Day 1 (Wednesday, August 15)

Time	Topic	Speaker	Location
Session 0	Introduction	Chair: Gary Bader	Red Room
9:00-9:15	Welcome to COMBINE 2012	Gary Bader	
9:15-9:30	COMBINE	Nicolas Le Novère	
Session 1	Biological Models and Simulations	Chair: Mike Hucka	Red Room
9:30-9:50	Update on SBML Level 3 and the SBML Test Suite	Mike Hucka	
9:50-10:10	Draft for discussion / SBML Specifications for Revised Multi, Simple Spatial and Multi-Spatial Extensions	Fengkai Zhang	
10:10-10:30	The Open Source Brain Initiative	Padraig Gleeson	
10:30-11:00	Break		Black Room
11:00-11:20	Experience with SBML Packages within iBioSim	Chris Myers	
11:20-11:40	Multiscale multicellular simulations using Cell Based Chaste	James Osborne	
11:40-12:00	Towards CellML 1.2	Jonathan Cooper	
12:00-12:20	The new JWS Online simulation interface: SBGN schema generation, MIRIAM annotation and SBML model specification	Franco B du Preez	
12:20-1:40	Lunch		Black Room
1:40-2:10	Tutorial: BioModels Database	Camille Laibe	
2:10-2:20	Discussion		
2:20-2:50	Break		Black Room
Session 2	Simulation Algorithm, Experiments and Results	Chair: Dagmar Waltemath	Red Room
2:50-3:10	Introduction to SED-ML	Dagmar Waltemath	
3:10-3:30	Nested Tasks Proposal for SED-ML	Frank T. Bergmann	
3:30-4:00	Possibilities for SED-ML	Jonathan Cooper	
4:00-5:00	Keynote: How to Be an Educated Ontology Consumer	Michael Grüninger	Red Room
5:00-6:00	Break		
6:00-7:30	Welcome reception and poster session		Red room
Dinner on your own			

Day 2 (Thursday, August 16)

Time	Topic	Speaker	Location
9:00-9:15	Welcome to Day 2	Gary Bader	Red Room
9:15-9:30	OGI Bioinformatics initiative	Rhonda Tannenbaum, Ontario Genomics Institute	Red Room
Session 2 (continued)	Simulation Algorithm, Experiments and Results	Chair: Dagmar Waltemath	Red Room
9:30-9:50	DDMoRe - Developing new representation standards in PK/PD	Maciej J Swat	
9:50-10:10	Bridging Experiments and Modelling: The SABIO-RK Reaction Kinetics Database	Martin Golebiewski	
10:10-10:30	SEEK and JERM: standards-compliant integration of systems biology data	Olga Krebs	
10:30-11:00	Break		Black Room

Session 3	Parallel breakouts		
11:00-12:20	Biological Models and Simulations		Red Room
11:00-12:20	Simulation Algorithm, Experiments and Results		White Room
11:00-12:20	Model and Pathway Visualization		Black room
11:00-12:20	Biological Pathways and Networks		6th floor conference room
12:20-1:40	Lunch		Black Room
Session 4	Software Tools and Databases	Chair: Martina Kutmon	Red Room
1:40-2:00	BiNoM, a Cytoscape plugin for accessing and analyzing pathways using standard systems biology formats	Eric Bonnet	
2:00-2:20	Budhat - a tool for SBML model version control	Dagmar Waltemath	
2:20-2:50	Break		Black Room
2:50-3:10	JUMMP just a model management platform	Eils Juergen	
3:10-3:30	PhosphoSitePlus Updates	Jon Korhhauser	
3:30-4:00	Recent developments in libSBML and JSBML	Frank Bergmann	
4:00-5:00	Keynote: Comprehensive measure and modeling of C. elegans behavior	Will Ryu	Red Room
5:00-7:00	Break - on your own		
7:30-onwards	Conference Dinner	All registered participants	Messis Restaurant (http://www.messisrestaurant.ca/)

Day 3 (Friday, August 17)

Time	Topic	Speaker	Location
9:00-10:00	Keynote: Not your mama's network biology – dynamic cell-cell interaction networks in development and disease.	Peter Zandstra	Red Room
Session 5	Model and Pathway Visualization	Chair: Huaiyu Mi	Red Room
10:10-10:30	NAViGaTOR	Igor Jurisica	
10:30-11:00	Break		Black Room
11:00-11:20	SBGN Update	Nicolas Le Novère	
11:20-12:00	Tutorial: SBGN-ED - a tool for the Systems Biology Graphical Notation	Tobias Czauderna	
12:00-12:20	Cytoscape.js - network and pathway visualization on the web	Max Franz	
12:20-1:40	Lunch		Black Room
Session 6	Biological Pathways and Networks	Chair: Gary Bader	Red Room
1:40-2:00	Pathway Commons and BioPAX, Validator Update + Factoid/Crowd source curation, Human Computation and Games	Gary Bader	
2:00-2:20	Paxtools	Emek Demir	
2:20-2:50	Break		Black Room
2:50-3:10	Multifunctional Proteins in Multilevel Networks	Raúl A. Ortiz-Merino	
3:10-3:30	Cytoscape 3.0	Gary Bader	
3:30-4:00	Integration of external references for BioPAX Pathways and Models	Michel Dumontier	
4:00-5:00	Keynote: Model-based Engineering of Metabolism	Radhakrishnan Mahadevan	Red Room
Dinner on your own			

Day 4 (Saturday, August 18)

Time	Topic	Speaker	Location
Session 7	Software Tools and Databases	Chair: Martin Golebiewski	Red Room
9:30-9:40	Reforming Reactome	Robin Haw	
9:50-10:30	Tutorial: Access Reactome Database via Application Programming Interfaces	Guanming Wu	
10:30-11:00	Break		Black Room
Session 8	Parallel breakouts		
11:00-12:20	Biological Models and Simulations		Red Room
11:00-12:20	Simulation Algorithm, Experiments and Results		Black Room
11:00-12:20	Model and Pathway Visualization		Red Room (dual use)
11:00-12:20	Biological Pathways and Networks		6th floor conference room
12:20-1:40	Lunch		Black Room
Session 9	Interoperability Between Standards	Chair: Nicolas Le Novère	Red Room
1:40-2:00	Semantic interoperability framework	Sarala Wimalaratne	
2:00-2:20	Towards ML-agnostic modelling	Mike Cooling	
2:20-2:50	MIRIAM Registry and Identifiers.org	Nick Juty	
2:50-3:10	Break		Black Room
3:10-3:30	Reusing SB Standards to Exchange PK/PD Models	Stuart Moodie	
3:30-3:50	The COMBINE archive	Nicolas Le Novère	
3:50-4:05	Bio2RDF's namespace SPARQL endpoint	François Belleau	
4:05-4:45	**Open discussion with all participants and workshop summary**		
4:45-	**End of workshop**		
Off to a patio! (Informal)			
Dinner on your own			

Day 5 (Sunday, August 19)

Time	Topic	Speaker	Location
ICSB/COMBINE Tutorials			
9:00-2:30	Modelling and Simulation of Quantitative Biological Models	Frank Bergmann, Michael Blinov, Akira Funahashi, Martin Golebiewski, Noriko Hiroi, Stefan Hoops, Ion Moraru, Franco du Preez, Sven Sahle	Red Room
10:00-2:00	Introduction to the Statistical Inference of Regulatory Networks	Frank Emmert-Streib	Black Room
ICSB starts at 3pm			