

**2nd COMBINE MEETING**

Heidelberg, Germany  
September 3–7, 2011

## HOW STANDARDS PROLIFERATE: (SEE: A/C CHARGERS, CHARACTER ENCODINGS, INSTANT MESSAGING, ETC.)





## COmputational Modeling in Biology NETwork (COMBINE) 2011

Please contribute your presentation or poster to:

<http://preceedings.nature.com/collections/combine-2011/documents/new>

discussions. The second COMBINE meeting took place in Heidelberg, DE from 3 to 7 September 2011. Twenty sessions covered the development of SED-ML, BioPAX, SBML, SBGN, and associated metadata standards; as well as emerging standardisation efforts in other fields of the life sciences.

Tags: *This collection has not been tagged.*

Order by: Date Title



### Biopax and Semantics

Ismael Navas-Delgado et al.

Biopax community is producing sets of data in RDF files, but most of them

# Acknowledgements

- SDBV Team of HITS (especially Elina Wetsch)
- Technical staff (Mario Wirth, Dominic Bopp)
- HITS Sysadmin Team (SCO group)
- HITS administration
- HITS management: Klaus Tschira and Andreas Reuter
- Studio Villa Bosch: Sylke Peters
- Kornelia Gorisch (HITS)
- Linda Taddeo (Caltech)
- **YOU**

## Organizing Committee:

Martin Golebiewski, Heidelberg Institute for Theoretical Studies (HITS), Germany

Michael Hucka, California Institute of Technology (Caltech), USA

Nicolas Le Novère, European Bioinformatics Institute (EMBL-EBI), UK

Sven Sahle, BioQuant at the University of Heidelberg, Germany

For the latest news please refer to the meeting web page:

[http://co.mbine.org/events/COMBINE\\_2011](http://co.mbine.org/events/COMBINE_2011)

## Financial Support:



Heidelberg Institute for  
Theoretical Studies

