

# COMBINE 2020

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

## OCTOBER 5 • MONDAY

<b>PINNED</b> 01:00 – 01:45	<b>I CellDesigner: A modeling tool for biochemical networks</b> <i>Speakers: Akira Funahashi</i>	Room 1
01:45 – 02:00	<b>T A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology</b> <i>Speakers: Michael Pan</i>	Room 1
02:00 – 02:15	<b>T Open Source and Sustainability</b> <i>Speakers: Jacob Barhak</i>	Room 1
02:15 – 02:30	<b>T Physiome - Make your model publications discoverable, reproducible, and reusable.</b> <i>Speakers: Karin Lundengård</i>	Room 1
02:30 – 02:45	<b>D Discussion</b>	Room 1
02:45 – 03:00	<b>B Break</b>	Room 1
03:00 – 03:15	<b>T OpenCOR: how to enable reproducible science using community standards and tools</b> <i>Speakers: Alan Garny</i>	Room 1
03:15 – 03:30	<b>T CellML 2.0</b> <i>Speakers: David Nickerson</i>	Room 1
03:30 – 03:45	<b>T Implementing OMEX metadata v1.1</b> <i>Speakers: John Gennari</i>	Room 1
03:45 – 04:00	<b>D Discussion</b>	Room 1
<b>PINNED</b> 04:00 – 06:00	<b>S Social space/BREAK</b>	Room 1
<b>PINNED</b> 06:00 – 06:45	<b>I COVID-19 Disease Map: the key role of standards in community-driven development of systems biology disease models</b> <i>Speakers: Marek Ostaszewski</i>	Room 1
06:45 – 07:00	<b>T PETA – Interoperable Specification of Parameter Estimation Problems in Systems Biology</b> <i>Speakers: Daniel Weindl</i>	Room 1
07:00 – 07:15	<b>T Spatial Model Editor</b> <i>Speakers: Liam Keegan</i>	Room 1
07:15 – 07:30	<b>T pyABC: likelihood-free inference</b> <i>Speakers: Emad Alamoodi</i>	Room 1
07:30 – 07:45	<b>D Discussion</b>	Room 1
07:45 – 08:00	<b>B Break</b>	Room 1
08:00 – 08:15	<b>T FAIRDOME: standard compliant data and model management</b> <i>Speakers: Olga Krebs</i>	Room 1
08:15 – 08:30	<b>T FAIR principles in literature-based kinetic modelling</b> <i>Speakers: Christoff Odendaal</i>	Room 1
08:30 – 08:45	<b>T Stochastic Modelling and Prediction of the COVID-19</b> <i>Speakers: Joab Odhiambo</i>	Room 1
08:45 – 09:00	<b>D Discussion</b>	Room 1
<b>PINNED</b> 09:00 – 10:00	<b>S Social space/BREAK</b>	Room 1

10:00 – 10:15	T	<b>Automated inference of Boolean models from molecular interaction maps using CaSQ</b> <i>Speakers: Anna Niarakis</i>	Room 1
10:15 – 10:30	T	<b>MEWpy: A Metabolic Engineering Workbench for Constraint-Based Strain Optimization</b> <i>Speakers: Vítor Pereira</i>	Room 1
10:30 – 10:45	T	<b>Tropo, a Python Framework for Tissue-Specific Reconstruction and Phenotype Prediction Using Omics Data</b> <i>Speakers: Vítor Vieira</i>	Room 1
10:45 – 11:00	D	<b>Discussion</b>	Room 1
11:00 – 11:15	B	<b>Break</b>	Room 1
11:15 – 11:30	T	<b>VSM: the intuitive, general-purpose curation technology</b> <i>Speakers: Steven Vercruyse</i>	Room 1
11:30 – 11:45	T	<b>Synthetic Biology Curation Tools (SYNBICT)</b> <i>Speakers: Nicholas Roehner</i>	Room 1
11:45 – 12:00	T	<b>Modelling the Relationship between Design and Assembly</b> <i>Speakers: Alexis Casas</i>	Room 1
12:00 – 12:15	D	<b>Discussion</b>	Room 1
<b>PINNED</b> 12:15 – 13:00	I	<b>Information and data standards used at Ginkgo Bioworks</b> <i>Speakers: Ariel Hecht</i>	Room 1
<b>PINNED</b> 13:00 – 14:00	S	<b>Social space/BREAK</b>	Room 1
14:00 – 14:15	T	<b>Creating SBOL Designs with Excel</b> <i>Speakers: Isabel Marleen Pöttsch</i>	Room 1
14:15 – 14:30	T	<b>SABIO-RK: Curation and Visualization of Reaction Kinetics Data</b> <i>Speakers: Ulrike Wittig</i>	Room 1
14:30 – 14:45	T	<b>EnzymeML – an SBML-based data exchange format for biocatalysis and enzymology</b> <i>Speakers: Juergen Pleiss</i>	Room 1
14:45 – 15:00	D	<b>Discussion</b>	Room 1
15:00 – 15:15	B	<b>Break</b>	Room 1
15:15 – 15:30	T	<b>Stochastic Differential Equations and their Application in Systems Biology</b> <i>Speakers: Stefan Hoops</i>	Room 1
15:30 – 15:45	T	<b>Towards in silico approaches for personalized medicine – Recommendations for verifying and validating predictive computational models in EU collaborative research</b> <i>Speakers: Catherine Collin</i>	Room 1
15:45 – 16:00	T	<b>Automated Extraction of Implicit Molecular Structure from Reaction Network Models</b> <i>Speakers: Ali Sinan Saglam</i>	Room 1
16:00 – 16:15	D	<b>Discussion</b>	Room 1
<b>PINNED</b> 16:15 – 17:00	I	<b>TBA</b> <i>Speakers: Nathan Hillson</i>	Room 1
<b>PINNED</b> 17:00 – 18:00	S	<b>Social space/BREAK</b>	Room 1
<b>PINNED</b> 18:00 – 18:15		<b>Opening session</b>	Room 1

<b>PINNED</b> 18:15 – 19:00	I	<b>Novel technologies for systematically building and simulating whole-cell models</b> <i>Speakers: Jonathan Karr</i>	Room 1
19:00 – 19:30	L	<b>Lightning talks (1)</b> <i>Speakers: Paul Stapor, Mudasir Shaikh, Michael Blinov, Gonzalo Vidal, Adrien Rougny, Joseph Hellerstein</i>	Room 1
19:30 – 19:45	D	<b>Discussion</b>	Room 1
19:45 – 20:00	B	<b>Break</b>	Room 1
20:00 – 20:30	L	<b>Lightning talks (2)</b> <i>Speakers: Malik-Sheriff, Rahuman S., Eirini Tsirvouli, Hugh Sorby, Adel Heydarabadipour, Joab Odhiambo</i>	Room 1
20:30 – 21:00	D	<b>Wrap-ups // Discussion</b>	Room 1
<b>PINNED</b> 21:00 – 21:45	I	<b>Putting energy into systems biology: biophysical models of cell systems for understanding, simulation and design</b> <i>Speakers: Edmund Crampin</i>	Room 1
21:45 – 22:00	T	<b>A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma</b> <i>Speakers: Fabian Fröhlich</i>	Room 1
22:00 – 22:15	T	<b>The Systems Biology Graphical Notation: a standardised representation of biological maps</b> <i>Speakers: Michael Blinov</i>	Room 1
22:15 – 22:30	T	<b>BioSimulators: a registry of containerized biosimulation tools with standard interfaces that enhance the reuse of biomodels</b> <i>Speakers: Bilal Shaikh</i>	Room 1
22:30 – 22:45	D	<b>Discussion</b>	Room 1
22:45 – 23:00	B	<b>Break</b>	Room 1
23:00 – 23:15	T	<b>Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior</b> <i>Speakers: Lian Zhouyang</i>	Room 1
23:15 – 23:30	T	<b>SBViper: Verification Testing of Kinetics Models in Systems Biology</b> <i>Speakers: Joseph L Hellerstein</i>	Room 1
23:30 – 23:45	T	<b>pyPESTO: A python package for Parameter Estimation and Uncertainty Quantification</b> <i>Speakers: Jakob Vanhoefer</i>	Room 1
23:45 – 00:00	D	<b>Discussion</b>	Room 1

## COMBINE 2020

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

## OCTOBER 6 • TUESDAY

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

<b>PINNED</b> 08:15 – 09:00	I <b>(Replay + Live Discussion) TBA</b> <i>Speakers: Nathan Hillson</i>	Room 1
<b>PINNED</b> 09:00 – 10:00	S <b>Social space/BREAK</b>	Room 1
<b>PINNED</b> 10:00 – 10:45	I <b>(Replay + Live Discussion) Putting energy into systems biology: biophysical models of cell systems for understanding, simulation and design</b> <i>Speakers: Edmund Crampin</i>	Room 1
10:45 – 11:00	T <b>(Replay) A thermodynamic Model of EGFR and ERK Signaling explains Adaptive and Genetic Resistance in Melanoma</b> <i>Speakers: Fabian Fröhlich</i>	Room 1
11:00 – 11:15	T <b>(Replay) The Systems Biology Graphical Notation: a standardised representation of biological maps</b> <i>Speakers: Michael Blinov</i>	Room 1
11:15 – 11:30	T <b>(Replay) BioSimulators: a registry of containerized biosimulation tools with standard interfaces that enhance the reuse of biomodels</b> <i>Speakers: Bilal Shaikh</i>	Room 1
11:30 – 11:45	D <b>Discussion</b>	Room 1
11:45 – 12:00	B <b>Break</b>	Room 1
12:00 – 12:15	T <b>(Replay) Datanator: an integrated database of molecular data for quantitatively modeling cellular behavior</b> <i>Speakers: Lian Zhouyang</i>	Room 1
12:15 – 12:30	T <b>(Replay) SBViper: Verification Testing of Kinetics Models in Systems Biology</b> <i>Speakers: Joseph L Hellerstein</i>	Room 1
12:30 – 12:45	T <b>(Replay) pyPESTO: A python package for Parameter Estimation and Uncertainty Quantification</b> <i>Speakers: Jakob Vanhoefer</i>	Room 1
12:45 – 13:00	D <b>Discussion</b>	Room 1
<b>PINNED</b> 13:00 – 14:00	S <b>Social space/BREAK</b>	Room 1
<b>PINNED</b> 14:00 – 14:45	I <b>(Replay + Live Discussion) CellDesigner: A modeling tool for biochemical networks</b> <i>Speakers: Akira Funahashi</i>	Room 1
14:45 – 15:00	T <b>(Replay) A modular, thermodynamic approach for constructing large-scale kinetic models in systems biology</b> <i>Speakers: Michael Pan</i>	Room 1
15:00 – 15:15	T <b>(Replay) Open Source and Sustainability</b> <i>Speakers: Jacob Barhak</i>	Room 1
15:15 – 15:30	T <b>(Replay) Physiome - Make your model publications discoverable, reproducible, and reusable.</b> <i>Speakers: Karin Lundengård</i>	Room 1
15:30 – 15:45	D <b>Discussion</b>	Room 1
15:45 – 16:00	B <b>Break</b>	Room 1
16:00 – 16:15	T <b>(Replay) OpenCOR: how to enable reproducible science using community standards and tools</b> <i>Speakers: Alan Garny</i>	Room 1
16:15 – 16:30	T <b>(Replay) CellML 2.0</b> <i>Speakers: David Nickerson</i>	Room 1
16:30 – 16:45	T <b>(Replay) Implementing OMEX metadata v1.1</b> <i>Speakers: John Gennari</i>	Room 1
16:45 – 17:00	D <b>Discussion</b>	Room 1

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

## COMBINE 2020

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

## OCTOBER 7 • WEDNESDAY

<b>PINNED</b> 00:00 – 01:00	S	<b>Social space/BREAK</b>	Room 1
<b>PINNED</b> 04:00 – 06:00	S	<b>Social space/BREAK</b>	Room 1
06:00 – 09:00	R	<b>SED-ML L1V4</b> <i>Speakers: Matthias König</i>	Room 1
<b>PINNED</b> 09:00 – 10:00	S	<b>Social space/BREAK</b>	Room 1
10:00 – 12:00	R	<b>Standards for curating flux balance constraint (FBC) models</b> <i>Speakers: Malik-Sheriff, Rahuman S.</i>	Room 1
10:00 – 13:00	R	<b>SBOL Libraries Roundtripping and Testing</b>	Room SBOL
12:00 – 13:00	R	<b>What is the best way to add thermodynamic information to an SBML model?</b> <i>Speakers: Moritz Beber</i>	Room 1
<b>PINNED</b> 13:00 – 14:00	S	<b>Social space/BREAK</b>	Room 1
14:00 – 17:00	R	<b>BioSimulations</b>	Room 2
14:00 – 17:00	R	<b>SBOL 3.0.1</b>	Room SBOL
14:00 – 17:00	R	<b>Towards in silico approaches for personalized medicine</b> <i>Speakers: Catherine Collin</i>	Room 1
<b>PINNED</b> 17:00 – 18:00	S	<b>Social space/BREAK</b>	Room 1
18:00 – 21:00	R	<b>Systems Biology Graphical Notations</b> <i>Speakers: Michael Blinov</i>	Room 2
18:00 – 21:00	U	<b>Building, exploring and sharing rule-based models of cellular signaling pathways (I/II)</b> <i>Speakers: Martin Meier-Schellersheim</i>	Room 1
18:00 – 21:00	U	<b>SBOL Version 3: Simplified Data Exchange for Bioengineering</b> <i>Speakers: Jacob Beal</i>	Room SBOL
21:00 – 23:00	R	<b>SBML Layout and Render Extensions</b> <i>Speakers: Herbert Sauro</i>	Room 1

## COMBINE 2020

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

## OCTOBER 8 • THURSDAY

<b>PINNED</b> 00:00 – 01:00	<b>S Social space/BREAK</b>	Room 1
01:00 – 03:00	<b>U Using Python HoloViz Technologies to Create Interactive Presentations</b> <i>Speakers: James Bednar, Jacob Barhak</i>	Room 1
<b>PINNED</b> 04:00 – 06:00	<b>S Social space/BREAK</b>	Room 1
06:00 – 08:00	<b>U COPASI - an update on recently added functionality</b> <i>Speakers: Pedro Mendes</i>	Room 1
08:00 – 09:00	<b>U Newt: view, design and analyze pathways in SBGN and more</b> <i>Speakers: Ugur Dogrusoz</i>	Room 1
<b>PINNED</b> 09:00 – 10:00	<b>S Social space/BREAK</b>	Room 1
10:00 – 13:00	<b>R SBOL Validation</b> <i>Speakers: Christopher Myers</i>	Room SBOL
12:00 – 13:00	<b>R Discussion about centralizing data for calibrating and validating models and enabling standards (1/2)</b> <i>Speakers: Jonathan Karr</i>	Room 1
<b>PINNED</b> 13:00 – 14:00	<b>S Social space/BREAK</b>	Room 1
14:00 – 17:00	<b>R Discussion about centralizing data for calibrating and validating models and enabling standards (2/2)</b> <i>Speakers: Jonathan Karr</i>	Room 1
14:00 – 17:00	<b>R ELIXIR Systems Biology Focus Group</b> <i>Speakers: John Hancock</i>	Room 2
14:00 – 17:00	<b>R SBOL Visual Parametric SVG</b> <i>Speakers: Christopher Myers</i>	Room SBOL
<b>PINNED</b> 17:00 – 18:00	<b>S Social space/BREAK</b>	Room 1
18:00 – 19:00	<b>U Equilibrator for Metabolic Network Analysis: Thermodynamic Profiling and Enzyme-Cost Minimization</b> <i>Speakers: Moritz Beber</i>	Room 1
18:00 – 21:00	<b>U Building, exploring and sharing rule-based models of cellular signaling pathways (II/II)</b> <i>Speakers: Martin Meier-Schellersheim</i>	Room 2
19:00 – 21:00	<b>U MAGINE: From time-series multi-omics to cellular mechanism of action</b> <i>Speakers: Alex Lubbock</i>	Room 1
19:00 – 21:00	<b>U SBOL Visual: Communicating engineered biological designs with diagrams</b> <i>Speakers: Thomas Gorochowski</i>	Room SBOL
21:00 – 23:00	<b>R SED-ML Breakout Session</b> <i>Speakers: Herbert Sauro, Matthias König</i>	Room 1
23:00 – 00:00	<b>R Model Annotation &amp; the OMEX Metadata Spec v1.1</b> <i>Speakers: John Gennari</i>	Room 1





# COMBINE 2020

R Breakout
 D Discussion
S Social space
U Tutorial

## OCTOBER 9 • FRIDAY

<b>PINNED</b> 00:00 – 01:00	<b>S Social space/BREAK</b>	Room 1
01:00 – 04:00	<b>U Center for Reproducible Biomedical Modeling Tutorial</b> <i>Speakers: Veronica Porubsky</i>	Room 1
<b>PINNED</b> 04:00 – 06:00	<b>S Social space/BREAK</b>	Room 1
06:00 – 09:00	<b>U libCellML: How to get started</b> <i>Speakers: Keri Moyle</i>	Room 1
<b>PINNED</b> 09:00 – 10:00	<b>S Social space/BREAK</b>	Room 1
10:00 – 13:00	<b>R SBOL 3 Examples and Use Cases</b> <i>Speakers: Christopher Myers</i>	Room SBOL
11:00 – 13:00	<b>R Reproducibility in Systems Biology Modelling</b> <i>Speakers: Malik-Sheriff, Rahuman S.</i>	Room 1
<b>PINNED</b> 13:00 – 14:00	<b>S Social space/BREAK</b>	Room 1
14:00 – 16:00	<b>R ModeleXchange - Are We Ready Yet?</b> <i>Speakers: Henning Hermjakob</i>	Room 1
14:00 – 17:00	<b>R SBOL Visual Workflow and Ontology</b> <i>Speakers: Christopher Myers</i>	Room SBOL
14:00 – 17:00	<b>R Workshop on standardised neuronal network specifications</b> <i>Speakers: Pdraig Gleeson</i>	Room 2
16:00 – 17:00	<b>R Improving annotation and COMBINE archives: Problems, open research ideas &amp; task brainstorming</b> <i>Speakers: John Gennari</i>	Room 1
<b>PINNED</b> 17:00 – 18:00	<b>S Social space/BREAK</b>	Room 1
18:00 – 19:00	<b>U FlapJack</b> <i>Speakers: Gonzalo Vidal</i>	Room 1
18:00 – 19:00	<b>U PySB: a mathematical framework for modeling biochemical reactions as python programs</b> <i>Speakers: Samantha Beik</i>	Room 2
19:00 – 21:00	<b>U Modelling with VCell</b> <i>Speakers: Michael Blinov</i>	Room 1
<b>PINNED</b> 21:00 – 21:30	<b>D Closing session</b>	Room 1