Welcome

2nd HARMONY MEETING

Meeting Website

www.co.mbine.org/events/HARMONY_2012

Twitter: #harmony2012

Symposium

- Tutorials
- Software libraries

- Lunch

- Talks
- Poster session/reception

Day 1

09:00 - 09:15 Welcome – Chris Evelo

09:15 - 10:00 SBGN-ED - Tutorial Falk Schreiber & Tobias Czauderna

10:00 - 10:45 BioModels Database Tutorial - Camille Laibe

11:15 - 11:25 Introduction libSBML - Sarah Keating

11:25 - 11:35 Introduction jSBML - Nicolas Rodriguez

11:35 - 11:45 Introduction libSBGN - Tobias Czauderna

11:45 - 11:55 Introduction libSedML - Frank Bergmann

12:00 - 12:30 SBML Test Suite Tutorial - Lucian Smith

12:30 - 13:30 Lunch

13:30 - 13:50 Welcome Lecture - Chris Evelo

13:50 - 14:10 BioPAX, Pathway Commons, Cytoscape & the future of scientific publishing - Gary Bader

14:15 - 14:35 Software for SBML today - Michael Hucka

14:40 - 15:00 Moving on with standard interoperability - Nicolas Le Novere

15:30 - 15:45 SBFC - Format Converter Framework - Nicolas Rodriguez

15:45 - 16:00 Paxtools - Gary Bader

16:00 - 16:15 MIRIAM Registry / Identifiers.org - Nicolas Le Novere

16:15 - 16:30 RepoSE - Michael Guravage

16:30 - 16:45 Semantic web and open data - Egon Willighagen

17:00 - 19:00 Reception and Poster Session

Organizers

- Gary Bader, University of Toronto, CA
- Michael Hucka, California Institute of Technology, USA
- Nicolas Le Novère, EMBL-EBI, UK

- Martina Kutmon, Maastricht University, NL
- Chris Evelo, Maastricht University, NL

- For latest news please refer to the meeting web page:
  http://co.mbine.org/events/HARMONY_2012

Sponsors

Special thanks to the **Maastricht University Congresbureau**, especially Erica van den Oever for her help.