FAIRDOM for Findable, Accessible, Interoperable, and Reusable Research Data

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CHARME MC meeting & workshop
October 1 -3 2018, Valetta, Malta

FAIRDOM


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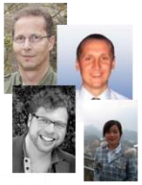
Standards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PALs, users developers

PLoS Med. 2005 Aug; 2(8): e124.
Published online 2005 Aug 30. doi: 10.1371/journal.pmed.0020124

PMCID: PMC1182327
PMID: 16060722

Why Most Published Research Findings Are False

John P. A. Ioannidis

SERIES | RESEARCH: INCREASING VALUE, REDUCING WASTE | VOLUME 383, ISSUE 9912, P166-175, JANUARY 11, 2014

PDF [219 KB]

Increasing value and reducing waste in research design, conduct, and analysis

Prof John P A Ioannidis, MD • Prof Sander Greenland, DrPH • Prof Mark A Hlatky, MD • Muin J Khoury, MD • Prof Malcolm R Macleod, PhD • Prof David Moher, PhD • et al. Show all authors

Published: January 08, 2014 • DOI: https://doi.org/10.1016/S0140-6736(13)62227-8 • Check for updates

Correctable weaknesses in the design, conduct, and analysis of biomedical and public health research studies can produce misleading results and waste valuable resources. Small effects can be difficult to distinguish from bias introduced by study design and analyses. An absence of detailed written protocols and poor documentation of research is common. Information obtained might not be useful or important, and statistical precision or power is often too low or used in a misleading way. Insufficient consideration might be given to both previous and continuing studies. Arbitrary choice of analyses and an overemphasis on random extremes might affect the reported findings. Several problems relate to the research workforce, including failure to involve experienced statisticians and methodologists, failure to train clinical researchers and laboratory scientists in research methods and design, and the involvement of stakeholders with conflicts of interest. Inadequate emphasis is placed on recording of research decisions and on reproducibility of research. Finally, reward systems incentivise quantity more than quality, and novelty more than reliability. We propose potential solutions for these problems, including improvements in protocols and documentation, consideration of evidence from studies in progress, standardisation of research efforts, optimisation and training of an experienced and non-conflicted scientific workforce, and reconsideration of scientific reward systems.

PLOS

Box 1. Some Research Practices that May Help Increase the Proportion of True Research Findings

- Large-scale collaborative research
- Adoption of replication culture
- Registration (of studies, protocols, analysis codes, datasets, raw data, and results)
- Sharing (of data, protocols, materials, software, and other tools)
- Reproducibility practices
- Containment of conflicted sponsors and authors
- More appropriate statistical methods
- Standardization of definitions and analyses
- More stringent thresholds for claiming discoveries or "successes"
- Improvement of study design standards
- Improvements in peer review, reporting, and dissemination of research
- Better training of scientific workforce in methods and statistical literacy

John P. A. Ioannidis How to Make More Published Research True, October 21, 2014 DOI: 10.1371/journal.pmed.1001747

FAIRDOM

www.nature.com/scientificdata

SCIENTIFIC DATA

OPEN

SUBJECT CATEGORIES
» Research data
» Publication characteristics

Comment: The FAIR Guiding Principles for scientific data management and stewardship

OPEN ACCESS Freely available online

PLOS | COMPUTATIONAL BIOLOGY

Editorial

Ten Simple Rules for Reproducible Computational Research

Geir Kjetil Sandve[1,2]*, Anton Nekrutenko[3], James Taylor[4], Eivind Hovig[1,5,6]

Box 2 | The FAIR Guiding Principles

To be Findable:
F1. (meta)data are assigned a globally unique and persistent identifier
F2. data are described with rich metadata (defined by R1 below)
F3. metadata clearly and explicitly include the identifier of the data it describes
F4. (meta)data are registered or indexed in a searchable resource

To be Accessible:
A1. (meta)data are retrievable by their identifier using a standardized communications protocol
A1.1 the protocol is open, free, and universally implementable
A1.2 the protocol allows for an authentication and authorization procedure, where necessary
A2. metadata are accessible, even when the data are no longer available

To be Interoperable:
I1. (meta)data use a formal, accessible, shared, and broadly applicable language for knowledge representation.
I2. (meta)data use vocabularies that follow FAIR principles
I3. (meta)data include qualified references to other (meta)data

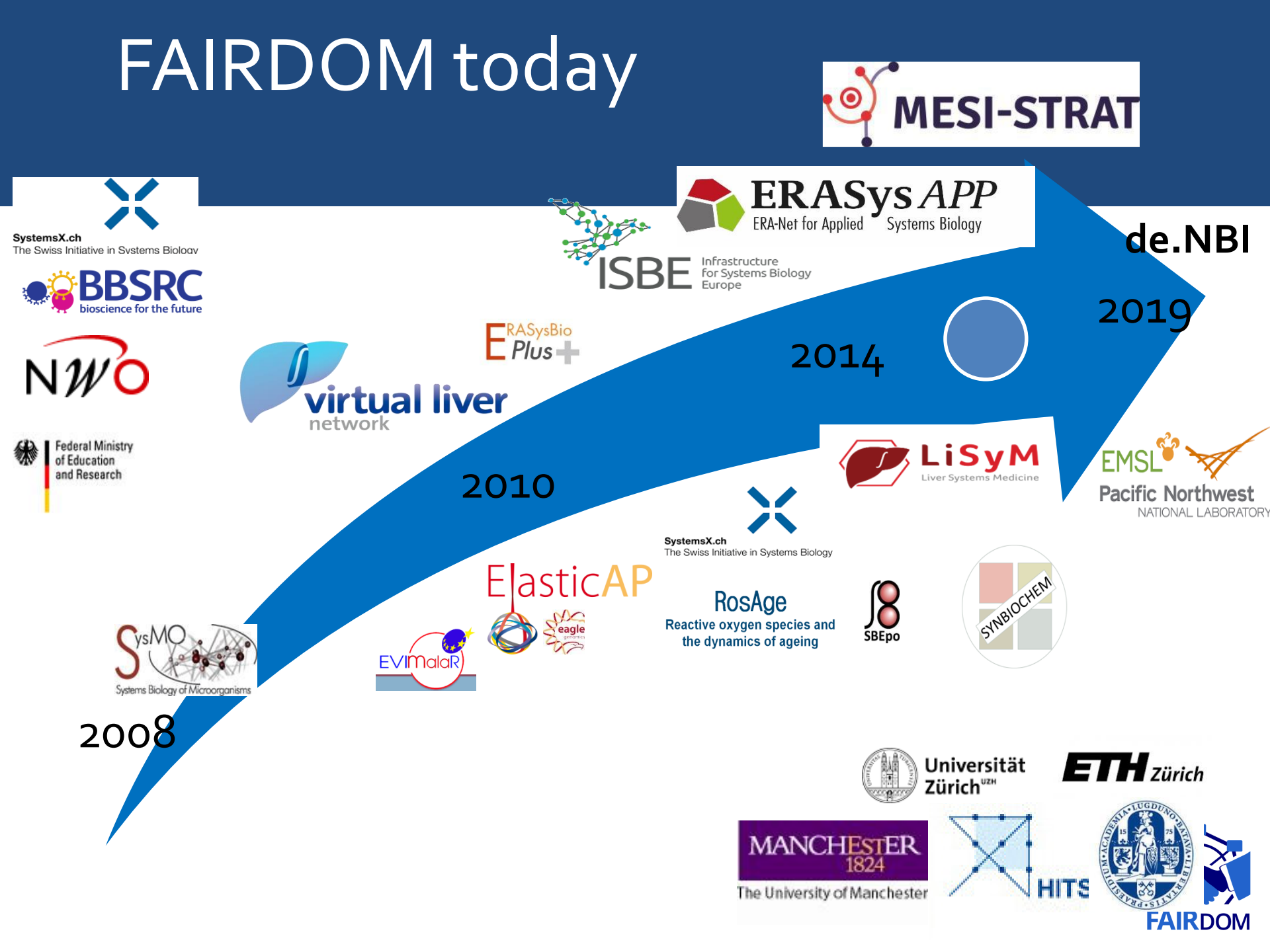
To be Reusable:
R1. meta(data) are richly described with a plurality of accurate and relevant attributes
R1.1. (meta)data are released with a clear and accessible data usage license
R1.2. (meta)data are associated with detailed provenance
R1.3. (meta)data meet domain-relevant community standards

1. For Every Result, Keep Track of How It Was Produced
2. Avoid Manual Data Manipulation Steps
3. Archive the Exact Versions of All External Programs Used
4. Version Control All Custom Scripts
5. Record All Intermediate Results, When Possible in Standardized Formats
6. For Analyses That Include Randomness, Note Underlying Random Seeds
7. Always Store Raw Data behind Plots
8. Generate Hierarchical Analysis Output, Allowing Layers of Increasing Detail to Be Inspected
9. Connect Textual Statements to Underlying Results
10. Provide Public Access to Scripts, Runs, and Results

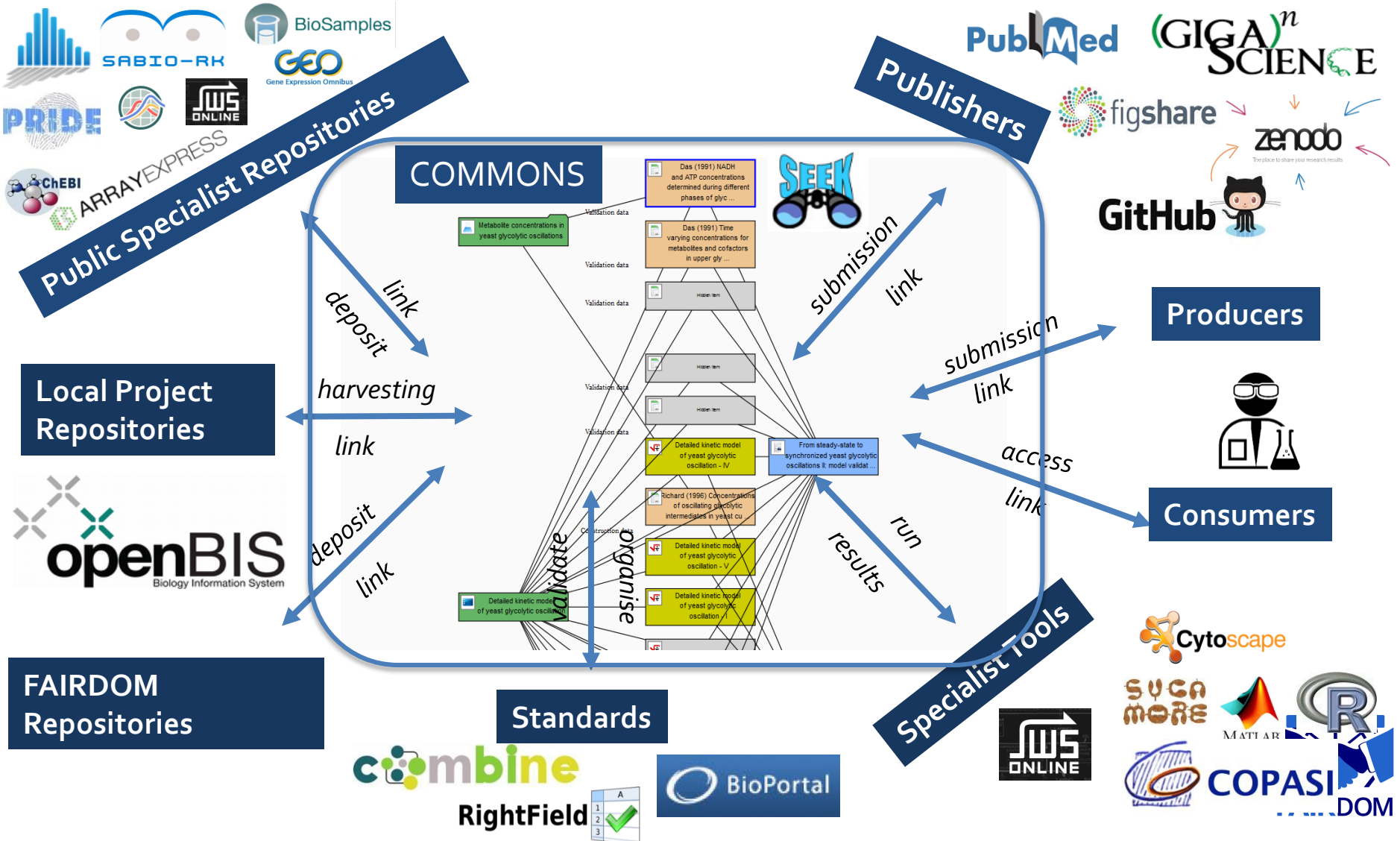
Findable (Citable)
Accessible (Trackable)
Interoperable (Intelligible)
Reusable (Reproducible)

FAIRDOM

FAIRDOM today



FAIRDOM Platform: Catalogue, Commons, Collections, Project-centric Data Management



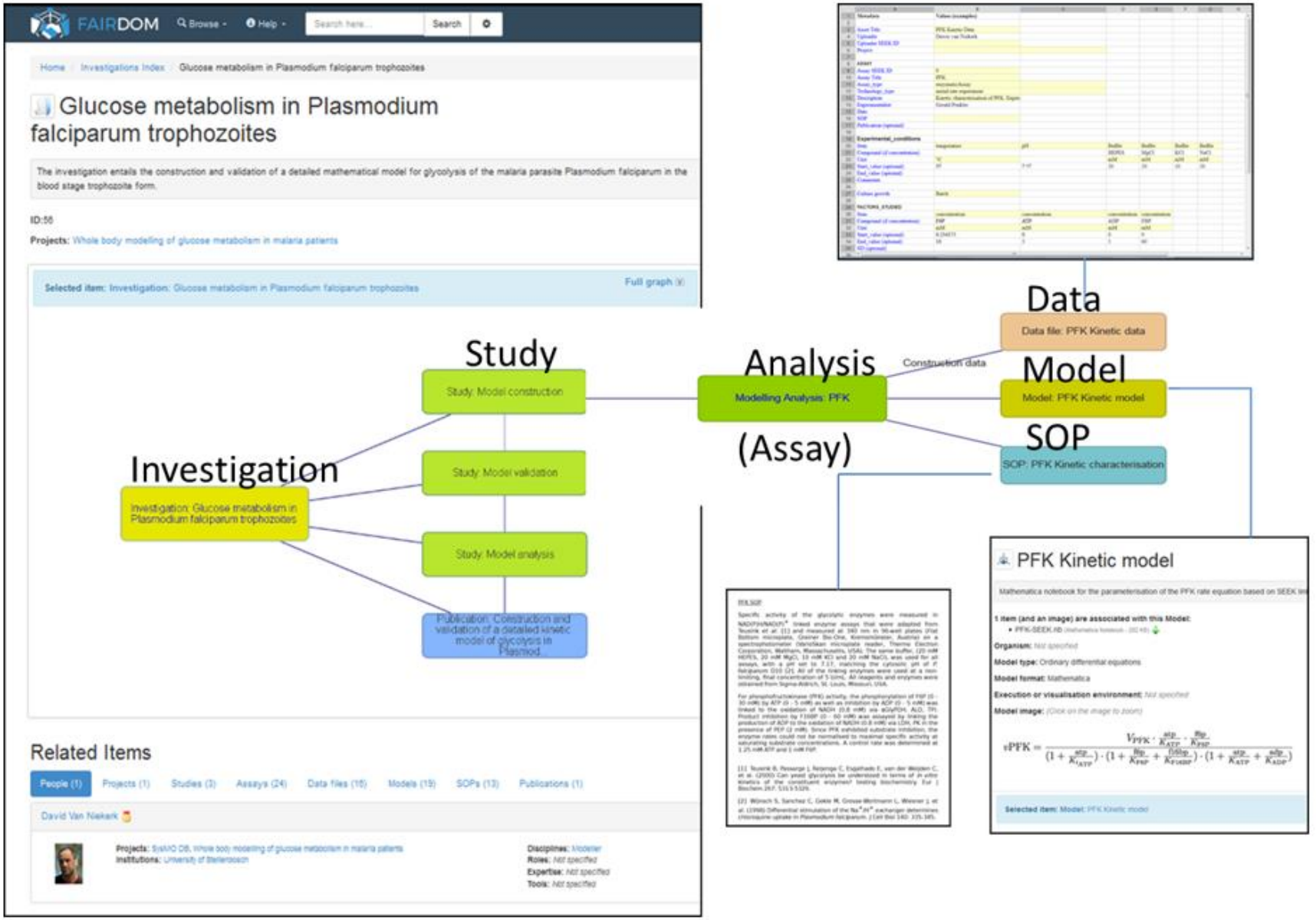
FAIRDOMHub

Common Space

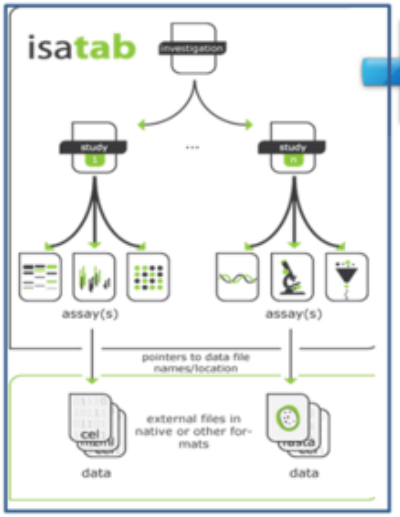
Find – Access – Interoperate – Reuse
Collaborate – Control – Organise – Retain

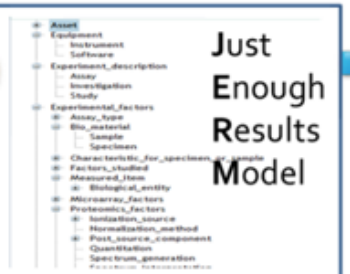
- Trusted long-term repository
- Repository space during and after project
- Project controlled spaces
- Working space for projects
- Show space for communicating results
- Collaboration space for partners
- Supp. materials space for publications
- Portal to project on-site repositories
- Portal to modelling tools + public archives
- Shared service

FAIRDOM


FAIRDOM
Browse
Help
Search here...
Search
Home
Investigations Index
Glucose metabolism in Plasmodium falciparum trophozoites
Glucose metabolism in Plasmodium falciparum trophozoites
The investigation entails the construction and validation of a detailed mathematical model for glycolysis of the malaria parasite Plasmodium falciparum in the blood stage trophozoite form.
ID:56
Projects: Whole body modelling of glucose metabolism in malaria patients
Selected item: Investigation: Glucose metabolism in Plasmodium falciparum trophozoites
Full graph
Related Items
People (1)
Projects (1)
Studies (3)
Assays (24)
Data files (16)
Models (19)
SOPs (13)
Publications (1)
David Van Niekerk
Projects: SysMO DB, Whole body modelling of glucose metabolism in malaria patients
Institutions: University of Stellenbosch
Disciplines: Modeller
Roles: Not specified
Expertise: Not specified
Tools: Not specified
Data
Data file: PFK Kinetic data
Analysis
Construction data
Model
Modelling Analysis: PFK
Model: PFK Kinetic model
SOP
(Assay)
SOP: PFK Kinetic characterisation
Study
Study: Model construction
Investigation
Investigation: Glucose metabolism in Plasmodium falciparum trophozoites
Study: Model validation
Study: Model analysis
Publication: Construction and validation of a detailed kinetic model of glycolysis in Plasmod...
PFK Kinetic model
1 item (and an image) are associated with this Model:
Organism: Not specified
Model type: Ordinary differential equations
Model format: Mathematica
Execution or visualisation environment: Not specified
Model image: (Click on the image to zoom)
Selected item: Model: PFK Kinetic model

Aggregation and scientific context. The Investigation, Studies, Assays **(ISA)** framework isused to allow research assets and experimental back ground to be aggregated and interlinked; providing descriptions, scientific context, relationships between assets, and includes clear credit to the scientists and projects involved.





Just Enough Results Model

Common elements & relationships between things produced and used in experiments.

Specific elements Community Standards

COMBINE
MIBBI
Etc....

Spreadsheet tooling for metadata templates and metadata harvesting

RightField, for embedding ontology term selection into spreadsheets, enabling JERM compliant annotation of data.
http://www.rightfield.org.uk

Standards

	Data	Models	Simulation	Results
Minimal Requirements	MIBBI: MIAME, MIAPE, 30+	MIRIAM	MIASE	
implements				
Standard Formats	identifiers.org, MAGE-TAB, isatab	SBGN, SBML, CellML, NeuroML, SBOL	SED-ML	SBRML
add meaning	BioPortal, OBO	SBO, OPB	KiSAO	TEDDY
Ontologies				

biosharing

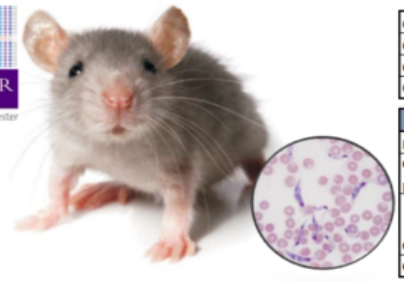
combine

FAIRDOM

Biosamples in SEEK

miniMECH-*Trypo*

Add a New Paper | Save Paper Review | Score Paper Review | Show All PaperReview | 17066074 | Load



	Paper #	Paper #	Paper #	Paper #
Quality of parasite information	84%	84%	58%	92%
Quality of host information	93%	93%	100%	93%
Quality of infection information	100%	100%	100%	100%
Quality of the experiment	92%	92%	87%	95%

Please input the information of the reviewed paper		Paper Information	Paper Information	Paper Information
Please provide the PMID	17066074	17066074	18343633	19365556
Choose the species of the parasite	Trypanosoma congolense	Trypanosoma congolense	Trypanosoma cruzi	Trypanosoma congolense
Choose the disease modeled	Animal African Trypanosomiasis	Animal African Trypanosomiasis	Human American Trypanosomiasis (Chagas disease)	Animal African Trypanosomiasis
Choose de experimental model	Animal model	Animal model	Animal model	Animal model

Item groups	Item#	Please answer the following questions according to the information reported in the experiment.	Please fill the fields the fields cannot be empty	Paper Reviews	Paper Reviews	Paper Reviews
General	1	Is the species of the parasite identified? (e.g. *Trypanosoma congolense*)	YES	YES	YES	YES
	2	Is the the strain of the parasite identified? (e.g. IL1180)	YES	YES	YES	YES
	3	Is the stage of the parasite used identified? (e.g. Trypomastigotes)	YES	YES	YES	YES
Animal	18	Is the age of the animal described? (e.g. 6-8 weeks old)				
	19	Is the gender of the animal described? (e.g. Female)				
	20.1	Is the housing conditions -light/dark cycle- described? (e.g. 12 hours				
	20.2	Is the housing conditions -temperature- described? (e.g. 25 °C)				
	20.3	Is the housing conditions -humidity- described? (e.g. 40-45 %)				
	20.4	Is the housing conditions -food/water access- described? (e.g. limite				
	20.5	Is the housing conditions -animals per cage- described? (e.g. 3 mice				
	20.6	Is the housing conditions -sex cage- described? (e.g. same-sex cage)				
	21	Is the method of sacrifice described? (e.g. Cervical dislocation)				
	22	Is the cell type identified? (e.g. HEK 293)				
	23	In primary culture, is the organ/tissue from which cells come identifie				
	24	In primary culture, is the method of purification of the cells described				

Information about the host

$$\text{Process} = \frac{\text{Interest}}{\text{Friction}} \times \text{Number people reach}$$

The Neylon Equation

IDFExcelExample2_jerm.xls

Print Import Copy Paste Format Undo Redo AutoSum Sort A-Z Sort Z-A Gallery Toolbox Zoom Help

Sheets | Charts | SmartArt Graphics | WordArt

	Example	Format	Constraint Typed in b	drop-down	automatica	Key Type	
Title	Transcription profiling of wild-type and ATF3 -	text	Not NULL		x	PK	Explanations
Design Type *	Transcription profiling of wild-type and ATF3 -	text	Not NULL		x	PK	Explanations
Factor Category *	compound_treatment_design	text	Not NULL	x	x	CV	PK - primary key
lame	COMPOUND	text	NOT NULL	x	x	CV	FK - foreign key
lame	Marzolf	text	Not NULL				CV - controlled vocabularies
itial	Bruz						
ion	Institute for Systems Biology						
	submitter						
ol Description Type *		text	NOT NULL				
cription Type *		text	NOT NULL	X	X	CV	
Description type *				X	X	CV	
escription				X	X	CV	
		text	X		X		
me							
Type *		text				CV	
col Description		text					
Protocol Parameters		integer	NOT NULL		X		
		text	NOT NULL	X			
SDRF File		text	NOT NULL	X			
data file							
ADF file		text	NOT NULL	X			
Term Source Name		integer	NOT NULL	X	X		
Term Source File		date	NOT NULL				
Term Source Version		integer	NOT NULL	X	X		
		integer		X	X		
				X	X		

- array_manufacturer
- biomaterial_provider
- biosequence_provider
- consortium_member
- consultant
- curator
- data_analyst
- data_coder
- funder
- hardware_manufacturer
- institution
- investigator
- software_manufacturer
- ✓ submitter

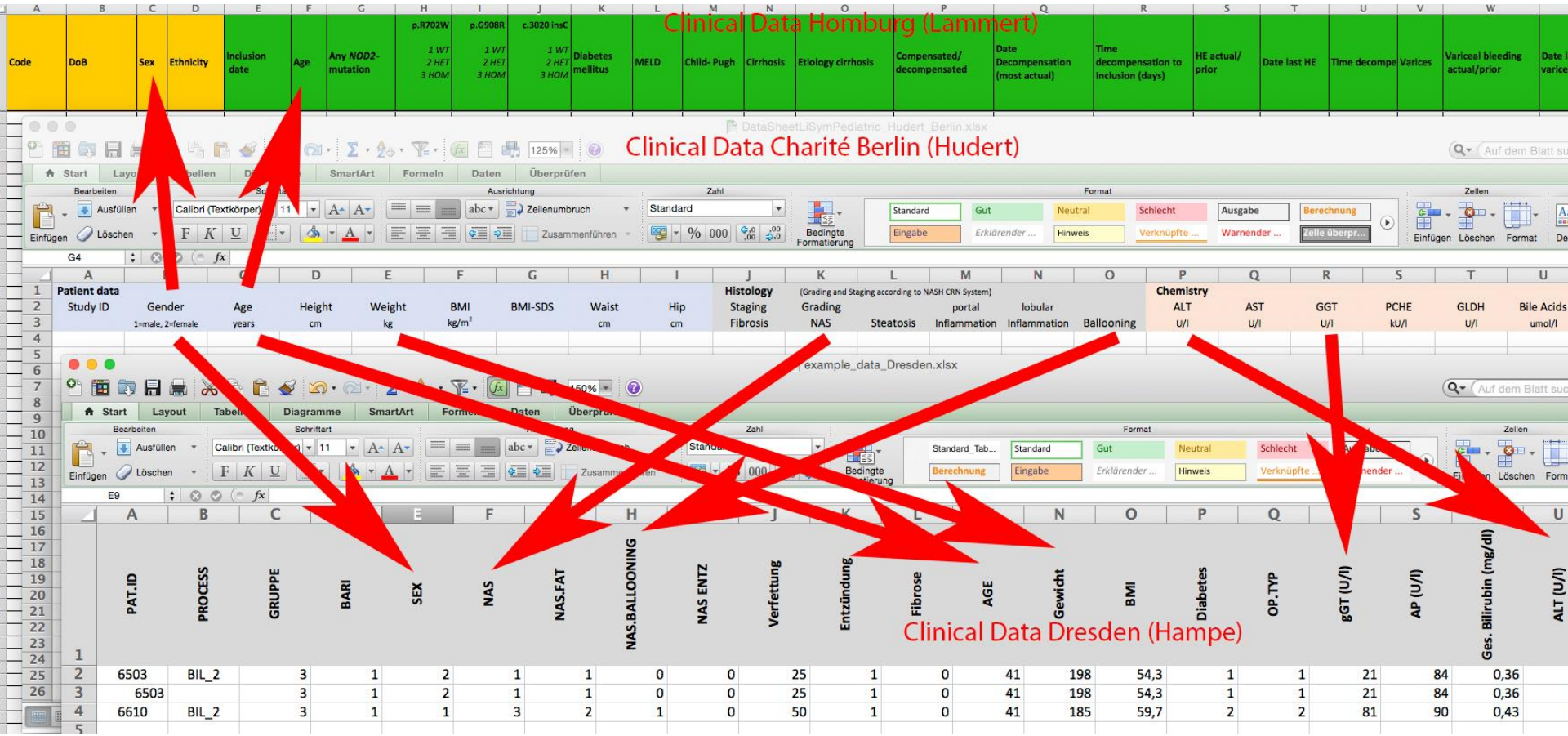
IDFExcelExample | SampleData | values

Normal View | Ready

RightField

FAIRDOM

Clinical Data → Many Centers, Many Formats



Mapping the different data formats to create one consolidated spreadsheet template of description data (describing donor attributes) for human clinical samples in LiSyM

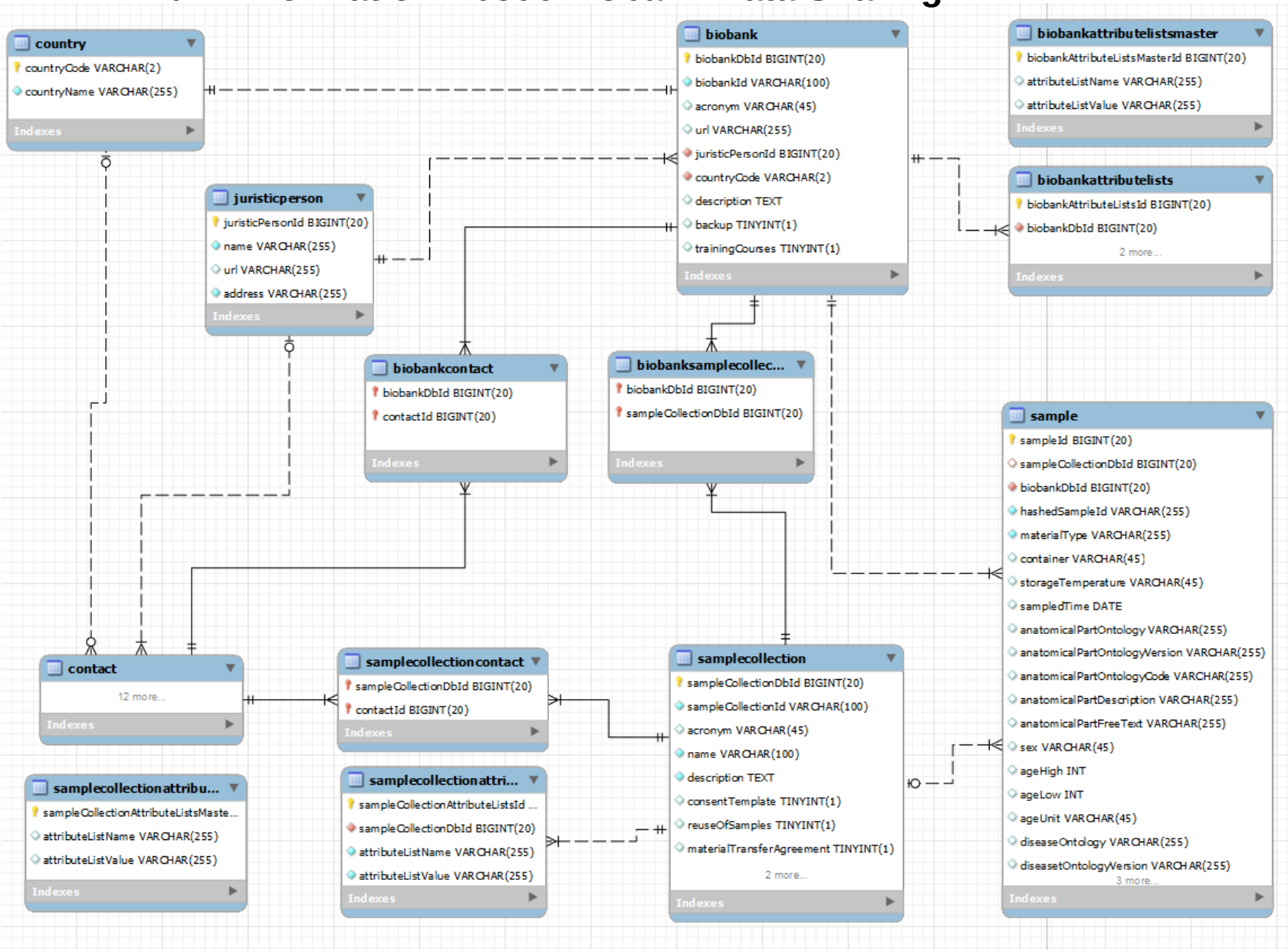
HITS

LiSyM
Liver Systems Medicine

SPONSORED BY THE
Federal Ministry of Education and Research

Standardized Sample Description: MIABIS

Minimum Information About Biobank Data Sharing



BBMRI-ERIC

HITS

Standard Operating Procedures Quality Control

Home > SOPs Index > Introduction of shRNAs, miRNAs or anti-microRNAs into primary human hepatocytes with lentivirus

Introduction of shRNAs, miRNAs or anti-microRNAs into primary human hepatocytes with lentivirus

Download SOP | View content

Here we used VSV-G-pseudotyped, EGFP-expressing lentiviral vectors to develop an efficient gene transfer protocol to modify gene expression in primary human hepatocytes (by RNAi). The protocol comprises the production of recombinant viruses as well as the steps for efficient delivery of short-hairpin RNA (shRNAs), microRNAs or anti-microRNAs to human hepatocytes. On average infection efficiencies of over 95% are achieved at relatively low multiplicity of infection (MOI), which effectively reduces the amount of preparative work required per experiment. Depending on the laboratory equipment available, we provide here two alternative workflows, which can be easily adapted in the lab. The procedure of virus production with subsequent titer determination takes approx. 6 to 10 working days. The procedure of viral infection of hepatocytes until effects can be measured takes approx. 3 to 5 days. This protocol should be helpful to study many aspects of functional genomics in primary human hepatocytes.

Contributors
[Maria Thomas]

Attributions
None

Scales

Filename: Lentiviral production and infection_SOP_04042011.pdf

Format: PDF document

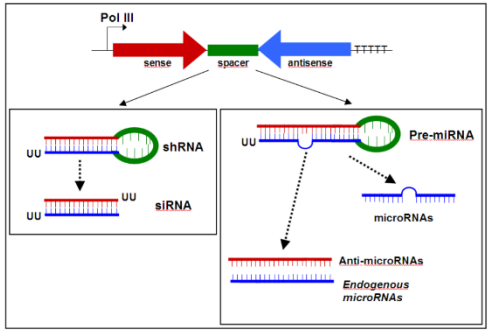


Fig.1: Schematic presentation of designed template sequences which are processed intracellularly into short hairpin RNAs, microRNAs or anti-microRNAs. The stem-loop structures consisting of both the sense and anti-sense strands of the targeted sequence are separated by a loop sequence.

MATERIALS

REAGENTS/KITS

BLOCK-iT™ Lentiviral RNAi Expression Kit (Invitrogen#49-4400)

ViraPower™ Lentiviral Gateway Expression Kit (Invitrogen#K49-6000)

miRZip™ Lentivector-based Anti- MicroRNAs (System Biosciences#MZIPxxxPA/AA-1)

ed microRNAs (System Biosciences#PMIRHxxxPA/AA-1)

PROCEDURE

NOTE: all the steps marked with "S" should be performed following recommended guidelines for working with BL-2 organisms (Germany: S2 lab).

1. Preparation of HEK293FT cells.

For cultivating HEK293FT cells, add G148 (Geneticin, final concentration 500 µg/ml) to the DMEM culture medium with components (see Reagent Setup). The cells should be passaged at least 1-2 times after thawing to adapt to the culture conditions. Three days prior to transfection, plate out the cells at a density of approximately $3{,}5*10^6$ cells/per 1 T175 flask in 30 ml of medium with components and G148 to achieve optimal phase of cellular growth.

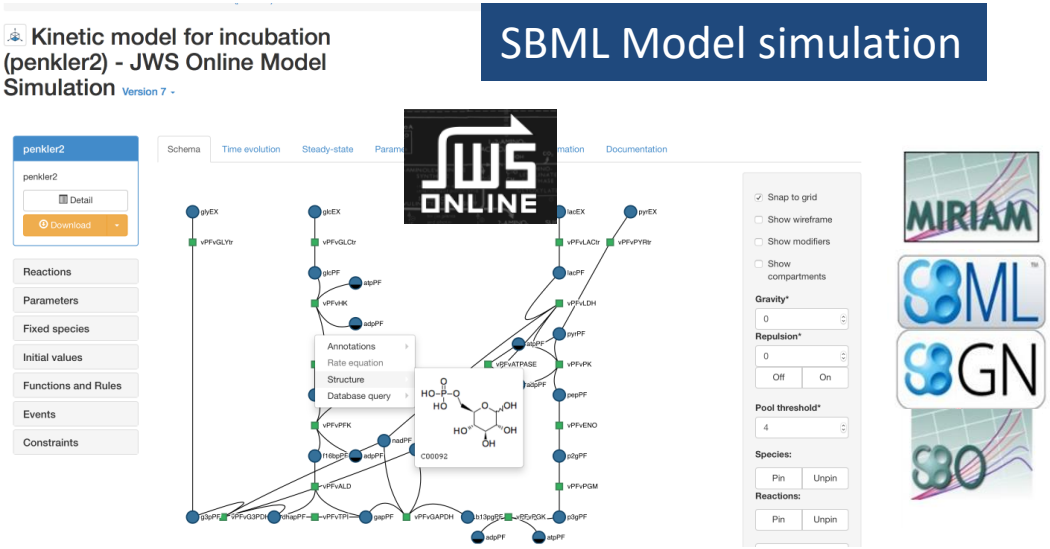
virtual liver network

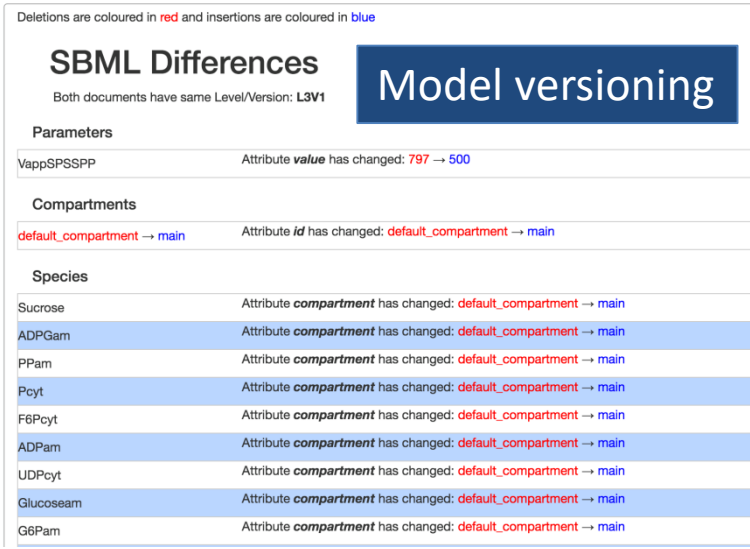
AIRDOM

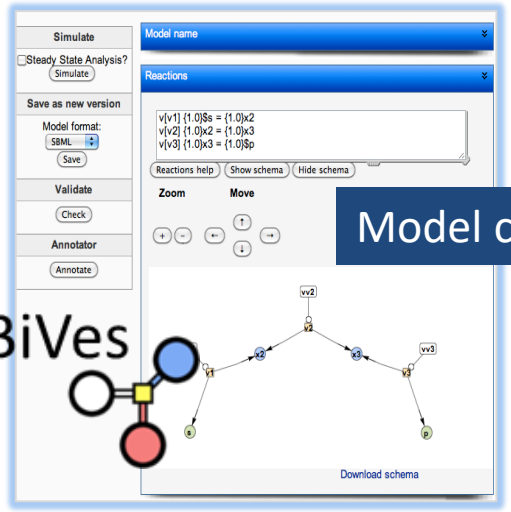
Reproducible models in FAIRDOM

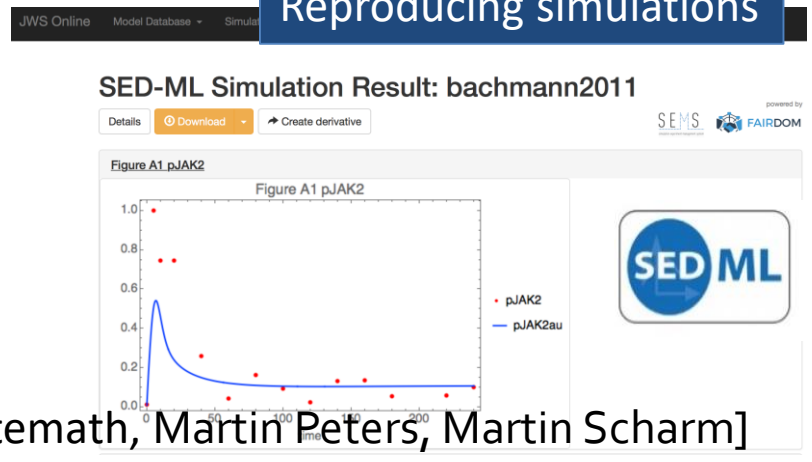
metadata annotation against standards
validation, comparison and simulation

JWS Online





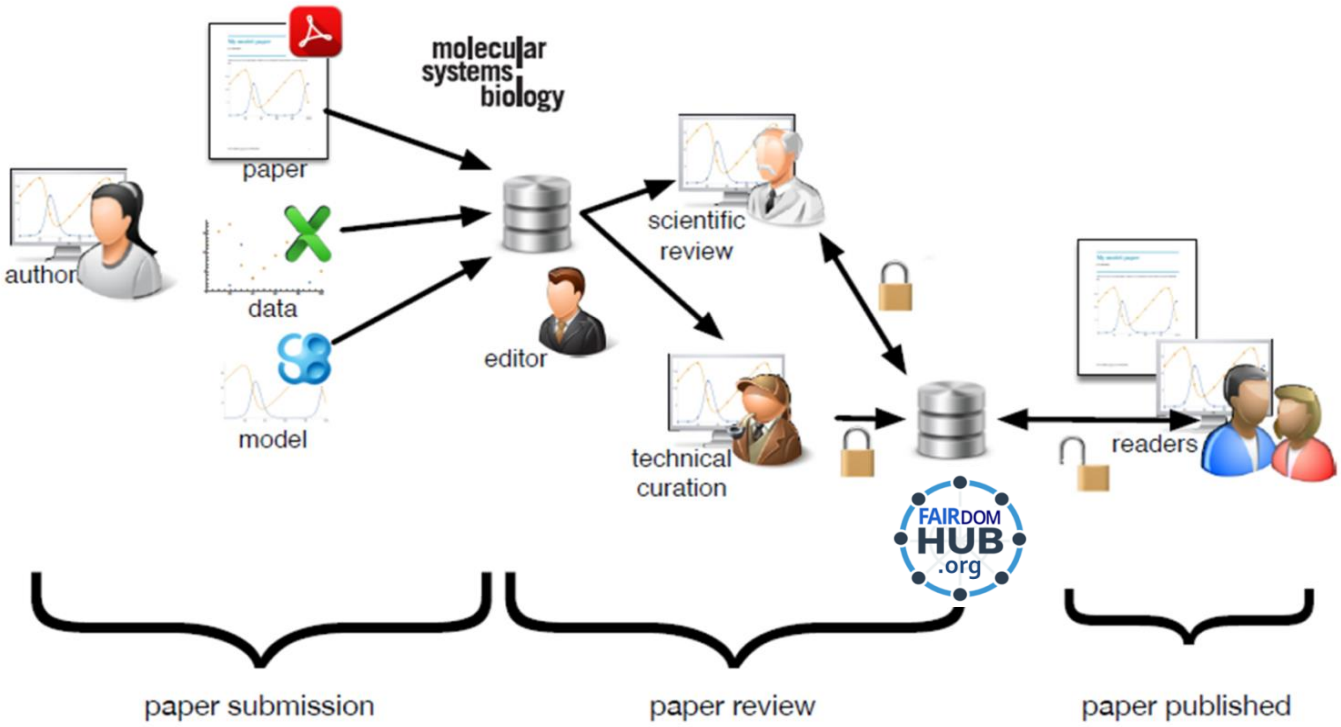




[Jacky Snoep, Dagmar Waltemath, Martin Peters, Martin Scharm]

FAIRDOM service : model curation

* store DOI citable supplementary files on FAIRDOMHub
** model and data curation
*** reproducible clickable figures in papers using SED-ML



[Jacky Snoep (Stellenbosch), Dagmar Waltemath, Martin Peters, Martin Scharm (Rostock)]

FAIRDOM

Credit and Attribution

Citing FAIRDOM Entries, living and snapshot entries, contributors

the FEBS Journal

Construction and validation of a detailed kinetic model of glycolysis in *Plasmodium falciparum*

Gerald Penkler[1,2], Francois du Toit[1], Waldo Adams[1], Marina Rautenbach[1], Daniel C. Palm[1], David D. van Niekerk[1] and Jacky L. Snoep[1,2,3]

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2 Molecular Cell Physiology, Vrije Universiteit Amsterdam, The Netherlands
3 MIB, University of Manchester, UK

Keywords
enzyme kinetics; glucose metabolism; model workflow; mathematical model; systems biology

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(Received 19 August 2014, revised 7 February 2015, accepted 13 February 2015)

doi:10.1111/febs.13237

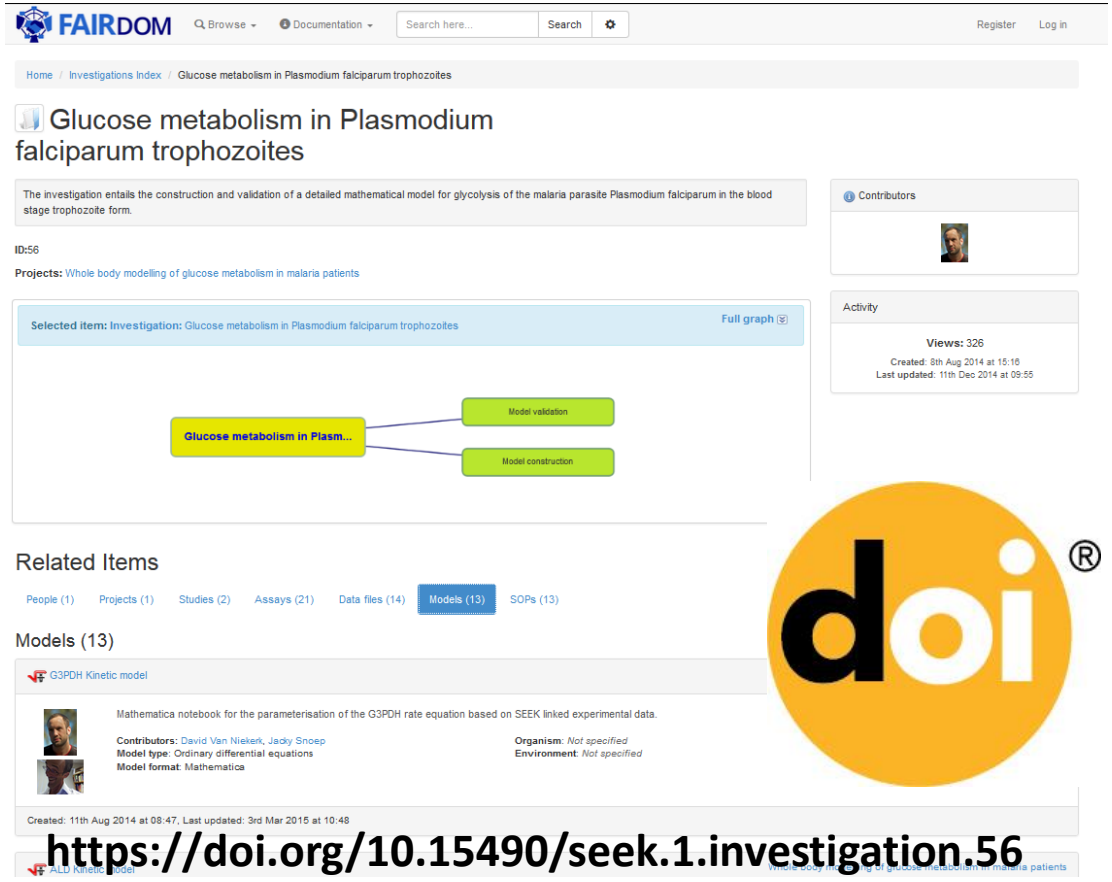
The enzymes in the Embden–Meyerhof–Parnas pathway of *Plasmodium falciparum* trophozoites were kinetically characterized and their integrated activities analyzed in a mathematical model. For validation of the model, we compared model predictions for steady-state fluxes and metabolite concentrations of the hexose phosphates with experimental values for intact parasites. The model, which is completely based on kinetic parameters that were measured for the individual enzymes, gives an accurate prediction of the steady-state fluxes and intermediate concentrations. This is the first detailed kinetic model for glucose metabolism in *P. falciparum*, one of the most prolific malaria-causing protozoa, and the high predictive power of the model makes it a strong tool for future drug target identification studies. The modelling workflow is transparent and reproducible, and completely documented in the SEEK platform, where all experimental data and model files are available for download.

Database
The mathematical models described in the present study have been submitted to the JWS Online Cellular Systems Modelling Database (http://jjj.bio.vu.nl/database/penkler). The investigation and complete experimental data set is available on SEEK (10.15490/seek.1.investigation.56).

Introduction

Despite several attempts at a complete eradication of the disease, malaria is still killing more than half a million people per year, mostly small children in sub-saharan Africa (World Health Organisation Malaria report 2013, http://www.who.int/malaria/publications/world_malaria_report_2013/en/). The disease is caused by parasitic protozoa of the *Plasmodium* genus, which have a complicated life cycle consisting of an insect vector and vertebrate host [1]. In the human host, parasite sporozoites first invade liver cells, but the malaria disease symptoms manifest only at a later stage during multiplication of the asexual stages of the parasite in red blood cells (RBCs). The blood life cycle consists of ring, trophozoite and schizont stages, and subsequent

Abbreviations
2PG, 2-phosphoglycerate; 3PG, 3-phosphoglycerate; ALD, fructose-bisphosphate aldolase; B13PG, 1,3-bisphosphoglycerate; DHAP, glycerone phosphate; ENO, phosphopyruvate hydratase; F16BP, fructose 1,6-bisphosphate; F6P, fructose 6-phosphate; G3P, glycerol 3-phosphate; G3PDH, glycerol 3-phosphate dehydrogenase; G6P, glucose 6-phosphate; GAP, D-glyceraldehyde 3-phosphate; GAPDH, glyceraldehyde 3-phosphate dehydrogenase; GLC, glucose; GLY, glycerol; HK, hexokinase; LAC, lactate; LDH, lactate dehydrogenase; MCT, monocarboxylate transporter; ODE, ordinary differential equation; PEP, phosphoenolpyruvate; PFK, 6-phosphofructokinase; PGI, glucose 6-phosphate isomerase; PGK, phosphoglycerate kinase; PGM, phosphoglycerate mutase; PK, pyruvate kinase; PYR, pyruvate; RBC, red blood cell; TCA, tricarboxylic acid; TPI, triose-phosphate isomerase.



https://doi.org/10.15490/seek.1.investigation.56

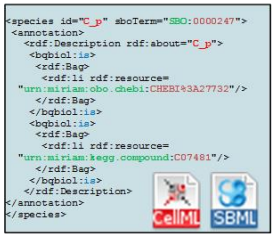
Penkler et al (2015) FEBSJ 282:1481-1511
https://dx.doi.org/10.1111/febs.13237

FAIRDOM

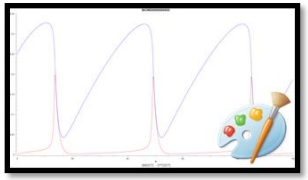
Packaging: CombineArchive

https://sems.uni-rostock.de/projects/combinearchive/

model



simulation results and data



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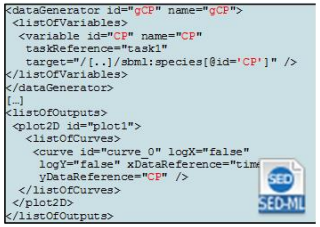
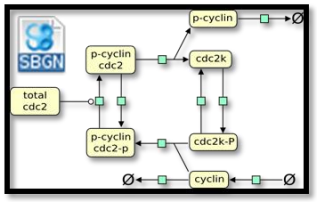
4		0,02	0,0000891215
5		0,03	0,0001330460
6		0,04	0,0001765560

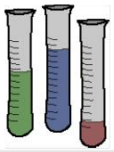
simulation description



graphical representation



wetlab data



	A	B	C
1	# Time	[M/CT]	[YT/CT]
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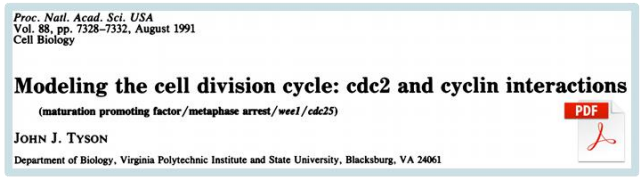
manuscript



Proc. Natl. Acad. Sci. USA
Vol. 88, pp. 7328–7332, August 1991
Cell Biology

Modeling the cell division cycle: cdc2 and cyclin interactions

(maturation promoting factor/metaphase arrest/*wee1*/*cdc25*)

PDF

JOHN J. TYSON

Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA 24061

BMC Bioinformatics

Software

Highly accessed | Open Access

COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project

Frank T Bergmann[1], Richard Adams[2], Stuart Moodie[3,4], Jonathan Cooper[5], Mihai Glont[3], Martin Golebiewski[6], Michael Hucka[7], Camille Laibe[3], Andrew K Miller[8], David P Nickerson[8], Brett G Olivier[9], Nicolas Rodriguez[10], Herbert M Sauro[11], Martin Scharm[12], Stian Soiland-Reyes[13], Dagmar Waltemath[12], Florent Yvon[3] and Nicolas Le Novère[103]*

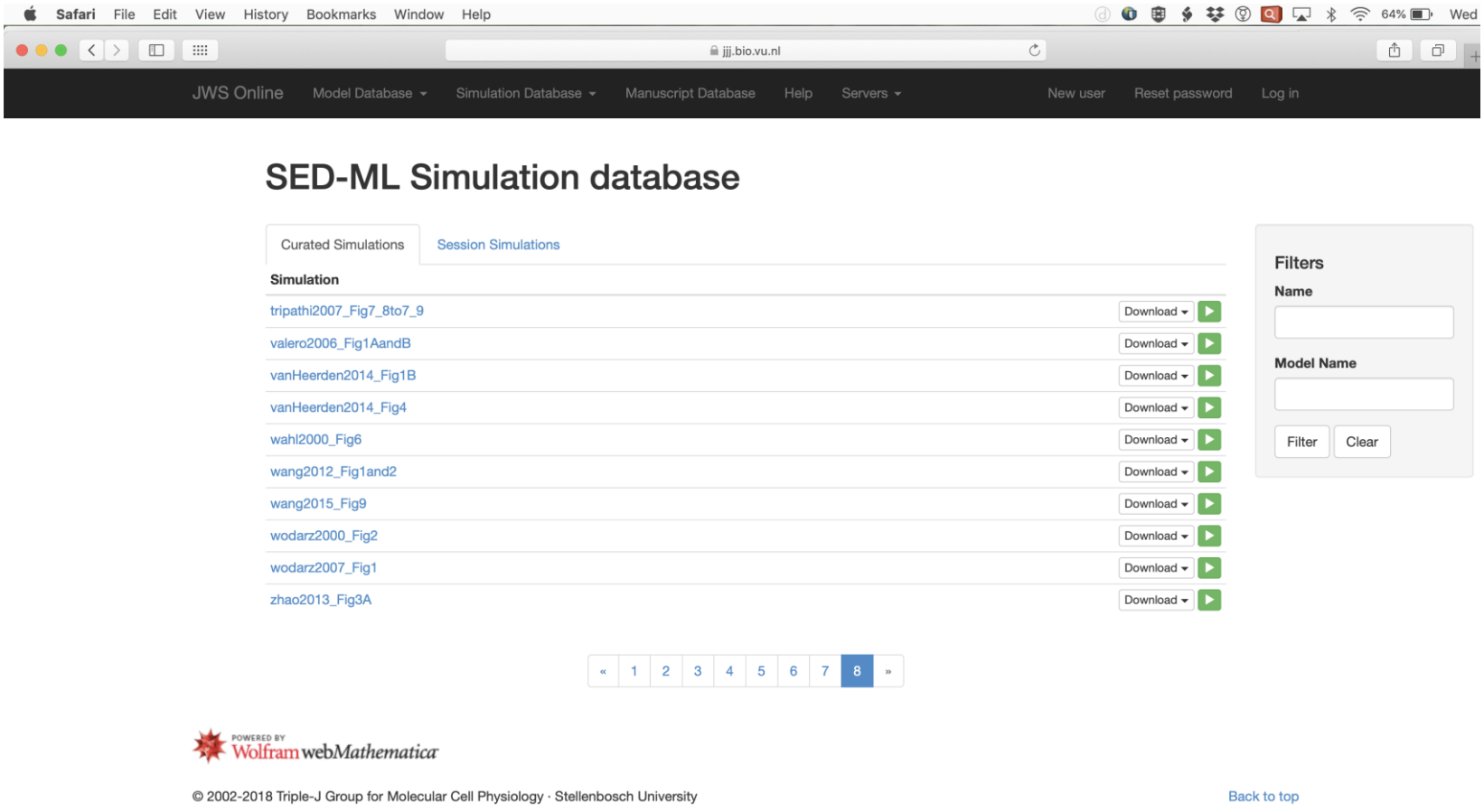
zip-like file with a manifest & metadata

- Bundling files
- Exchanging data
- Keeping provenance
- Shipping results

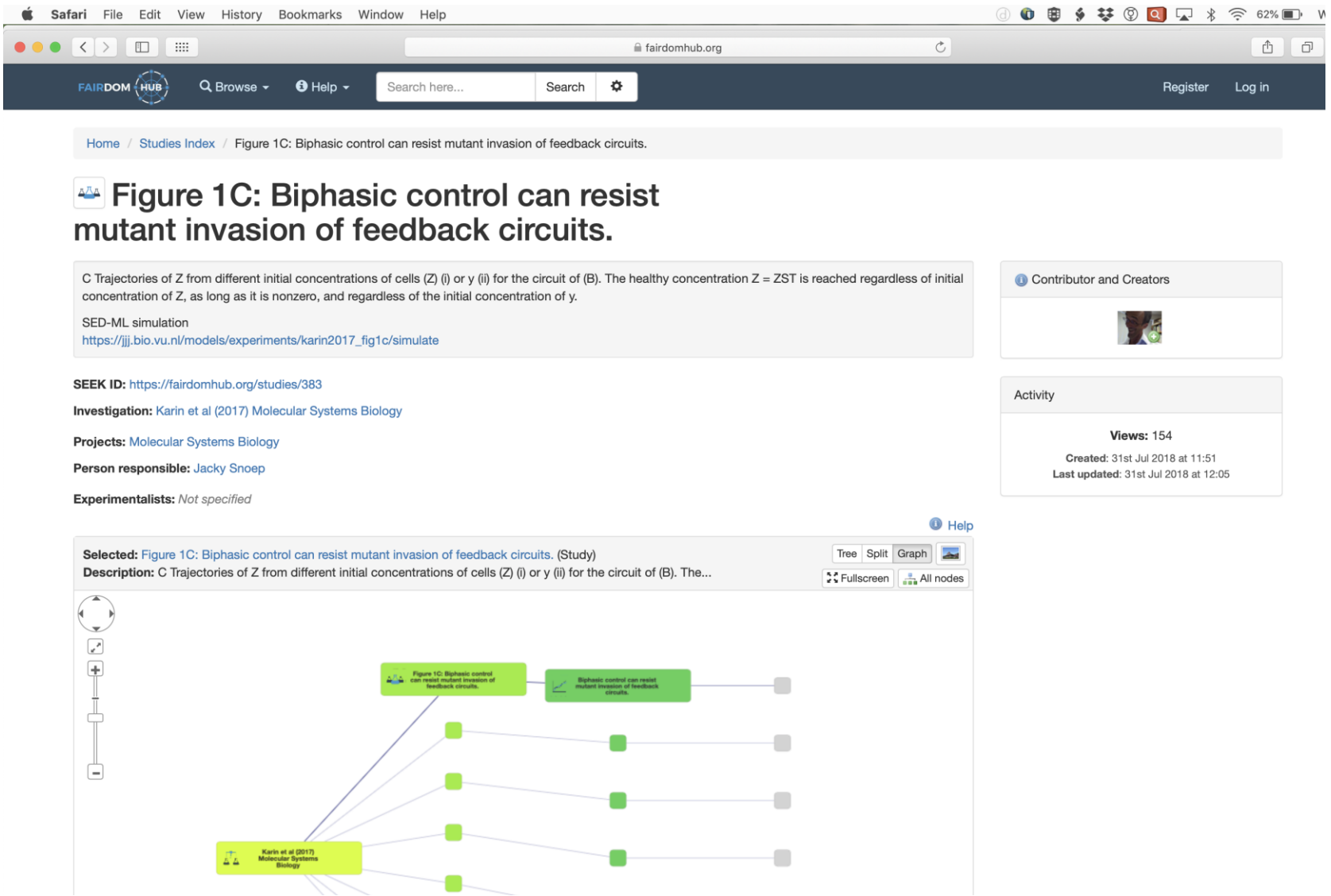
Scharm M, Wendland F, Peters M, Wolfien M, Theile T, Waltemath D
SEMS, University of Rostock

Bergmann, F. T., Adams, R., Moodie, S., Cooper, J., Glont, M., Golebiewski, M., ... & Olivier, B. G. (2014). COMBINE archive and OMEX format: one file to share all information to reproduce a modeling project. *BMC bioinformatics*,*15*(1), 1.

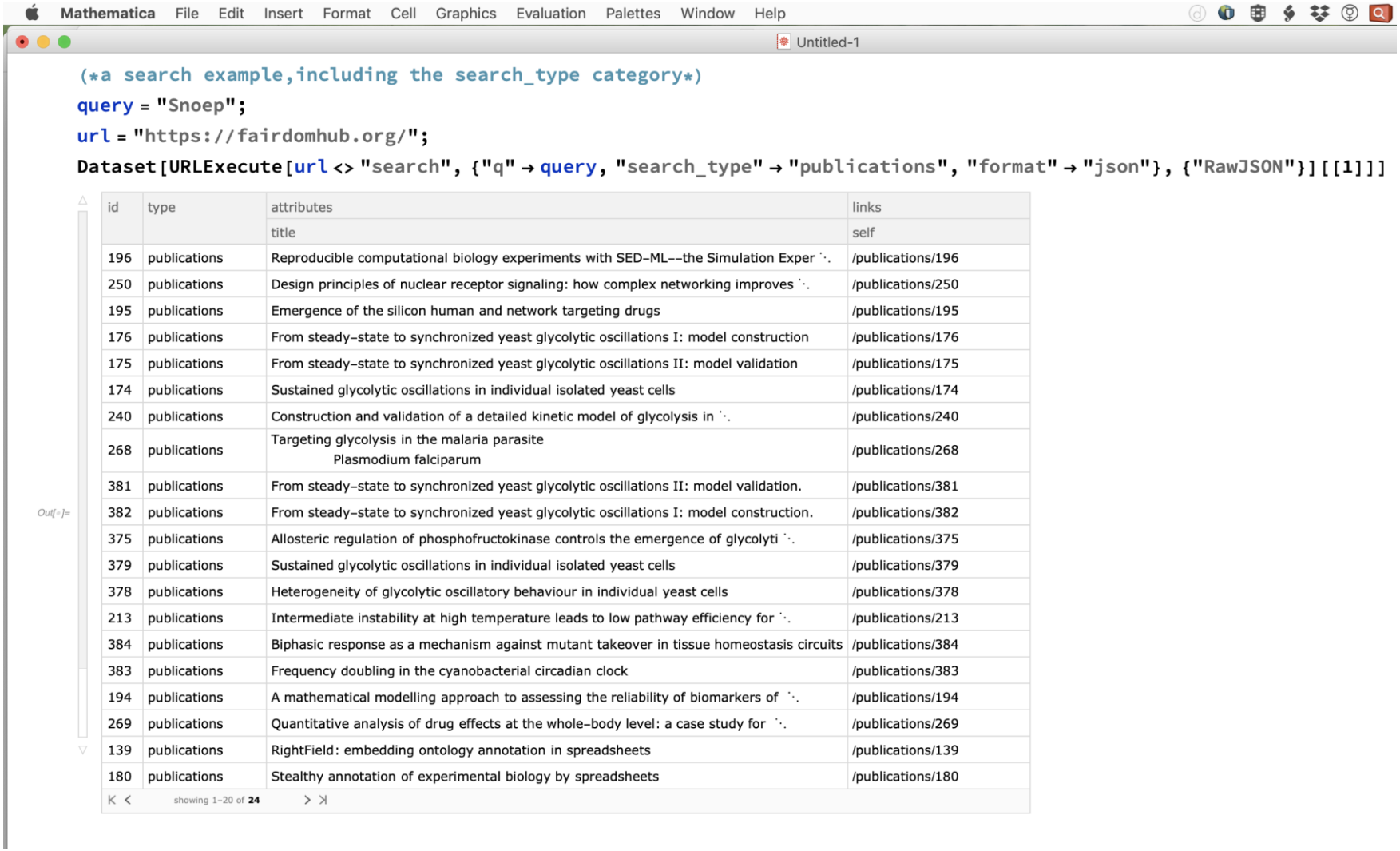
More than 200 curated SED-ML simulations, each reproducing a publication figure



Direct simulation of SED-ML files in SEEK, links model (e.g. JWS) and experimental data files (e.g. SEEK) to reproduce manuscript figures



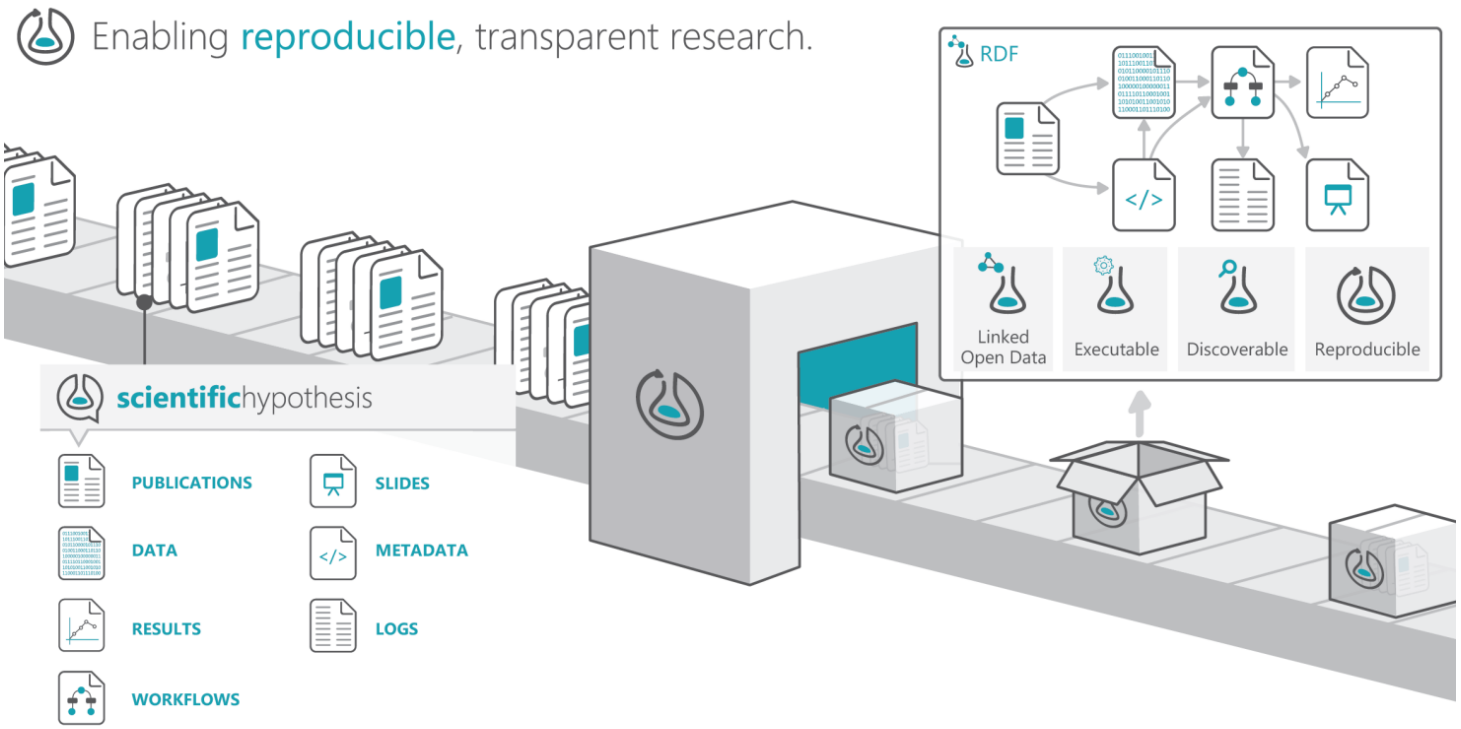
API search example in Mathematica



id	type	attributes	links
		title	self
196	publications	Reproducible computational biology experiments with SED-ML--the Simulation Exper ⋱	/publications/196
250	publications	Design principles of nuclear receptor signaling: how complex networking improves ⋱	/publications/250
195	publications	Emergence of the silicon human and network targeting drugs	/publications/195
176	publications	From steady-state to synchronized yeast glycolytic oscillations I: model construction	/publications/176
175	publications	From steady-state to synchronized yeast glycolytic oscillations II: model validation	/publications/175
174	publications	Sustained glycolytic oscillations in individual isolated yeast cells	/publications/174
240	publications	Construction and validation of a detailed kinetic model of glycolysis in ⋱	/publications/240
268	publications	Targeting glycolysis in the malaria parasite Plasmodium falciparum	/publications/268
381	publications	From steady-state to synchronized yeast glycolytic oscillations II: model validation.	/publications/381
382	publications	From steady-state to synchronized yeast glycolytic oscillations I: model construction.	/publications/382
375	publications	Allosteric regulation of phosphofructokinase controls the emergence of glycolyti ⋱	/publications/375
379	publications	Sustained glycolytic oscillations in individual isolated yeast cells	/publications/379
378	publications	Heterogeneity of glycolytic oscillatory behaviour in individual yeast cells	/publications/378
213	publications	Intermediate instability at high temperature leads to low pathway efficiency for ⋱	/publications/213
384	publications	Biphasic response as a mechanism against mutant takeover in tissue homeostasis circuits	/publications/384
383	publications	Frequency doubling in the cyanobacterial circadian clock	/publications/383
194	publications	A mathematical modelling approach to assessing the reliability of biomarkers of ⋱	/publications/194
269	publications	Quantitative analysis of drug effects at the whole-body level: a case study for ⋱	/publications/269
139	publications	RightField: embedding ontology annotation in spreadsheets	/publications/139
180	publications	Stealthy annotation of experimental biology by spreadsheets	/publications/180

showing 1–20 of **24**

Packaging: Research Objects

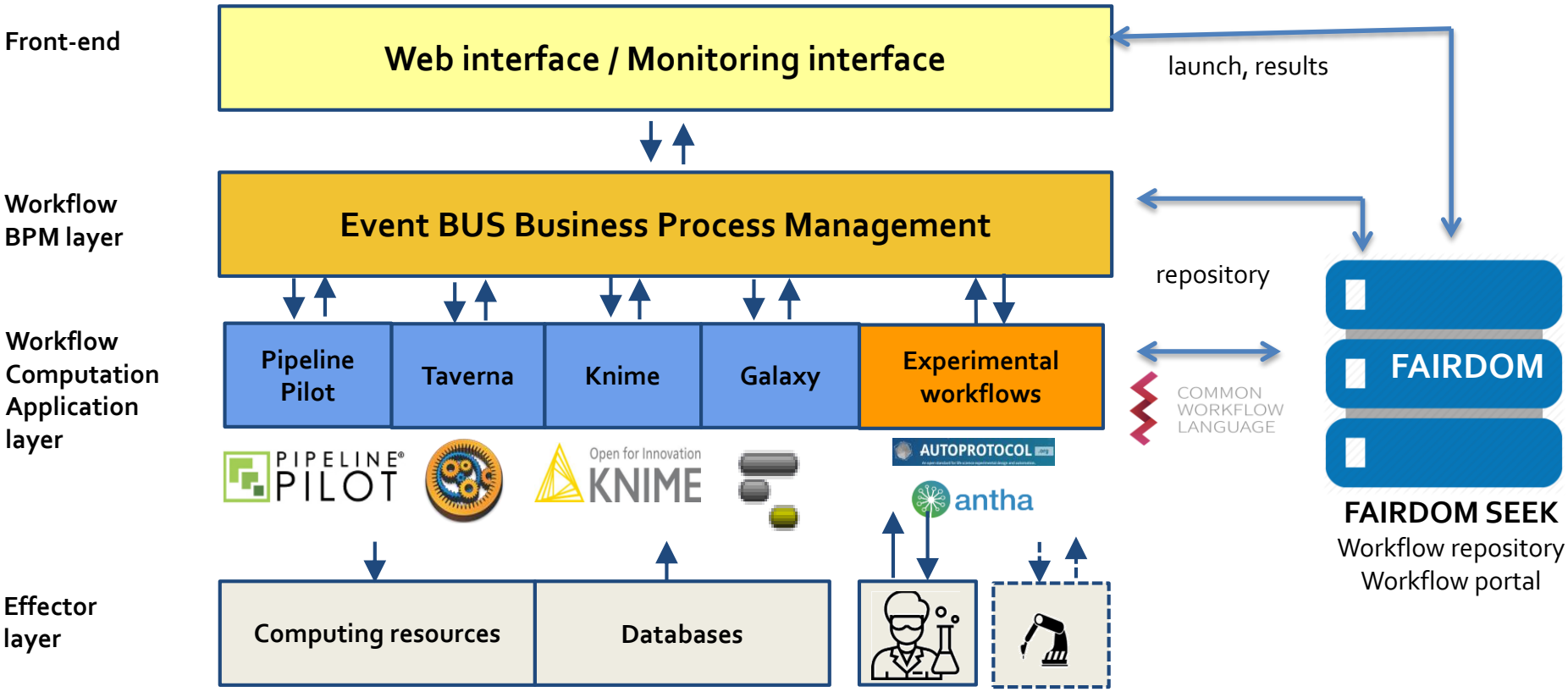


Standards-based metadata framework for
bundling (scattered) resources with context and citation

http://researchobject.org

Use a workflow – the vision!

preferrably a workflow management system
preferrably described using Common Workflow Language



[Jean Loup Fallon, Carole Goble]

FAIRDOM

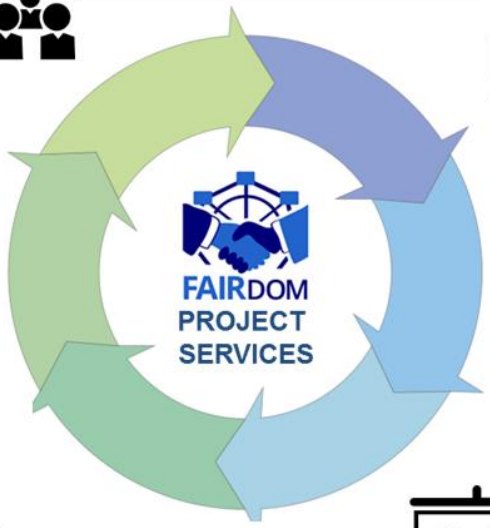
FAIRDOM support

Understanding the project, its collaborations, its assets, and its workflows

Helping projects promote their project, skills and results

Designing and deploying the technical platforms and the right tools

Maintaining, archiving and securing access to FAIRDOMHub



Working with researchers and technicians to design and adopt practices and procedures and curate models and data.

Customising on-site project installations

Training researchers and students

Managing, developing and updating the platforms and tools

FAIRDOM

12 steps to being FAIR
plan to be born FAIR

1. plan data management lifecycle: plan, cost and implement pathways and storage including what you will archive, what you will throw away, how you will collect metadata and how you will curate throughout
2. use standard identifiers and identifier standards
3. use metadata standards with data provenance
4. catalogue / register data with metadata
5. have access and sharing policies with licenses
6. use data (assets) management platforms and tools that work together
7. deposit into public archives
8. have a sustainability / end project plan
9. resource and support, and that also means people too
10. embed data management into work practices and do some training
11. give credit
12. check if you have sensitive data issues

Sounds hard.... what can **I** do?

FAIRDOM

We are part of/liaising with numerous initiatives