COMBINE 2020

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** *Speakers: Akira Funahashi*	Room 1
01:45 – 02:00	T	**A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology** *Speakers: Michael Pan*	Room 1
02:00 – 02:15	T	**Open Source and Sustainability** *Speakers: Jacob Barhak*	Room 1
02:15 – 02:30	T	**Physiome - Make your model publications discoverable, reproducible, and reusable.** *Speakers: Karin Lundengård*	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** *Speakers: Alan Garny*	Room 1
03:15 – 03:30	T	**CellML 2.0** *Speakers: David Nickerson*	Room 1
03:30 – 03:45	T	**Implementing OMEX metadata v1.1** *Speakers: John Gennari*	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** *Speakers: Marek Ostaszewski*	Room 1
06:45 – 07:00	T	**PEtab – Interoperable Specification of Parameter Estimation Problems in Systems Biology** *Speakers: Daniel Weindl*	Room 1
07:00 – 07:15	T	**Spatial Model Editor** *Speakers: Liam Keegan*	Room 1
07:15 – 07:30	T	**pyABC: likelihood-free inference** *Speakers: Emad Alamoodi*	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** *Speakers: Christoff Odendaal*	Room 1
08:15 – 08:30	T	**FAIRDOM: standard compliant data and model management** *Speakers: Olga Krebs*	Room 1
08:30 – 08:45	T	**Stochastic Modelling and Prediction of the COVID-19** *Speakers: Joab Odhiambo*	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** *Speakers: Anna Niarakis*	Room 1
10:15 – 10:30	T	**MEWpy: A Metabolic Engineering Workbench for Constraint-Based Strain Optimization** *Speakers: Vítor Pereira*	Room 1
10:30 – 10:45	T	**Troppo, a Python Framework for Tissue-Specific Reconstruction and Phenotype Prediction Using Omics Data** *Speakers: Vítor Vieira*	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** *Speakers: Steven Vercruysse*	Room 1
11:30 – 11:45	T	**Synthetic Biology Curation Tools (SYNBICT)** *Speakers: Nicholas Roehner*	Room 1
11:45 – 12:00	T	**Modelling the Relationship between Design and Assembly** *Speakers: Alexis Casas*	Room 1
12:00 – 12:15	D	**Discussion**	Room 1
PINNED 12:15 – 13:00	I	**Information and data standards used at Ginkgo Bioworks** *Speakers: Ariel Hecht*	Room 1
PINNED 13:00 – 14:00	S	**Social space/BREAK**	Room 1
14:00 – 14:15	T	**Creating SBOL Designs with Excel** *Speakers: Isabel Marleen Pötzsch*	Room 1
14:15 – 14:30	T	**SABIO-RK: Curation and Visualization of Reaction Kinetics Data** *Speakers: Ulrike Wittig*	Room 1
14:30 – 14:45	T	**EnzymeML – an SBML-based data exchange format for biocatalysis and enzymology** *Speakers: Juergen Pleiss*	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** *Speakers: Stefan Hoops*	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** *Speakers: Catherine Collin*	Room 1
15:45 – 16:00	T	**Automated Extraction of Implicit Molecular Structure from Reaction Network Models** *Speakers: Ali Sinan Saglam*	Room 1
16:00 – 16:15	D	**Discussion**	Room 1
PINNED 16:15 – 17:00	I	**TBA** *Speakers: Nathan Hillson*	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** *Speakers: Jonathan Karr*	Room 1
19:00 – 19:30	L	**Lightning talks (1)** *Speakers: Paul Stapor, Mudasir Shaikh, Michael Blinov, Gonzalo Vidal*	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)** *Speakers: Malik-Sheriff, Rahuman S., Eirini TsirvJoab Odhiamboouli, Hugh Sorby, Adel Heydarabadipour, Joab Odhiambo*	Room 1
20:30 – 21:00	D	**Wrap-ups // Discussion**	Room 1
PINNED 21:00 – 21:45	I	**TBA** *Speakers: Edmund Crampin*	Room 1
21:45 – 22:00	T	**A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma** *Speakers: Fabian Fröhlich*	Room 1
22:00 – 22:15	T	**The Systems Biology Graphical Notation: a standardised representation of biological maps** *Speakers: Michael Blinov*	Room 1
22:15 – 22:30	T	**BioSimulators: a registry of containerized biosimulation tools with standard interfaces that enhance the reuse of biomodels** *Speakers: Bilal Shaikh*	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** *Speakers: Lian Zhouyang*	Room 1
23:15 – 23:30	T	**SBViper: Verification Testing of Kinetics Models in Systems Biology** *Speakers: Joseph L Hellerstein*	Room 1
23:30 – 23:45	T	**pyPESTO: A python package for Parameter Estimation and Uncertainty Quantification** *Speakers: Jakob Vanhoefer*	Room 1
23:45 – 00:00	D	**Discussion**	Room 1

COMBINE 2020

| 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** *Speakers: Anna Niarakis*	Room 1
01:15 – 01:30	T	**(Replay) MEWpy: A Metabolic Engineering Workbench for Constraint-Based Strain Optimization** *Speakers: Vítor Pereira*	Room 1
01:30 – 01:45	T	**(Replay) Troppo, a Python Framework for Tissue-Specific Reconstruction and Phenotype Prediction Using Omics Data** *Speakers: Vítor Vieira*	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** *Speakers: Steven Vercruysse*	Room 1
02:30 – 02:45	T	**(Replay) Synthetic Biology Curation Tools (SYNBICT)** *Speakers: Nicholas Roehner*	Room 1
02:45 – 03:00	T	**(Replay) Modelling the Relationship between Design and Assembly** *Speakers: Alexis Casas*	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** *Speakers: Ariel Hecht*	Room 1
PINNED 04:00 – 06:00	S	**Social space/BREAK**	Room 1
06:00 – 06:15	T	**(Replay) Creating SBOL Designs with Excel** *Speakers: Isabel Marleen Pötzsch*	Room 1
06:15 – 06:30	T	**(Replay) SABIO-RK: Curation and Visualization of Reaction Kinetics Data** *Speakers: Ulrike Wittig*	Room 1
06:30 – 06:45	T	**(Replay) EnzymeML – an SBML-based data exchange format for biocatalysis and enzymology** *Speakers: Juergen Pleiss*	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** *Speakers: Stefan Hoops*	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** *Speakers: Catherine Collin*	Room 1
07:45 – 08:00	T	**(Replay) Automated Extraction of Implicit Molecular Structure from Reaction Network Models** *Speakers: Ali Sinan Saglam*	Room 1
08:00 – 08:15	D	**Discussion**	Room 1

PINNED 08:15 – 09:00	I	**(Replay + Live Discussion) TBA** *Speakers: Nathan Hillson*			Room 1
PINNED 09:00 – 10:00	S	**Social space/BREAK**			Room 1
PINNED 10:00 – 10:45	I	**(Replay + Live Discussion) TBA** *Speakers: Edmund Crampin*			Room 1
10:45 – 11:00	T	**(Replay) A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma** *Speakers: Fabian Fröhlich*			Room 1
11:00 – 11:15	T	**(Replay) The Systems Biology Graphical Notation: a standardised representation of biological maps** *Speakers: Michael Blinov*			Room 1
11:15 – 11:30	T	**(Replay) BioSimulators: a registry of containerized biosimulation tools with standard interfaces that enhance the reuse of biomodels** *Speakers: Bilal Shaikh*			Room 1
11:30 – 11:45	D	**Discussion**			Room 1
11:45 – 12:00	B	**Break**			Room 1
12:00 – 12:15	T	**(Replay) Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior** *Speakers: Lian Zhouyang*			Room 1
12:15 – 12:30	T	**(Replay) SBViper: Verification Testing of Kinetics Models in Systems Biology** *Speakers: Joseph L Hellerstein*			Room 1
12:30 – 12:45	T	**(Replay) pyPESTO: A python package for Parameter Estimation and Uncertainty Quantification** *Speakers: Jakob Vanhoefer*			Room 1
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** *Speakers: Akira Funahashi*			Room 1
14:45 – 15:00	T	**(Replay) A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology** *Speakers: Michael Pan*			Room 1
15:00 – 15:15	T	**(Replay) Open Source and Sustainability** *Speakers: Jacob Barhak*			Room 1
15:15 – 15:30	T	**(Replay) Physiome - Make your model publications discoverable, reproducible, and reusable.** *Speakers: Karin Lundengård*			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** *Speakers: Alan Garny*			Room 1
16:15 – 16:30	T	**(Replay) CellML 2.0** *Speakers: David Nickerson*			Room 1
16:30 – 16:45	T	**(Replay) Implementing OMEX metadata v1.1** *Speakers: John Gennari*			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** *Speakers: Jason Papin*	Room 1
18:45 – 19:00	T	**LibSBML 2020 and beyond** *Speakers: Sarah Keating*	Room 1
19:00 – 19:15	T	**pySBOL3: A Python library for SBOL 3** *Speakers: Tom Mitchell*	Room 1
19:15 – 19:30	T	**Latest developments with the Python modeling package: Tellurium** *Speakers: Herbert Sauro*	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** *Speakers: Linhao Meng*	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** *Speakers: Paul F Lang*	Room 1
20:30 – 20:45	T	**Missing talk 2** *Speakers: TBA*	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** *Speakers: Marek Ostaszewski*	Room 1
21:45 – 22:00	T	**(Replay) PEtab – Interoperable Specification of Parameter Estimation Problems in Systems Biology** *Speakers: Daniel Weindl*	Room 1
22:00 – 22:15	T	**(Replay) Spatial Model Editor** *Speakers: Liam Keegan*	Room 1
22:15 – 22:30	T	**(Replay) pyABC: likelihood-free inference** *Speakers: Emad Alamoodi*	Room 1
22:30 – 22:45	D	**Discussion**	Room 1
22:45 – 23:00	B	**Break**	Room 1
23:00 – 23:15	T	**(Replay) FAIR principles in literature-based kinetic modelling** *Speakers: Christoff Odendaal*	Room 1
23:15 – 23:30	T	**(Replay) FAIRDOM: standard compliant data and model management** *Speakers: Olga Krebs*	Room 1
23:30 – 23:45	T	**(Replay) Stochastic Modelling and Prediction of the COVID-19** *Speakers: Joab Odhiambo*	Room 1
23:45 – 00:00	D	**Discussion**	Room 1

COMBINE 2020

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** *Speakers: Matthias König*		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** *Speakers: Malik-Sheriff, Rahuman S.*		Room 1
10:00 – 13:00	R	**SBOL Libraries Roundtriping and Testing**		Room SBOL
12:00 – 13:00	R	**What is the best way to add thermodynamic information to an SBML model?** *Speakers: Moritz Beber*		Room 1
PINNED 13:00 – 14:00	S	**Social space/BREAK**		Room 1
14:00 – 17:00	R	**SBOL Visual Parametric SVG**		Room SBOL
14:00 – 17:00	R	**Towards in silico approaches for personalized medicine** *Speakers: Catherine Collin*		Room 1
PINNED 17:00 – 18:00	S	**Social space/BREAK**		Room 1
18:00 – 21:00	R	**Systems Biology Graphical Notations** *Speakers: Michael Blinov*		Room 2
18:00 – 21:00	U	**Building, exploring and sharing rule-based models of cellular signaling pathways** *Speakers: Martin Meier-Schellersheim*		Room 1
18:00 – 21:00	U	**SBOL Version 3: Simplified Data Exchange for Bioengineering** *Speakers: Jacob Beal*		Room SBOL
21:00 – 23:00	R	**SBML Layout and Render Extensions** *Speakers: Herbert Sauro*		Room 1

COMBINE 2020

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** *Speakers: Jacob Barhak*	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** *Speakers: Pedro Mendes*	Room 1
08:00 – 09:00	U **Newt: view, design and analyze pathways in SBGN and more** *Speakers: Ugur Dogrusoz*	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)** *Speakers: Jonathan Karr*	Room 1
10:00 – 13:00	R **SBOL Visual Workflow and Ontology** *Speakers: Christopher Myers*	Room SBOL
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)** *Speakers: Jonathan Karr*	Room 1
14:00 – 17:00	R **ELIXIR Systems Biology Focus Group** *Speakers: John Hancock*	Room 2
14:00 – 17:00	R **SBOL 3.0.1** *Speakers: Christopher Myers*	Room SBOL
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** *Speakers: Moritz Beber*	Room 1
18:00 – 21:00	U **Building, exploring and sharing rule-based models of cellular signaling pathways** *Speakers: Martin Meier-Schellersheim*	Room 2
19:00 – 21:00	U **MAGINE: From time-series multi-omics to cellular mechanism of action** *Speakers: Alex Lubbock*	Room 1
19:00 – 21:00	U **SBOL Visual: Communicating engineered biological designs with diagrams** *Speakers: Thomas Gorochowski*	Room SBOL
21:00 – 23:00	R **SED-ML Breakout Session** *Speakers: Herbert Sauro, Matthias König*	Room 1
23:00 – 00:00	R **Model Annotation & the OMEX Metadata Spec v1.1** *Speakers: John Gennari*	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** *Speakers: Veronica Porubsky*	Room 1
PINNED 04:00 – 06:00	S	**Social space/BREAK**	Room 1
06:00 – 09:00	U	**libCellML: How to get started** *Speakers: Keri Moyle*	Room 1
PINNED 09:00 – 10:00	S	**Social space/BREAK**	Room 1
10:00 – 13:00	R	**SBOL 3 Validation** *Speakers: Christopher Myers*	Room SBOL
11:00 – 13:00	R	**Reproducibility in Systems Biology Modelling** *Speakers: Malik-Sheriff, Rahuman S.*	Room 1
PINNED 13:00 – 14:00	S	**Social space/BREAK**	Room 1
14:00 – 16:00	R	**ModeleXchange - Are We Ready Yet?** *Speakers: Henning Hermjakob*	Room 1
14:00 – 17:00	R	**SBOL 3 Examples and Use Cases** *Speakers: Christopher Myers*	Room SBOL
14:00 – 17:00	R	**Workshop on standardised neuronal network specifications** *Speakers: Padraig Gleeson*	Room 2
16:00 – 17:00	R	**Improving annotation and COMBINE archives: Problems, open research ideas & task brainstorming** *Speakers: John Gennari*	Room 1
PINNED 17:00 – 18:00	S	**Social space/BREAK**	Room 1
18:00 – 19:00	U	**FlapJack** *Speakers: Gonzalo Vidal*	Room 1
18:00 – 19:00	U	**PySB: a mathematical framework for modeling biochemical reactions as python programs** *Speakers: Samantha Beik*	Room 2
19:00 – 21:00	U	**Modelling with VCell** *Speakers: Michael Blinov*	Room 1
PINNED 21:00 – 21:30	D	**Closing session**	Room 1