



**Maastricht University**



**HARMONY2012**  
21-25 May Maastricht



# Welcome

## 2<sup>nd</sup> HARMONY MEETING

# Meeting Website



The screenshot shows the homepage of the COMBINE website. At the top is the COMBINE logo, which consists of a stylized network of green and yellow nodes followed by the word "combine" in a sans-serif font. To the right of the logo is the tagline "the computational modeling in biology network". Below this is a dark green navigation bar with white text links: "HARMONY 2012", "Standards", "Documents", "Tools", "Events", and "About". On the right side of this bar is a search box and a green "Search" button. On the left side of the page is a sidebar with a dark green header "COMBINE" and a list of links: "Standards", "Events", "Documents", "Tools", "About", "Help", "Sign-in", and "Home". The main content area has a breadcrumb trail "Home > HARMONY 2012: The Hackathon on Resources for Modeling in Biology". Below this is a green banner with the text "HARMONY 2012: The Hackathon on Resources for Modeling in Biology". Under the banner, the text reads: "Department of Bioinformatics - BiGCaT  
Maastricht, The Netherlands  
May 21-25, 2012". A paragraph follows: "In 2010, the systems biology standards communities inaugurated a new, broader series of meetings to replace, among other events, the individual SBML and SBGN workshops and BioPAX meetings." Another paragraph states: "HARMONY is a hackathon-type meeting, with a focus on development of the standards, interoperability and infrastructure. There is generally not many general discussions or oral presentations during HARMONY; instead, the time is devoted to allowing hands-on hacking and interaction between people focused on practical development of software and standards. The HARMONY 2012 meeting will be hosted by the Department of Bioinformatics from Maastricht University."

Home > HARMONY 2012: The Hackathon on Resources for Modeling in Biology

## HARMONY 2012: The Hackathon on Resources for Modeling in Biology

Department of Bioinformatics - BiGCaT  
Maastricht, The Netherlands  
May 21-25, 2012

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[www.co.mbine.org/events/HARMONY\\_2012](http://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 Novère

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 Novère

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](http://co.mbine.org/events/HARMONY_2012)

# Sponsors



*Gemeente Maastricht*



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