

B Break
D Discussion
I Invited Talk
L Lightning talks
S Social space
T Talk

OCTOBER 5 • MONDAY

PINNED 01:00 – 01:45	I TBA <i>Speakers: Akira Funahashi</i>	Room 1
01:45 – 02:00	T A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology <i>Speakers: Michael Pan</i> Abstract: Comprehensive large-scale mathematical models of biomolecular systems have the potential to direct future advances in health and biotechnology, but are currently difficult to develop. It is generally acknowledged that kinetic models should be constructed by reusing and coupling together existing models of smaller systems, i.e. in a modular fashion. However, models of biological systems are often expressed in different formalisms and therefore do not naturally interface with each other. In this talk, I argue that the conservation laws of physics provide a unified interface for models to communicate. The bond graph - a graphical, energy-based modelling framework that is well-established in the field of engineering - is introduced as a means of enabling this approach. The approach will be illustrated in the development of a model of the MAPK signalling cascade. Target audience: kinetic modellers, tool developers	Room 1
02:00 – 02:15	T Open Source and Sustainability <i>Speakers: Jacob Barhak</i>	Room 1
02:15 – 02:30	T Physiome - Make your model publications discoverable, reproducible, and reusable. <i>Speakers: Karin Lundengård</i>	Room 1
02:30 – 02:45	D Discussion	Room 1
02:45 – 03:00	B Break	Room 1
03:00 – 03:15	T OpenCOR: how to enable reproducible science using community standards and tools <i>Speakers: Alan Garny</i>	Room 1
03:15 – 03:30	T CelIML 2.0 <i>Speakers: David Nickerson</i>	Room 1
03:30 – 03:45	T Implementing OMEX metadata v1.1 <i>Speakers: John Gennari</i>	Room 1
03:45 – 04:00	D Discussion	Room 1
PINNED 04:00 – 06:00	S Social space/BREAK	Room 1
PINNED 06:00 – 06:45	I COVID-19 Disease Map: the key role of standards in community-driven development of systems biology disease models <i>Speakers: Marek Ostaszewski</i>	Room 1
06:45 – 07:00	T PEtat – Interoperable Specification of Parameter Estimation Problems in Systems Biology <i>Speakers: Daniel Weindl</i>	Room 1
07:00 – 07:15	T Spatial Model Editor <i>Speakers: Liam Keegan</i>	Room 1
07:15 – 07:30	T pyABC: likelihood-free inference <i>Speakers: Emad Alamoodi</i>	Room 1
07:30 – 07:45	D Discussion	Room 1
07:45 – 08:00	B Break	Room 1
08:00 – 08:15	T FAIR principles in literature-based kinetic modelling <i>Speakers: Christoff Odendaal</i>	Room 1

08:15 – 08:30	T	FAIRDOM: standard compliant data and model management <i>Speakers: Olga Krebs</i>	Room 1
08:30 – 08:45	T	Stochastic Modelling and Prediction of the COVID-19 <i>Speakers: Joab Odhiambo</i>	Room 1
08:45 – 09:00	D	Discussion	Room 1
PINNED 09:00 – 10:00	S	Social space/BREAK	Room 1
10:00 – 10:15	T	Automated inference of Boolean models from molecular interaction maps using CaSQ <i>Speakers: Anna Niarakis</i>	Room 1
10:15 – 10:30	T	MEWpy: A Metabolic Engineering Workbench for Constraint-Based Strain Optimization <i>Speakers: Vítor Pereira</i>	Room 1
10:30 – 10:45	T	Troppo, a Python Framework for Tissue-Specific Reconstruction and Phenotype Prediction Using Omics Data <i>Speakers: Vítor Vieira</i>	Room 1
10:45 – 11:00	D	Discussion	Room 1
11:00 – 11:15	B	Break	Room 1
11:15 – 11:30	T	VSM: the intuitive, general-purpose curation technology <i>Speakers: Steven Vercruysse</i>	Room 1
11:30 – 11:45	T	Synthetic Biology Curation Tools (SYNBICT) <i>Speakers: Nicholas Roehner</i>	Room 1
11:45 – 12:00	T	Modelling the Relationship between Design and Assembly <i>Speakers: Alexis Casas</i>	Room 1
12:00 – 12:15	D	Discussion	Room 1
PINNED 12:15 – 13:00	I	Information and data standards used at Ginkgo Bioworks <i>Speakers: Ariel Hecht</i>	Room 1
PINNED 13:00 – 14:00	S	Social space/BREAK	Room 1
14:00 – 14:15	T	Creating SBOL Designs with Excel <i>Speakers: Isabel Marleen Pöttsch</i>	Room 1
14:15 – 14:30	T	SABIO-RK: Curation and Visualization of Reaction Kinetics Data <i>Speakers: Ulrike Wittig</i>	Room 1
14:30 – 14:45	T	EnzymeML – an SBML-based data exchange format for biocatalysis and enzymology <i>Speakers: Juergen Pleiss</i>	Room 1
14:45 – 15:00	D	Discussion	Room 1
15:00 – 15:15	B	Break	Room 1
15:15 – 15:30	T	Stochastic Differential Equations and their Application in Systems Biology <i>Speakers: Stefan Hoops</i>	Room 1
15:30 – 15:45	T	Towards in silico approaches for personalized medicine – Recommendations for verifying and validating predictive computational models in EU collaborative research <i>Speakers: Catherine Collin</i>	Room 1
15:45 – 16:00	T	Automated Extraction of Implicit Molecular Structure from Reaction Network Models <i>Speakers: Ali Sinan Saglam</i>	Room 1
16:00 – 16:15	D	Discussion	Room 1

PINNED 16:15 – 17:00	I	TBA <i>Speakers: Nathan Hillson</i>	Room 1
PINNED 17:00 – 18:00	S	Social space/BREAK	Room 1
PINNED 18:00 – 18:15		Opening session	Room 1
PINNED 18:15 – 19:00	I	TBA <i>Speakers: Jonathan Karr</i>	Room 1
19:00 – 19:30	L	Lightning talks (1) <i>Speakers: Paul Stapor, Mudasir Shaikh, Joseph L Hellerstein, Michael Blinov, Gonzalo Vidal</i>	Room 1
19:30 – 19:45	D	Discussion	Room 1
19:45 – 20:00	B	Break	Room 1
20:00 – 20:30	L	Lightning talks (2) <i>Speakers: Malik-Sheriff, Rahuman S., Eirini TsirvJoab Odhiamboouli, Hugh Sorby, Adel Heydarabadipour, Joab Odhiambo</i>	Room 1
20:30 – 21:00	D	Wrap-ups // Discussion	Room 1
PINNED 21:00 – 21:45	I	TBA <i>Speakers: Edmund Crampin</i>	Room 1
21:45 – 22:00	T	A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma <i>Speakers: Fabian Fröhlich</i>	Room 1
22:00 – 22:15	T	The Systems Biology Graphical Notation: a standardised representation of biological maps <i>Speakers: Michael Blinov</i>	Room 1
22:15 – 22:30	T	BioSimulators: a registry of containerized biosimulation tools with standard interfaces that enhance the reuse of biomodels <i>Speakers: Bilal Shaikh</i>	Room 1
22:30 – 22:45	D	Discussion	Room 1
22:45 – 23:00	B	Break	Room 1
23:00 – 23:15	T	Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior <i>Speakers: Lian Zhouyang</i>	Room 1
23:15 – 23:30	T	SBViper: Verification Testing of Kinetics Models in Systems Biology <i>Speakers: Joseph L Hellerstein</i>	Room 1
23:30 – 23:45	T	pyPESTO: A python package for Parameter Estimation and Uncertainty Quantification <i>Speakers: Jakob Vanhoefer</i>	Room 1
23:45 – 00:00	D	Discussion	Room 1

B Break **D** Discussion **I** Invited Talk **S** Social space **T** Talk

OCTOBER 6 • TUESDAY		
PINNED 00:00 – 01:00	S Social space/BREAK	Room 1
01:00 – 01:15	T (Replay) Automated inference of Boolean models from molecular interaction maps using CaSQ <i>Speakers: Anna Niarakis</i>	Room 1
01:15 – 01:30	T (Replay) MEWpy: A Metabolic Engineering Workbench for Constraint-Based Strain Optimization <i>Speakers: Vítor Pereira</i>	Room 1
01:30 – 01:45	T (Replay) Troppo, a Python Framework for Tissue-Specific Reconstruction and Phenotype Prediction Using Omics Data <i>Speakers: Vítor Vieira</i>	Room 1
01:45 – 02:00	D Discussion	Room 1
02:00 – 02:15	B Break	Room 1
02:15 – 02:30	T (Replay) VSM: the intuitive, general-purpose curation technology <i>Speakers: Steven Vercruysse</i>	Room 1
02:30 – 02:45	T (Replay) Synthetic Biology Curation Tools (SYNBICT) <i>Speakers: Nicholas Roehner</i>	Room 1
02:45 – 03:00	T (Replay) Modelling the Relationship between Design and Assembly <i>Speakers: Alexis Casas</i>	Room 1
03:00 – 03:15	D Discussion	Room 1
PINNED 03:15 – 04:00	I (Replay + Live Discussion) Information and data standards used at Ginkgo Bioworks <i>Speakers: Ariel Hecht</i>	Room 1
PINNED 04:00 – 06:00	S Social space/BREAK	Room 1
06:00 – 06:15	T (Replay) Creating SBOL Designs with Excel <i>Speakers: Isabel Marleen Pöttsch</i>	Room 1
06:00 – 06:15	T (Replay) EnzymeML – an SBML-based data exchange format for biocatalysis and enzymology <i>Speakers: Juergen Pleiss</i>	Room 1
06:15 – 06:30	T (Replay) SABIO-RK: Curation and Visualization of Reaction Kinetics Data <i>Speakers: Ulrike Wittig</i>	Room 1
06:45 – 07:00	D Discussion	Room 1
07:00 – 07:15	B Break	Room 1
07:15 – 07:30	T (Replay) Stochastic Differential Equations and their Application in Systems Biology <i>Speakers: Stefan Hoops</i>	Room 1
07:30 – 07:45	T (Replay) Towards in silico approaches for personalized medicine – Recommendations for verifying and validating predictive computational models in EU collaborative research <i>Speakers: Catherine Collin</i>	Room 1
07:45 – 08:00	T (Replay) Automated Extraction of Implicit Molecular Structure from Reaction Network Models <i>Speakers: Ali Sinan Saglam</i>	Room 1
08:00 – 08:15	D Discussion	Room 1

PINNED 08:15 – 09:00	I (Replay + Live Discussion) TBA <i>Speakers: Nathan Hillson</i>	Room 1
PINNED 09:00 – 10:00	S Social space/BREAK	Room 1
PINNED 10:00 – 10:45	I (Replay + Live Discussion) TBA <i>Speakers: Edmund Crampin</i>	Room 1
10:45 – 11:00	T (Replay) A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma <i>Speakers: Fabian Fröhlich</i>	Room 1
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12:45 – 13:00	D Discussion	Room 1
PINNED 13:00 – 14:00	S Social space/BREAK	Room 1
PINNED 14:00 – 14:45	I (Replay + Live Discussion) TBA <i>Speakers: Akira Funahashi</i>	Room 1
14:45 – 15:00	T (Replay) A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology <i>Speakers: Michael Pan</i>	Room 1
15:00 – 15:15	T (Replay) Open Source and Sustainability <i>Speakers: Jacob Barhak</i>	Room 1
15:15 – 15:30	T (Replay) Physiome - Make your model publications discoverable, reproducible, and reusable. <i>Speakers: Karin Lundengård</i>	Room 1
15:30 – 15:45	D Discussion	Room 1
15:45 – 16:00	B Break	Room 1
16:00 – 16:15	T (Replay) OpenCOR: how to enable reproducible science using community standards and tools <i>Speakers: Alan Garny</i>	Room 1
16:15 – 16:30	T (Replay) CellML 2.0 <i>Speakers: David Nickerson</i>	Room 1
16:30 – 16:45	T (Replay) Implementing OMEX metadata v1.1 <i>Speakers: John Gennari</i>	Room 1
16:45 – 17:00	D Discussion	Room 1

PINNED 17:00 – 18:00	S Social space/BREAK	Room 1
PINNED 18:00 – 18:45	I TBA <i>Speakers: Jason Papin</i>	Room 1
18:45 – 19:00	T LibSBML 2020 and beyond <i>Speakers: Sarah Keating</i>	Room 1
19:00 – 19:15	T pySBOL3: A Python library for SBOL 3 <i>Speakers: Tom Mitchell</i>	Room 1
19:15 – 19:30	T Latest developments with the Python modeling package: Tellurium <i>Speakers: Herbert Sauro</i>	Room 1
19:30 – 19:45	D Discussion	Room 1
19:45 – 20:00	B Break	Room 1
20:00 – 20:15	T Integration of sequence visualization into SynBioHub <i>Speakers: Linhao Meng</i>	Room 1
20:15 – 20:30	T BpForms and BcForms: a toolkit for concretely describing non-canonical polymers and complexes to facilitate global biochemical networks <i>Speakers: Paul F Lang</i>	Room 1
20:30 – 20:45	T Missing talk 2 <i>Speakers: TBA</i>	Room 1
20:45 – 21:00	D Discussion	Room 1
PINNED 21:00 – 21:45	I (Replay + Live Discussion) COVID-19 Disease Map: the key role of standards in community-driven development of systems biology disease models <i>Speakers: Marek Ostaszewski</i>	Room 1
21:45 – 22:00	T (Replay) PEtAb – Interoperable Specification of Parameter Estimation Problems in Systems Biology <i>Speakers: Daniel Weindl</i>	Room 1
22:00 – 22:15	T (Replay) Spatial Model Editor <i>Speakers: Liam Keegan</i>	Room 1
22:15 – 22:30	T (Replay) pyABC: likelihood-free inference <i>Speakers: Emad Alamoodi</i>	Room 1
22:30 – 22:45	D Discussion	Room 1
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23:15 – 23:30	T (Replay) FAIRDOM: standard compliant data and model management <i>Speakers: Olga Krebs</i>	Room 1
23:30 – 23:45	T (Replay) Stochastic Modelling and Prediction of the COVID-19 <i>Speakers: Joab Odhiambo</i>	Room 1
23:45 – 00:00	D Discussion	Room 1

R Breakout **S** Social space **U** Tutorial

OCTOBER 7 • WEDNESDAY

PINNED 00:00 – 01:00	S	Social space/BREAK	Room 1
01:00 – 04:00	R	BioSimulations	Room 1
PINNED 04:00 – 06:00	S	Social space/BREAK	Room 1
06:00 – 09:00	R	SED-ML L1V4	Room 1
PINNED 09:00 – 10:00	S	Social space/BREAK	Room 1
10:00 – 12:00	R	Standards for curating flux balance constraint (FBC) models	Room 1
10:00 – 13:00	R	SBOL Libraries Roundtripping and Testing	Room 2
12:00 – 13:00	R	What is the best way to add thermodynamic information to an SBML model?	Room 1
PINNED 13:00 – 14:00	S	Social space/BREAK	Room 1
14:00 – 17:00	R	SBOL Visual Parametric SVG	Room 2
14:00 – 17:00	R	Towards in silico approaches for personalized medicine	Room 1
PINNED 17:00 – 18:00	S	Social space/BREAK	Room 1
18:00 – 21:00	R	Systems Biology Graphical Notations	Room 3
18:00 – 21:00	U	Building, exploring and sharing rule-based models of cellular signaling pathways	Room 1
18:00 – 21:00	U	SBOL Version 3: Simplified Data Exchange for Bioengineering	Room 2
21:00 – 23:00	R	SBML Layout and Render Extensions	Room 1

R Breakout **S** Social space **U** Tutorial

OCTOBER 8 • THURSDAY

PINNED 00:00 – 01:00	S Social space/BREAK	Room 1
01:00 – 03:00	U Using Python HoloViz Technologies to Create Interactive Presentations	Room 1
PINNED 04:00 – 06:00	S Social space/BREAK	Room 1
06:00 – 08:00	U COPASI - an update on recently added functionality	Room 1
08:00 – 09:00	U Newt: view, design and analyze pathways in SBGN and more	Room 1
PINNED 09:00 – 10:00	S Social space/BREAK	Room 1
10:00 – 13:00	R Discussion about centralizing data for calibrating and validating models and enabling standards (1/2)	Room 1
10:00 – 13:00	R SBOL Visual Workflow and Ontology	Room 2
PINNED 13:00 – 14:00	S Social space/BREAK	Room 1
14:00 – 17:00	R Discussion about centralizing data for calibrating and validating models and enabling standards (2/2)	Room 1
14:00 – 17:00	R ELIXIR Systems Biology Focus Group	Room 1
14:00 – 17:00	R SBOL 3.0.1	Room 1
PINNED 17:00 – 18:00	S Social space/BREAK	Room 1
18:00 – 19:00	U Equilibrator for Metabolic Network Analysis: Thermodynamic Profiling and Enzyme-Cost Minimization	Room 1
18:00 – 21:00	U Building, exploring and sharing rule-based models of cellular signaling pathways	Room 1
19:00 – 21:00	U MAGINE: From time-series multi-omics to cellular mechanism of action	Room 1
19:00 – 21:00	U SBOL Visual: Communicating engineered biological designs with diagrams	Room 1
21:00 – 23:00	R SED-ML Breakout Session	Room 1
23:00 – 00:00	R Model Annotation & the OMEX Metadata Spec v1.1	Room 1

COMBINE 2020

R Breakout **D** Discussion **S** Social space **U** Tutorial

OCTOBER 9 • FRIDAY

PINNED 00:00 – 01:00	S Social space/BREAK	Room 1
01:00 – 04:00	U Center for Reproducible Biomedical Modeling Tutorial	Room 1
PINNED 04:00 – 06:00	S Social space/BREAK	Room 1
06:00 – 09:00	U libCellML: How to get started	Room 1
PINNED 09:00 – 10:00	S Social space/BREAK	Room 1
10:00 – 13:00	R SBOL 3 Validation	Room 1
11:00 – 13:00	R Reproducibility in Systems Biology Modelling	Room 1
PINNED 13:00 – 14:00	S Social space/BREAK	Room 1
14:00 – 16:00	R Modelexchange - Are We Ready Yet?	Room 1
14:00 – 17:00	R SBOL 3 Examples and Use Cases	Room 1
14:00 – 17:00	R Workshop on standardised neuronal network specifications	Room 1
16:00 – 17:00	R Improving annotation and COMBINE archives: Problems, open research ideas & task brainstorming	Room 1
PINNED 17:00 – 18:00	S Social space/BREAK	Room 1
18:00 – 19:00	U FlapJack	Room 1
18:00 – 19:00	U PySB: a mathematical framework for modeling biochemical reactions as python programs	Room 1
19:00 – 21:00	U Modelling with VCell	Room 1
PINNED 21:00 – 21:30	D Closing session	Room 1