Universität Rostock Traditio et Innovatio

SYSTEMS BIOLOGY BIOINFORMATICS ROSTOCK

SEMS simulation experiment management system

The CombineArchive Toolkit

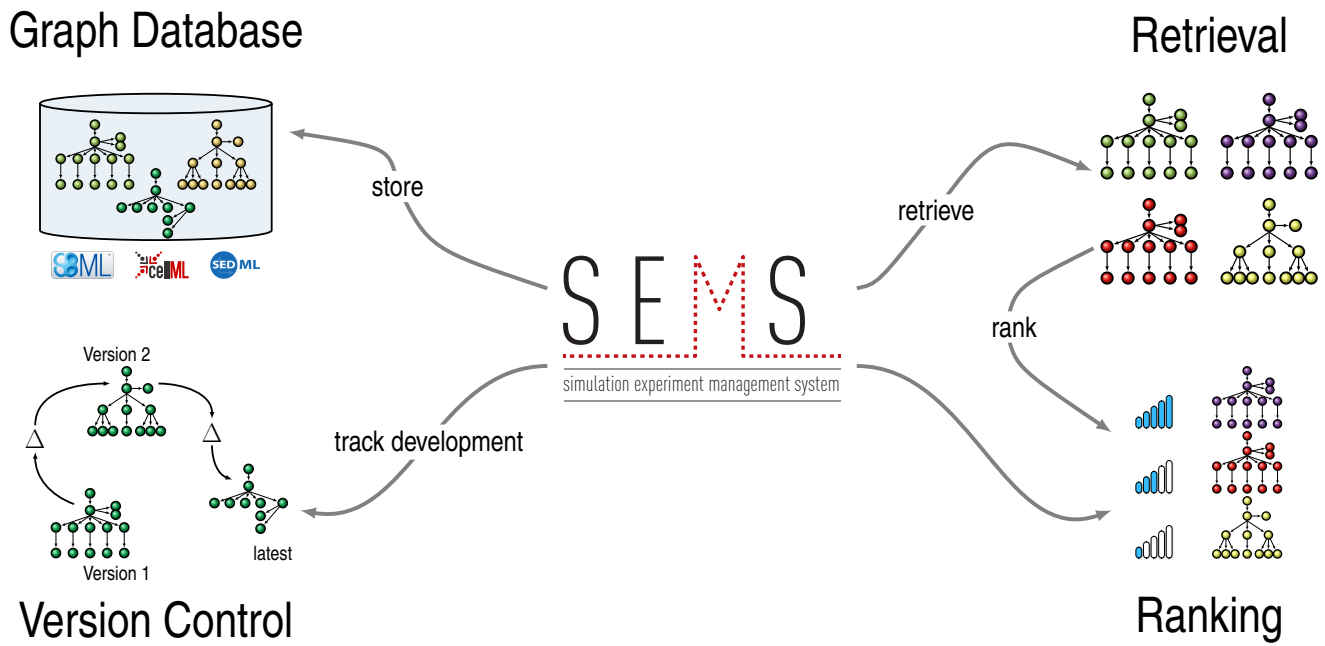
facilitating the transfer of research results.

MARTIN SCHARM

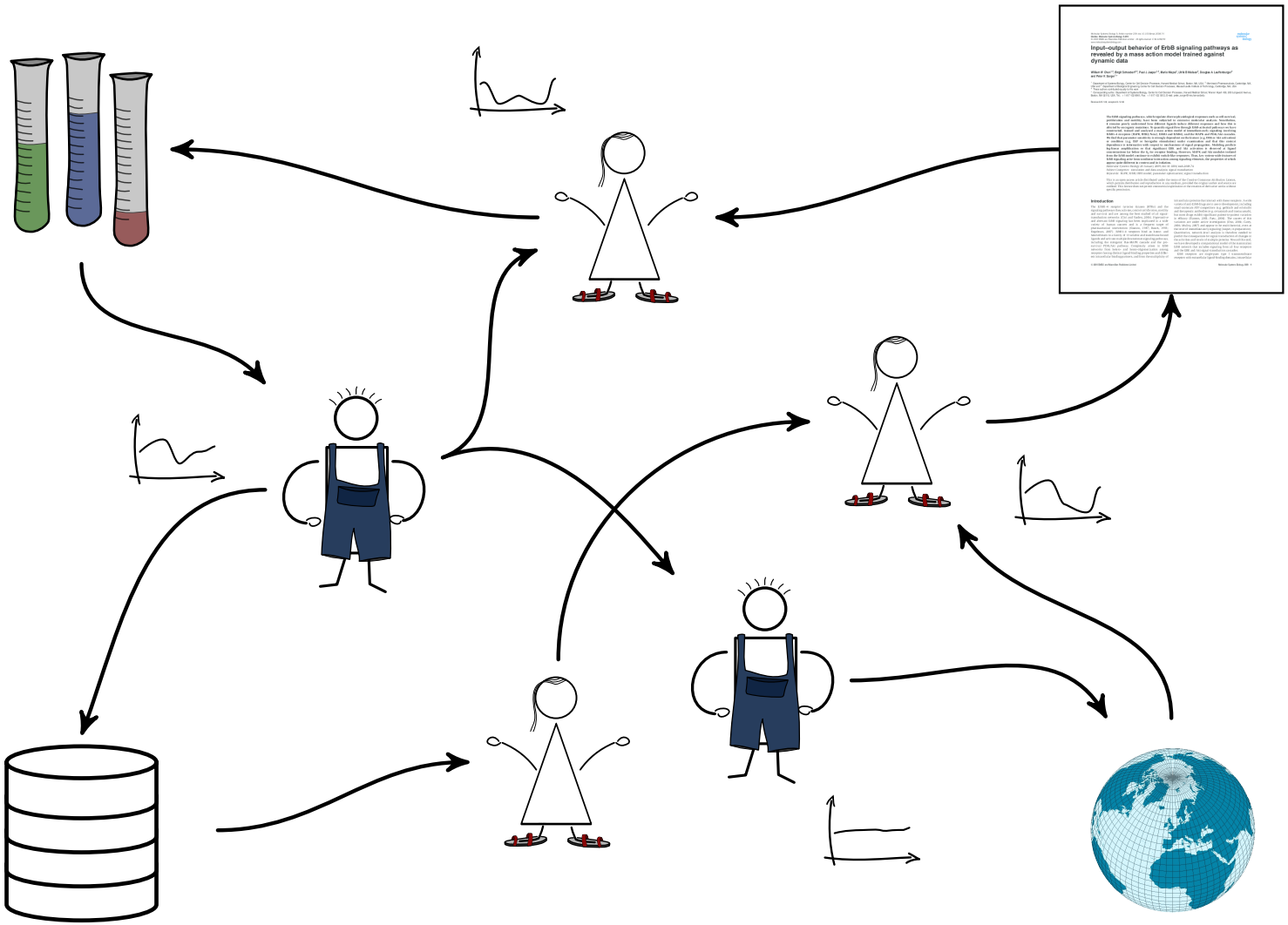
Department of Systems Biology & Bioinformatics, University of Rostock

http://sems.uni-rostock.de

Foundry Workshop, Heidelberg

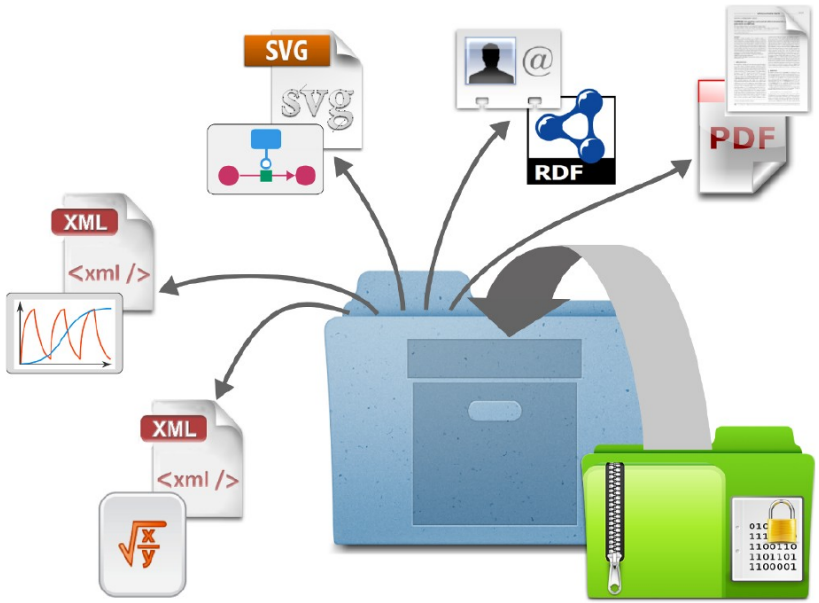

Graph Database
store
SEMS
simulation experiment management system
retrieve
Retrieval
rank
Version 2
track development
Version 1
latest
Version Control
Ranking

How do you share your data?



The COMBINE Archive

one file to share them all



arXiv.org > cs > arXiv:1407.4992

Search or Article-id

Computer Science > Digital Libraries

COMBINE archive: One File To Share Them All

Frank T. Bergmann, Richard Adams, Stuart Moodie, Jonathan Cooper, Mihai Glont, Martin Golebiewski, Michael Hucka, Camille Laibe, Andrew K. Miller, David P. Nickerson, Brett G. Olivier, Nicolas Rodriguez, Herbert M. Sauro, Martin Scharm, Stian Soiland-Reyes, Dagmar Waltemath, Florent Yvon, Nicolas Le Novère

(Submitted on 18 Jul 2014)

- ZIP container (**O**pen **M**odelling **EX**change Format)
- Contents:
  - manifest.xml – information about files and their formats
  - Meta data files – clerical information
  - The files – necessary to reproduce a modelling result
- Already supported by BioModels SED ML

- Java library:
  - Extract single files / whole archive
  - Browse through the archive
  - Add and remove files
  - Rename and organise files
  - Attach and retrieve meta data
- Desktop Application
- Web Interface

Martin Scharm

Florian Wendland

Martin Peters

Website: sems.uni-rostock.de/cat

Publication: peerj.com/preprints/514

PREPRINT - *PeerJ PrePrints* is not a peer-reviewed venue.

The CombineArchive Toolkit - facilitating the transfer of research results

Martin Scharm, Florian Wendland, Martin Peters, Markus Wolfien, Tom Theile, Dagmar Waltemath

What does my tool do? The CombineArchive Toolkit facilitates the transfer of research results.

What are the neighbors of the tool? Our library can be integrated in websites, databases, and other software projects to add support for COMBINE Archives. The user interfaces provide intuitive access to COMBINE Archives for end users.

Who are the users of the tool? Every scientist can use the CombineArchive Toolkit to share reproducible research results. Software developers may integrate our library into their tools.

What is the current sustainability concept? The format as well as our tools are open and free to use for everyone interested in reproducibility.

How does this fit in with ELIXIR/ISBE/National efforts? The combine archive format was co-developed by active members of ELIXIR, ISBE, and the BMBF. Thus, this format is supposed to become the standard format in these societies.

Thank you for your attention!

SEMS group

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Ron Henkel
Martin Peters
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Rebekka Alm
Olaf Wolkenhauer

combine
SysMO SEEK Systems Biology of Microorganisms
cellML
BioModels

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Bundesministerium für Bildung und Forschung