HITS
Heidelberg Institute for
Theoretical Studies

Data management intro

Wolfgang Müller, HITS

Think beyond the limits!

FAIRDOM Initiative

http://fair-dom.org

Findable
Accessible
Interoperable
Reusable

Data
Operations
Models

- develop a community
- establish an internationally sustained Data and Model Management service

- Partners from U Manchester, HITS, U Zürich, ETH Zürich
- Funded by BMBF, ISBE, BBSRC, SystemsX (CH)
- Part of ELIXIR as “Node Resource” in UK and DE

Topics

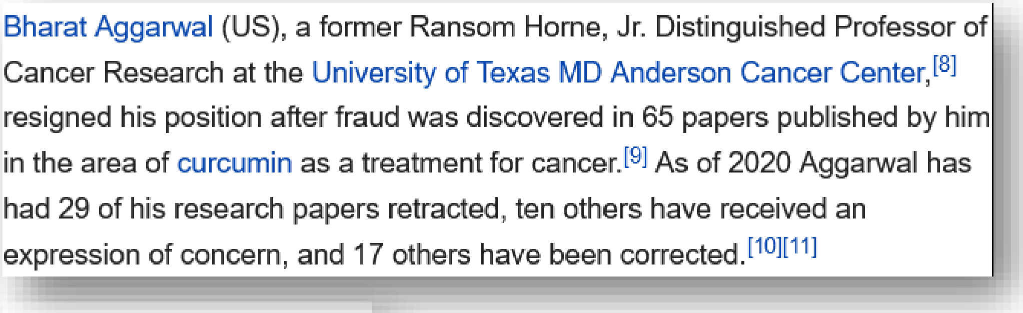
- Why data management?
- Some general thoughts leading up to the SEEK day and the openBIS day

The reason: Reproducibility Crisis

- In a variety of subject matters
    - Many positive findings are false

    - Many papers to be trusted
    - But many not to be trusted
    - High profile misconduct incidents

- Need for fast way to access data
    - Proving reproducibility
    - Making control easier
    - Making QC easier within labs



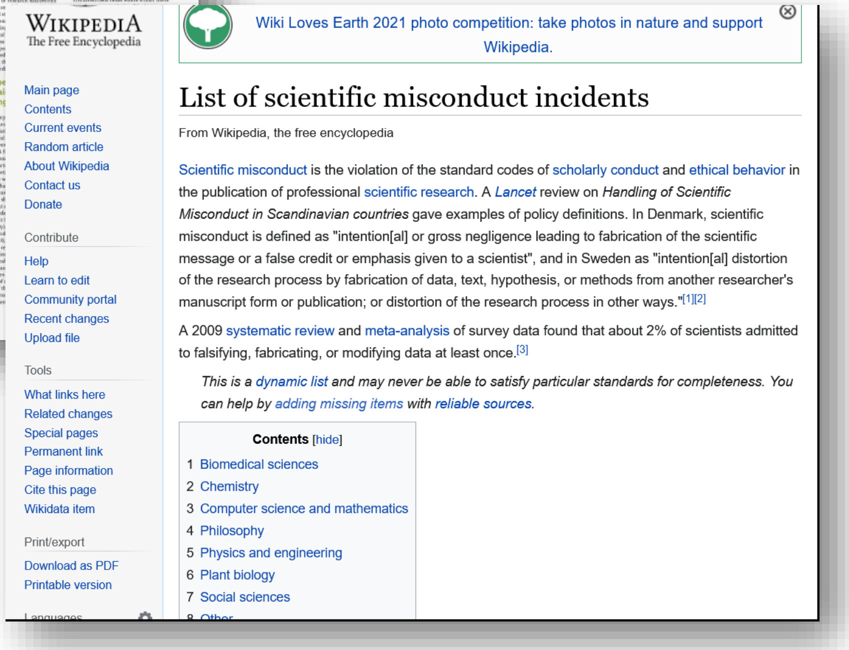
Bharat Aggarwal (US), a former Ransom Horne, Jr. Distinguished Professor of Cancer Research at the University of Texas MD Anderson Cancer Center,[8] resigned his position after fraud was discovered in 65 papers published by him in the area of curcumin as a treatment for cancer.[9] As of 2020 Aggarwal has had 29 of his research papers retracted, ten others have received an expression of concern, and 17 others have been corrected.[10][11]

Open access, freely available online

Essay

Why Most Published Research Findings Are False

John P. A. Ioannidis



Wikipedia
The Free Encyclopedia

Main page
Contents
Current events
Random article
About Wikipedia
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Tools
What links here
Related changes
Special pages
Permanent link
Page information
Cite this page
Wikidata item

Print/export
Download as PDF
Printable version

Wiki Loves Earth 2021 photo competition: take photos in nature and support Wikipedia.

List of scientific misconduct incidents

From Wikipedia, the free encyclopedia

Scientific misconduct is the violation of the standard codes of scholarly conduct and ethical behavior in the publication of professional scientific research. A *Lancet* review on *Handling of Scientific Misconduct in Scandinavian countries* gave examples of policy definitions. In Denmark, scientific misconduct is defined as "intention[al] or gross negligence leading to fabrication of the scientific message or a false credit or emphasis given to a scientist", and in Sweden as "intention[al] distortion of the research process by fabrication of data, text, hypothesis, or methods from another researcher's manuscript form or publication; or distortion of the research process in other ways."[1][2]

A 2009 systematic review and meta-analysis of survey data found that about 2% of scientists admitted to falsifying, fabricating, or modifying data at least once.[3]

This is a dynamic list and may never be able to satisfy particular standards for completeness. You can help by adding missing items with reliable sources.

Contents [hide]

Consequence: drive for FAIR data

- Next slides:
- What is FAIR
- And what do funders ask for, at the example of DFG

What is FAIR?
Data should be like money

To be useful, money must be…

findable

accessible

interoperable

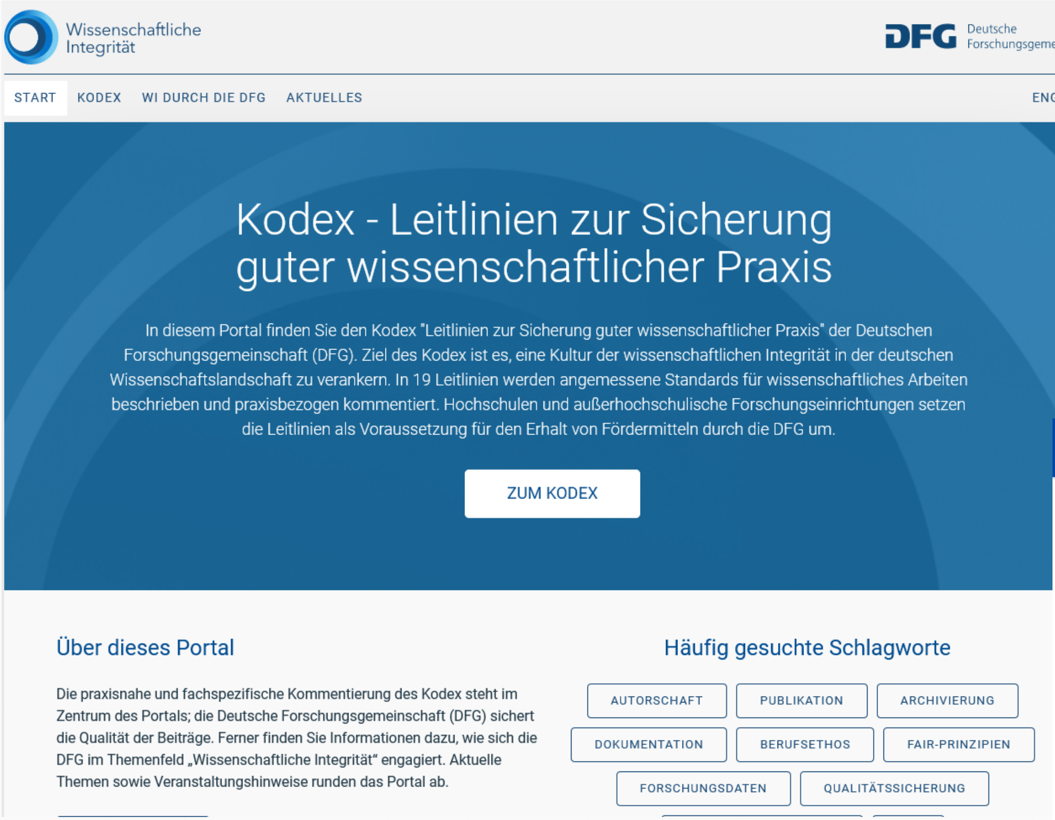
reusable

But data is more

Principle	Meaning
Findable	Identified, metadata enriched, searchable
Accessible	Locatable, standardized protocols
Interoperable	Metadata rich, sustained, metadata survives data
Reusable	Licensed data&metadata, versatile metadata

The stick

Funders want this



Wissenschaftliche Integrität

DFG Deutsche Forschungsgemeinschaft

START KODEX WI DURCH DIE DFG AKTUELLES ENGLISH

Kodex - Leitlinien zur Sicherung guter wissenschaftlicher Praxis

In diesem Portal finden Sie den Kodex "Leitlinien zur Sicherung guter wissenschaftlicher Praxis" der Deutschen Forschungsgemeinschaft (DFG). Ziel des Kodex ist es, eine Kultur der wissenschaftlichen Integrität in der deutschen Wissenschaftslandschaft zu verankern. In 19 Leitlinien werden angemessene Standards für wissenschaftliches Arbeiten beschrieben und praxisbezogen kommentiert. Hochschulen und außerhochschulische Forschungseinrichtungen setzen die Leitlinien als Voraussetzung für den Erhalt von Fördermitteln durch die DFG um.

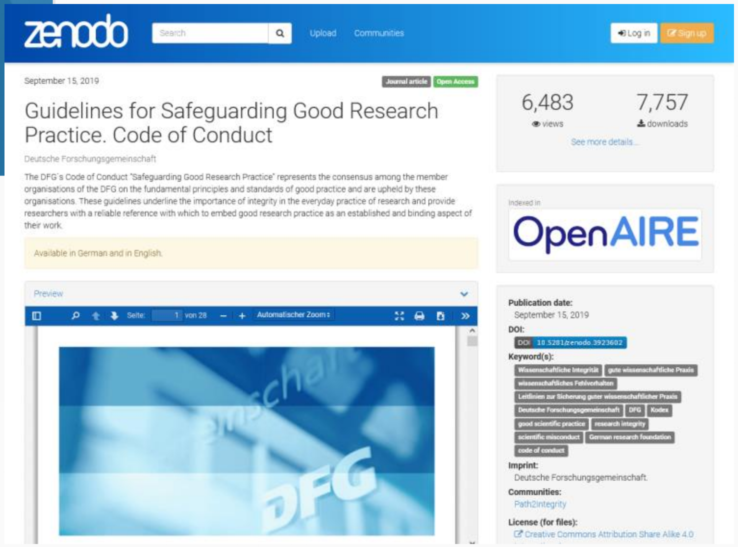
ZUM KODEX

Über dieses Portal

Die praxisnahe und fachspezifische Kommentierung des Kodex steht im Zentrum des Portals; die Deutsche Forschungsgemeinschaft (DFG) sichert die Qualität der Beiträge. Ferner finden Sie Informationen dazu, wie sich die DFG im Themenfeld „Wissenschaftliche Integrität" engagiert. Aktuelle Themen sowie Veranstaltungshinweise runden das Portal ab.

Häufig gesuchte Schlagworte

AUTORSCHAFT PUBLIKATION ARCHIVIERUNG DOKUMENTATION BERUFSETHOS FAIR-PRINZIPIEN FORSCHUNGSDATEN QUALITÄTSSICHERUNG



September 15, 2019

Journal article Open Access

Guidelines for Safeguarding Good Research Practice. Code of Conduct

Deutsche Forschungsgemeinschaft

The DFG´s Code of Conduct "Safeguarding Good Research Practice" represents the consensus among the member organisations of the DFG on the fundamental principles and standards of good practice and are upheld by these organisations. These guidelines underline the importance of integrity in the everyday practice of research and provide researchers with a reliable reference with which to embed good research practice as an established and binding aspect of their work.

Available in German and in English.

Preview

Seite: 1 von 28 Automatischer Zoom

6,483 views

7,757 downloads

See more details...

Indexed in OpenAIRE

Publication date: September 15, 2019

DOI: DOI 10.5281/zenodo.3923602

Keyword(s): Wissenschaftliche Integrität | gute wissenschaftliche Praxis | wissenschaftliches Fehlverhalten | Leitlinien zur Sicherung guter wissenschaftlicher Praxis | Deutsche Forschungsgemeinschaft | DFG | Kodex | good scientific practice | research integrity | scientific misconduct | German research foundation | code of conduct

Imprint: Deutsche Forschungsgemeinschaft.

Communities: Path2integrity

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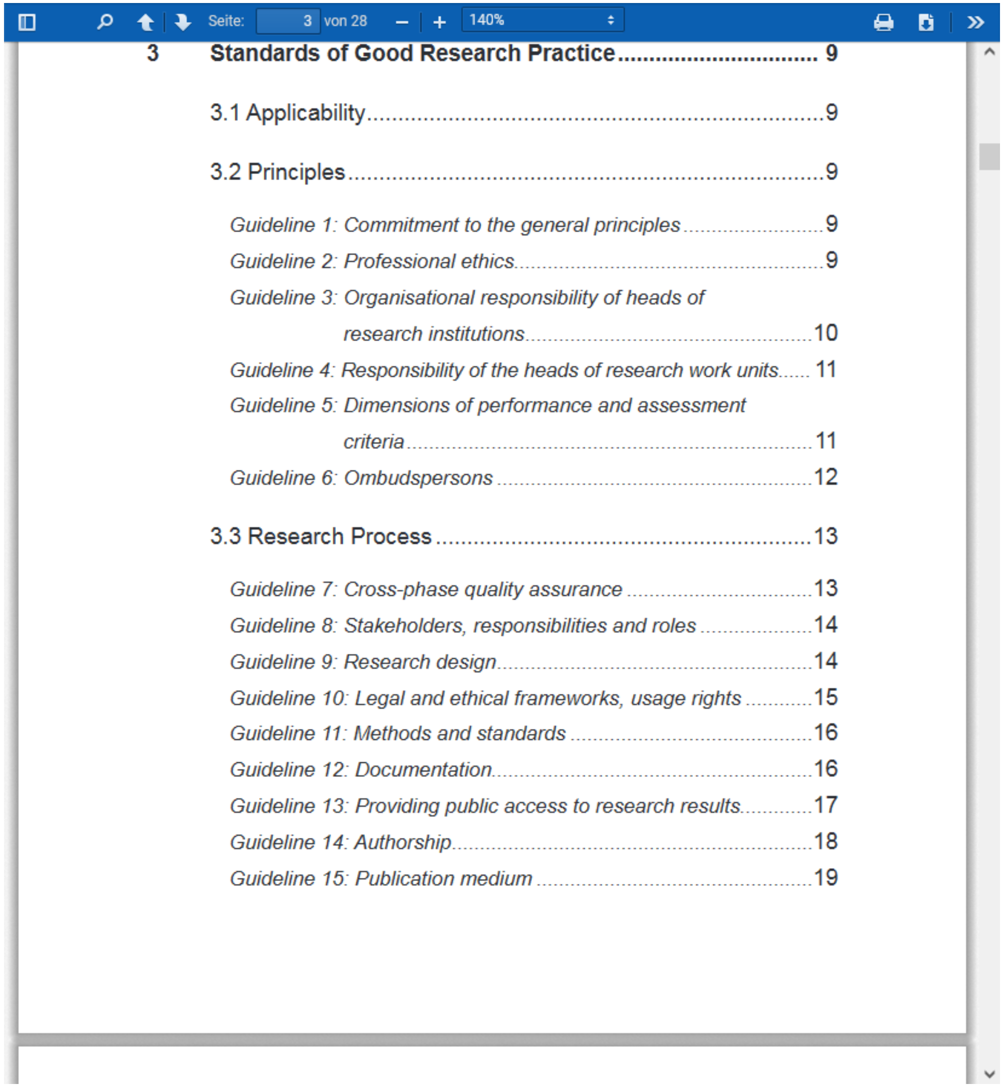
Rough overview of GSP guidelines of DFG



Seite: 3 von 28

140%

- Comprehensive standards of good research practice
- Many suggestsions with an impact on data management:
  - Quality control
  - Long-term preservation
  - Publishing of research

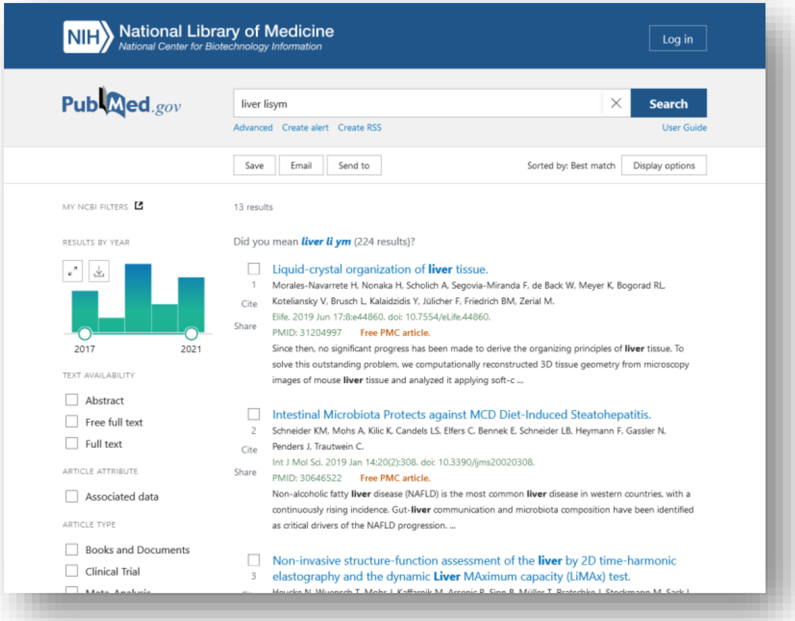
The carrot

Imagine: You want to discover a project/group/institute

For example: LiSyM

Publications

- PubMed: „Liver Lisym“ → 13 results



13 results

Did you mean ***liver li ym*** (224 results)?

□ 1 Cite Share

Liquid-crystal organization of **liver** tissue.
Morales-Navarrete H, Nonaka H, Scholich A, Segovia-Miranda F, de Back W, Meyer K, Bogorad RL, Koteliansky V, Brusch L, Kalaidzidis Y, Jülicher F, Friedrich BM, Zerial M.
Elife. 2019 Jun 17;8:e44860. doi: 10.7554/eLife.44860.
PMID: 31204997 Free PMC article.
Since then, no significant progress has been made to derive the organizing principles of **liver** tissue. To solve this outstanding problem, we computationally reconstructed 3D tissue geometry from microscopy images of mouse **liver** tissue and analyzed it applying soft-c ...

□ 2 Cite Share

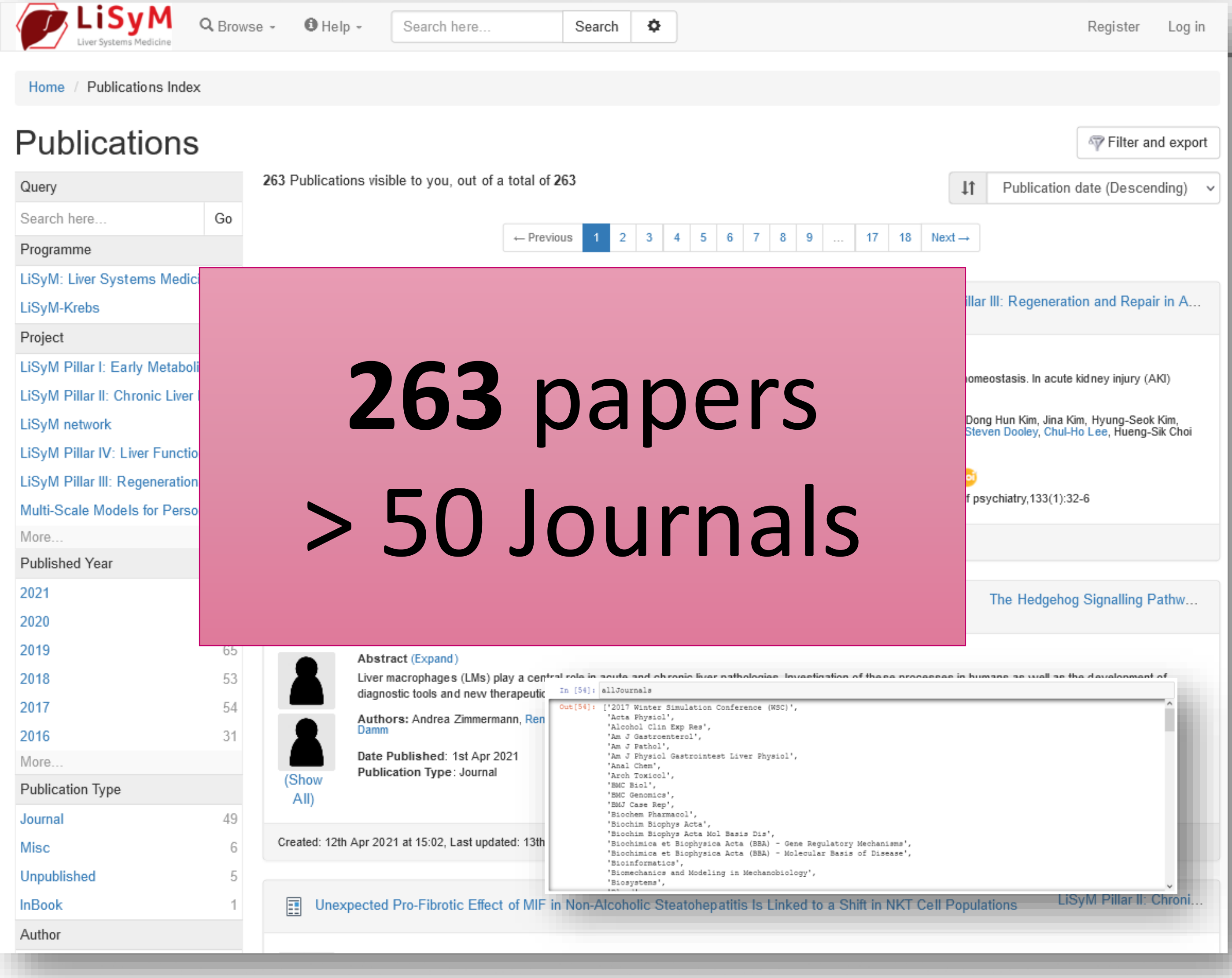
Intestinal Microbiota Protects against MCD Diet-Induced Steatohepatitis.
Schneider KM, Mohs A, Kilic K, Candels LS, Elfers C, Bennek E, Schneider LB, Heymann F, Gassler N, Penders J, Trautwein C.
Int J Mol Sci. 2019 Jan 14;20(2):308. doi: 10.3390/ijms20020308.
PMID: 30646522 Free PMC article.
Non-alcoholic fatty **liver** disease (NAFLD) is the most common **liver** disease in western countries, with a continuously rising incidence. Gut-**liver** communication and microbiota composition have been identified as critical drivers of the NAFLD progression. ...

□ 3

Non-invasive structure-function assessment of the **liver** by 2D time-harmonic elastography and the dynamic **Liver** MAximum capacity (LiMAx) test.
Heucke N, Wuensch T, Mohr J, Kaffarnik M, Arsenic R, Sinn B, Müller T, Pratschke J, Stockmann M, Sack I

SEEK

263 papers
> 50 Journals



LiSyM Liver Systems Medicine · Browse · Help · Search here... · Search · Register · Log in

Home / Publications Index

Publications

Filter and export

263 Publications visible to you, out of a total of 263

Publication date (Descending)

← Previous 1 2 3 4 5 6 7 8 9 ... 17 18 Next →

Query	
Search here... Go	
Programme	
LiSyM: Liver Systems Medici	
LiSyM-Krebs	
Project	
LiSyM Pillar I: Early Metaboli	
LiSyM Pillar II: Chronic Liver	
LiSyM network	
LiSyM Pillar IV: Liver Functio	
LiSyM Pillar III: Regeneration	
Multi-Scale Models for Perso	
More...	
Published Year	
2021	
2020	
2019	65
2018	53
2017	54
2016	31
More...	
Publication Type	
Journal	49
Misc	6
Unpublished	5
InBook	1
Author	

llar III: Regeneration and Repair in A...

omeostasis. In acute kidney injury (AKI)

Dong Hun Kim, Jina Kim, Hyung-Seok Kim, Steven Dooley, Chul-Ho Lee, Hueng-Sik Choi

f psychiatry,133(1):32-6

The Hedgehog Signalling Pathw...

Abstract (Expand)

Liver macrophages (LMs) play a central role in acute and chronic liver pathologies. Investigation of these processes in humans as well as the development of diagnostic tools and new therapeutic

Authors: Andrea Zimmermann, Ren Damm

(Show All)

Date Published: 1st Apr 2021

Publication Type: Journal

Created: 12th Apr 2021 at 15:02, Last updated: 13th

```
In [54]: allJournals

Out[54]: ['2017 Winter Simulation Conference (WSC)',
          'Acta Physiol',
          'Alcohol Clin Exp Res',
          'Am J Gastroenterol',
          'Am J Pathol',
          'Am J Physiol Gastrointest Liver Physiol',
          'Anal Chem',
          'Arch Toxicol',
          'BMC Biol',
          'BMC Genomics',
          'BMJ Case Rep',
          'Biochem Pharmacol',
          'Biochim Biophys Acta',
          'Biochim Biophys Acta Mol Basis Dis',
          'Biochimica et Biophysica Acta (BBA) - Gene Regulatory Mechanisms',
          'Biochimica et Biophysica Acta (BBA) - Molecular Basis of Disease',
          'Bioinformatics',
          'Biomechanics and Modeling in Mechanobiology',
          'Biosystems',
```

Unexpected Pro-Fibrotic Effect of MIF in Non-Alcoholic Steatohepatitis Is Linked to a Shift in NKT Cell Populations

LiSyM Pillar II: Chroni...

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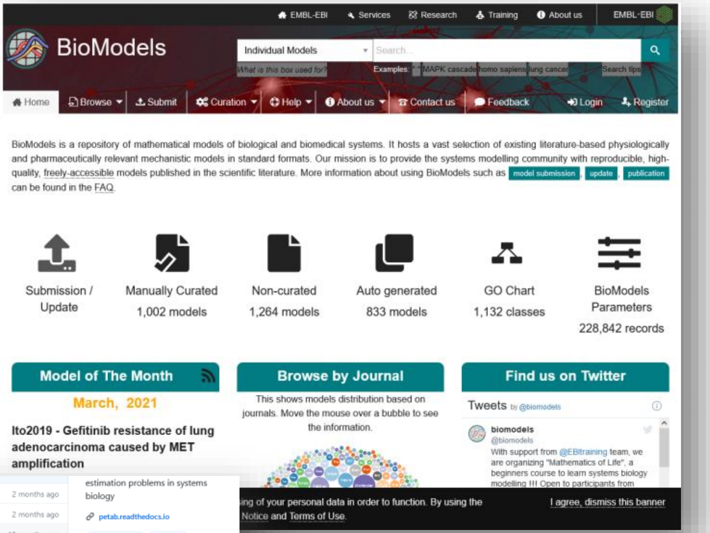
Now, let‘s look at

- Models
- Data

Models: Model DBs & GitHub/GitLab

HITS



BioModels is a repository of mathematical models of biological and biomedical systems. It hosts a vast selection of existing literature-based physiologically and pharmaceutically relevant mechanistic models in standard formats. Our mission is to provide the systems modelling community with reproducible, high-quality, freely-accessible models published in the scientific literature. More information about using BioModels such as model submission, update, publication can be found in the FAQ.

Submission / Update	Manually Curated	Non-curated	Auto generated	GO Chart	BioModels Parameters
	1,002 models	1,264 models	833 models	1,132 classes	228,842 records

Model of The Month

March, 2021

Ito2019 - Gefitinib resistance of lung adenocarcinoma caused by MET amplification

Browse by Journal

This shows models distribution based on journals. Move the mouse over a bubble to see the information.

Find us on Twitter

Tweets by @biomodels

biomodels
@biomodels
With support from @EBItraining team, we are organizing "Mathematics of Life", a beginners course to learn systems biology modelling !!! Open to participants from

…ing of your personal data in order to function. By using the … Notice and Terms of Use.

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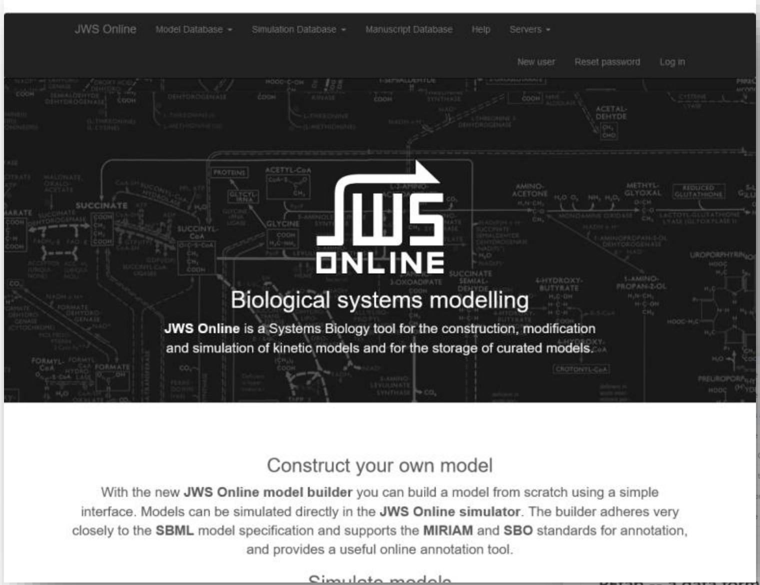


Biological systems modelling

JWS Online is a Systems Biology tool for the construction, modification and simulation of kinetic models and for the storage of curated models.

Construct your own model

With the new **JWS Online model builder** you can build a model from scratch using a simple interface. Models can be simulated directly in the **JWS Online simulator**. The builder adheres very closely to the **SBML** model specification and supports the **MIRIAM** and **SBO** standards for annotation, and provides a useful online annotation tool.

Simulate models

…python-package-related files (#518)	2 months ago
…python-package-related files (#518)	2 months ago
…and add residual calculation function (#345)	15 months ago
…python-package-related files (#518)	2 months ago
…CHANGELOG	2 months ago
…test results and add contribution guide (#389)	14 months ago
…mmit	3 years ago
…python-package-related files (#518)	2 months ago

…estimation problems in systems biology

petab.readthedocs.io

Releases 30

PEtab v0.1.14 Latest
on 12 Jan

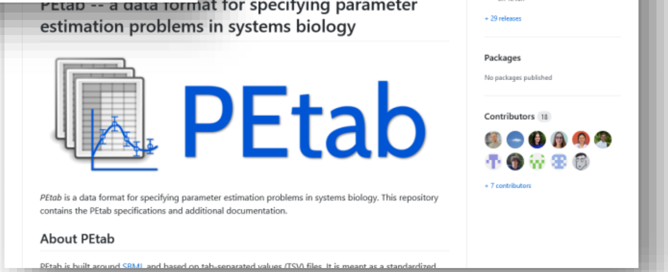
+ 29 releases

Packages

No packages published

Contributors 18

+ 7 contributors

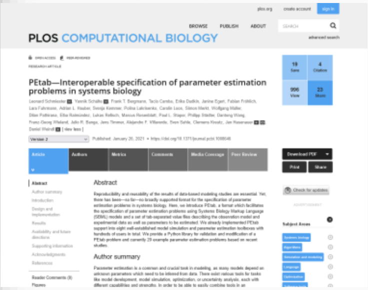


PEtab -- a data format for specifying parameter estimation problems in systems biology

PEtab is a data format for specifying parameter estimation problems in systems biology. This repository contains the PEtab specifications and additional documentation.

About PEtab

PEtab is built around SBML and based on tab-separated values (TSV) files. It is meant as a standardized



PLOS COMPUTATIONAL BIOLOGY

PEtab—Interoperable specification of parameter estimation problems in systems biology

Leonard Schmiester, Yannik Schälte, Frank T. Bergmann, Tacio Camba, Erika Dudkin, Janine Egert, Fabian Fröhlich, Lara Fuhrmann, Adrian L. Hauber, Svenja Kemmer, Polina Lakrisenko, Carolin Loos, Simon Merkt, Wolfgang Müller, Dilan Pathirana, Elba Raimúndez, Lukas Refisch, Marcus Rosenblatt, Paul L. Stapor, Philipp Städter, Dantong Wang, Franz-Georg Wieland, Julio R. Banga, Jens Timmer, Alejandro F. Villaverde, Sven Sahle, Clemens Kreutz, Jan Hasenauer, Daniel Weindl [view less]

Version 2 Published: January 26, 2021 • https://doi.org/10.1371/journal.pcbi.1008646

Abstract

Reproducibility and reusability of the results of data-based modeling studies are essential. Yet, there has been—so far—no broadly supported format for the specification of parameter estimation problems in systems biology. Here, we introduce PEtab, a format which facilitates the specification of parameter estimation problems using Systems Biology Markup Language (SBML) models and a set of tab-separated value files describing the observation model and experimental data as well as parameters to be estimated. We already implemented PEtab support into eight well-established model simulation and parameter estimation toolboxes with hundreds of users in total. We provide a Python library for validation and modification of a PEtab problem and currently 20 example parameter estimation problems based on recent studies.

Author summary

Parameter estimation is a common and crucial task in modeling, as many models depend on unknown parameters which need to be inferred from data. There exist various tools for tasks like model development, model simulation, optimization, or uncertainty analysis, each with different capabilities and strengths. In order to be able to easily combine tools in an

LiSyM Liver Systems Medicine

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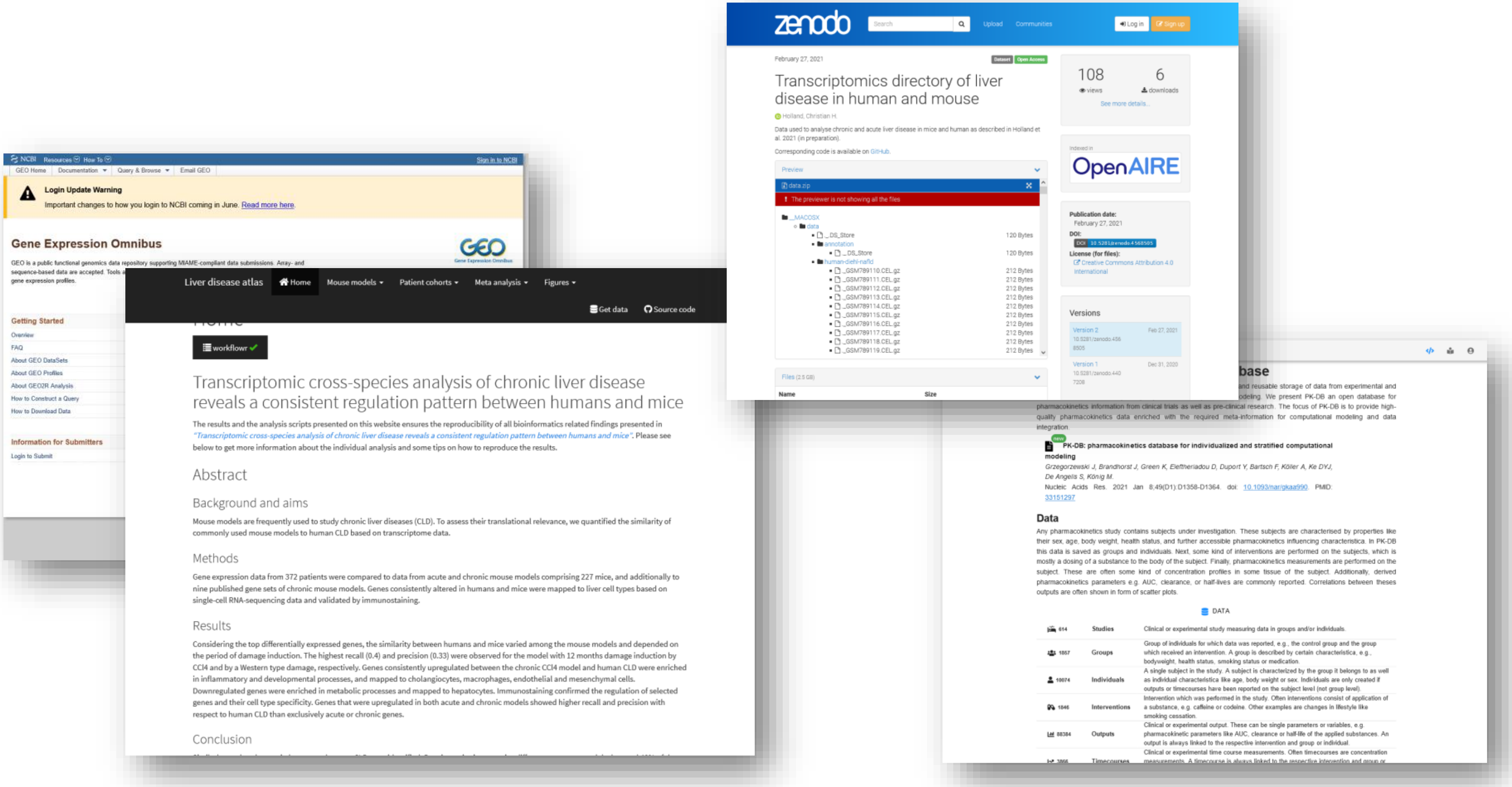
and Research

Datacollections, Zenodo, web apps



Login Update Warning

Important changes to how you login to NCBI coming in June. Read more here.

Gene Expression Omnibus

GEO is a public functional genomics data repository supporting MIAME-compliant data submissions. Array- and sequence-based data are accepted. Tools a

gene expression profiles.

Getting Started

- Overview
- FAQ
- About GEO DataSets
- About GEO Profiles
- About GEO2R Analysis
- How to Construct a Query
- How to Download Data

Information for Submitters

- Login to Submit

Transcriptomic cross-species analysis of chronic liver disease reveals a consistent regulation pattern between humans and mice

The results and the analysis scripts presented on this website ensures the reproducibility of all bioinformatics related findings presented in *"Transcriptomic cross-species analysis of chronic liver disease reveals a consistent regulation pattern between humans and mice"*. Please see below to get more information about the individual analysis and some tips on how to reproduce the results.

Abstract

Background and aims

Mouse models are frequently used to study chronic liver diseases (CLD). To assess their translational relevance, we quantified the similarity of commonly used mouse models to human CLD based on transcriptome data.

Methods

Gene expression data from 372 patients were compared to data from acute and chronic mouse models comprising 227 mice, and additionally to nine published gene sets of chronic mouse models. Genes consistently altered in humans and mice were mapped to liver cell types based on single-cell RNA-sequencing data and validated by immunostaining.

Results

Considering the top differentially expressed genes, the similarity between humans and mice varied among the mouse models and depended on the period of damage induction. The highest recall (0.4) and precision (0.33) were observed for the model with 12 months damage induction by CCl4 and by a Western type damage, respectively. Genes consistently upregulated between the chronic CCl4 model and human CLD were enriched in inflammatory and developmental processes, and mapped to cholangiocytes, macrophages, endothelial and mesenchymal cells. Downregulated genes were enriched in metabolic processes and mapped to hepatocytes. Immunostaining confirmed the regulation of selected genes and their cell type specificity. Genes that were upregulated in both acute and chronic models showed higher recall and precision with respect to human CLD than exclusively acute or chronic genes.

Conclusion

February 27, 2021

Transcriptomics directory of liver disease in human and mouse

Holland, Christian H.

Data used to analyse chronic and acute liver disease in mice and human as described in Holland et al. 2021 (in preparation).

Corresponding code is available on GitHub.

! The previewer is not showing all the files

```
■ __MACOSX
  ○ ■ data
      ▪ ._DS_Store                120 Bytes
      ▪ ■ annotation
          ▪ ._DS_Store            120 Bytes
      ▪ ■ human-diehl-nafld
          ▪ ._GSM789110.CEL.gz    212 Bytes
          ▪ ._GSM789111.CEL.gz    212 Bytes
          ▪ ._GSM789112.CEL.gz    212 Bytes
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          ▪ ._GSM789119.CEL.gz    212 Bytes
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Files (2.5 GB)

Name	Size

108 views

6 downloads

See more details...

Indexed in

Publication date: February 27, 2021

DOI: DOI 10.5281/zenodo.4568505

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Versions

Version 2 Feb 27, 2021
10.5281/zenodo.4568505

Version 1 Dec 31, 2020
10.5281/zenodo.4407208

base

and reusable storage of data from experimental and odeling. We present PK-DB an open database for pharmacokinetics information from clinical trials as well as pre-clinical research. The focus of PK-DB is to provide high-quality pharmacokinetics data enriched with the required meta-information for computational modeling and data integration.

new **PK-DB: pharmacokinetics database for individualized and stratified computational modeling**
Grzegorzewski J, Brandhorst J, Green K, Eleftheriadou D, Duport Y, Bartsch F, Köller A, Ke DYJ, De Angelis S, König M.
Nucleic Acids Res. 2021 Jan 8;49(D1):D1358-D1364. doi: 10.1093/nar/gkaa990. PMID: 33151297

Data

Any pharmacokinetics study contains subjects under investigation. These subjects are characterised by properties like their sex, age, body weight, health status, and further accessible pharmacokinetics influencing characteristica. In PK-DB this data is saved as groups and individuals. Next, some kind of interventions are performed on the subjects, which is mostly a dosing of a substance to the body of the subject. Finally, pharmacokinetics measurements are performed on the subject. These are often some kind of concentration profiles in some tissue of the subject. Additionally, derived pharmacokinetics parameters e.g. AUC, clearance, or half-lives are commonly reported. Correlations between theses outputs are often shown in form of scatter plots.

DATA

614	**Studies**	Clinical or experimental study measuring data in groups and/or individuals.
1857	**Groups**	Group of individuals for which data was reported, e.g., the control group and the group which received an intervention. A group is described by certain characteristica, e.g., bodyweight, health status, smoking status or medication.
10074	**Individuals**	A single subject in the study. A subject is characterized by the group it belongs to as well as individual characteristica like age, body weight or sex. Individuals are only created if outputs or timecourses have been reported on the subject level (not group level).
1846	**Interventions**	Intervention which was performed in the study. Often interventions consist of application of a substance, e.g. caffeine or codeine. Other examples are changes in lifestyle like smoking cessation.
88384	**Outputs**	Clinical or experimental output. These can be single parameters or variables, e.g. pharmacokinetic parameters like AUC, clearance or half-life of the applied substances. An output is always linked to the respective intervention and group or individual.
3866	**Timecourses**	Clinical or experimental time course measurements. Often timecourses are concentration measurements. A timecourse is always linked to the respective intervention and group or

Summarising

- Many specialized data sources
- Many useful data locations
- Quite some data merged – curated

- Looking at all of them: too cumbersome

- Data management enables to have
  - **one place to find them all**
  - **one place to standardize**

- Needs to be adapted to
  - Remote data
  - Local data

FAIRDOM
SEEK

Be the hub for heterogeneous, big projects, store data & models, too

FAIRDOM

Be the data management for groups (and possibly bigger)

openBIS

Now

- Talk by Piotr Zadora, DKFZ
  Covering the use of openBIS
  in the Klingmüller Department at DKFZ

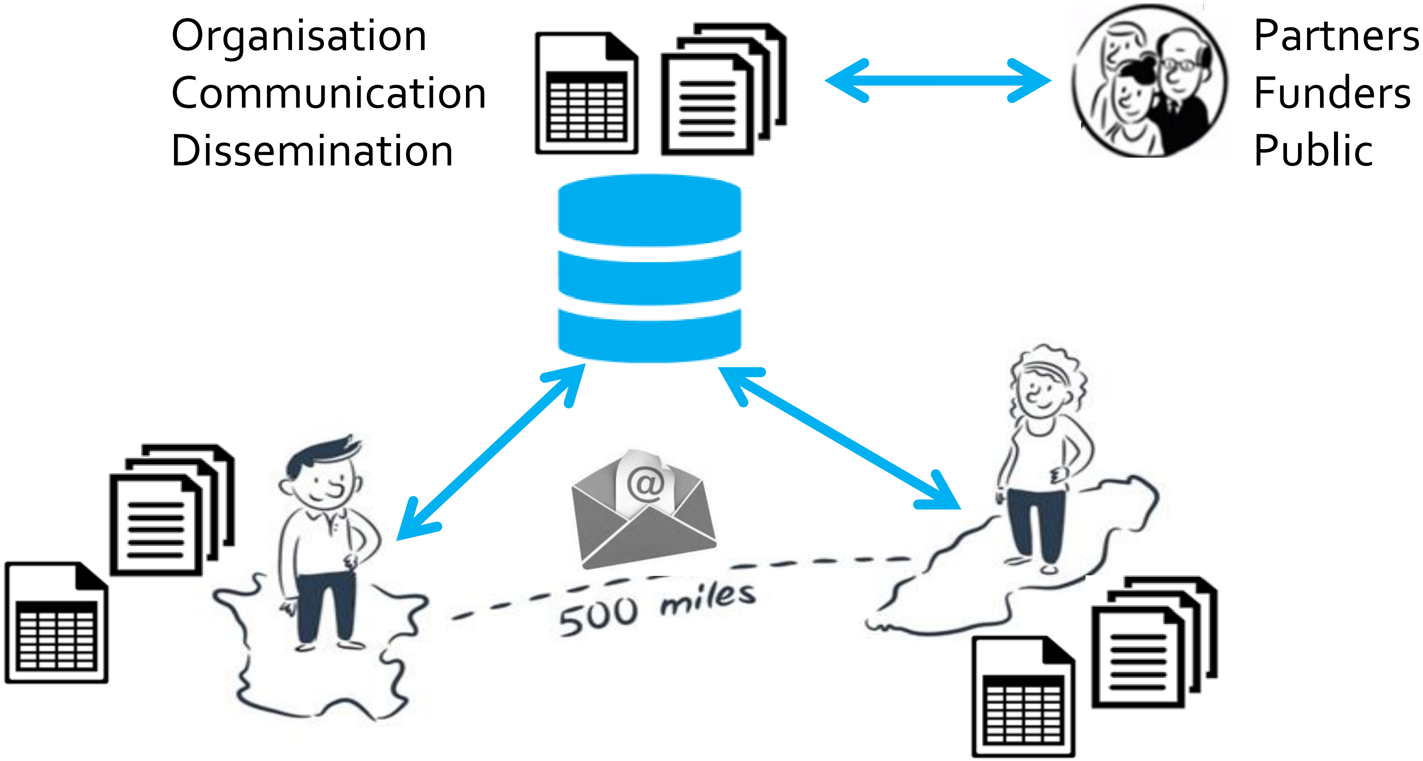
- Then some more work about challenges to address in DM or DMM

- Then „the SEEK day“
- Followed by „the openBIS day“

Some more general words about DM

- Strong push by lead
- Onboarding by proficient users
- Jupyter Notebooks in openBIS
- Data models
  (FAIRDOM support but scientific tech organiser, internally, too)

Goal:
Project Data Management



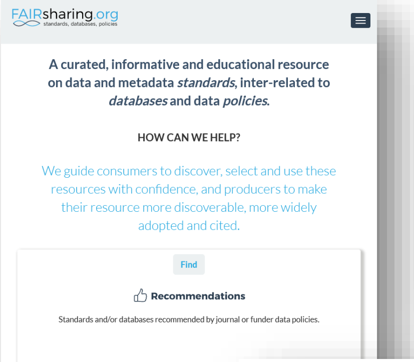
Organisation
Communication
Dissemination

Partners
Funders
Public

Current, comprehensive, FAIR

Challenges to adress

- Social & organisational
- Conceptual
  - Data structures
  - Ontologies
  - Standards
- Tooling
  - Which tools to use
  - How to combine



FAIRsharing.org
standards, databases, policies

A curated, informative and educational resource on data and metadata *standards*, inter-related to *databases* and data *policies*.

HOW CAN WE HELP?

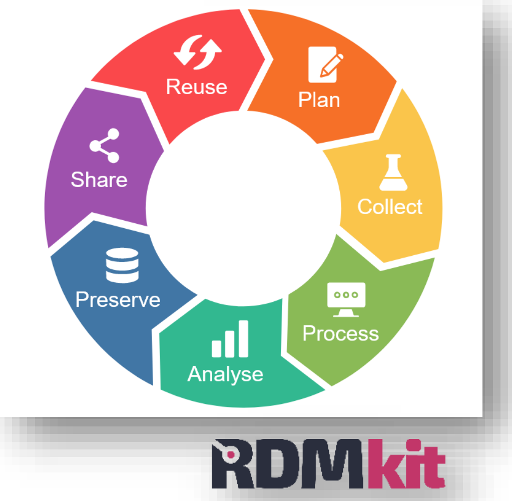
We guide consumers to discover, select and use these resources with confidence, and producers to make their resource more discoverable, more widely adopted and cited.

Find

Recommendations

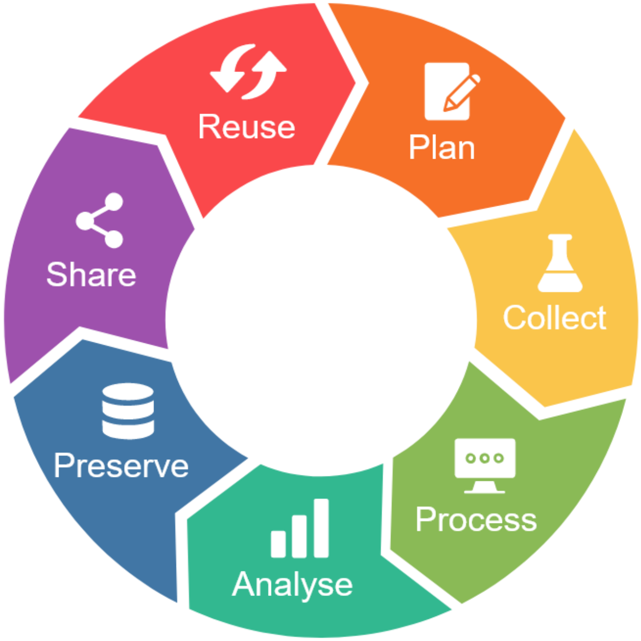
Standards and/or databases recommended by journal or funder data policies.

Discover



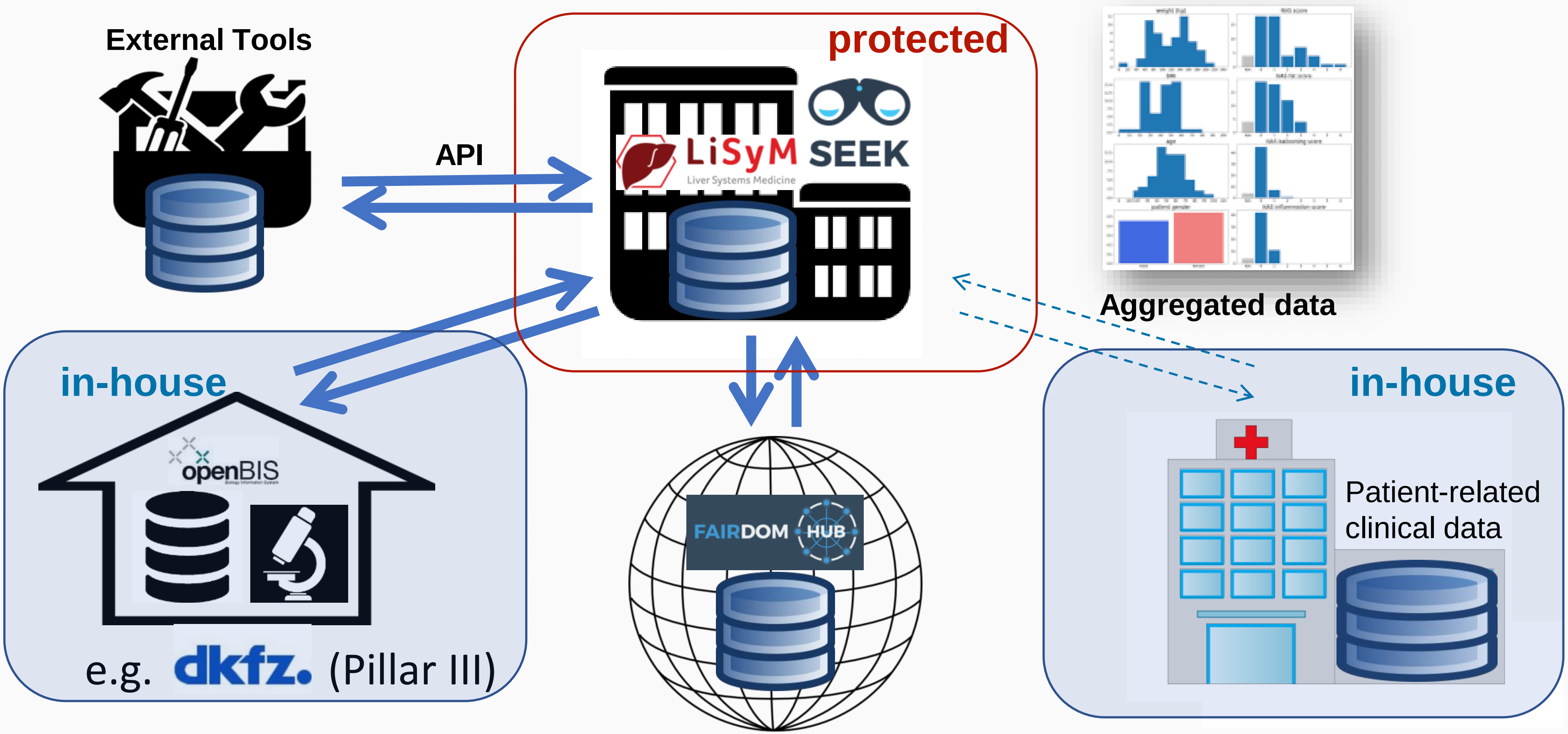
Assembling data management processes

- Collect raw and processed (secondary) data, models & metadata together with experimental context
- Organise and link assets
- Prepare reproducible publications
- Use standardised metadata
- Share with colleagues and public
- Integrate with legacy, home grown, external systems
- Reuse tools and community archives



RDMkit
https://rdmkit.elixir-europe.org

Structuring deployment: LiSyM Example



External Tools

API

protected

Aggregated data

in-house

in-house

Patient-related clinical data

e.g. dkfz. (Pillar III)

LiSyM Liver Systems Medicine

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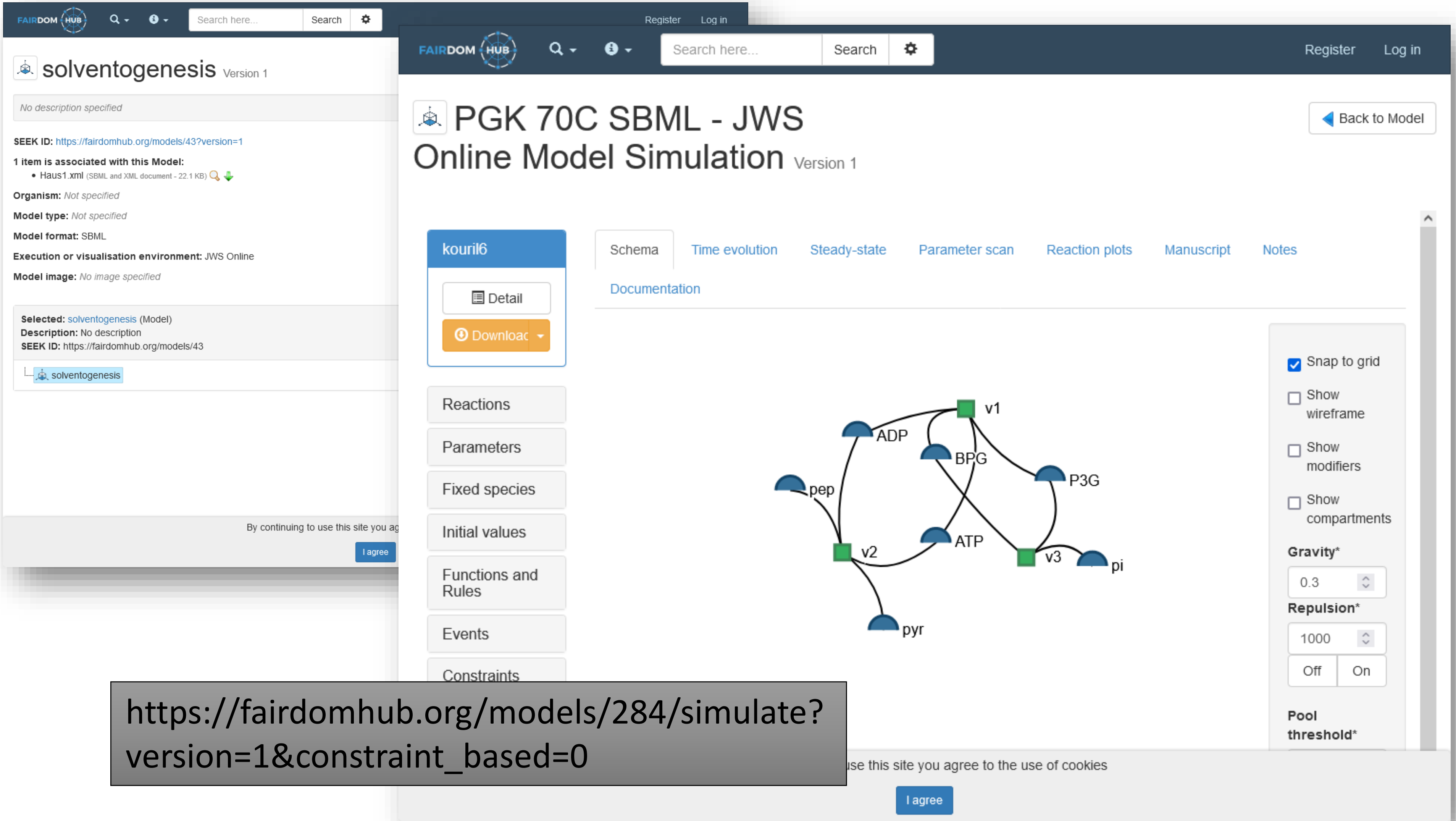
Assembling vs. Integrating: integrated JWS modelling tool in SEEK-based FAIRDOMHub



solventogenesis Version 1

No description specified

SEEK ID: https://fairdomhub.org/models/43?version=1

1 item is associated with this Model:

- Haus1.xml (SBML and XML document - 22.1 KB)

Organism: *Not specified*

Model type: *Not specified*

Model format: SBML

Execution or visualisation environment: JWS Online

Model image: *No image specified*

Selected: solventogenesis (Model)
Description: No description
SEEK ID: https://fairdomhub.org/models/43

solventogenesis

By continuing to use this site you ag

I agree

PGK 70C SBML - JWS Online Model Simulation Version 1

☑ Snap to grid

□ Show wireframe

□ Show modifiers

□ Show compartments

Gravity* 0.3

Repulsion* 1000

Off On

Pool threshold*

use this site you agree to the use of cookies

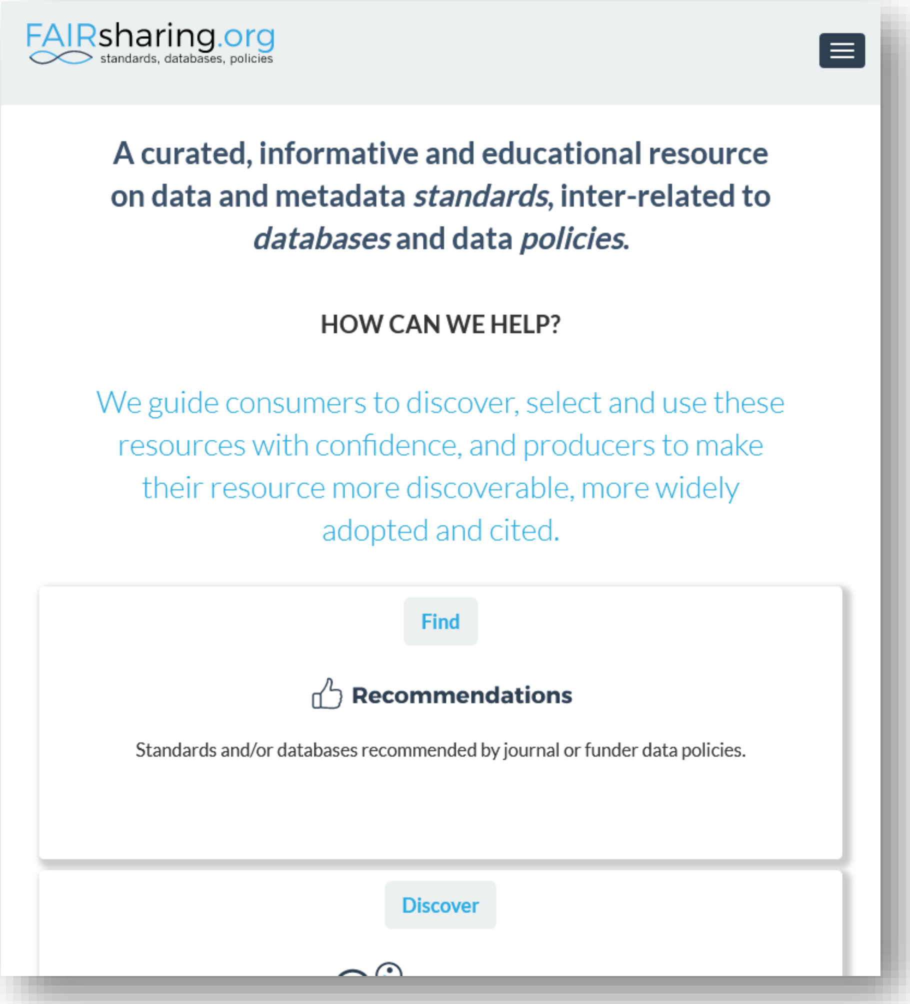
I agree

https://fairdomhub.org/models/284/simulate?version=1&constraint_based=0

Ontologies and standards: FAIRsharing.org

How to structure your data?
Reuse other people's work

- Community standards
  - 1532 Standards
    (e.g. the MIBBI standards)
  - 1773 Databases
  - 140 Policies



A curated, informative and educational resource on data and metadata *standards*, inter-related to *databases* and data *policies*.

HOW CAN WE HELP?

We guide consumers to discover, select and use these resources with confidence, and producers to make their resource more discoverable, more widely adopted and cited.

Recommendations

Standards and/or databases recommended by journal or funder data policies.

Social

- **Insight:** Data management means **change**

- **Challenge: How to include people?**
  - How to get information
  - Useful suggestions how to do better
  - Refinement of workflows
  - **Strive for painless ingestion and useful outcome**

- **Proposal:** Have responsibles on per-project basis
- Regular meetings with data management responsibles
- Who should be responsible?
  Depends on **<u>your</u>** organisation

The FAIRDOM approach: Have „PALs“, a focus group in the project

PALs kickoff of FAIRDOM 2013

Organisational: Data sharing policy

Example: LiSyM DSP, derived from ERASysAPP DSP

- Expression of intent
- Who is responsible?
- Who shares with whom?
- When?
- What?
- What in case of disagreement?

LiSyM
Liver Systems Medicine

Data Sharing Policy

Principles adopted by LiSyM
for sharing data, models and processes

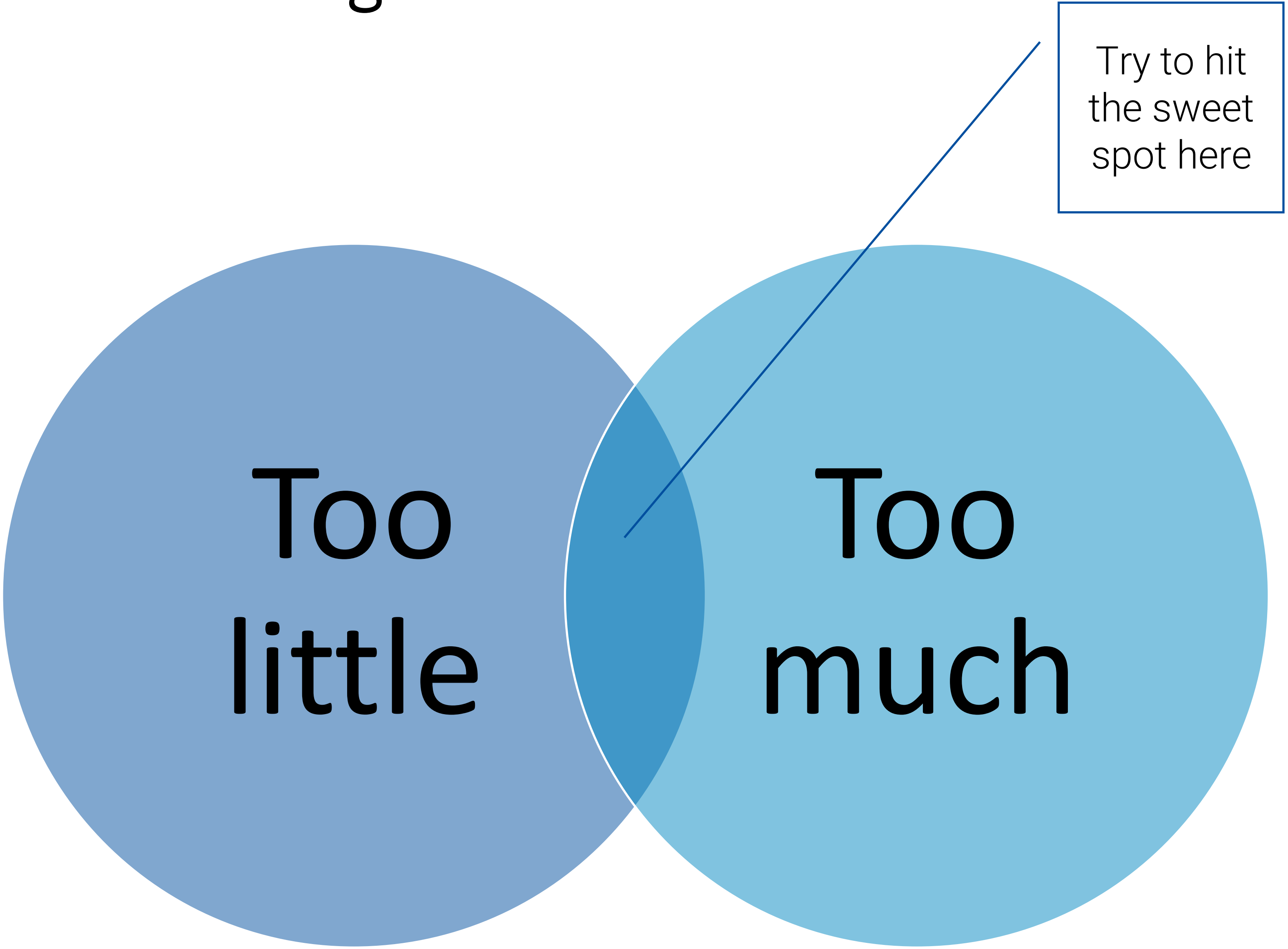
December 2017

Federal Ministry
of Education
and Research

PtJ
Projektträger Jülich
Forschungszentrum Jülich

1 Page |

Spend the right amount of effort on this



Now: Front End

Find, Access and Organise assets

FAIRDOM

SEEK

- Upload data
- Link to data regardless of physical store
- Sharing
- ISA structure
- Yellow pages and collaboration
- Supplementary data for publications
- Standards-compliant

Thanks, Questions?

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KTS

Bundesministerium für Bildung und Forschung

elixir

de.NBI

GERMAN NETWORK FOR BIOINFORMATICS INFRASTRUCTURE