

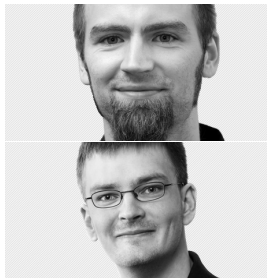
# The CombineArchive Toolkit

facilitating the transfer of research results.

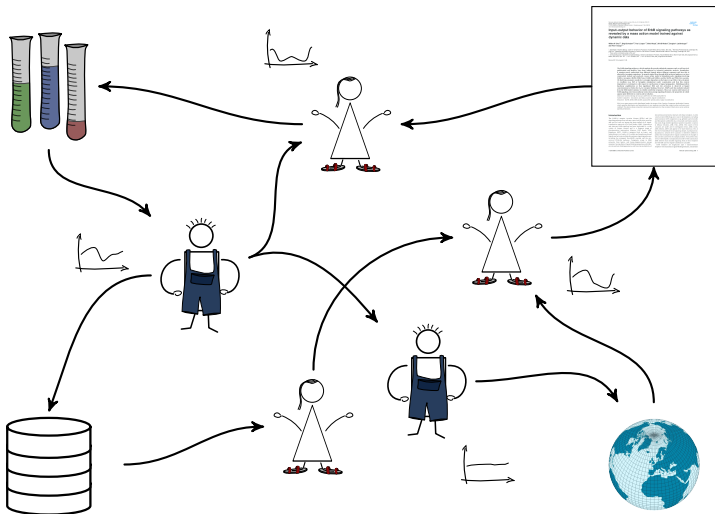
**MARTIN SCHARM, FLORIAN WENDLAND**

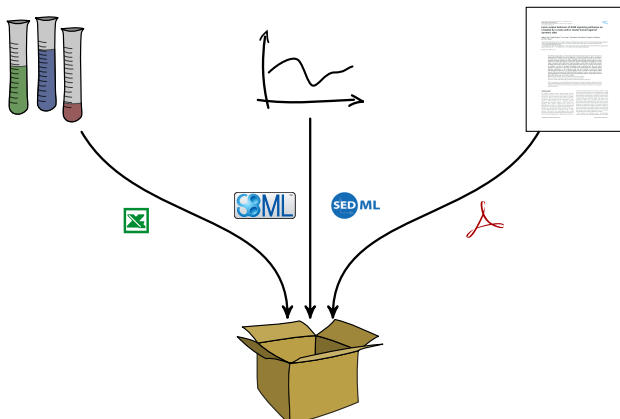
Department of Systems Biology & Bioinformatics, University of Rostock

<http://sems.uni-rostock.de>



SBI Research Seminar  
WS 2014/2015








arXiv.org > cs > arXiv:1407.4992

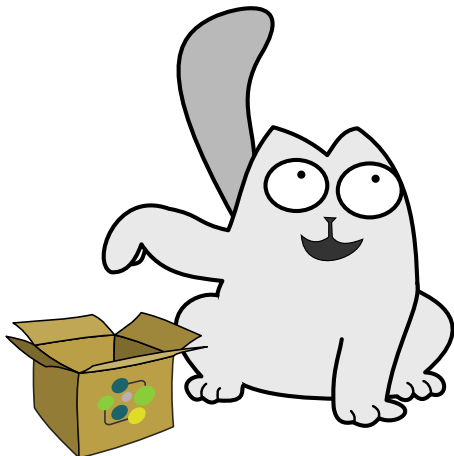
Search or Article-Id

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

- **OMEX: Open Modelling EXchange Format**
- Contents:
  - manifest.xml – information about files and their formats
  - Meta data files – clerical information
  - The files – necessary to reproduce a modelling result
- Already convinced   



Martin Scharm



Dagmar Waltemath



Florian Wendland



Tom Theile



Martin Peters



Markus Wolfien

- Java library:
  - Organise files
  - Attach and retrieve meta data
  - Build, validate, and repair archive
- Desktop Application
- Web Interface

Website: [sems.uni-rostock.de/cat](http://sems.uni-rostock.de/cat)



Martin Scharm



Dagmar Waltemath



Florian Wendland



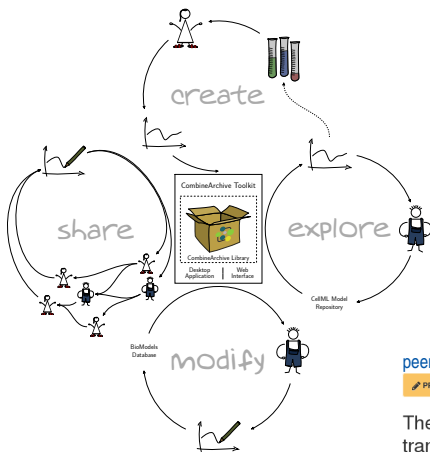
Tom Theile



Martin Peters



Markus Wolfien



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Martin Peters



Markus Wolfien

[peerj.com/preprints/514](http://peerj.com/preprints/514)

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The CombineArchive Toolkit - facilitating the transfer of research results

Martin Scharm<sup>1</sup>, 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

Dagmar Waltemath  
Ron Henkel  
Martin Peters  
Markus Wolfien  
Rebekka Alm  
Olaf Wolkenhauer




 combine

 SysMO  
DE  
Systems Biology of Microorganisms

 SEEK

 cellML

 BioModels

 @SemsProject  
<http://sems.uni-rostock.de>

 PTJ  
Projektträger Jülich  
Forschungszentrum Jülich



Bundesministerium  
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