, too.

In all figures, the captions are very useful but very long. According to F1000 style guide, these captions should be short. If the style is applied, the captions should be moved into inline text (with more discussion).

In figure 3, the separation between the form (on the right) and the screen shot (on the left) is unclear. It's hard to read this figure and understand it quickly.

The graph in figure 4 is too detailed for reproduction in a PDF. For users that want to study it more, it would be helpful if the supplementary material would contain the .cys file from which it was generated.

Competing Interests: I am the chief architect and project manager for Cytoscape, and am interested in seeing high quality apps added to the Cytoscape app store and made available to Cytoscape users.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Discuss this Article

Version 1

Reader Comment 12 Aug 2016

Andreas Dräger, University of Tuebingen, Germany

This work aligns very well with two earlier works, namely the integration of SABIO-RK access into

1. the pathway modeling tool CellDesigner, see <https://www.ncbi.nlm.nih.gov/pubmed/17822394/> and
2. the rate law generator SBMLsqueezer, see <https://www.ncbi.nlm.nih.gov/pubmed/26452770/>.

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