



SEEK for Science: A Data Management Platform to support Open and Reproducible Science

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The University of Manchester

UK

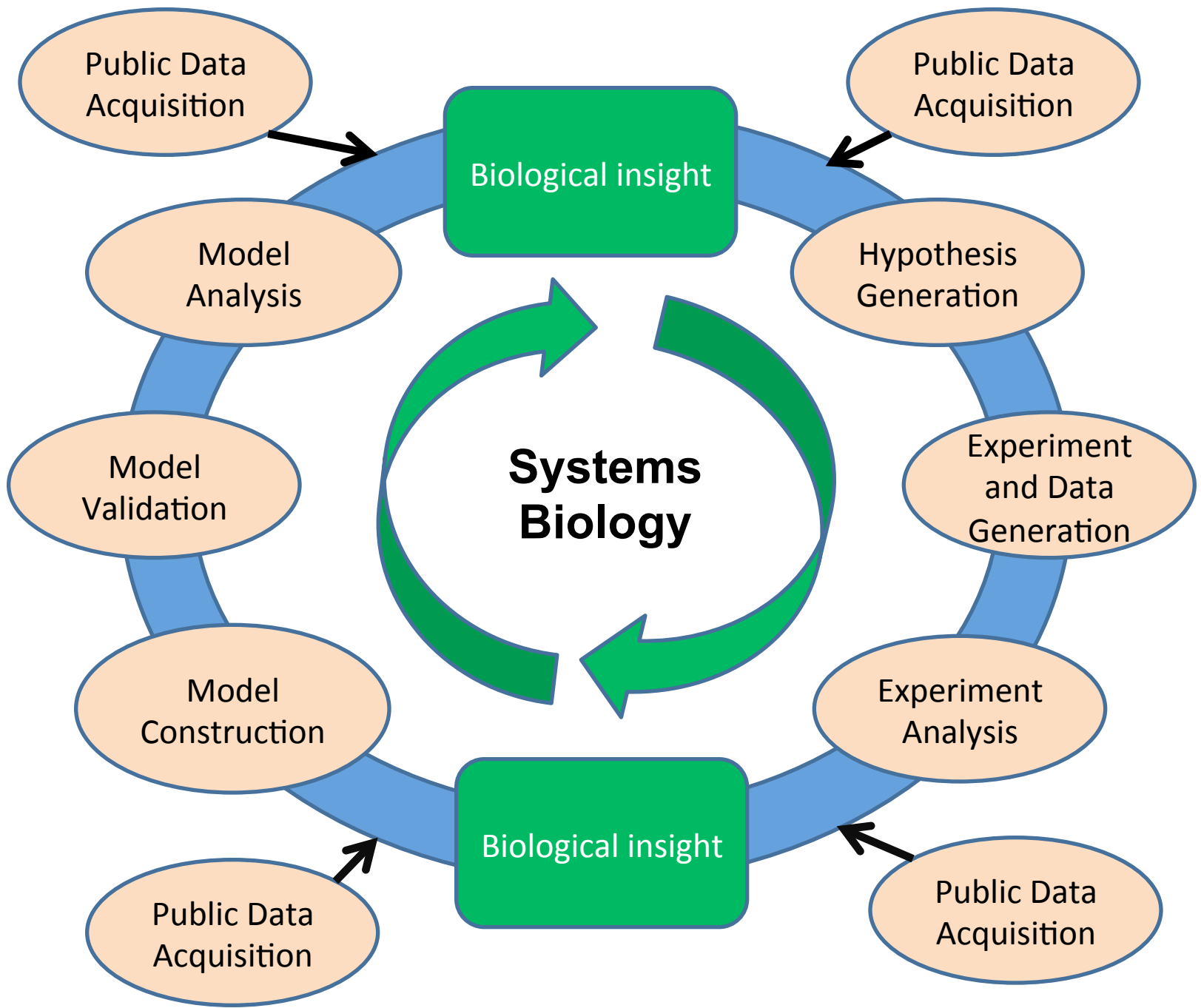
MANCHESTER
1824

The University of Manchester



Modelling

Experimental



Sponsors and Motivation



- EU ERANet programme
- 122 organisations
- 16 multi-inst. consortia
- independent projects in a two-round funding initiative



- BMBF “Großprojekt”
- ~45 organisations
- ~70 groups
- multiscale rep of the liver
- multiscale data, models
- imaging data

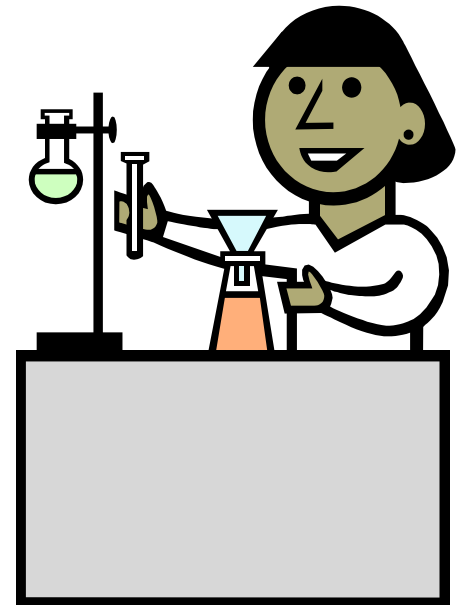
Funders

- *Preserve* results beyond projects.
- *Organise & link* data, models, processes.
- *Exchange & search* initiative's assets.
- *Share & disseminate* results
- *Improve* standard curation practice.
- *Pool* capacities.
- *Handle home-brewed* solutions with mixed resourcing and no access



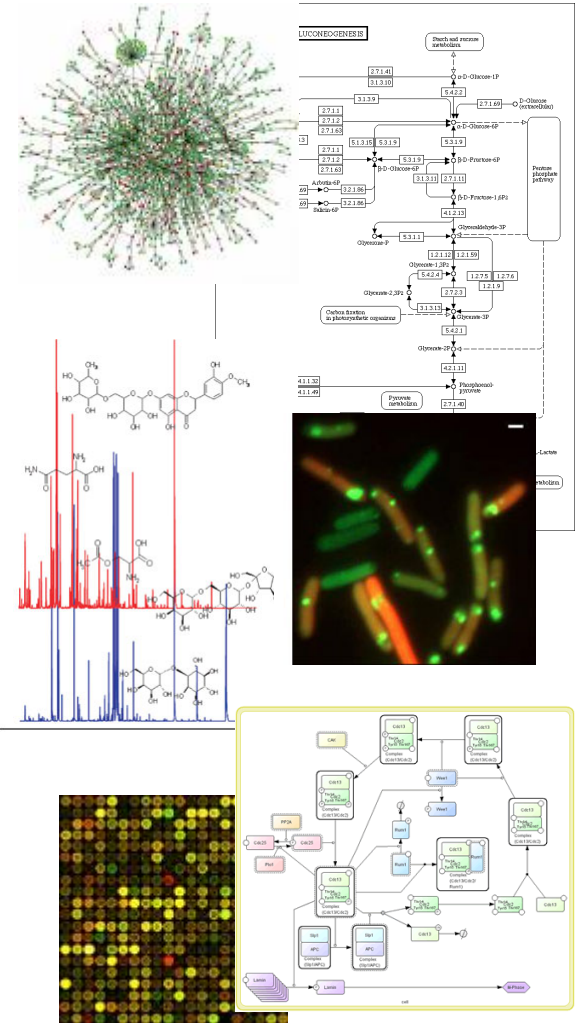
People

- Dynamic distributed groups of modellers and experimentalists.
- Mixed teams of experimentalists and modellers
- Cherished own home-grown and unstable data solutions
 - wikis, CMS, databases, spreadsheets, files)
- Access & visibility control over shared content



Content

- Locally hosted private repositories
- Public archives
- From single-cell to human
- Samples, Specimens, Standard Op Procedures
- Small Data: Reactome...: files, spreadsheets
- Big Data: NGS, Mass Spec...: Specialist repositories, files
- Models: ODE, SBML, Native Matlab, PDE, Multi-scale
- In progress: versioning, track provenance and parameters
- Published: citation, links to publications





The Web-based SEEK Platform

Ruby on RAILS 3.2, BSD,

<https://bitbucket.org/seek4science/seek>

<http://www.seek4science.org>

Find, share and exchange **Data**, **Models** and **Processes** within the [SysMO Consortium](#).



Yellow pages Experiment details **Assets** Activities Documentation

Data files **Models** SOPs Publications Biosamples

All External Search

Log in / Register

Login:

Password:

Remember me:

Alternatively...

Log in using OpenID

Log in

Need an account?

Sign up

Forgotten password?

Tags [show all]

Bacillus subtilis Biochemistry
Biochemistry and protein analysis
Bioinformatics chemostat
Computational and theoretical
biology Computational Systems
Biology Data Management
dynamics and control of
biological ne... Fermentation
Genetic modification Genetics
Mathematica Mathematical
modelling Matlab Metabolomics
Microarray analysis
Microbiology Molecular
Biology Molecular biology

[Home](#) > [Models Index](#) > TPI Kinetic Model



TPI Kinetic Model

Download Model

1 item (and an image) are associated with this Model:

Filename: tpi-model.nb

Format: Binary file type

Size: 26.0 KB



Organism: *Sulfolobus solfataricus*

Model type: Ordinary differential equations

Model format: Mathematica

Execution or visualisation environment: *Not specified*

Model image: *(Click on the image to zoom)*

$$v_{TPI} = \frac{V_{Mf} \cdot \frac{GAP}{K_{M,GAP}} - V_{Mr} \cdot \frac{DHAP}{K_{M,DHAP}}}{\left(1 + \frac{GAP}{K_{M,GAP}} + \frac{DHAP}{K_{M,DHAP}} + \frac{3PG}{K_{i,3PG}} + \frac{PEP}{K_{i,PEP}}\right)}$$

Description:

Mathematical model for TPI kinetics, GAP and DHAP saturation and inhibition with 3PG and PEP

Uploader and creators



Attributions

None

Views: 41 **Downloads:** 4

Created: 1st August 2013 at 16:54

Last used: 6th October 2013 at 13:57

<https://seek.sysmo-db.org/models/114>

Cataloguing

Find my peers

Creating and sharing
SOPs across projects

Track my
specimens

Track different
versions of my
model

yellow pages, manage SOPs and link them to investigations, studies, assays,
specimens and samples

Browse experimental data without
downloading them

How data, models and SOPs fit
together

Data viewing functionality
ISA: Link Studies to their data, models,
SOPs, samples, publications

Which data belong to which
publication

Reproducibility

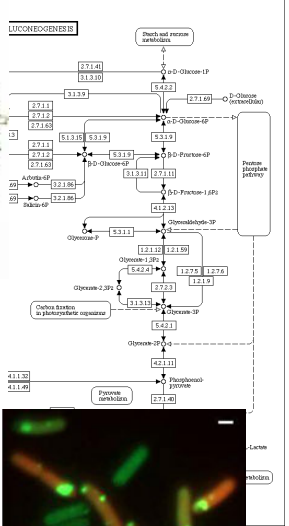
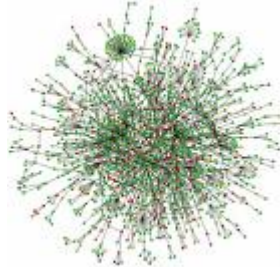
Cross-cataloguing/link, Packaging

- People, experiments procedures, data, models, samples, publications
- Common elements: enzyme rate equations; values for the K_m / V_{max} (concentration of substrate / maximal velocity of activity speed) of that enzyme



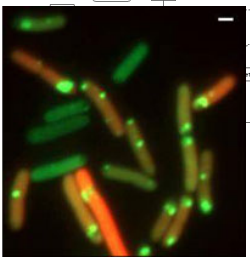
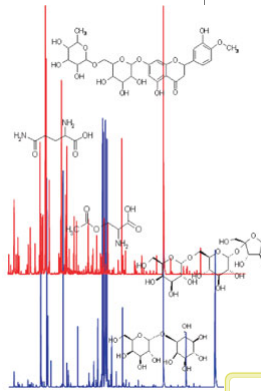
Model simulation

- Integrated simulators & data comparisons
- Differentiate construction, validation & predicted data



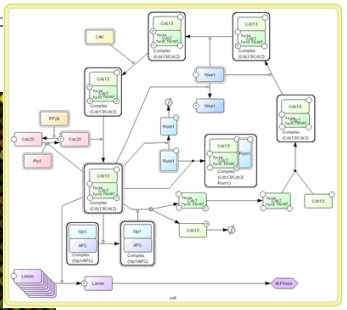
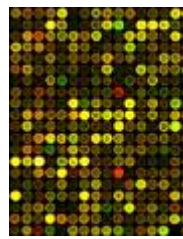
Standards compliance

- SBML, SED-ML, SBGN, MIBBI, ISA, MIRIAM, CellML, COMBINE
- Curation support: tools & services.



Access and Archiving

- Deposition to public repositories
- Gateway/cross-link to public archives & lab repositories
- Public archive for publishers, funders, researchers, trainers.

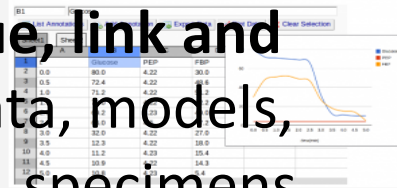


Reproducibility Card

yellow pages
of peers
projects,
experts



catalogue, link and index data, models, samples, specimens, sops, experiments, publications using standards



project mgt,
access control
reporting, citation
governance &
policies



simulate models
differentiate
construction,
validation &
predicted data



curate &
annotate data
and models using
standards with
compliance tools



manage, store and
exchange different
types and scales of
data



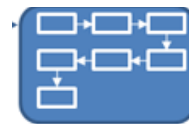
integrate local and
project tools and
data systems



incorporate public
data and model
repositories & tools
deposition



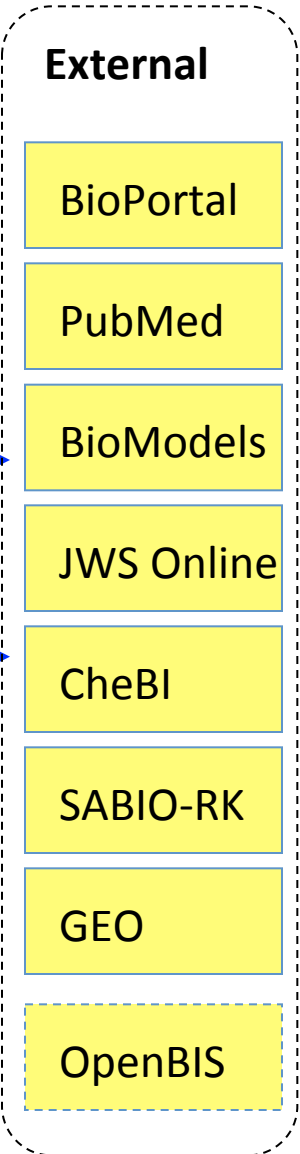
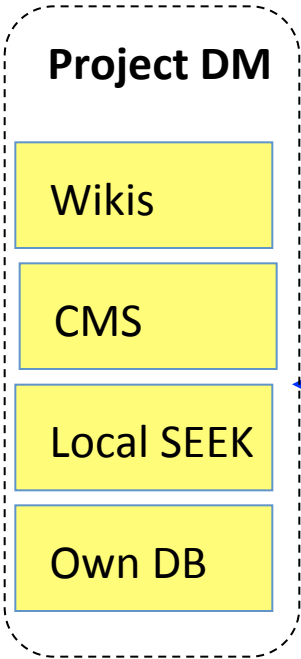
scaled-out
collection &
analytics using third
party platforms





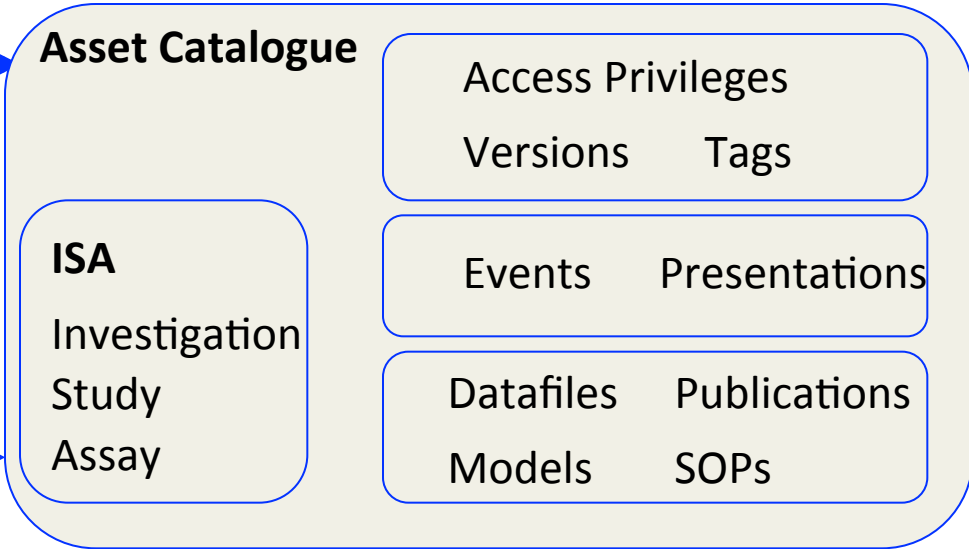
Web Interface

REST API



SEEK

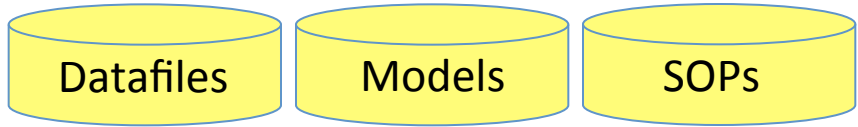
Yellow Pages People Projects Institutions



JERM Extract, Harvest, Index

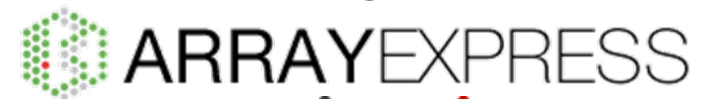
APIs and Links

Direct Upload

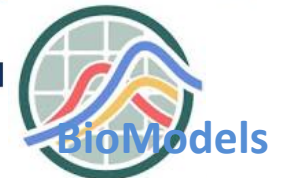


Plug-in, Play nice

- Gateway plugin framework
 - Tight and loose coupling
 - RAILS plugin or bundled GEM
- Metadata framework
 - JERM and ISA
- Different instances
 - Single query across all model repositories
 - One click deposition



JWS Online
OneStop
DataFuse



Data....

- Public and new data
- Factors studied
 - Linked -> SABIO-RK and ChEBI
- Samples and Specimens
 - Extends EBI/NCBI BioSamples
- Treatment Extraction
- Tagging with **vocabularies**
- **Spreadsheet**-based data-view
- Big Data
 - Upload and by email, Share by trusted link, Link to external repository
- Access
 - DOIs and Temp links for reviews

Add new entry manually

Item	Unit	Start value	End value	SD
concentration	mol			

Please enter the concentration of which:

Methycarbinol (Ethanol) x

Saccharomyces cerevisiae

Details about this organism

Synonyms (4)
"lager beer yeast", "brewer's yeast", "yeast", "baker's yeast"

Related Synonyms (8)
"Saccharomyces oviformis", "Saccharomyces uvarum var. melibicus cerevisiae", "Saccaromyces cerevisiae", "Candida robusta", "Sac"

Definitions (0)
None defined

[Visualise ontology term](#) | [NCBI taxonomy browser](#)

Name	Provider name	Provider's strain ID
YJM789	Not specified	Not specified
FY2 diploid	Not specified	Not specified
FY2 diploid	Not specified	Not specified

experimental assay type

- experimental assay type
- culture growth
- fluxomics
- genomics
- comparative genomics
- DNA sequencing
- genotyping
- primer design
- SNP detection
- interactomics
- protein-protein interaction profiling
- metabolomics
- cell growth optimisation
- metabolite profiling
- catabolic response

B1 Glucose

Sheet1	Sheet2	A	B	C	D	E	F
		t	Glucose	PEP	FBP		
		0.0	80.0	4.22	30.0		
		0.5	72.4				
		1.0	71.2				
		1.5	70.0				
		2.0	69.2				
		2.5	66.0				
		3.0	32.0				
		3.5	12.3				
		4.0	11.2				
		4.5	10.9				
		5.0	10.8				

VL File Transfer

File Edit SEEK Welcome Andreas!

Drop user

Wolfgang Müller Johannes Bausch Martin Golebiewski

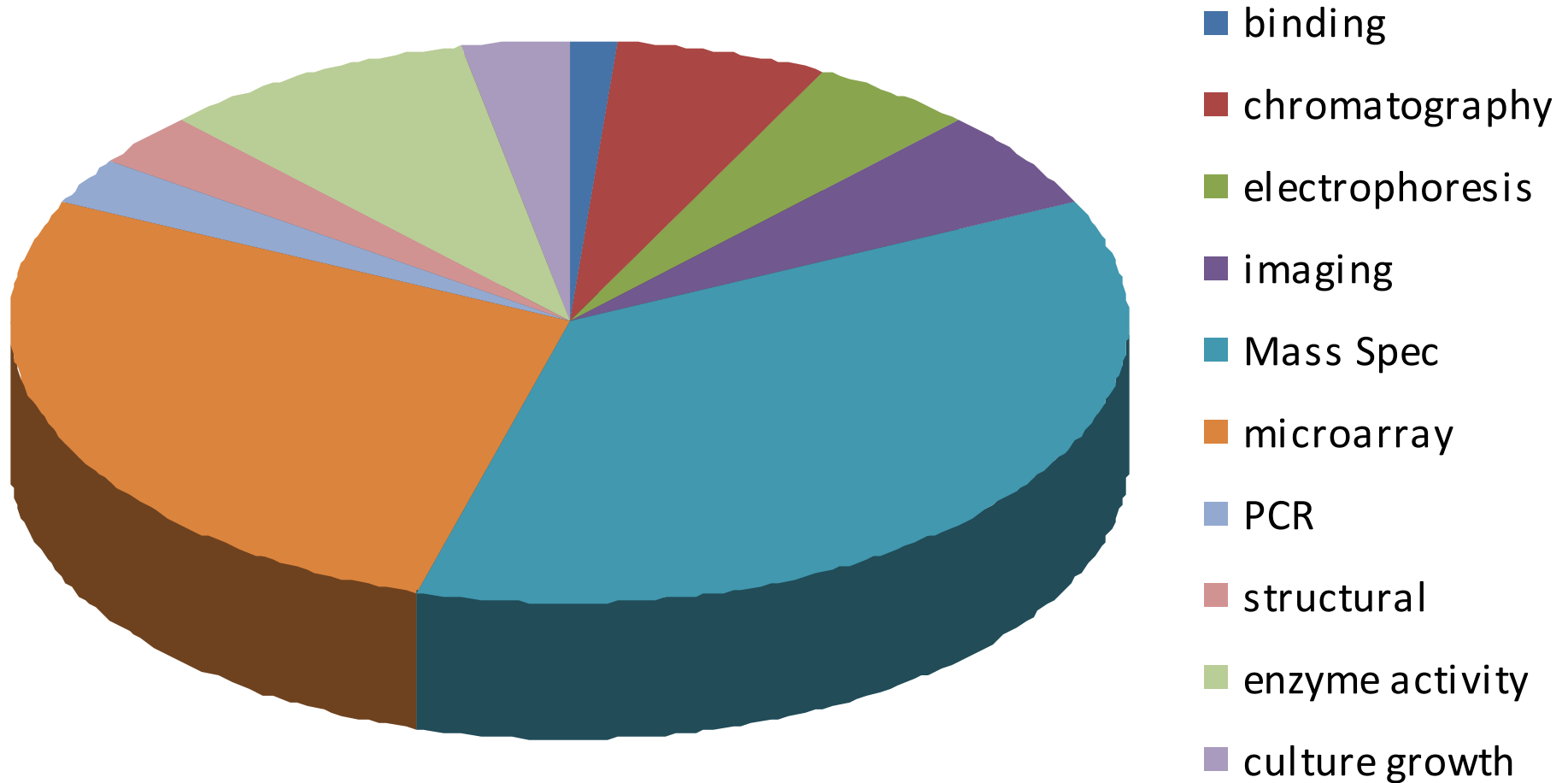
File upload

Sending file: ProgressReport.odp

64%

#	File name	Size (kB)	Recipient	Date sent	St
1	Citations.txt	3	Martin Golebiewski	Wed Dec 01 09:55...	File sent
2	ProgressReport.odp	1676	Martin Golebiewski		File trans

SysMO projects Assay and Technology Type



Unclassified not included

Models....

Repositories

- Biomodels, JWS Online, local SEEK

JWS Online Simulator

- SBML support
- Auto generation of SBGN schemas for user models
- SED-ML export

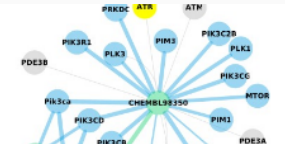
DataFuse

- Link and compare construction and validation data with models
- Run models with parameter values from spreadsheets

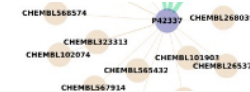
Find, share and exchange Data, Models and Processes within the SysMOOD Testing.

Download as CSV | View Results

Visualise Model with Cytoscape Web



Cytoscape



Download Model

Simulate Model on JWS

Simulate Model on Sycamore

Simulate

Steady State Analysis?

Simulate

Save as new version

Model format: SBML

Save

Validate

Check

Annotator

Annotate



Model name

Reactions

```
v[v1] {1.0}$s = {1.0}x2
v[v2] {1.0}x2 = {1.0}x3
v[v3] {1.0}x3 = {1.0}$p
```

Reactions help Show schema Hide schema

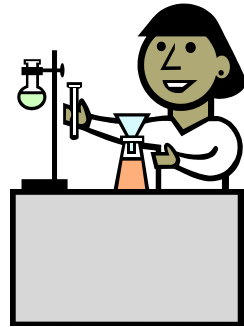
Zoom Move

vv1 v2 v3 x2 x3

Standard Formats and Vocabularies

Experiment Data

Models



SED-ML

Exchange



MIBBI Standards
OBO Controlled
Vocabularies

Exchange

Construction
Comparison
Verification
Prediction

Exchange

SBML

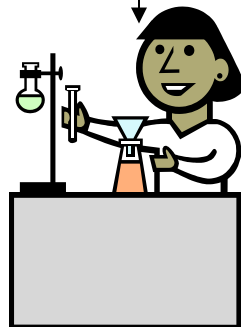
MIRIAM

SBGN

SemanticSBML

CellML

**Just
Enough
Results
Model**



Exchange



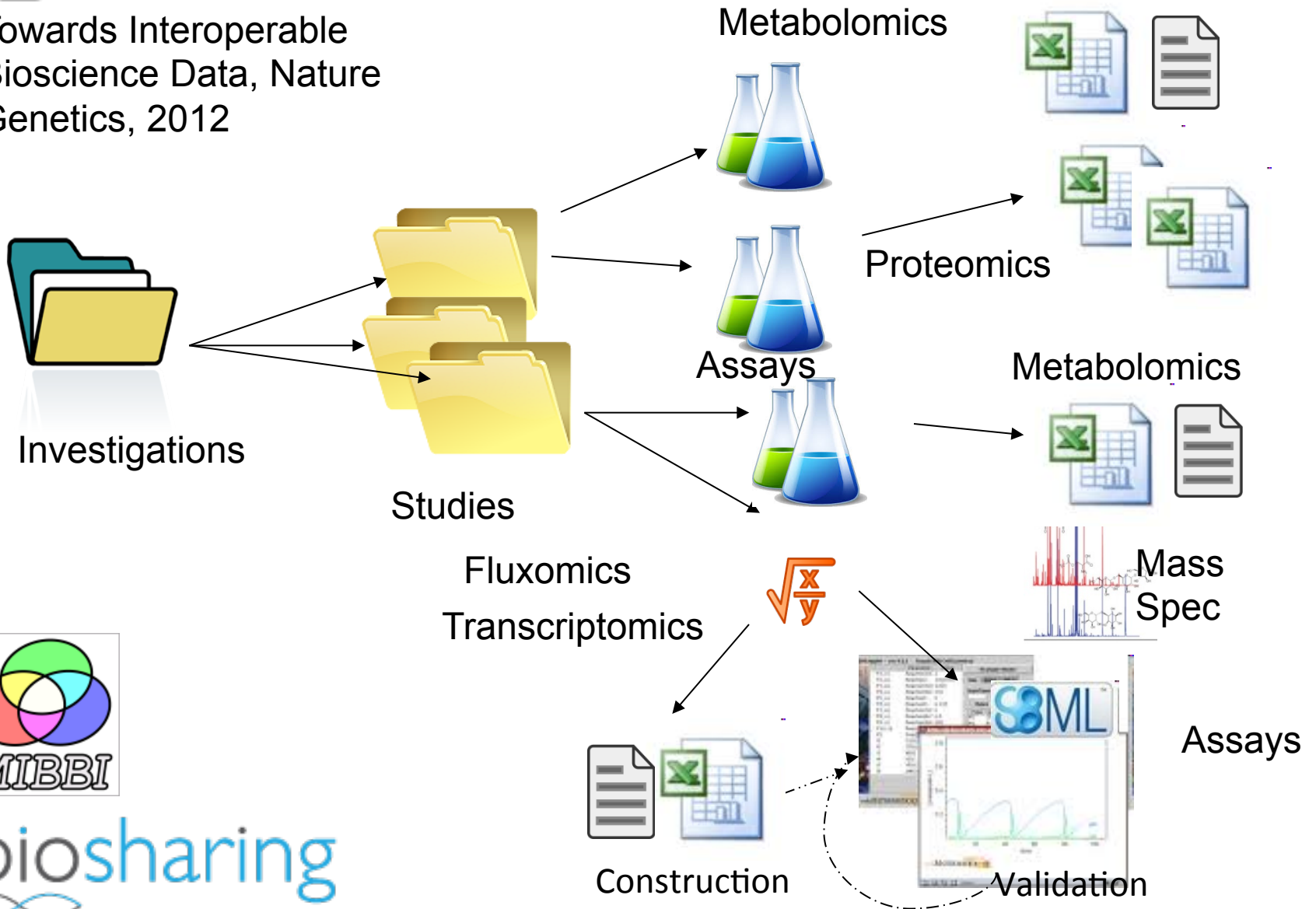
ISA-TAB

Simulation Experiment Description Markup Language



Standards, Structure, Interlink

Towards Interoperable
Bioscience Data, Nature
Genetics, 2012





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Remember me:

Alternatively...

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Tags [show all]

- Bacillus subtilis Biochemi
- Biochemistry and protein an
- Bioinformatics Computati
- and theoretical biology
- Computational Systems Bio
- Data Management dynamic
- control of biological ne.
- Fermentation Genetic
- modification Genetics
- Mathematica Mathematic
- modelling Matlab Metabol
- Microarray analysis
- Microbiology
- Molecular Biolog

[Home](#) > Data files Index

Latest A B C D E F G H I J K L M N O P Q R S T U V W X Y Z Other All



Activation / Inhibition of 4 LDH enzymes in the presence of phosphate ions (Pi).

Uploader: Anna Feldman-Salit

Creator: Anna Feldman-Salit

Other creators: Not specified

Version: 1

Projects: SysMO-LAB

View

Download

The Table represents the simulation results of how the presence of phosphate ions (Pi) in the solution might affect the activity of four LDH enzymes. This includes the



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Tags [show all]

- Bacillus subtilis Biochemistry
- Biochemistry and protein analysis
- Bioinformatics Computational
- and theoretical biology
- Computational Systems Biology
- Data Management dynamics and
- control of biological ne...
- Fermentation Genetic
- modification Genetics
- Mathematica Mathematical
- modelling Matlab Metabolomics

[Home](#) > [Models Index](#) > BSA115-sigB-adaptation



BSA115-sigB-adaptation

Download Model

The zip file contains model files and an experiment file. Unpack it in a directory and navigate with matlab to there. Use the 'matlab_execution_guide.m' for simulation and visualisation of the model. This file is written in matlab cell mode, so it is not a stand alone function.

Three models have been developed to test their capacity to reproduce the experimental data from Study: 'Controlled sigmaB induction in shake flask' with Assay: 'IPTG induction of sigmaB in BSA115'.

One model assumes a post-transcriptional inhibition (PTI) in the expression of the lacZ reporter gene. The PTI is either due to induced instability of lacZ mRNA or LacZ protein after activation of sigmaB. A hypothetical sigmaB dependent protein RegB is responsible for PTI. It is either a RNase or protease in this model.

One model assumes a transcription inhibitory effect on sigmaB dependent expression by a sigmaB dependent protein called RegB. This protein might bind to the sigma factor to decrease its efficacy in inducing transcription.

One model assumes that a protease called RegB acts specifically on sigmaB. This protease is also induced by sigmaB.

All models is based on mass-action (nearly so). Parameter for IPTG concentration is [100,200,1000], kbs, the expression parameter of Pspac-dependent sigmaB is fixed at 100. All other six parameters are estimated with two of the three experiments as training set (IPTG 0.1 and 0.2 mM) and one experiment as test set (IPTG 1mM). Parameter estimation is performed with SBToolbox2 using multiple rounds of particle swarm algorithm (pswarm).

1 item is associated with this Model:

Filename: BSA115-sigB-adaptation.zip

Upload

sigB

Views: 19

Created:

Last update:

Last used:

Log in / Register

Login:

 Password:

 Remember me:
 Alternatively...
 Log in using OpenID

Need an account?
Sign up
 Forgotten password?

Tags [show all]

- Bacillus subtilis
- Biochemistry
- Biochemistry and protein analysis
- Bioinformatics
- Computational and theoretical biology
- Computational Systems Biology
- Data Management
- dynamics and control of biological ne...
- Fermentation
- Genetic modification
- Genetics
- Mathematica
- Mathematical modelling
- Matlab
- Metabolomics
- Microarray analysis
- Microbiology**
- Molecular Biology**
- Molecular biology techniques (RNA/DNA...)
- Molecular microbiology
- ODE parameter estimation
- Proteomics
- Systems Biology
- Transcriptomics

Organisms

- Bacillus subtilis
- Clostridium acetobutylicum
- Enterococcus faecalis
- Escherichia coli
- Lactic Acid Bacteria



Yeast Glycolytic Oscillations

Investigating oscillations at the level of yeast populations and individual cells

ID: 50

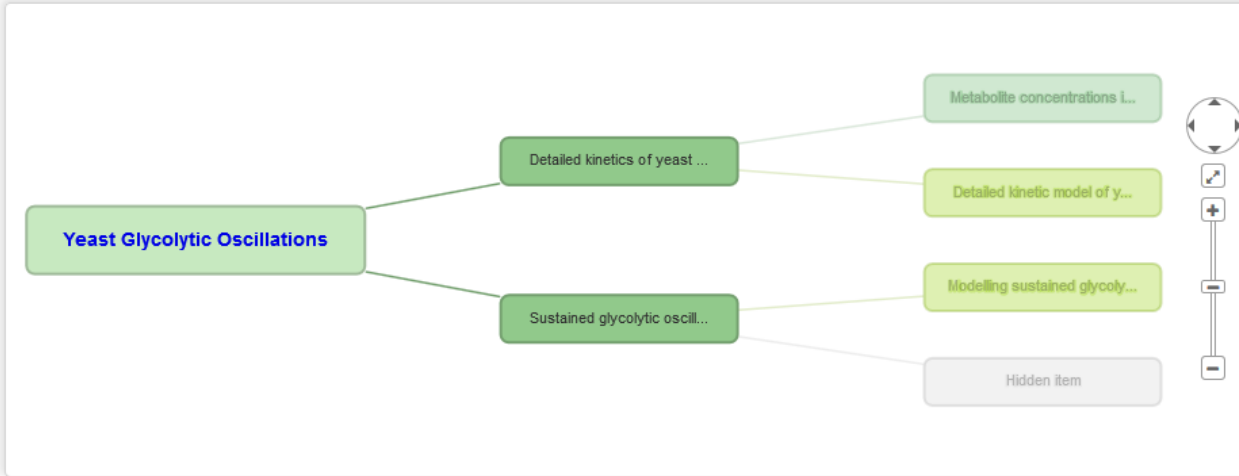
Projects: SysMO DB

Creators



Views: 136

Created: 20th Feb 2013 at 15:33



Chosen item

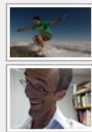
Investigation: Yeast Glycolytic Oscillations

Connected items

- Study:** Sustained glycolytic oscillations in individual isolated yeast cells
- Study:** Detailed kinetics of yeast glycolytic oscillation

Related items

- People (1)
- Projects (1)
- Studies (2)
- Assays (3+1)
- Data files (3+8)
- Models (10+1)
- Publications (3)



Das (1991) NADH and ATP concentrations determined during different phases of glycolytic oscillation in yeast extracts

View
 Download

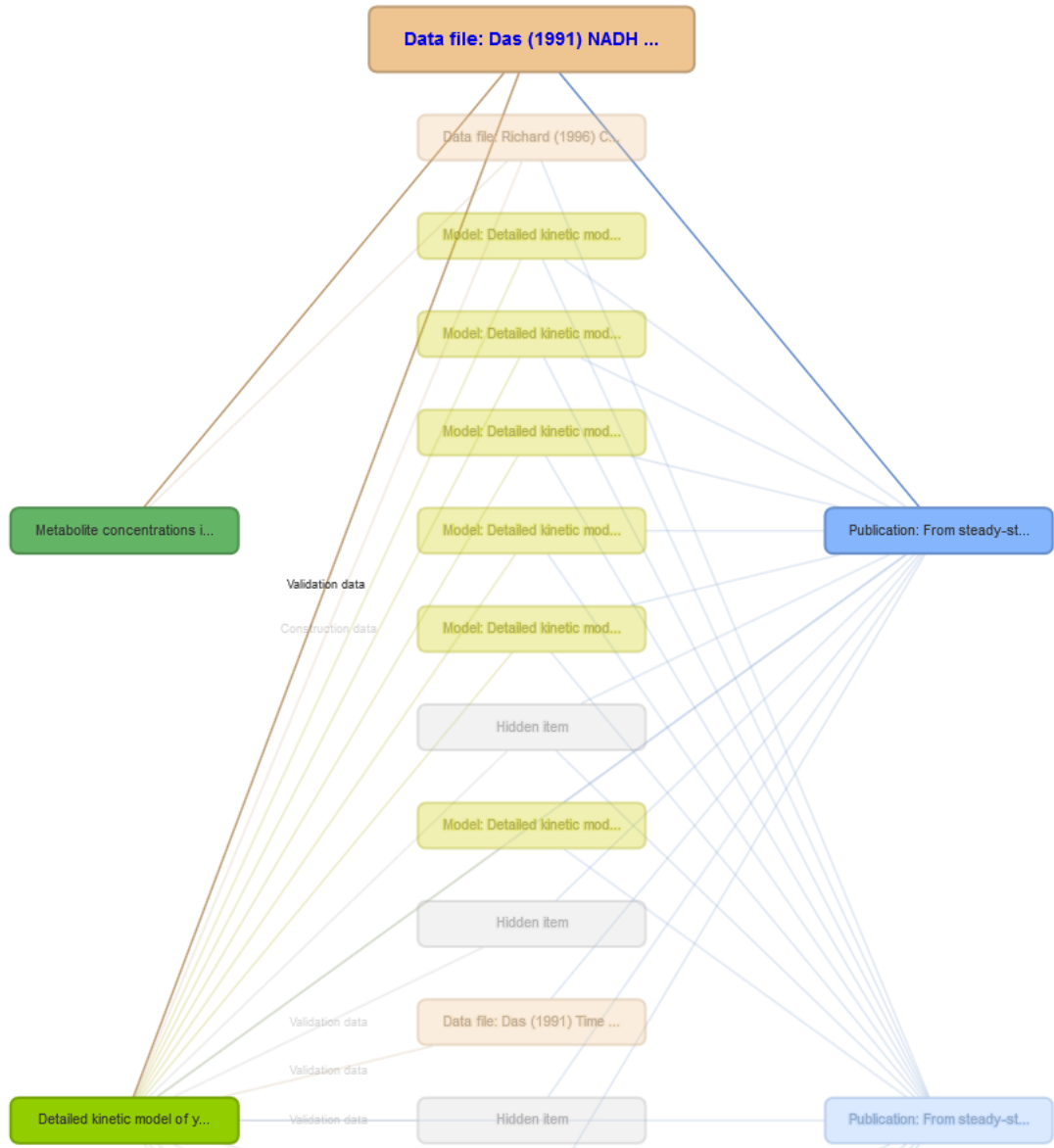
Uploader: Franco Du Preez
 Creators: Franco Du Preez, Jacky Snoep

Version: 2
 Projects: SysMO DB

modification Genetics
 Mathematica Mathematical
 modelling Matlab Metabolomics
 Microarray analysis
Microbiology
 Molecular Biology
 Molecular biology techniques
 (RNA/DNA... Molecular
 microbiology ODE parameter
 estimation Proteomics Systems
 Biology Transcriptomics

Organisms

Bacillus subtilis
 Clostridium acetobutylicum
 Enterococcus faecalis
 Escherichia coli
 Lactic Acid Bacteria
 Lactobacillus plantarum
 Lactococcus lactis
 Pseudomonas fluorescens
 Pseudomonas putida
 Saccharomyces cerevisiae
 Streptococcus pneumoniae
 Streptococcus pyogenes
 Streptomyces coelicolor
 Sulfolobus solfataricus
 Trypanosoma brucei



Chosen item

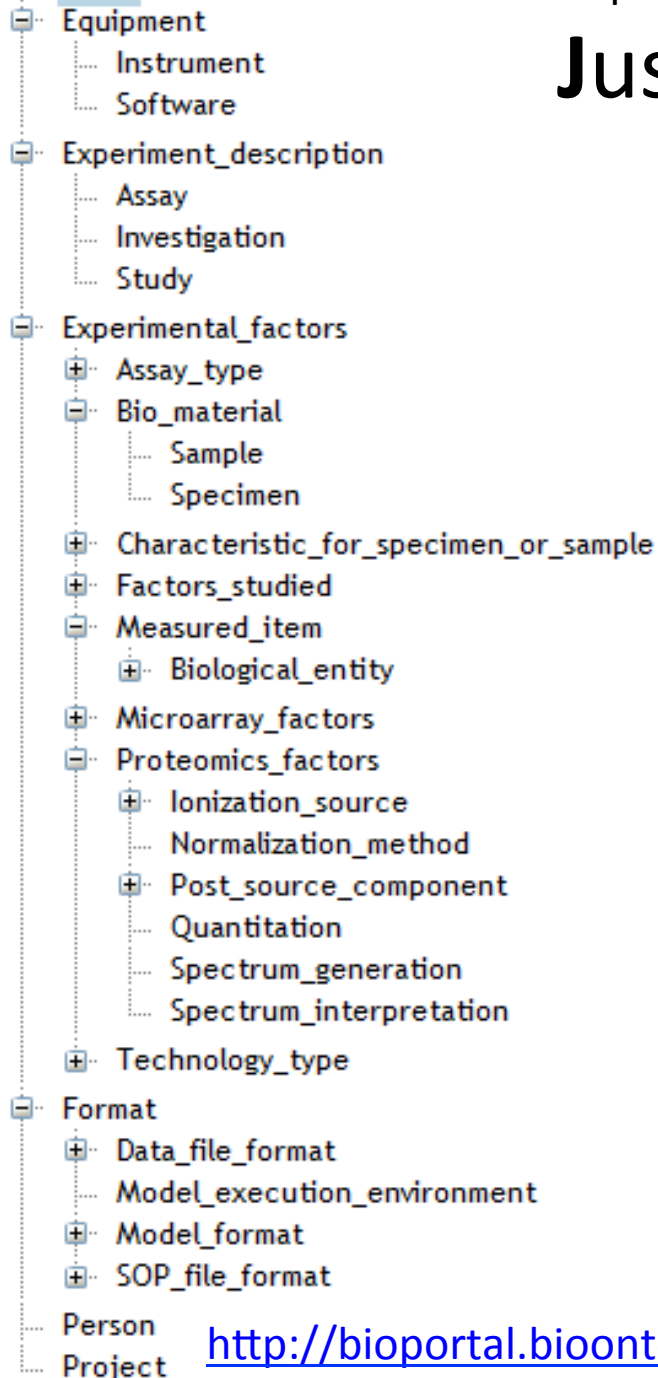
Data file: Das (1991) NADH and ATP concentrations determined during different phases of glycolytic oscillation in yeast extracts

Connected items

Publication: From steady-state to synchronized yeast glycolytic oscillations II: model validation
Modelling Analysis: Detailed kinetic model of yeast glycolytic oscillation
Experimental Assay: Metabolite concentrations in yeast glycolytic oscillations



Asset 262 classes and 43 properties



Just Enough Results Model

- Overarching Application Ontology
- Describes and enriches the relationships between things produced and used in experiments
 - experiment descriptions
 - provenance of projects
 - data, models, results, samples, protocols, standard operating procedures, publication...
- For the experiments themselves
 - reuse community ontologies, markups, mim, identifiers
 - MGED/EFO, PSI-MS, SBO, CheBI ids etc

<http://bioportal.bioontology.org/ontologies/JERM> expressed in OWL



Type of data	What was measured	Values in the datasets	Biological sample and treatments applied
Microarray, growth curve, enzyme activity...	Gene expression, OD, metabolite concentration...	Units, time series, repeats...	
<i>Common elements</i>			

Just Enough Results Model
 Describes and enriches the relationships between things produced and used in experiments.

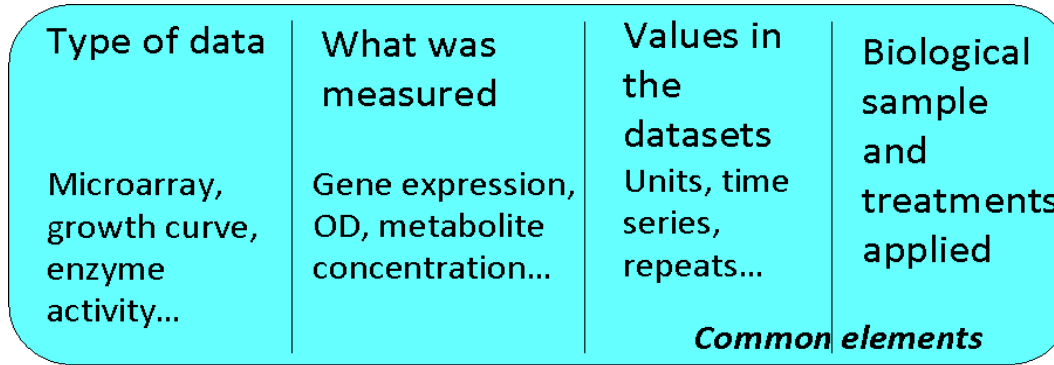
reuse community ontologies, markups, mim, identifiers

Enzymic reactions
 reactions catalyzed, substrates, products, inhibitions
CheBI ids

Microarray
 QC methods normalisation
MGED/EFO

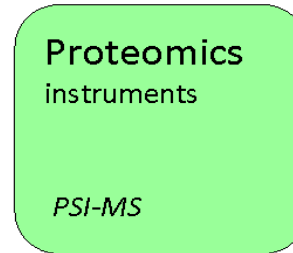
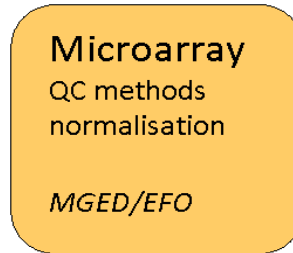
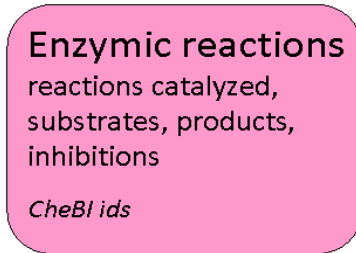
Proteomics
 instruments
PSI-MS

Data type specific elements



Just Enough Results Model
Describes and enriches the relationships between things produced and used in experiments.

reuse community ontologies, markups, mim, identifiers



Data type specific elements

metadata sheets

1	Assay Title	PGK
2	Assay SEEK ID	16
3	Assay Title	PGK
4	Assay type	enzymaticAssay
5	Technology_type	enzymaticAssay
6	Description	Extracellular Metabolite concentration flux balance analysis
7	Experimentalist	fluomics
8	Date	gene expression profiling
9	SOP	genome-scale enzyme activity profiling
10	Experimental_conditions	peromics
11	Item	perostyling
12	Compound (if concentration)	concentration
13	Unit	3PG
14	Start_value (optional)	mM
15	End_value (optional)	5
16	Culture growth	5
17	FACTORS_STUDIED	Chemostat
18	Item	concentration
19	Compound (if concentration)	ATP
20	Unit	mM

sample sheets

1	Sample Name	Organism	NCBI_ID	Strain	Enzymes	Phenotype	Genotype	Treatments (Factors_studied)
2	A01	Organism						
3	B01	Bacillus subtilis						
4	C01	Clostridium acetobutylicum						
5	D01	Enterococcus faecalis						
6	E01	Escherichia coli						
7	A02	Lactococcus lactis						
8	B02	Pseudomonas fluorescens						
9	C02	Pseudomonas putida						
10	D02	Saccharomyces cerevisiae						
11	E02	Organism						
12		Organism						
13		Organism						
14		Organism						
15		Organism						

Note: this sheet allows you to describe your samples in as much detail as required. Sample names can be...

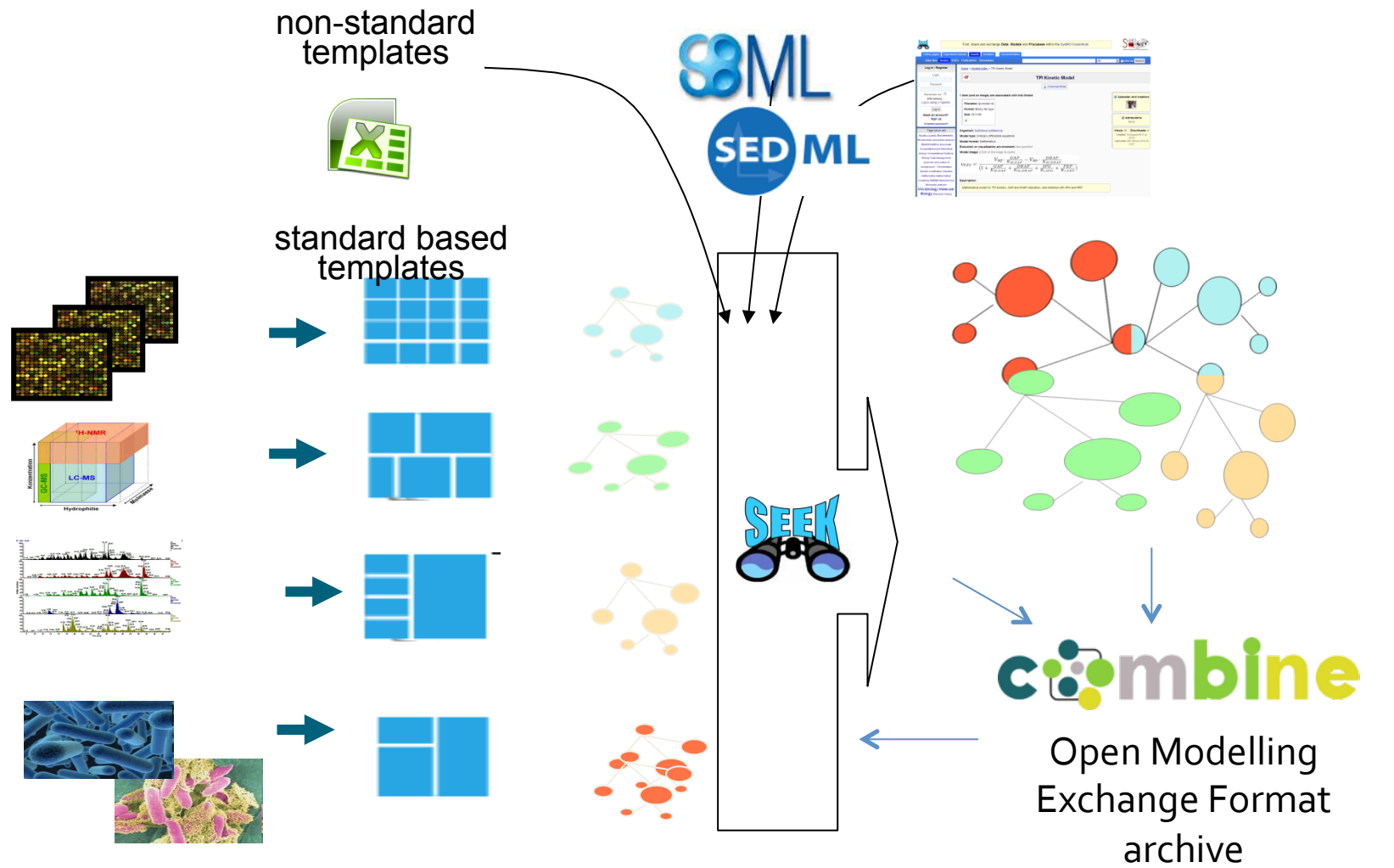
indexes

data sheets

	A	B	C
1	Samples	Measurements (e.g. Concentration)	
2		Units	
3	A01		
4	B01		
5	C01		
6	D01		
7	E01		
8	A02		

RightField





Different types of data
 Plugins to registered data repositories

Extract and auto-catalogue metadata

Define relationships, cross-link, aggregate, query

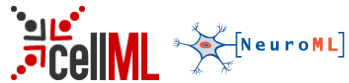


Sys Bio Research Objects

<http://www.researchobject.org>

Systems Biology:

A common archive format for reuse across tools



Adobe UCF



ePUB

OASIS

ODF



ORE

W3C[®]

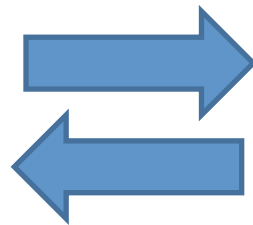
PROV



JSON-LD

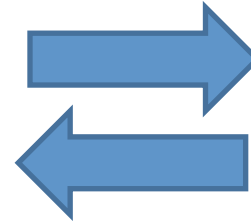


OMEX archive



researchobject

Research Object Bundle



zenodo



- Aggregation
- Annotations/provenance
- Ad-hoc domain-specific specification

RightField

<http://rightfield.org.uk/>



Semantic Annotation by Stealth Instrumented Spreadsheets

- Desktop tool
- Embed ranges of ontology terms into spreadsheets
- Annotate data with terms through drop-down lists
- Automatically extract semantically annotated metadata from annotated spreadsheets (and produce RDF)

metadata sheets

2	Asset Title	PGK_ATP
3	Uploader	A SEEK Scientist
4	Uploader SEEK ID	
5	Project	
6	ASSAY	
7	Assay SEEK ID	16
8	Assay Title	PGK
9	Assay_type	enzymaticAssay
10	Technology_type	Enzymatic Assay
11	Description	Extracellular Metabolite concentration
12	Experimentalist	flux balance analysis
13	Date	Ruonans
14	SOP	gene expression profiling
15	Experimental_conditions	genome-scale enzyme activity profiling
16	Item	genomics
17	Compound (if concentration)	concentration
18	Unit	3PG
19	Start_value	Organism
20	End_value	
21	Culture	
22	FACTORS	
23	Item	NCBI_ID
24	Compound	Strain
25	Unit	Genotype
26	Start_value	Phenotype
27	End_value	organism/cell part
28	Culture	Treatments (Factors studied)

sample sheets

1	Sample Name	NCBI_ID	Strain	Genotype	Phenotype	organism/cell part	Treatments (Factors studied)
3	A01	Organism					
4	B01	Bacillus subtilis					
5	C01	Clostridium acetobutylicum					
6	D01	Escherichia coli					
7	E01	Lactococcus lactis					
8	A02	Pseudomonas fluorescens					
9	B02	Pseudomonas putida					
10	C02	Saccharomyces cerevisiae					
11	D02	Organism					
12	E02	Organism					

indexes

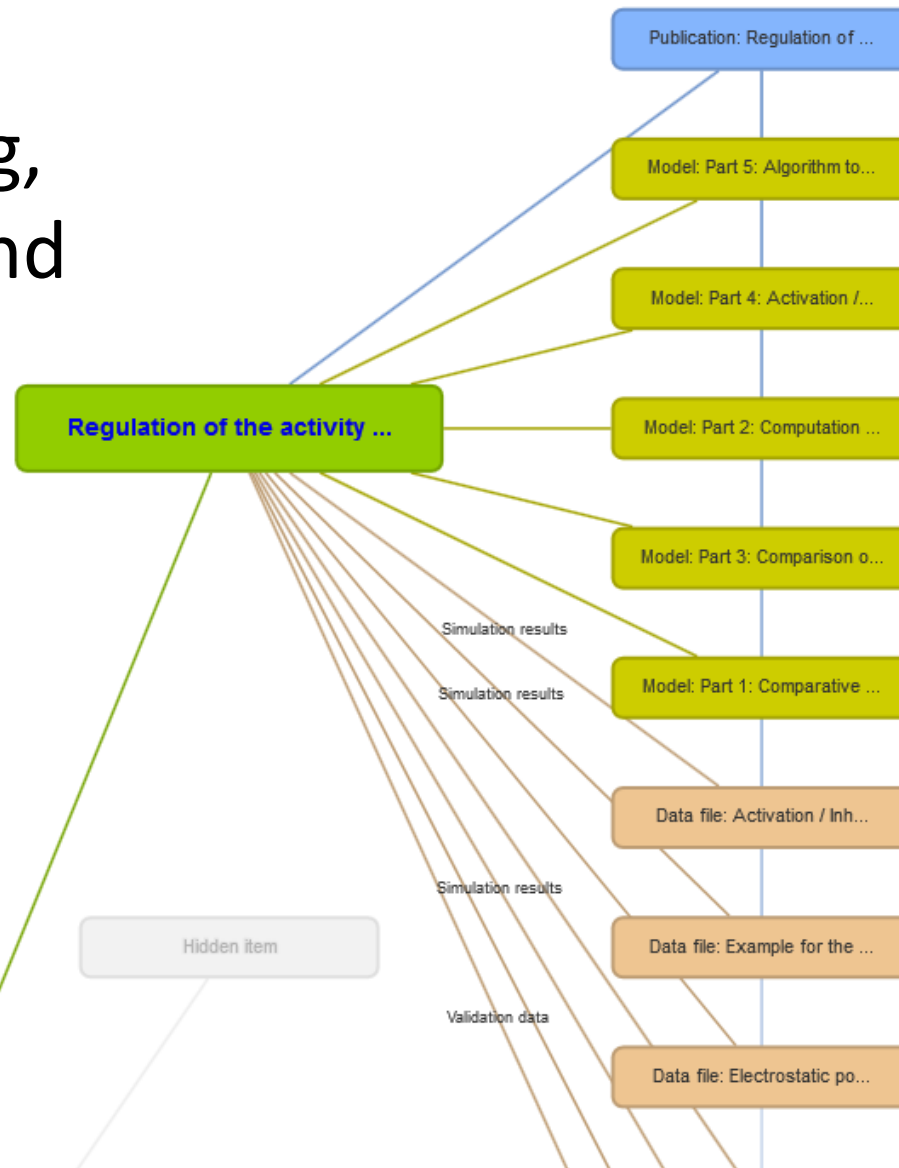
	A	B	C
1	Samples	Measurements (e.g. Concentration)	
2		Units	
3	A01		
4	B01		
5	C01		
6	D01		
7	E01		
8	A02		

data sheets

Question	Lucene	RDF
Which experiments were carried out on <i>E.coli</i> (organism X)?	+	+
What proteomic (experiment x) data is available? What types of transcriptomics (assay type x) experiments were performed?	+/+	+/+
Who has experimental data on gene/protein/metabolite X	+/+/+	+/+/+
What data was used to construct the model and what data was used to validate it?	+	+
Who is in the COSMIC (project X) project?	+	+
Are there any models on yeast (models on X)?	+	+
What SOP were used in experiment X? are there any protocols for Mass Spectroscopy (tech type X) experiments?	-	+
Which microarray data files show up-regulation in genes with Gene ontology molecular function X	-	+
Who is in more than one SysMO project?	-	+
What are the factors studied in the MOSES project (project X)?	-	+
What range of concentrations of metabolites (extra- and intracellular) are detectable from organism XXX	-	+
How good is the correlation between transcriptome levels, proteome levels and enzyme activities in organism X in study Y? Is a time delay observed?	-	-

Reproducible (Open?) Research

Data sharing,
openness and
careers
incentive



See Titus and Phil talks

Chosen item

Modelling Analysis:

Regulation of the activity of lactate dehydrogenases from four lactic acid bacteria

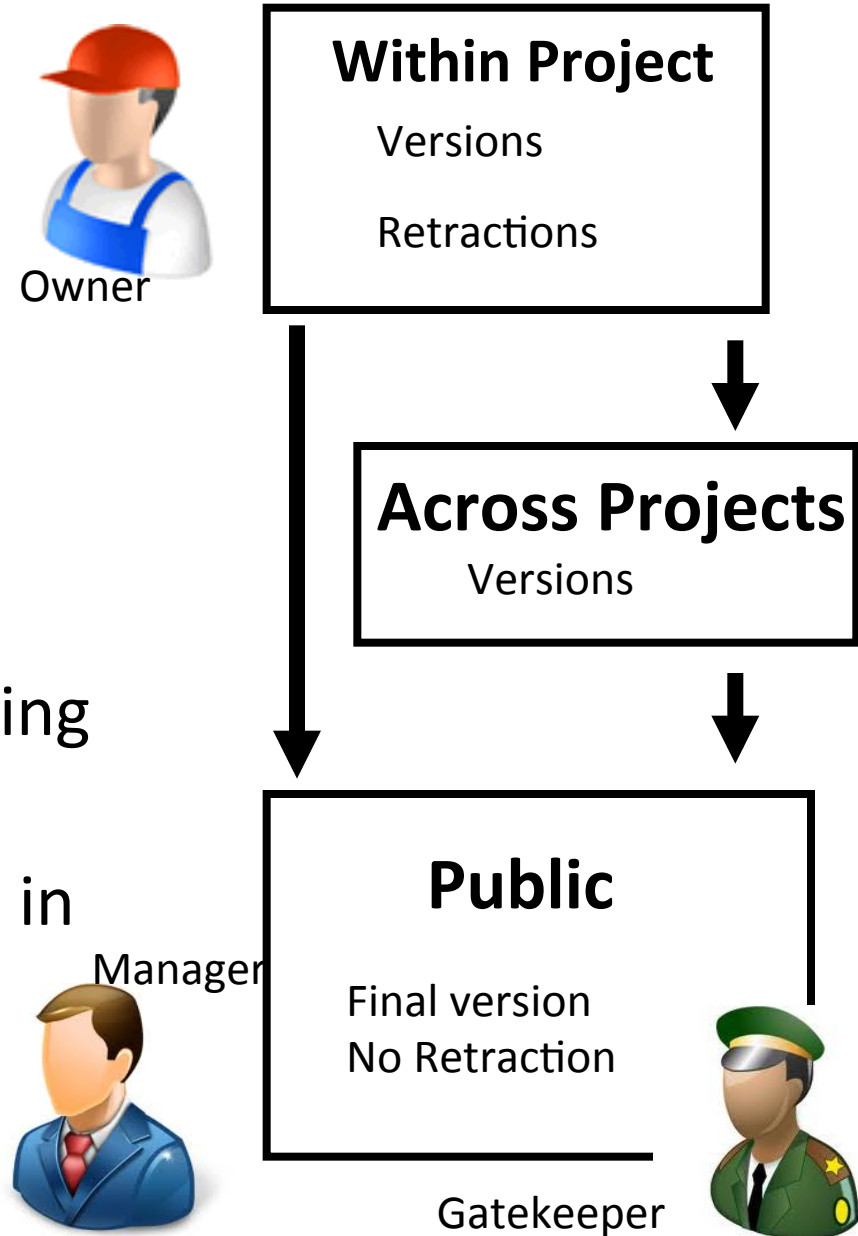
Connected items

Data file: The effects of fructose-1,6-bisphosphate, phosphate and ionic strength on enzyme activity differ for the three L-DHs from three

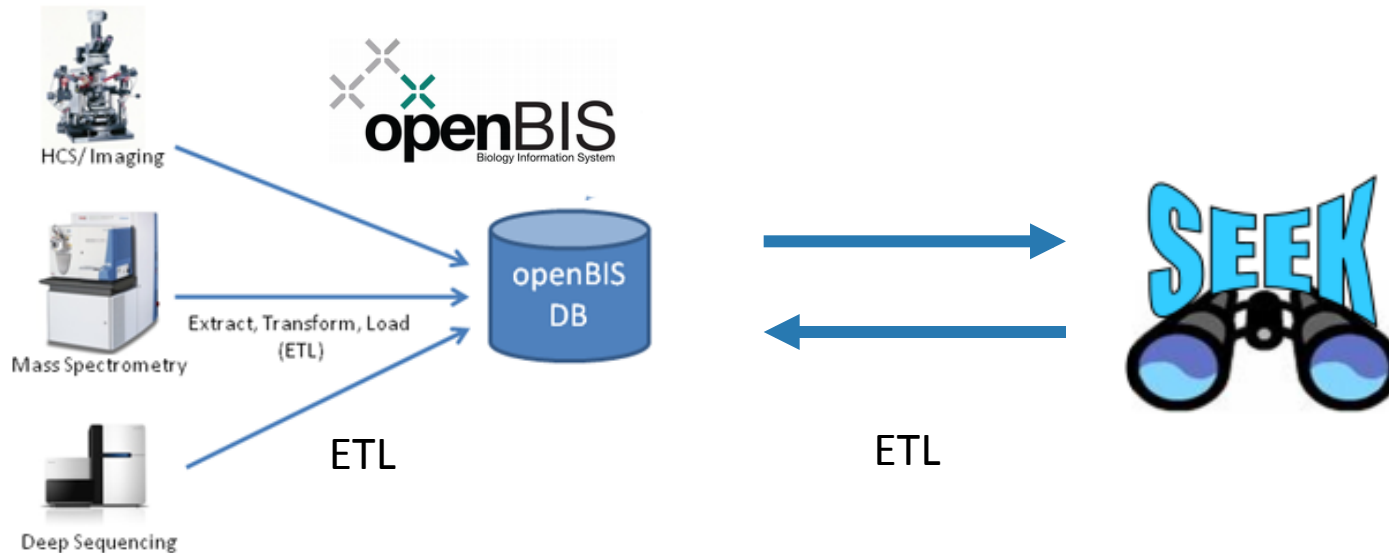
Open Research: Research Groups & Lifecycles

- Sharing policy
- Visibility, Downloadability
- Fine grained permissions

- Protocols for
 - Management transfer
 - Visibility feedback and sharing workflows
 - Publication data deposition in external public stores
 - Batch publishing



OpenBIS and SEEK



Open BIS back-end: Extract, Transform and Load tooling direct from the instrumentation, along with data analysis pipelines. Automatic archiving. Handles large data.

SEEK front-end: A rich web interface for describing, finding, linking and promoting ongoing research and outcomes.



Open Source Customisable Platform

<https://bitbucket.org/seek4science/seek>

Briefings in Bioinformatics Advance Access published October 9, 2012
BRIEFINGS IN BIOINFORMATICS, page 1 of 14
doi:10.1093/bib/bbs064

Yeast Glycolysis



Vrije Universiteit, Amsterdam

Data management strategies for multinational large-scale systems biology projects

Wasco Wruck, Martin Peuker and Christian R.A. Regenbrecht

Submitted: 13th July 2012; Received (in revised form): 4th September 2012



Key Points

- Incentives to share data can be given by data citation credits (datacite).
- Open access to research data can be advanced via making sharing a condition of funding.
- Data management systems might be made attractive via alleviating and improving researchers' work, e.g. support for standard formats and publications.
- The reviewed systems proved useful for systems biology projects at least in dedicated environments, SysMO-SEEK out-of-the-box provides most useful features for large-scale systems biology projects.

ElasticAP RosAge
Reactive oxygen species and the dynamics of ageing



FORSYS MACS

SBCancer. SIFSYS biotec


<http://bib.oxfordjournals.org/content/early/2012/10/09/bib.bbs064.full.p>



Open Source Customisable Platform

<https://bitbucket.org/seek4science/seek>

Home Workflows Runs Contact Log in / Register

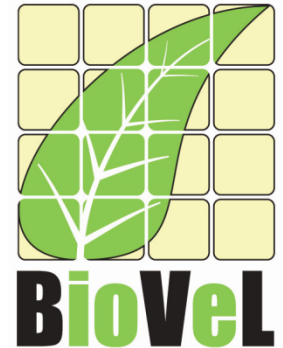


Welcome to the BioVeL Portal
For technical support or questions about the BioVeL Project, please visit the contact page.

Choose an analysis...

- Taxonomic Refinement
- Ecological Niche Modelling
- Metagenomics
- Phylogenetics

Home Workflows Runs Contact Log in / Register



Home Workflows Runs Contact Log in / Register

Workflows

Search workflows... Search Clear

- Bioclim workflow with interaction** (Ecological Niche Modelling)
This workflow takes as input a file containing species occurrence points to create a model with the openModeller Web Service using the Bioclim algorithm. Environmental layers and mask are selected during the workflow. Points are filtered so that only environmentally unique points are used to create
...
Uploaded 25 Mar 2014 14:34:43 UTC Run workflow
- BioVeL ESW DIFF - ENM Statistical Workflow with raster difference computation** (Ecological Niche Modelling)
The ENM Statistical Difference Workflow (ESW DIFF) allows the computation of the extent and intensity of change in species potential distribution through computation of the differences between two raster layers using the R statistical environment (R Core Team 2013). The difference file is computed
...
Uploaded 25 Mar 2014 14:27:29 UTC Run workflow
- BioVeL ESW STACK - ENM Statistical Workflow with raster stack computation** (Ecological Niche Modelling)
The ENM Statistical Stack Workflow (ESW STACK) allows the computation of the extent, intensity and a cumulated potential species distribution through computation of a average sum layer from the input raster layers using the R statistical environment (R Core Team 2013). The sum layer is computed from
...
Uploaded 5 Feb 2014 10:41:59 UTC Run workflow
- Data Refinement Workflow v15** (Taxonomic Refinement)
The aim of the (Taxonomic) Data Refinement Workflow is to provide a streamlined workflow environment for preparing observational and specimen data sets for use in scientific analysis on the Taverna platform. The workflow has been designed in a way that
• accepts input data in a recognized format.
...
Uploaded 8 May 2014 13:16:37 UTC Run workflow

Currently showing
All workflows

Filter by category

- Taxonomic Refinement
- Ecological Niche Modelling
- Metagenomics
- Phylogenetics
- Population Modelling
- Ecosystem Modelling
- Other

Filter by uploader

- Robert Haines
- Finn Bacall
- Sarah Bourlat
- Saverio Vicario
- Francisco Quevedo

Show all users

Logo of the European Union

BioVeL has received funding from the European Union's Seventh Framework Programme for research, technological development and demonstration under grant agreement no. 283359.



Open Facility for European Systems Biology data & model management seeded by EU programmes

- **Platform**

- SEEK + openBIS + new features & styling

- **Resource**

- EuroSEEK + pool of community resources (including established SEEKs).

- Independent researchers. Secure data.

- **Facility**

- Curation & support services, training



SystemsX.ch
The Swiss Initiative in System Biology





Open Facility for European Systems Biology data & model management seeded by EU programmes

- **Community**

- workshops, user and developer forums, knowledge network, standards & policy, training, FAIRDOM Foundation, **Model Carpentry**.

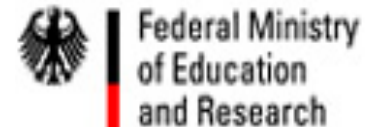
- **Sys Bio Developers Foundry workshop**

- 6-7 October Heidelberg

- http://fair-dom.org/wiki/Foundry_workshop

- **RI**

- working with other EU RIs, an EU network of national facilities, funding models.



SystemsX.ch
The Swiss Initiative in System Biology





Carole Goble



Jacky Snoep



Wolfgang
Mueller



Peter Kunszt

Natalie
Stanford



Stuart Owen



Olga Krebs



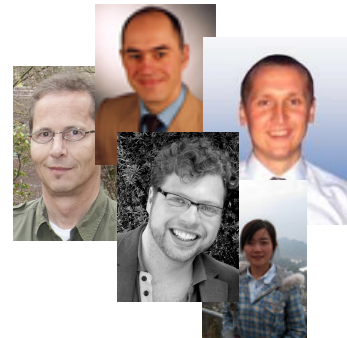
Quyen Nguyen



Bernd Rinn



also contributing:
UK SEEK team



also contributing:
VLN SEEK team



Katy Wolstencroft

