



# EDITORIAL

**We are delighted to welcome the worldwide systems biology community in Lyon for ICSB2018!**

The Lyon University has a long-standing tradition in promoting mathematics and informatics for biology, from the biometrics pioneered by Jean-Marie LEGAY to the first DNA sequence database created by Richard GRANTHAM and Christian GAUTIER. The Lyon community in systems biology, now federated by BioSyL ([www.biosyl.org](http://www.biosyl.org)), was naturally established on such a fertile ground. It has further developed with the involvement of both the Inria national computer science institute and the Institute for Complex Systems (IXXI).

This was paralleled by strong investment in training, with the creation in 2000 of a Bioinformatics and Modeling course at the 'Institut National des Sciences Appliquées de Lyon' and of a license/master curriculum in Mathematics and Computer Sciences at the University Claude Bernard Lyon 1.

Finally, Lyon has hosted international conferences in systems biology since the early 2000s, starting with the IPG series (Integrative Post-Genomics, 2004-2010) and the LyonSysBio conference since 2014.

For all these scientific reasons, and not to mention the fantastic extra-scientific life quality in Lyon, our city has been chosen to host the **19<sup>th</sup> International Conference on Systems Biology in 2018**.

We have appointed an extraordinary Scientific Program Committee that enthusiastically agreed to help us shape the overall program of that edition. We tried to cover both established and more emerging fields of research that are of interest to the systems biology community at large.

We hope everyone will feel welcome and will return home with vivid memories of the 19<sup>th</sup> edition of the ICSB.

On behalf of the local organizing committee,

**Olivier GANDRILLON**, co-chair ICSB2018 Lyon

**Jan TRAAS**, co-chair ICSB2018 Lyon

# Scientific Program Committee

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National Cancer Institute (NCI), National Institutes of Health (NIH), Bethesda, USA

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Imperial College London, UK

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University of Amsterdam, The Netherlands

**Grégory BATT,**

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**Ellen DECAESTECKER,**

KU Leuven, Belgium

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**Nir FRIEDMAN,**

Weizmann Institute of Science, Rehovot, Israel

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**Ronald GERMAIN,**

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**Stefan HOHMANN,**

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University of Tokyo, Japan

**Anne SIEGEL,**

CNRS and IRISA (Institute of Research in Informatics and Random Systems), Rennes, France

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Swiss Federal Institute of Technology, Lausanne, Switzerland

**Peter SWAIN,**

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INRA and École Normale Supérieure de Lyon, France

**Gaël YVERT,**  
CNRS and École Normale Supérieure de Lyon, France

# Tutorials and Satellite Workshops

ICSB 2018 is pleased to announce the list of Tutorials and Satellite Workshops, to be held on Saturday, October 27, just before the Conference.

Please note these will take place at Ecole Normale Supérieure de Lyon while the conference will take place at Cité Internationale.

More details available by clicking on the titles below:

• [Workshop -- Systems Biology of Transcription Regulation](#)

Organizer: **Ekaterina SHELEST**

• [FAIRDOM Workshop -- FAIR Data Management in Life-Sciences](#)

Organizer: **Natalie STANFORD**

• [COMBINE & de.NBI Tutorial -- Modeling and Simulation Tools in Systems Biology](#)

Organizer: **Martin GOLEBIEWSKI**

• [JuFLUX Tutorial -- Introduction to 13C Metabolic Flux Analysis with the JuFlux Platform](#)

Organizer: **Katharina NÖH**

• [Advanced modelling with COPASI](#)

Organizer: **Sven SAHLE**



## SUNDAY OCTOBER 28

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am	Welcome - Coffee break		
10:00 am	Opening ceremony		
10:50 am	Julie THERIOT, Seattle, USA		
11:50 am	Andrew OATES, Lausanne, Switzerland		
12:30 pm	Lunch		
02:00 pm	Poster session		
03:30 pm	Coffee break		
04:00 pm	Multiscale Systems Biology	Developmental Systems Biology A	Systems Neurosciences
05:50 pm	David SUTER, Lausanne, Switzerland		
From 06:30 pm	Welcome cocktail		

## MONDAY OCTOBER 29

08:30 am	Welcome		
09:00 am	Takashi HIIRAGI, Heidelberg, Germany		
09:40 am	Ottoline LEYSER, Cambridge, UK		
10:20 am	Coffee break		
10:50 am	Methodological developments for Systems Biology A	Systems Medicine A	Modelling Networks and Circuits A
12:30 pm	Lunch		
02:00 pm	Poster session		
02:30 pm	Bioaster session: systems biology for infectious diseases and microbiology		
03:30 pm	Coffee break		
04:00 pm	Developmental Systems Biology B	Multi-omics	Evolutionary and Ecological Systems Biology
05:50 pm	Mariko OKADA, Osaka, Japan		

## TUESDAY OCTOBER 30

08:30 am	Welcome		
09:00 am	James SHARPE, Barcelona, Spain		
09:40 am	Marie-Anne FELIX, Paris, France		
10:20 am	Coffee break		
10:50 am	Single-cell Systems Biology	Quantitative Systems Physiology	Systems Biology for Synthetic Biology
12:30 pm	Lunch		
02:00 pm	Cultural Program		
From 08:00 pm	Gala reception		

## WEDNESDAY OCTOBER 31

08:30 am	Welcome		
09:00 am	Ines THIELE, Esch-sur-Alzette, Luxembourg		
09:40 am	Uwe SAUER, Zurich, Switzerland		
10:20 am	Coffee break		
10:50 am	Methodological developments for Systems Biology B	Systems Medicine B	Modelling Networks and Circuits B
12:30 pm	Lunch		
02:00 pm	Poster session		
03:30 pm	Coffee break		
04:00 pm	Methodological developments for Systems Biology C	Systems Medicine C	Modelling Networks and Circuits C
05:50 pm	Barbara PRAINSACK, Vienna, Austria		

## THURSDAY NOVEMBER 1

08:30 am	Welcome		
09:00 am	Mustafa KHAMMASH, Basel, Switzerland		
09:40 am	Nathalie BALABAN, Jerusalem, Israel		
10:20 am	Coffee break		
10:50 am	Johan ELF, Uppsala, Sweden		
11:50 am	Closing ceremony		
12:30 pm	Lunch		

## SUNDAY OCTOBER 28

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am - 10:00 am	Welcome - Coffee break		
10:00 am - 10:50 am	Opening ceremony		
10:50 am - 11:50 am	<p><b>Chair: Olivier GANDRILLON, Lyon, France</b>  <b>Julie THERIOT, Seattle, USA</b>  <i>The fast and the furious: dissecting the mechanics and dynamics of rapid cell locomotion</i></p>		
11:50 am - 12:30 pm	<p><b>Chair: Olivier GANDRILLON, Lyon, France</b>  <b>Andrew OATES, Lausanne, Switzerland</b>  <i>Clocks and timers in development</i></p>		
12:30 pm - 02:00 pm	Lunch		
02:00 pm - 03:30 pm	Poster session		
03:30 pm - 04:00 pm	Coffee break		
04:00 pm - 05:40 pm	<p><b>Multiscale Systems Biology</b>  <b>Chair: Marija CVJJOVIC, Gothenburg, Sweden</b>  <b>Matteo BARBERIS, Amsterdam, Netherlands</b>            04:00 pm - 04:20 pm  <i>Deciphering yeast physiology by a multi-scale framework integrating cell cycle and metabolism</i></p> <p><b>David HENRIQUES, Vigo, Spain</b>            04:20 pm - 04:40 pm  <i>Enabling the comparison of conventional and non-conventional winemaking <i>Saccharomyces</i> species with genome-scale models</i></p> <p><b>Frédérique CLEMENT, Palaiseau, France</b>            04:40 pm - 05:00 pm  <i>A multiscale mathematical model of neural progenitor dynamics during the development of the cerebral cortex in mice</i></p> <p><b>Annabelle BALLESTA, Villejuif, France</b>            05:00 pm - 05:20 pm  <i>A multi-scale systems pharmacology approach for personalizing cancer chronotherapy</i></p>	<p><b>Developmental Systems Biology A</b>  <b>Chair: Benjamin AUDIT, Lyon, France</b>  <b>Erika TSINGOS, Heidelberg, Germany</b>            04:00 pm - 04:20 pm  <i>Coordination of different stem cell niches during homeostatic growth of the adult fish eye</i></p> <p><b>Elias FRIMAN, Lausanne, Switzerland</b>            04:20 pm - 04:40 pm  <i>OCT4 is required at the M-G1 transition to reestablish chromatin accessibility at enhancers in pluripotent stem cells</i></p> <p><b>Mahé RACCAUD, Lausanne, Switzerland</b>            04:40 pm - 05:00 pm  <i>Mitotic chromosome binding predicts transcription factor dynamics, target site occupancy and ability to modify chromatin accessibility</i></p> <p><b>Didier GONZE, Brussels, Belgium</b>            05:00 pm - 05:20 pm  <i>Modeling cell fate specification during early embryonic development in mouse</i></p> <p><b>Honda NAOKI, Kyoto, Japan</b>            05:20 pm - 05:40 pm  <i>Noise-resistant developmental reproducibility in vertebrate somite formation</i></p>	<p><b>Systems Neurosciences</b>  <b>Chair: Olivier GANDRILLON, Lyon, France</b>  <b>Melanie STEFAN, Edinburgh, United Kingdom</b>            04:00 pm - 04:20 pm  <i>Modelling hyperpolarisation-gated synaptic plasticity in motor learning</i></p> <p><b>Uiryong KANG, Daejeon, South Korea</b>            04:20 pm - 04:40 pm  <i>Robustness of controllability in structural brain networks</i></p> <p><b>Marti JETT, Washington, United States</b>            04:40 pm - 05:00 pm  <i>Systems biology applied to post-traumatic stress disorder to stratify into subtypes</i></p> <p><b>Dennis VITKUP, New York, United States</b>            05:00 pm - 05:20 pm  <i>Gene networks, neuron types, and brain circuits underlying common psychiatric disorders</i></p>
05:50 pm - 06:30 pm	<p><b>Chair: Olivier GANDRILLON, Lyon, France</b>  <b>David SUTER, Lausanne, Switzerland</b>  <i>Protein homeostasis at the single cell level</i></p>		
From 06:30 pm	Welcome cocktail		

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am - 09:00 am	Welcome		
09:00 am - 09:40 am	<p><b>Chair: Jan TRAAS, Lyon, France</b> <b>Takashi HIIRAGI, Heidelberg, Germany</b></p> <p><i>Self-organisation in mouse development</i></p>		
09:40 am - 10:20 am	<p><b>Chair: Jan TRAAS, Lyon, France</b> <b>Ottoline LEYSER, Cambridge, UK</b></p> <p><i>Auxin and the self-organisation of plant form</i></p>		
10:20 am - 10:50 am	Coffee break		
10:50 am - 12:30 pm	<p><b>Methodological developments for Systems Biology A</b> <b>Chair: Frédérique CLEMENT, Palaiseau, France</b> <b>Hugo DOURADO, Düsseldorf, Germany</b> 10:50 am - 11:10 am <i>Enzyme and substrate concentrations in cellular reaction networks at maximal growth rate</i></p> <p><b>Romain YVINEC, Nouzilly, France</b> 11:10 am - 11:30 am <i>Using dynamical reaction network to infer drugs selectivity in pharmacology</i></p> <p><b>Corinna SCHMALOHR, Cologne, Germany</b> 11:30 am - 11:50 am <i>Detecting epistasis using random forest</i></p> <p><b>Elif OZKIRIMLI, Istanbul, Turkey</b> 11:50 am - 12:10 pm <i>SMILES-based prediction of drug-target interaction binding affinity</i></p>	<p><b>Systems Medicine A</b> <b>Chair: Matteo BARBERIS, Amsterdam, Netherlands</b> <b>Eyal SIMONOVSKY, Beer Sheva, Israel</b> 10:50 am - 11:10 am <i>Large-scale analysis of human gene expression variability associates highly variable drug targets with lower drug effectiveness and safety</i></p> <p><b>Xin LAI, Erlangen, Germany</b> 11:10 am - 11:30 am <i>Mathematical modelling of E2F1 repression by cooperative microRNA pairs in the context of anticancer chemotherapy resistance</i></p> <p><b>Juan MARTINEZ, Mexico City, Mexico</b> 11:30 am - 11:50 am <i>Controllability analysis of the core gene regulatory network underlying epithelial-to-mesenchymal transition in the context of epithelial cancer</i></p> <p><b>Dirk FEY, Dublin, Ireland</b> 11:50 am - 12:10 pm <i>Patient-specific modelling of the network dynamics induced by chemotherapeutic drugs in primary and relapsed tumours</i></p> <p><b>Lan NGUYEN, Melbourne, Australia</b> 12:10 pm - 12:30 pm <i>Optimizing drug combinations for cancer treatment using integrative network modelling</i></p>	<p><b>Modelling Networks and Circuits A</b> <b>Chair: Daniel JOST, La Tronche, France</b> <b>Om PATANGE, Cambridge, United Kingdom</b> 10:50 am - 11:10 am <i>E. coli can survive stress by noisy growth modulation</i></p> <p><b>Johannes BORGQVIST, Gothenburg, Sweden</b> 11:10 am - 11:30 am <i>The triangle of ageing: a model of the accumulation of damaged proteins in Saccharomyces cerevisiae shows how retention enables replicative ageing</i></p> <p><b>Mona TONN, London, United Kingdom</b> 11:30 am - 11:50 am <i>Emergence of non-genetic heterogeneity in metabolic reactions</i></p> <p><b>Christian EULER, Toronto, Canada</b> 11:50 am - 12:10 pm <i>Functional topology of the E. coli small molecule regulatory network</i></p> <p><b>Congxin LI, Heidelberg, Germany</b> 12:10 pm - 12:30 pm <i>Transcriptional regulation out of equilibrium: theory and experiment</i></p>
12:30 pm - 02:00 pm	Lunch		

## MONDAY OCTOBER 29

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
02:00 pm - 03:30 pm	Poster session		
02:30 pm - 03:30 pm		<p><b>Bioaster session: systems biology for infectious diseases and microbiology</b></p> <p><b>Nathalie GARCON, Lyon, France</b> <i>Systems biology in vaccines: toward population/personalized vaccination?</i></p> <p><b>Wivine BURNY, Brussels, Belgium</b> <i>Correlates of adjuvanticity : a comparison of 4 adjuvanted vaccines in humans</i></p> <p><b>Nitin S. BALIGA, Seattle, USA</b> <i>A multiscale systems approach to overcome emergence of antimicrobial resistance in TB</i></p>	
03:30 pm - 04:00 pm	Coffee break		
04:00 pm - 05:40 pm	<p><b>Developmental Systems Biology B</b> Chair: Didier GONZE, Brussels, Belgium</p> <p><b>Lidia YAMAMOTO, Leuven, Belgium</b> 04:00 pm - 04:20 pm <i>Simulating cellular movements in early C. elegans embryogenesis</i></p> <p><b>Sophie PANTALACCI, Lyon, France</b> 04:20 pm - 04:40 pm <i>Making and erasing patterns in the tooth field: lessons from Edar dynamics and mathematical modeling</i></p> <p><b>Olivier ALI, Lyon, France</b> 04:40 pm - 05:00 pm <i>3D mechanical stress patterning during flower morphogenesis</i></p> <p><b>Edgar HERRERA DELGADO, London, United Kingdom</b> 05:00 pm - 05:20 pm <i>Enhancer function underpins essential properties of gene regulatory networks for patterning precision</i></p> <p><b>Lutz BRUSCH, Dresden, Germany</b> 05:20 pm - 05:40 pm <i>Wet-tip versus dry-tip regimes of osmotically driven bile flow in the liver</i></p>	<p><b>Multi-omics</b> Chair: Pedro MENDES, Farmington, United States</p> <p><b>Chris PLAISIER, Tempe, United States</b> 04:00 pm - 04:20 pm <i>Causal and mechanistic pan-cancer immune regulatory network deciphered using systems genetics network analysis (SYGNAL)</i></p> <p><b>Katsuyuki YUGI, Yokohama, Japan</b> 04:20 pm - 04:40 pm <i>Dynamic metabolomics and phosphoproteomics reveal that insulin primes the adipocyte for glucose metabolism</i></p> <p><b>Jean-Michel ARBONA, Lyon, France</b> 04:40 pm - 05:00 pm <i>Emergence of the spatio-temporal replication program: role of origin distribution heterogeneity and 3D chromatin structure</i></p> <p><b>Magali RICHARD, La Tronche, France</b> 05:00 pm - 05:20 pm <i>PenDA, a rank-based method for personalized differential analysis: application to lung cancer</i></p> <p><b>Pascale CRÉPIEUX, Nouzilly, France</b> 05:20 pm - 05:40 pm <i>A hormone-regulated transcriptome in primary cells highlights a positive feedback loop of signaling components operating at the level of translation</i></p>	<p><b>Evolutionary and Ecological Systems Biology</b> Chair: Ellen DECAESTECKER, Kortrijk, Belgium</p> <p><b>Brian JI, New York, United States</b> 04:00 pm - 04:20 pm <i>Quantifying spatiotemporal dynamics and noise in microbiome studies using replicate sampling</i></p> <p><b>Juan POYATOS, Madrid, Spain</b> 04:20 pm - 04:40 pm <i>High-order interactions and the predictability of function in microbial consortia</i></p> <p><b>German PLATA, New York, United States</b> 04:40 pm - 05:00 pm <i>The percolation of metabolism and bacterial lifestyle and evolvability</i></p> <p><b>Marco GALARDINI, Cambridge, United Kingdom</b> 05:00 pm - 05:20 pm <i>Systematic evaluation of conditional gene essentiality changes across genetic backgrounds in Saccharomyces cerevisiae</i></p> <p><b>Gabriel CARVALHO, Villeurbanne, France</b> 05:20 pm - 05:40 pm <i>Natural transformation: acquisition and removal of mobile genetic elements in stochastic environments</i></p>
05:50 pm - 06:30 pm	<p>Chair: Fabien CRAUSTE, Lyon, France <b>Mariko OKADA, Osaka, Japan</b> <i>Quantitative transcription control mediated by signaling network</i></p>		



## TUESDAY OCTOBER 30

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am - 09:00 am	Welcome		
09:00 am - 09:40 am	<p><b>Chair: Sophie PANTALACCI, Lyon, France</b> <b>James SHARPE, Barcelona, Spain</b> <i>Limb development, Turing patterns, and computer modelling</i></p>		
09:40 am - 10:20 am	<p><b>Chair: Sophie PANTALACCI, Lyon, France</b> <b>Marie-Anne FELIX, Paris, France</b> <i>Variational properties in a developmental system with six precursor cells</i></p>		
10:20 am - 10:50 am	Coffee break		
10:50 am - 12:30 pm	<p><b>Single-cell Systems Biology</b> <b>Chair: Nathalie BALABAN, Jerusalem, Israel</b> <b>Rinat ARBEL-GOREN, Rehovot, Israel</b> 10:50 am - 11:10 am <i>Noise and correlated gene expression in a one-dimensional organism</i></p> <p><b>Nacho MOLINA, Strasbourg, France</b> 11:10 am - 11:30 am <i>Experimental and theoretical study of nuclear diffusion dynamics of transcription factors</i></p> <p><b>Marie GUILBERT, Villeneuve d'Ascq, France</b> 11:30 am - 11:50 am <i>Cell-to-cell variability in the activation of the heat shock response</i></p> <p><b>Aneta KOSESKA, Dortmund, Germany</b> 11:50 am - 12:10 pm <i>Spatially distributed network between EGFR and phosphatases optimizes growth factor sensing at criticality</i></p> <p><b>Lorenz RIPKA, Mainz, Germany</b> 12:10 pm - 12:30 pm <i>Integration of GDF11 and TGF-<math>\beta</math> - on the SMAD-signaling pathway - modelling population average and variability based on single cell data</i></p>	<p><b>Quantitative Systems Physiology</b> <b>Chair: Delphine ROPERS, Montbonnot, France</b> <b>Vakil TAKHAVEEV, Groningen, Netherlands</b> 10:50 am - 11:10 am <i>What causes metabolic oscillations in the eukaryotic cell?</i></p> <p><b>Andrea WEISSE, London, United Kingdom</b> 11:10 am - 11:30 am <i>Stochasticity of cellular growth: sources, propagation and consequences</i></p> <p><b>Shiny MARTIS B., Lyon, France</b> 11:30 am - 11:50 am <i>Interplay of local and global regulators in pectin catabolism during plant infection by <i>Dickeya dadantii</i></i></p> <p><b>Bruno MARTINS, Cambridge, United Kingdom</b> 11:50 am - 12:10 pm <i>Circadian regulation of cell size, division timing and growth in cyanobacteria</i></p>	<p><b>Systems Biology for Synthetic Biology</b> <b>Chair: Igor GORYANIN, Okinawa, Japan</b> <b>Qiong YANG, Ann Arbor, United States</b> 10:50 am - 11:10 am <i>An artificial cell-cycle system: how network structures modulate the clock functions</i></p> <p><b>Carlos TOSCANO OCHOA, Barcelona, Spain</b> 11:10 am - 11:30 am <i>On the feasibility of complex synthetic biological circuits</i></p> <p><b>Britte BOUCHAUT, Delft, Netherlands</b> 11:30 am - 11:50 am <i>Perceptions of inherent safety: a comparison study from the bioengineering field</i></p> <p><b>Dvir SCHIRMAN, Revadim, Israel</b> 11:50 am - 12:10 pm <i>Optimization of gene expression through cost-effective promoter architectures</i></p> <p><b>Claude LORMEAU, Zurich, Switzerland</b> 12:10 pm - 12:30 pm <i>Model-based design of robust synthetic biological circuits</i></p>
12:30 pm - 02:00 pm	Lunch		
02:00 pm - 08:00 pm	Cultural Program		
From 08:00 pm	Gala reception		

## WEDNESDAY OCTOBER 31

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am - 09:00 am	Welcome		
09:00 am - 09:40 am	<p><b>Chair: Daniel KAHN, Lyon, France</b>  <b>Ines THIELE, Esch-sur-Alzette, Luxembourg</b>  <i>Personalized whole-body models integrate metabolism, physiology, and the gut microbiome</i></p>		
09:40 am - 10:20 am	<p><b>Chair: Daniel KAHN, Lyon, France</b>  <b>Uwe SAUER, Zurich, Switzerland</b>  <i>Metabolic coordination through metabolite-protein interactions</i></p>		
10:20 am - 10:50 am	Coffee break		
10:50 am - 12:30 pm	<p><b>Methodological developments for Systems Biology B</b>  <b>Chair: Mustafa KHAMMASH, Basel, Switzerland</b>  <b>Satya SAMAL, Aachen, Germany</b>            10:50 am - 11:10 am  <i>Sensitive parameters and tipping points of biochemical networks with potential applications in precision medicine</i></p> <p><b>Anne POUPON, Nouzilly, France</b>            11:10 am - 11:30 am  <i>Parameter estimation in dynamical models for systems biology - the delicate balance between identifiability and predictivity</i></p> <p><b>Ozgur AKMAN, Exeter, United Kingdom</b>            11:30 am - 11:50 am  <i>The parameter explosion problem: extending the scope of GRN modelling by combining reduced models with evolutionary computation</i></p> <p><b>Martial GUILLAUD, Vancouver, Canada</b>            11:50 am - 12:10 pm  <i>Hyperspectral cell sociology analysis of histological specimens</i></p> <p><b>Serge PELET, Lausanne, Switzerland</b>            12:10 pm - 12:30 pm  <i>Dynamic single cell analysis of a cell fate decision system</i></p>	<p><b>Systems Medicine B</b>  <b>Chair: Jacqueline MARVEL, Lyon, France</b>  <b>Teresa LEHNERT, Jena, Germany</b>            10:50 am - 11:10 am  <i>Characterization of different sepsis phases by virtual infection modeling of the innate immune response in human whole blood</i></p> <p><b>Anna MEDYUKHINA, Jena, Germany</b>            11:10 am - 11:30 am  <i>Automated image analysis of mast cell - dendritic cell interactions reveals weapon transfer in immune system</i></p> <p><b>Chloé AUDEBERT, Villeurbanne, France</b>            11:30 am - 11:50 am  <i>Non-linear mixed effects models to study inter-individual variability in CD8 T cell immune responses in mice</i></p> <p><b>Chen-Hsiang YEANG, Taipei, Taiwan</b>            11:50 am - 12:10 pm  <i>Modelling bistable tumour population dynamics to design effective treatment strategies</i></p> <p><b>Marcel SCHILLING, Heidelberg, Germany</b>            12:10 pm - 12:30 pm  <i>The complex life of Smad isoforms determines gene expression in hepatocellular carcinoma</i></p>	<p><b>Modelling Networks and Circuits B</b>  <b>Chair: Ina KOCH, Frankfurt, Germany</b>  <b>Jonas BÉAL, Paris, France</b>            10:50 am - 11:10 am  <i>Instantiation of patient-specific logical models with multi-omics data allows clinical stratification of patients</i></p> <p><b>Oleksii RUKHLENKO, Dublin, Ireland</b>            11:10 am - 11:30 am  <i>Structure-based kinetic modelling reveals kinase inhibitor combinations to overcome oncogenic RAS signalling</i></p> <p><b>Yaroslav NIKOLAEV, Zurich, Switzerland</b>            11:30 am - 11:50 am  <i>Systems NMR: simultaneous quantitative monitoring of RNA, protein, and metabolite dynamics for biomolecular network analysis</i></p> <p><b>Daniel JOST, La Tronche, France</b>            11:50 am - 12:10 pm  <i>Assigning function to natural allelic variation via dynamic modeling of gene network induction</i></p> <p><b>Ulysse HERBACH, Lyon, France</b>            12:10 pm - 12:30 pm  <i>Inferring gene regulatory networks using single-cell data: from mechanistic modelling to statistics</i></p>
12:30 pm - 02:00 pm	Lunch		

## WEDNESDAY OCTOBER 31

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
02:00 pm - 03:30 pm	Poster session		
03:30 pm - 04:00 pm	Coffee break		
04:00 pm - 05:40 pm	<p><b>Methodological developments for Systems Biology C</b> Chair: Anne POUPON, Nouzilly, France</p> <p><b>Laurent GUYON, Grenoble, France</b> 04:00 pm - 04:20 pm <i>miRNA selection using miRNA network a priori showed improved reliability and identify functionally related miRNAs</i></p> <p><b>Andras GYORGY, Abu Dhabi, United Arab Emirates</b> 04:20 pm - 04:40 pm <i>Optimal part characterization with shared cellular resources</i></p> <p><b>Arthur GOLDBERG, New York, United States</b> 04:40 pm - 05:00 pm <i>A multialgorithmic simulator for whole-cell biochemical models</i></p> <p><b>Silas Boye NISSEN, Copenhagen, Denmark</b> 05:00 pm - 05:20 pm <i>Four simple rules that are sufficient to generate the mammalian blastocyst</i></p> <p><b>Jörn STARRUSS, Dresden, Germany</b> 05:20 pm - 05:40 pm <i>Morpheus: a user-friendly and extensible simulation framework for declarative modelling in multiscale and multicellular systems biology</i></p>	<p><b>Systems Medicine C</b> Chair: Maria Manuela NOGUEIRA, Lyon, France</p> <p><b>Fortunato BIANCONI, Perugia, Italy</b> 04:00 pm - 04:20 pm <i>Machine learning pipeline for pathways analysis with reverse phase microarray data of non-small cell lung cancer cell lines and different drugs</i></p> <p><b>Michiel ADRIAENS, Maastricht, Netherlands</b> 04:20 pm - 04:40 pm <i>Putting the squeeze on RNA-seq data: mapping individualized genetic and epigenetic regulation in complex diseases</i></p> <p><b>Avijit PODDER, New Delhi, India</b> 04:40 pm - 05:00 pm <i>Therapeutic understanding of human dopaminergic system in neurological diseases - a systems biology approach</i></p> <p><b>Pedro MENDES, Farmington, United States</b> 05:00 pm - 05:20 pm <i>Transforming physiological models from mice to humans - the case of iron homeostasis</i></p> <p><b>Dominik LUTTER, Neuherberg, Germany</b> 05:20 pm - 05:40 pm <i>A circadian metabolomics atlas of the body under chronic nutrient stress</i></p>	<p><b>Modelling Networks and Circuits C</b> Chair: Ralf STEUER, Berlin, Germany</p> <p><b>Niklas KORSBO, Cambridge, United Kingdom</b> 04:20 pm - 04:40 pm <i>Precise adaptation in stem cell control</i></p> <p><b>Martin ZAUSER, Heidelberg, Germany</b> 04:40 pm - 05:00 pm <i>Automated image analysis and modeling of calcium waves in plant roots</i></p> <p><b>Jian-Geng CHIOU, Durham, United States</b> 05:00 pm - 05:20 pm <i>Principles that govern competition or co-existence in Rho-GTPase driven polarization in the budding yeast</i></p> <p><b>Atsushi MOCHIZUKI, Kyoto, Japan</b> 05:20 pm - 05:40 pm <i>Controlling cell fate specification system based on network structure</i></p>
05:50 pm - 06:30 pm	<p>Chair: Annamaria CARUSI, Sheffield, UK</p> <p><b>Barbara PRAINSACK, Vienna, Austria</b> <i>Is precision medicine "open"?</i></p>		

## THURSDAY NOVEMBER 1

	AUDITORIUM LUMIERE	AUDITORIUM PASTEUR	SALON PASTEUR
08:30 am - 09:00 am	Welcome		
09:00 am - 09:40 am	<b>Chair: Andrea WEISSE, London, UK</b> <b>Mustafa KHAMMASH, Basel, Switzerland</b> <i>Rationally-designed biomolecular control systems</i>		
09:40 am - 10:20 am	<b>Chair: Andrea WEISSE, London, UK</b> <b>Nathalie BALABAN, Jerusalem, Israel</b> <i>To grow or not to grow: phenotypic variability of growth in single cells</i>		
10:20 am - 10:50 am	Coffee break		
10:50 am - 11:50 am	<b>Chair: Jan TRAAS, Lyon, France</b> <b>Johan ELF, Uppsala, Sweden</b> <i>Adventures with single molecules in bacterial cells</i>		
11:50 am - 12:30 pm	<b>Closing ceremony</b>		
12:30 pm - 02:00 pm	Lunch		

Création : IlluScientia



## SUNDAY, OCTOBER 28

02:00 pm - 03:30 pm

### Single-cell Systems Biology

**CEL 1 - Mohit NAVANDAR, Mainz, Germany**

*Computational screening of signature genes for rare cell population involved during neurogenesis*

**CEL 5 - Katharina NÖH, Jülich, Germany**

*An integrated platform for dynamic microfluidics based single-cell experimentation*

**CEL 7 - Angel STANOEV, Dortmund, Germany**

*Spatial unification of coupling interactions between EGFR and PTPs establishes a growth factor sensing network*

**CEL 9 - Shaoying WANG, Lyon, France**

*Single cell data generation for the calibration and development of a multiscale model of effector and memory CD8 T cell differentiation*

**CEL 11 - Merve YUCE, Istanbul, Turkey**

*Monitoring of flagellar motility using microfluidic technology*

**CEL 13 - Christian SCHWALL, Cambridge, United Kingdom**

*Sigma factor mediated memory*

**CEL 15 - Gael YVERT, Lyon, France**

*Expression variability of B-cell surface proteins displays genetic variation among humans*

**CEL 17 - Shori NISHIMOTO, Yokohama, Japan**

*Predicting the future direction of cell movement with convolutional neural networks*

**CEL 19 - Nicolas SAPAY, Lyon, France**

*Benchmarking of unsupervised cytometry data analysis methods for the comparison of population*

**CEL 21 - Pol GRASLAND-MONGRAIN, Lyon, France**

*«Cellquake elastography»: an ultrafast method to image cell elasticity*

### Developmental Systems Biology

**DEV 1 - Andras HARTMANN, Esch-sur-Alzette, Luxembourg**

*A method to predicting cell-fate determinants in cell differentiation*

**DEV 3 - Juan MARTINEZ, Mexico City, Mexico**

*Identification of gene morphogenetic activity functionalities through reachability analysis: the Arabidopsis thaliana flower morphogenesis case*

**DEV 9 - Frédérique ROBIN, Palaiseau, France**

*Structured cell population dynamics applied to the early development of ovarian follicles*

**DEV 11 - Silas Boye NISSEN, Copenhagen, Denmark,**

*Theory bridging cell polarities with development of robust complex morphologies*

**DEV 13 - Angélique RICHARD, Villeurbanne, France**

*Erythroid differentiation displays a peak of energy consumption concomitant with glycolytic metabolism rearrangements*

**DEV 15 - Lutz BRUSCH, Dresden, Germany**

*Multi-scale modeling of planar cell polarity dynamics in planarians*

**DEV 17 - Hadrien OLIVERI, Lyon, France**

*Emergent properties of stress-based regulation of growth in multicellular plant morphogenesis*

### Evolutionary and Ecological Systems Biology

**EVO 1 - Axelle MARCHANT, Québec, Canada**

*Duplication of homomeric proteins: retention of paralogs and evolution of protein-protein interactions*

**EVO 3 - Charlotte RAMON, Zurich, Switzerland**

*Functional alignment of genome-scale metabolic networks*

**EVO 11 - Cheol-Min GHIM, Ulsan, South Korea**

*Selection of heterozygosity in cis-regulatory sequences*

**EVO 13 - Ellen DECAESTECKER, Kortrijk, Belgium**

*Host genotype shapes the assembly of both the gut microbiota and the surrounding bacterioplankton in the freshwater crustacean Daphnia magna*

**EVO 15 - Karoly KOVACS, Szeged, Hungary**

*Suboptimal transcriptional regulation contributes to the fitness cost following gene deletion in yeast*

### Systems Medicine

**MED 3 - Mareike SIMON, Berlin, Germany**

*Mathematical modeling of the energy metabolism of neuroblastoma cells*

**MED 5 - Sugyun AN, Daejeon, South Korea**

*Identification of a novel target for senotherapeutics in fibroblasts*

**MED 9 - Arran HODGKINSON, Montpellier, France**

*Multi-affinity ligand systems may confer evolutionary advantage: a case study in interferon*

**MED 11 - Jana WOLF, Berlin, Germany**

*Quantitative modelling of the NF- $\kappa$ B system as a basis for the analysis of pathway mutations*

**MED 15 - Akinori NISHI, Yoshiwara, Japan**

*Systems biology of herbal medicine: elucidating the transcriptome and metabolome signature of the complex effect of traditional Japanese medicine*

**MED 17 - Martin EBERHARDT, Erlangen, Germany**

*Profiling of patient plasma exosomes to predict melanoma relapses*

**MED 19 - Koji ISHIYA, Tokyo, Japan**

*A robust age-prediction model based on methylation data from multiple tissues*

**MED 27 - Ana Sofia FIGUEIREDO, Mannheim, Germany**

*System medicine approaches identify PRKDC, ZEB2 and VSTM1 as transcriptional biomarkers discerning septic shock from SIRS in circulating granulocytes*

**MED 33 - Ozlem OZBEK, Istanbul, Turkey**

*Synthesis of liposome-polymeric nanoparticle hybrid systems for therapeutic applications*

**MED 35 - Florian SALOPIATA, Heidelberg, Germany**

*The influence of EGF/HGF receptor abundance on efficacy of targeted therapy in NSCLC cell lines*

**MED 37 - Rupert OVERALL, Dresden, Germany**

*The adult neurogenesis map*

# Poster Sessions

## **MED 39 - Sabine STÜBLER, Potsdam, Germany**

*Systems biology model of the mucosal immune system in the context of inflammatory bowel disease*

## **MED 41 - Francesca FRAU, Frankfurt am Main, Germany**

*Investigating the association of two genetic risk scores with anthropometry, insulin sensitivity and MRI derived fat distribution*

## **MED 43 - Thomas LEPOUTRE, Villeurbanne, France**

*Mathematical model of tumor immune interaction in chronic myeloid leukemia: application to treatment cessation*

## **MED 45 - Alexia GIANNOULA, Barcelona, Spain**

*Temporal comorbidity analysis of disease trajectories using semantic, genetic and phenotypic similarities: an application to prostate cancer*

## **Methodological developments for Systems Biology**

### **METH 1 - Martin GOLEBIEWSKI, Heidelberg, Germany**

*The NormSys registry for modeling standards in systems and synthetic biology*

### **METH 3 - Irina SUROVTSOVA, Heidelberg, Germany**

*Investigating functional connections in biological networks using transfer entropy: pitfalls and how to avoid them*

### **METH 7 - Nikolaos TSIANTIS, Vigo, Spain**

*Inferring dynamics in metabolic networks via optimality principles: the interplay of constraints and trade-offs*

### **METH 9 - Shirin FALLAHI, Bergen, Norway**

*Bayesian flux balance analysis; concepts and computation*

### **METH 11 - Gaoxiang ZHOU, Pittsburgh, United States**

*Sensitivity analysis of discrete models and application in biological networks*

### **METH 15 - Reihaneh MOSTOLIZADEH, Tübingen, Germany**

*Prediction of infection outcome by computational modeling of *Yersinia enterocolitica* infection*

### **METH 17 - Ronan DUCHESNE, Lyon, France**

*Identifiability in mixed effect models: the example of in vitro erythropoiesis*

### **METH 19 - Sandra CASTILLO, Espoo, Finland**

*Predictive models for protein sequences using knowledge distillation*

### **METH 21 - Katharina NÖH, Jülich, Germany**

*JuFLUX: a one-stop-shop framework for <sup>13</sup>C metabolic flux analysis*

### **METH 25 - Martin BEYSS, Jülich, Germany**

*Design of isotopic labeling experiments for metabolic flux analysis: a ménage à trois*

### **METH 27 - Axel THEORELL, Jülich, Germany**

*Advances in Markov Chain Monte Carlo techniques for systems biology: shifting the limits*

### **METH 29 - Hristo TODOROV, Mainz, Germany**

*Detecting treatment effects in preclinical neurotrauma models using univariate vs. multivariate statistics*

## **METH 31 - Adrien ROUGNY, Tokyo, Japan**

*The Systems Biology Graphical Notation: a standardised representation of biological maps*

## **METH 35 - Maximilian HILLEMANN, Lübeck, Germany**

*Image-based analysis of individual movement patterns of *C. elegans**

## **Modelling Networks and Circuits**

### **MOD 3 - Ruth GROSSEHOLZ, Heidelberg, Germany**

*Modeling hormone-induced cell elongation in plant epidermis root cells using ODEs*

### **MOD 5 - Laura TUFFERY, Dublin, Ireland**

*Mathematical modelling of pathway interactions and activation dynamics to predict cell responses to chemotherapeutic treatments in breast cancer cells*

### **MOD 7 - Lara BRUEZIERE, Lyon, France**

*A logical modeling approach to prepare and accelerate the design of ODE models. Application to the bile acids metabolism*

### **MOD 9 - Barbara SCHNITZER, Göteborg, Sweden**

*A theoretical approach to understand the role of the retention mechanism in the rejuvenation process*

### **MOD 11 - Roman RAINER, Berlin, Germany**

*Modelling the central carbon metabolism of three cancer cells using <sup>13</sup>C data*

### **MOD 15 - Marc LEFRANC, Villeneuve-d'Ascq, France**

*Heterodimer autorepression loop: a robust and flexible pulse-generating genetic module*

### **MOD 17 - Elba RAIMUNDEZ ALVAREZ, München, Germany**

*Modeling the EGFR signaling pathway in gastric cancer*

### **MOD 19 - Yoshitaka INOUE, Ikoma, Japan**

*Comparison of fluxome simulation and metabolome analysis using murine glioblastoma initiating cells*

### **MOD 21 - Djomangan Adama OUATTARA, Lyon, France**

*An automatic platform for genome-scale metabolic model reconstruction and analysis*

### **MOD 23 - Deniz SECILMIS, Stockholm, Sweden**

*A subset selection method for accurate gene regulatory network inference of uninformative datasets*

### **MOD 25 - Miguel CASTRESANA AGUIRRE, Stockholm, Sweden**

*Impact of network clustering methods on network-based pathway enrichment analysis tools*

### **MOD 31 - Rosa MARTINEZ-CORRAL, Barcelona, Spain**

*Self-amplifying pulsatile protein dynamics without positive feedback*

### **MOD 33 - Daniel MORGAN, Stockholm, Sweden**

*Perturbation-based gene regulatory network inference to reliably predict oncogenic mechanisms*

### **MOD 37 - Lilija APRUPE, Heidelberg, Germany**

*Computational modeling of the Hippo-YAP/TAZ pathway*

### **MOD 41 - Alvaro FLETCHER, Irvine, United States**

*A subnetwork-based approach for studying concentration robustness*

**MOD 43 - Celine HERNANDEZ, Paris, France**

*Dynamical modelling of T cell co-inhibitory pathways to predict anti-tumour responses to checkpoint inhibitors*

**MOD 45 - Mohamed Tahar LADJIMI, Lille, France**

*Predictive modelling of the effect of heat stress time profiles on cell survival*

**MOD 47 - Maksim ZAKHARTSEV, Ås, Norway**

*Reconstruction of whole-genome metabolic model of Atlantic salmon *Salmo salar* (SALARECON)*

**MOD 49 - Yuishi IWASAKI, Hitachi, Japan**

*Stochastic binary switching behavior of nonlinear neuron explains different responses to same stimulation in *C. elegans**

**MOD 51 - Arthur GOLDBERG, New York, United States**

*The Human Whole-Cell Modeling Project*

**MOD 53 - Roberto ORNELAS-GUEVARA, Mexico City, Mexico**

*Modelling the cytosolic [Ca<sup>2+</sup>] responses induced by *Shigella* invasion in epithelial cells*

**MOD 55 - Guilherme ARAUJO, São Carlos, Brazil**

*Stochastic analysis of a minimal model of indirect negative self-regulation*

**MOD 57 - Eric FANCHON, Grenoble, France**

*A model for iron regulation in animal cells*

## Multiscale Systems Biology

**MULT 1 - Balazs SZIGETI, New York, United States**

*Towards a whole-cell model of *Mycoplasma pneumoniae**

**MULT 3 - Hauke BUSCH, Lübeck, Germany**

*Low-level mitochondrial heteroplasmy modulates DNA replication, glucose metabolism and lifespan in mice*

**MULT 5 - Adrian LOPEZ GARCIA DE LOMANA, Seattle, United States**

*Ribosome-based regulation of cell state transitions*

**MULT 7 - Luis Cristobal MONRAZ, Paris, France**

*Atlas of Cancer Signaling Network: a resource of multi-scale biological maps to study disease mechanisms*

## Multi-omics

**OMIC 1 - Amphun CHAIBOONCHOE, Abu Dhabi, United Arab Emirates**

*Adaptive laboratory evolution generates a fast-growing *Chlamydomonas* mutant that accumulates lipids*

**OMIC 3 - Mohamed Amine BENADJAUD, Fontenay-aux-Roses, France**

*Temporal omics data integration using functional data analysis. Application to radiation-induced transcriptomic and proteomic time-course expressions*

**OMIC 9 - Stefano COLELLA, Montpellier, France**

*Data analysis automation and databases as key tools to multiple sources genomics data integration: starting from the legume model *Medicago truncatula**

**OMIC 11 - Clémentine DECAMPS, Eybens, France**

*Cellular heterogeneity and stochasticity in normal and tumorous tissues*

**OMIC 13 - Karin ORTMAYR, Zurich, Switzerland**

*Charting the cross-functional map between transcriptional regulators and cancer cell metabolism*

**OMIC 15 - Alain SEWER, Neuchâtel, Switzerland**

*Toward a computational multi-omics integrative framework for systems toxicology*

**OMIC 17 - Fatemeh ZAMANZAD GHAVIDEL, Bergen, Norway**

*Gene-specific correlation analysis of mRNA and protein levels in colorectal cancer cell lines*

**OMIC 19 - Saowalak KALAPANULAK, Bangkok, Thailand**

*Unraveling transcriptional regulation of starch metabolic genes in cassava through computational prediction with yeast-one hybrid validation*

**OMIC 21 - Krutik PATEL, Newcastle, United Kingdom**

*Integrative network analysis of time course microRNA and mRNA data using multiple tools*

**OMIC 23 - Brendan RYBACK, Zurich, Switzerland**

*Systematic identification of flux regulation through enzyme phosphorylation*

**OMIC 25 - Susanne KLINGENBERG, Mainz, Germany**

*Big data integration and trans-omics analysis for reconstructing relevant pathways and networks underlying neurodegenerative diseases*

**OMIC 29 - Daniel CRUZ, Ghent, Belgium**

*Profiling individual plants to probe plant stress responses and their interaction under field conditions*

**OMIC 31 - Nina KUSCH, Aachen, Germany**

*A two-step modelling approach to predict drug sensitivity in human cancer cell lines*

**OMIC 33 - Guillaume DEVAILLY, Castanet Tolosan, France**

*Heat adaptation in pigs: phenotypes, genotypes, blood transcriptomics and metabolomics*

**OMIC 35 - Masamitsu HARADA, Ikoma-shi, Japan**

*Integrated statistical model based on transcriptome and metabolome in the biophylaxis metabolism of *Angelica actiloba**

**OMIC 37 - Yang JIN, Ås, Norway**

*A systemic study of lipid metabolism regulation in salmon larvae and early juvenile fed vegetable oil*

**OMIC 39 - Yang JIN, Ås, Norway**

*A systemic change of fatty acid metabolism regulation in Atlantic salmon after CRISPR/Cas9-mediated knockout of *elovl2*,  $\Delta 5$ -*fads* and  $\Delta 6$ -*fads* genes*

**OMIC 41 - Ekaterina SHELEST, Leipzig, Germany**

*New tools for integrative view on regulatory mechanisms involved in interspecies molecular interactions*

# Poster Sessions

## Quantitative Systems Physiology

### PHYS 1 - Masahiro ITABASHI, Yokohama, Japan

*Development of an analyzing system of single cell lineage to uncover generation mechanism of the diversity in ATP concentration in Escherichia coli*

### PHYS 3 - Ralf STEUER, Berlin, Germany

*Cellular resource allocation and metabolic trade-offs during diurnal phototrophic growth*

### PHYS 5 - Istvan KLEIJN, London, United Kingdom

*Global gene-expression regulation as a response to nitrogen limitation in fission yeast*

### PHYS 7 - Maren DIETHER, Zürich, Switzerland

*Comprehensive mapping of the protein-metabolite interactome of E. coli central carbon metabolism*

### PHYS 9 - Miki UMETANI, Tokyo, Japan

*Long-term non-genetic adaptation of antibiotic-stressed Escherichia coli*

### PHYS 13 - Duncan HOLBROOK-SMITH, Zurich, Switzerland,

*Prediction of drug targets through comparison of drug and induced overexpression metabolic profiles*

### PHYS 15 - Dor RUSS, Technion City, Israel

*Universal laws of antimicrobial multi-drug additivity*

### PHYS 17 - Dieter WEBER, Aachen, Germany

*Application of mass spectrometry based metabolomics and fluxomics for biotechnological strain improvement*

### PHYS 19 - Antonio RIGUEIRO MESEJO, East Lansing, United States

*Analyzing the potential productivity of CAM photosynthesis using mathematical modeling*

## MONDAY, OCTOBER 29

02:00 pm - 03:30 pm

## Single-cell Systems Biology

### CEL 2 - Gael YVERT, Lyon, France

*Polygenic standing variation can turn a homogeneous environmental response into a binary, highly stochastic one*

### CEL 4 - Marcin TABAKA, Cambridge, United States

*Scalable visualization and exploration of single-cell "omics" data*

### CEL 8 - Luis MONTANO, Edinburgh, United Kingdom

*Dynamic signal integration drives an anticipatory response in Saccharomyces cerevisiae glucose transport*

### CEL 10 - Tetsuya KOBAYASHI, Tokyo, Japan

*Inferring hidden states of cells from direct lineage tracking data*

### CEL 14 - Hsiao-Chun HUANG, Taipei, Taiwan

*Kinesin-5 contributes to spindle-length scaling in the evolution of cancer toward metastasis*

### CEL 16 - Shori NISHIMOTO, Yokohama, Japan

*Predicting the future direction of cell movement with convolutional neural networks*

### CEL 18 - Muge KASIM, Istanbul, Turkey

*Analysis of the effects of inhibitor drugs against ribosome biogenesis by using self-organized maps*

### CEL 20 - Christophe VEDRINE, Paris, France

*Single-cell dynamics of cytokine-secreting immune cells*

### CEL 22 - Mirko FRANCESCONI, Lyon, France

*What makes a cell plastic?*

## Developmental Systems Biology

### DEV 2 - Yuta TOKUOKA, Yokohama, Japan

*Convolutional neural network-based instance segmentation algorithm to acquire quantitative criteria of early mouse development*

### DEV 4 - Uwe BENARY, Berlin, Germany

*Exploring pancreatic and hepatic cell fate decisions during embryonic development in a systems biological approach*

### DEV 6 - Subashika GOVINDAN, Lausanne, Switzerland

*Role of OCT4 in establishing and maintaining chromatin architecture during stem cell self-renewal*

### DEV 7 - Sophie COLOMBIÉ, Villenave-d'Ornon, France

*Modelling protein turnover in developing tomato fruit*

### DEV 8 - Juan MARTINEZ, Mexico City, Mexico

*Exploring cell cycle gene regulatory network dynamics through the algebraic analysis of its structural reachability properties*

### DEV 10 - Martin ROBERT, Sendai, Japan

*Metabolic activity within Escherichia coli macrocolonies and biofilms*

### DEV 14 - Marie DELATTRE, Lyon, France

*Comparative biophysics of the mitotic spindle in nematode embryos*



**DEV 16 - Jean-Daniel JULIEN, Goettingen, Germany**

*A mechanochemical model for the organization of contractions and fluid flows in Physarum polycephalum*

**DEV 18 - Majid NAZEMI, Antwerpen, Belgium**

*Delayed bone formation partly explains tibial anterolateral bowing associated with neurofibromatosis type 1*

## Evolutionary and Ecological Systems Biology

**EVO 4 - Anatoly SOROKIN, Doloprudny, Russia**

*Modelling of functional evolution of electrogenic bacterial communities*

**EVO 6 - Marta EIDE, Bergen, Norway**

*Modelling the chemical defense networks - a comparative dynamic visualisation of the involved genes and interactions in two fish species and humans*

**EVO 8 - Tobi LOUW, Stellenbosch, South Africa**

*Microbial ecology of reticulation networks under conditions of intermittent water supply*

**EVO 10 - Dinara USMANOVA, New York, United States**

*Determinants of protein evolutionary rate in multicellular organisms*

**EVO 12 - Evgenii ZAFIROV, Ekaterinburg, Russia**

*The problems of transport of substances through the cell membrane at the early stages of evolution from the point of view of system biology*

**EVO 14 - Guillaume BESLON, Villeurbanne, France**

*In silico experimental evolution shows that complexity can rise even in simple environments*

## Systems Medicine

**MED 2 - Fortunato BIANCONI, Perugia, Italy**

*CRA toolbox: a MATLAB package for conditional robustness analysis of mathematical models in cancer systems biology*

**MED 6 - Anja ZEILFELDER, Heidelberg, Germany**

*Disentangling the complex impact of drug-induced liver injury compounds on IL-6 responses*

**MED 8 - Zhixu NI, Leipzig, Germany**

*Lipidomics oriented metabolic model of adipocyte*

**MED 10 - Elin NYMAN, Linköping, Sweden**

*Perturbation biology links temporal protein changes to drug responses in a melanoma cell line*

**MED 12 - Cho-Yi CHEN, Taipei, Taiwan**

*Analysis of brain transcriptomes reveals candidate genes and pathways influenced by cerebrovascular diseases*

**MED 16 - Annikka POLSTER, Göteborg, Sweden**

*A stepwise integrative analysis pipeline for exploring host-microbiota interaction and symptom association*

**MED 18 - Loredana MARTIGNETTI, Paris, France**

*Global analysis of protein and mRNA expression levels in medulloblastoma reveals distinct activated pathways between tumor subgroups*

**MED 20 - Anatoly SOROKIN, Doloprudny, Russia**

*Comparison of lipid metabolism disruption in various brain tumors*

**MED 23 - Marc LEFRANC, Villeneuve-d'Ascq, France**

*A mathematical model of the liver circadian clock linking feeding and fasting cycles to clock function*

**MED 24 - Cesar PICHARDO, Canterbury, United Kingdom**

*QSP models versus empirical models for statistical clinical extrapolation: tools to aid decision making from early drug discovery to patient care*

**MED 26 - Man-Sun KIM, Daejeon, South Korea**

*Identification of common and cancer type-specific gene expression programs according to cancer stage*

**MED 28 - David COHEN, Fontenay-aux-Roses, France**

*A systems biology study of the effect of iodide on the development of foetal brain development in rats*

**MED 30 - Elif ESVAP, Istanbul, Turkey**

*Prostate cancer: network analysis of molecular pathways and identification of novel biomarkers and drug targets*

**MED 31 - Lara BRUEZIERE, Lyon, France**

*In silico exploration of immunotherapeutics combinations in lymphoma*

**MED 32 - Begum YAGCI, Istanbul, Turkey**

*In silico identification of possible pharmacological chaperones for neutral sphingomyelinase 2*

**MED 34 - Charlotte NACHTEGAEL, Brussels, Belgium**

*Unraveling the oligogenic potential of developmental disorders*

**MED 36 - Estelle PUJOS-GUILLOT, Theix, France**

*Metabolic characterization of metabolic syndrome: evidence from cross-sectional and longitudinal data*

**MED 38 - Alvar J. ALONSO-LAVIN, Getafe, Spain**

*Constraint-based modelling of redox couple perturbations anticipates cellular ageing and anti-ageing interventions*

**MED 40 - Charlotte HEWEL, Mainz, Germany**

*Crosstalk between host miRNAs and the gut microbiome in neurodegenerative diseases*

**MED 42 - Rémy JARDILLIER, Saint-Martin-d'Hères, France**

*Guarantee on the false discovery rate (FDR) and pairwise interactions in the penalized Cox model*

**MED 44 - Harukazu SUZUKI, Yokohama, Japan**

*Transcriptional landscape of macrophage activations*

# Poster Sessions

## Methodological developments for Systems Biology

### **METH 2 - Samuel MIRAVET VERDE, Barcelona, Spain**

*Unravelling the hidden universe of small proteins in bacterial genomes*

### **METH 6 - Eugenia OSHURKO, Lyon, France**

*KAMI: a bio-curation tool for cellular signalling*

### **METH 8 - Olufemi BOLAJI, Berlin, Germany**

*Drug target detection in metabolic networks as an optimality problem*

### **METH 10 - Thomas LIGON, Munich, Germany**

*Status report: parameter estimation of a large-scale mechanistic model for mast cells in asthma*

### **METH 12 - Jun SEITA, Tokyo, Japan**

*System-level gene expression profiling by gene expression commons for RNA-seq*

### **METH 14 - Susanne GERBER, Mainz, Germany**

*Toward a scalable multiscale analysis of biomolecular data*

### **METH 16 - Krystian KUBICA, Wroclaw, Poland**

*In search for optimal parameters in three-compartmental model of cholesterol homeostasis*

### **METH 20 - Egils STALIDZANS, Jelgava, Latvia**

*Improvement of model based design quality constraining kinetic and stoichiometric models during optimization*

### **METH 22 - Lisa TURNHOFF, Aachen, Germany**

*Translational modeling of drug efficacy in cancer*

### **METH 26 - Julia SCHLICHTING, Berlin, Germany**

*Synchronization effects on model parametrization for the yeast cell cycle*

### **METH 28 - Olivier GUIPAUD, Fontenay-aux-Roses, France**

*Temporal clustering analysis of endothelial cell gene expression under a conventional radiotherapy dose fraction using Gaussian process clustering*

### **METH 30 - Jürgen PAHLE, Heidelberg, Germany**

*CoRC - the Copasi R Connector*

### **METH 32 - Daniel WEINDL, Neuherberg, Germany**

*Efficient parameterization of large-scale dynamic models using relative protein, phospho-protein and proliferation measurements*

### **METH 33 - Ivan BORISOV, Moscow, Russia**

*An algorithm for practical identifiability analysis and confidence intervals evaluation based on constrained optimization*

### **METH 34 - Johan PERRIER, La Ravoire, France**

*Real-time metabolism assessment using NMR analyzes: application to the optimization of energy usage in mammalian cell-free protein synthesis systems*

### **METH 36 - Hirotsada MORI, Ikoma, Japan**

*New E. coli bar-code deletion mutant library and its application of the monitoring of population dynamics by deep sequencing*

## Modelling Networks and Circuits

### **MOD 1 - Evgeny METELKIN, Moscow, Russia**

*SBML viewer is a tool for transformation of systems biology models to human-readable format*

### **MOD 4 - Nadine VEITH, Heidelberg, Germany**

*Distribution of control in the sulfur assimilation in Arabidopsis thaliana depends on environmental conditions*

### **MOD 6 - Arnaud BONNAFFOUX, Oullins, France**

*WASABI: a dynamic iterative framework for gene regulatory network inference*

### **MOD 12 - Diane ADJAVON, Lille, France**

*Quantifying information transfer in in silico gene regulatory networks*

### **MOD 14 - Martin GOLEBIEWSKI, Heidelberg, Germany**

*SABIO-RK - kinetic data for systems biology*

### **MOD 18 - Niek WELKENHUYSEN, Gothenburg, Sweden**

*Robustness of nutrient signalling is maintained by interconnectivity between signal transduction pathways*

### **MOD 20 - Thibault ETIENNE, Grenoble, France**

*Coordination of mRNA stability and cell physiology in bacteria: a modelling study*

### **MOD 22 - David LAO-MARTIL, Eindhoven, Netherlands**

*Narrowing down uncertainty in yeast central carbon metabolism: an extended kinetic model to understand effects of dynamic environments*

### **MOD 24 - Samar TAREEN, Maastricht, Netherlands**

*Logical modelling and network analysis of cellular metabolic flexibility*

### **MOD 26 - Wolfram LIEBERMEISTER, Jouy-en-Josas, France**

*Enzyme economy in metabolic networks*

### **MOD 32 - Agris PENTJUSS, Jelgava, Latvia**

*Application of parallel runs of global stochastic optimization methods in COPASI wrapper SpaceScanner for termination of optimization task*

### **MOD 35 - Guillem HURALT, London, United Kingdom**

*Bayesian modelling to predict the evolution of eczema severity*

### **MOD 36 - Namhee KIM, Daejeon, South Korea**

*Network modeling and systems analysis reveal epithelial-to-mesenchymal transition spectrum and novel synergistic targets for its reversion*

### **MOD 38 - Kirsten THOBE, Berlin, Germany**

*Analysis of interconnections and dependencies between NF- $\kappa$ B signaling pathways using logical modeling*

### **MOD 40 - William ASHWORTH, Yomitan, Japan**

*Analysis of potential drug targets for non-alcoholic fatty liver disease in a computational model*

### **MOD 42 - Arne SCHOCH, Heidelberg, Germany**

*Kinetic models for frequency-decoding in calcium signalling - how topology and parameterization allow for band-pass activation*

### **MOD 44 - Rushina SHAH, Cambridge, United States**

*Investigating strategies for cell fate conversion through the theoretical analysis of multistable gene regulatory networks*

**MOD 50 - Ciaran WELSH, Newcastle, United Kingdom**

*Exploring temporal differences between gene activity of neonatal, senescent and adult fibroblasts using high throughput qPCR and mechanistic modelling*

**MOD 52 - Marta MATOS, Kgs Lyngby, Denmark**

*Elementary mass action stoichiometric simulation models predict non-negligible concentrations of enzyme-bound metabolites*

**MOD 54 - Melaz TAYAKOUT-FAYOLLE, Villeurbanne, France**

*Dynamical modeling of the immune system in case of septicemia*

**MOD 56 - Kulwadee THANAMIT, Jena, Germany**

*Predicting nutritional uptakes of *Bacillus subtilis* by integrating gene expression profiles into metabolic constrained-based models*

**MOD 58 - Torkel LOMAN, Cambridge, United Kingdom**

*Modelling the  $\sigma B$  mediated stress response in *Bacillus subtilis**

## Multiscale Systems Biology

**MULT 2 - Andrew MILLAR, Edinburgh, United Kingdom**

*Beyond GRN-to-phenotype with circadian models, from genome sequence to ecology*

**MULT 6 - Simon GIREL, Villeurbanne, France**

*Regulation of cellular heterogeneity by uneven molecular partitioning during the CD8 T-cell immune response*

**MULT 8 - Marion DARNAUD, Lyon, France**

*New gnotobiotic mouse model to explore interactions between microbiome and host physiology in childhood stunting induced by chronic undernutrition*

## Multi-omics

**OMIC 2 - Fumiko MATSUZAKI, Fukuoka, Japan**

*Transomics: integrated analysis through multiple molecular layers*

**OMIC 4 - Susanne GERBER, Mainz, Germany**

*Latent linkage highlights strong relations between DNA polymorphisms and the chromatin structure*

**OMIC 6 - Seyed LOGHMANI, Heidelberg, Germany**

*Studying the effect of integrating omics data into genome scale models in the example of an *in silico* model of *Enterococcus faecalis* using CoPE-FBA*

**OMIC 8 - Christoph OGRIS, Neuherberg, Germany**

*Improving multi-omics data integration via regression models using prior knowledge*

**OMIC 10 - Jeremie BECKER, Lyon, France**

*Multi-omic pathway enrichment analysis*

**OMIC 12 - Pascale CRÉPIEUX, Nouzilly, France**

*A design principle of GPCR signaling through beta-arrestins*

**OMIC 14 - Kjersti RISE, Trondheim, Norway**

*Cell lines vs tissue - a comparative study of gene expression using FunHoP*

**OMIC 16 - Jinhyuk BHIN, Amsterdam, Netherlands**

*Integrative multi-omics approach to identify the factors responsible for PARPi resistance in BRCA1-deficient breast cancers*

**OMIC 18 - Treenut SAITHONG, Bang Khun Thian, Thailand**

*Highlighting the condition-specific protein-protein interaction by integrating expression data into the interactome network: a case of AGPase protein*

**OMIC 20 - Kazushi MATSUMURA, Yokohama, Japan**

*Integrated omics analysis for assessing the biological impact of repeated whole cigarette smoke exposure on a 3D bronchial tissue culture*

**OMIC 24 - Wael ISMAIL, Manama, Bahrain**

*Differential proteomics reveals sulfur source-dependent physiological adaptations in the fuel biodesulfurizing *Rhodococcus sp.* IGTS8*

**OMIC 26 - Leonhard WACHUTKA, Garching, Germany**

*Genome-wide two-step pre-mRNA splicing kinetics in human cells*

**OMIC 28 - David FOURNIER, Mainz, Germany**

*Epigenetic landscape of low versus high-order chromatin folding*

**OMIC 30 - Valentina KLAUS, Munich, Germany**

*Elucidating genetic control of metabolic networks under different dietary conditions*

**OMIC 32 - Sebastien LEMAIRE, Lyon, France**

*Role of DNMT3B and hnRNPH in regulation of exons embedded in GC-rich introns*

**OMIC 34 - Kanak MUNGIKAR, Mainz, Germany**

*Deciphering transcriptional and epigenetic remodeling of actin dependent genes during neuronal diseases*

**OMIC 36 - Maren SITTE, Göttingen, Germany**

*Identification of target genes and signaling networks of Wnt11 in human breast cancer progression*

**OMIC 38 - Jens RIESER, Frankfurt am Main, Germany**

*Protein-Protein Interaction (PPI) network analysis for *Salmonella* infected cells*

**OMIC 40 - Adam KING, Wilmslow, United Kingdom**

*Multi-omic characterisation of bladder and lung carcinomas using a novel scanning quadrupole DIA acquisition method*

# Poster Sessions

## Quantitative Systems Physiology

**PHYS 2 - Rahuman SHERIFF, Cambridge, United Kingdom**

*Mathematical modelling of cell cycle: past and future*

**PHYS 4 - Matteo BARBERIS, Amsterdam, Netherlands**

*The multiplex phase interlocker - a novel and robust molecular design synchronizing transcriptional with cell cycle oscillators*

**PHYS 8 - Leticia GALERA-LAPORTA, Barcelona, Spain**

*Membrane potential as an indicator of the cellular state*

**PHYS 14 - Pablo YUBERO, Madrid, Spain**

*How gene expression's response to cell physiological status determines gene order and its conservation in microbes*

**PHYS 16 - S. Andreas ANGERMAYR, Cologne, Germany**

*A growth-mediated negative feedback loop lowers the sensitivity to antibiotics*

**PHYS 18 - Dong-Yeon LEE, La Jolla, United States**

*Single cell membrane potential dynamics under stress in bacteria*

**PHYS 20 - Yannick BRÜGGEMANN, Dortmund, Germany**

*Vesicular trafficking dynamics enable context-dependent regulation of ErbB receptor activity and signaling*

## WEDNESDAY, OCTOBER 31

02:00 pm - 03:30 pm

In order to give more visibility to the authors' research, on Wednesday, October 31, the poster session will be **open to all presenters** who would like to have another opportunity to exchange with the conference attendees.



ICSB 2018 has prepared 2 exclusive guided tours, to be held on Tuesday, October 30. Sign up for those tours on the online registration platform. Limited spots available.

## Lyon sightseeing city - From 02:00 pm to 06:00 pm

*Departure from La Cité Internationale.*

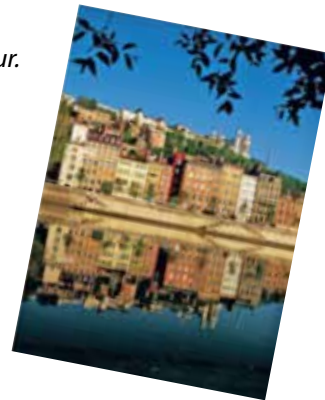
Sightseeing guided tour of the city where you will discover the peninsula, from the Place des Terraux to the Place Bellecour, the banks of the Saone and the Rhone, the Fourviere hill, the Old Lyon listed as World Heritage by UNESCO.

From the esplanade of Fourvière, you will admire a breathtaking panorama of the city shaped by over 2000 years of history, its two rivers and hills.

Discovery of the Basilica, a tribute to the Virgin Mary.

Visit of the Old Town with its "Traboules".

*Way back to the Cité Internationale with a stop on the way at Place Bellecour.*



## Beaujolais and the Golden Stones - From 02:00 pm to 06:30 pm

*Departure from Lyon Cité Internationale.*

On this tour, you will discover all the beauty and richness of South of Beaujolais landscapes. The golden stone villages are divine at sunrise, magnificent in the reflections of the sunset.

Their yellow ochre colour is absolutely unique and earned the name of Beaujolais Tuscany given to the region.

You will stop in the medieval village of Oingt, classified as one of the most beautiful villages in France. Perched on a hill and surrounded by the Beaujolais vineyards, Oingt has kept from its medieval past the ancient chapel of the castle, the fortified door, and a dungeon. In the heart of the village, ochre yellow facades houses are home of craftsmen and artists.

On this tour, you will discover this part of the vineyards with a wine tasting in a traditional cellar. *Way back to Lyon (1<sup>st</sup> stop Place Bellecour and then Cité Internationale).*



# Gala reception – The Selcius

On October 30, ICSB 2018 invites you to its gala dinner, to be held at The Selcius, located in the heart of the Confluence neighbourhood.

Sign up on the online registration platform. Limited spots available.

Historically, the Selcius building was a saline warehouse, where salt was transported by boat from the south to the north of France. Recognizable by its unusual architecture, its characteristic arches have been preserved during the rehabilitation of the Docks of the Saone river, nowadays known as Docks of the Confluence.

**The Selcius** welcomes you in an exceptional venue of more than 1000m<sup>2</sup>. Discover the exquisite restaurant and its open kitchen, but also «**Le Chai**» wine bar with a unique perspective and the outstanding view on the banks of the Saone river.



Création : IlluScientia



## Date

The conference will be held from Sunday, October 28, 2018 till Thursday, November 1, 2018

## Venue

### Lyon Convention Centre at the Cité Internationale (Entrance H on the map)

50, Quai Charles de Gaulle  
69463 Lyon cedex 06  
France

(Except the tutorials and satellite workshops that will take place at Ecole Normale Supérieure de Lyon on Saturday, October 27 2018).

## Getting to the venue

### From the airport:

An express tramway, RHONEXPRESS, links the Lyon-Saint-Exupéry International Airport to the Central Lyon Part-Dieu railway station in 25 minutes with departures every 15 minutes.

### Access and schedule available at the Rhônexpress website:

<https://www.rhonexpress.fr/en/access-and-schedules/23>

### From railway stations - by public transport:

**Bus C1** from Part Dieu railway station - Bus stop Cité internationale | Centre de Congrès

**Bus C2** from Part Dieu railway station - Bus stop Cité internationale | Transbordeur

**Bus C4** from metro/tramway station Jean Macé - Bus stop Cité internationale | Centre de Congrès

**Bus C5** from metro station Cordeliers - Bus stop Cité internationale | Centre de Congrès

**Bus C26** from metro/tramway station Grange Blanche - Bus stop Cité internationale | Transbordeur

**Bus 70** from Part Dieu railway station - Bus stop Cité internationale | Transbordeur

### Get more information by accessing the TCL network website:

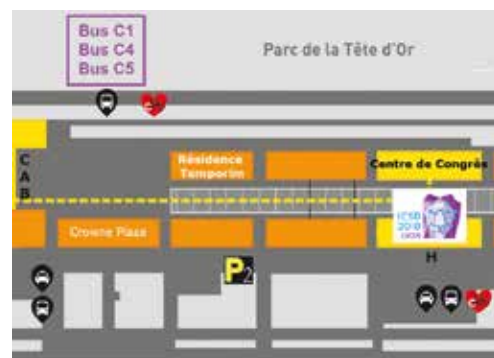
<http://www.tcl.fr/en>

### From the highway:

Périphérique Nord sortie Porte de Saint-Clair

GPS coordinates: Latitude: 45.7851676 | Longitude: 4.8528885

1:30 from Geneva, 3:00 from Turin, 4:00 from Paris, 4:30 from Milan, 5:00 from Barcelona



## Parking

### Nearby parking lots:

Parking Cité Internationale P0, P1 and P2  
Parking Indigo

## Taxis

A Taxi station is available at the level of the congress center and amphitheater.  
Taxi Radio: +33(0)4 72 10 86 86  
Allo Taxi: +33(0)4 78 28 23 23  
Taxi Lyonnais: +33(0)4 78 26 81 81

## Tourism Office

### OnlyLyon Tourisme & Congrès

Place Bellecour - BP 2254  
Phone: +33(0)4 72 77 69 69  
E-mail: [info@lyon-france.com](mailto:info@lyon-france.com)

## Organization Secretariat

### Live/by GL events

59, quai Rambaud - CS 80059  
69285 Lyon cedex 02 - France  
[contact@icsb2018-france.com](mailto:contact@icsb2018-france.com)  
[livebyglevenets.com](http://livebyglevenets.com)

# Partners

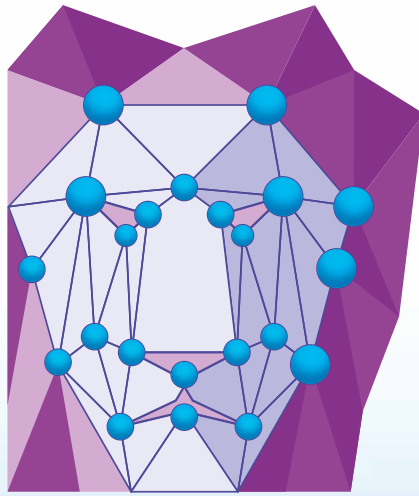


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