

# CSBio 2019 Program Overview

Belvedere Room, Valrose Park, 28 avenue Valrose, 06108 Nice, France



## Wednesday December 4, 2019

**15:00 – 16:00** Welcome Desk and Coffee (Reception room)

**16:00 – 18:00** Workshop by Francine Diener. Title: Why are slow-fast dynamical models and their canards interesting tools to understand neuronal spiking behavior

## Thursday December 5, 2019

**08:30 – 09:00** Welcome Desk

**09:00 – 09:15** Opening speech by Elisabetta De Maria.

**09:15 – 10:15** Keynote talk by François Fages. Title: Turing-completeness of chemical reaction networks in natural cells and artificial vesicles

**10:15 – 10:45** Coffee break (Reception room)

**10:45 – 12:45** FULL PAPERS SESSION 1

**BIOLOGICAL NETWORKS AND PATHWAYS** Chair: François Fages

- (3) Sofia Almeida, Madalena Chaves and Franck Delaunay. Period Control of the Coupled Clock and Cell Cycle Systems.
- (2) Stephanie Kamgnia Wonkap and Gregory Butler. BENIN: combining knockout gene expression data with time series gene expression for the gene regulatory network inference.
- (1) Juris Viksna, Gatis Melkus, Peteris Rucevskis, Edgars Celms, Kārlis Čerāns, Karlis Freivalds, Paulis Ķikusts, Lelde Lace, Martins Opmanis and Darta Rituma. Graph-based network analysis of transcriptional regulation pattern divergence in duplicated yeast gene pairs.
- (8) Marc Diener and Francine Diener. Canard bifurcation in the FitzHugh-Nagumo model for

spikes generation in neurons.

**12:45 - 14:00** Lunch (Reception room)

**14:00 - 15:00** Keynote talk by Nathalie Théret. Title: A framework for modelling large-scale signaling networks.

**15:00 – 16:00** FULL PAPERS SESSION 2

**TUMOR CLASSIFICATION** Chair: Jonathan Chan

- (7) Kristofer Linton-Reid, Harry Clifford and Joe Thompson. Enhanced Cancer Subtyping via PanTranscriptomics Data Fusion, Monte-Carlo Consensus Clustering, and Auto Classifier Creation.
- (5) Imene Zenbout, Abdelkrim Bouramoul, and Souham Meshoul. Targeted unsupervised features learning for gene expression data analysis to predict cancer stage.

**16:00 – 16:30** Coffee break (Reception room)

**16:30 – 17:30** FLASH PRESENTATIONS SESSION 1 (Chair: Ivan Cimrak)

- Mohammad Hassan Baig, Moniba Rahim, Dong Jae Jun, and Mohd Sajid Khan. Design and Evaluation of Formidable anti-diabetic tripeptide - Foiling the Game of Glycation.
- Khwanthana Grataitong, Krittalak Chakrabandhu, Anne-Odile Hueber, and Wattana Weerachatanukul. Protein prediction and structural analysis of modified MrNV viral capsids with GE11 peptide for targeting colorectal cancer cells.
- David Pratella, Veronique Duboc, Marco Milanesio, John Boudjarane, Veronique Paquis-Flucklinger, and Silvia Bottini. Clinical setting specific semi-supervised approach to model synthetic genomes of pregnant women to determine confidence intervals for NIPT.
- Thiptanawat Phongwattana and Jonathan H. Chan. Development of Biomedical Corpus Enlargement Platform Using BERT for Bio-entity Recognition.
- Joëlle Despeyroux, Amy Felty, Pietro Lio, and Carlos Olarte. Computational/Mathematical Logic for Biomedicine.

**19:30** Social dinner at Negresco



## Friday December 6, 2019

**08:30 – 09:00** Welcome desk

**09:00 – 10:00** Keynote talk by Hiroshi Matsuno. Title: Petri nets for cellular process modeling

**10:00 – 10:30** Coffee break (Reception room)

**10:30 – 12:00** FULL PAPERS SESSION 3

**GENOMICS AND PROTEOMICS** Chair: Hiroshi Matsuno

- (11) Sivakorn Kozuevanich, Jonathan H. Chan and Asawin Meechai. Feature selection in GSNFS-based marker identification.
- (4) Leandro Correa, Denis Pallez, Laurent Tichit, Olivier Soriani and Claude Pasquier. Population-based meta-heuristic for active modules identification.
- (9) Kimberly Mackay, Mats Carlsson and Anthony Kusalik. GeneRHi-C: 3D GENomE Reconstruction from Hi-C data.

**12:00 – 13:30** Lunch (Reception room)

**13:30 – 14:30** Industrial talk by Sylvain Benito. Title: Quantitative pharmacology: difficulties and use-cases.

**14:30 – 15:30** FULL PAPERS SESSION 4

**BIO-MEDICINE** Chair: Sylvain Benito

- (6) Katie Ovens, Daniel Hogan, Farhad Maleki, Ian McQuillan and Anthony Kusalik. pineplot: An R package for visualizing symmetric relationships.
- (10) Mohammad Kawsar Sharif Siam, Eva Rahman Kabir and Nashrah Mustafa. Scaffold of N-(2-(2-(tosylcarbamoyl)hydrazinyl)ethyl)isonicotinamide reveals anticancer effects through selective inhibition of FAP.

**15:30 – 16:00** Coffee break (Reception room)

**16:00 – 17:00** FLASH PRESENTATIONS SESSION 2 (Chair: Annabelle Ballesta)

- Gabriella Sferra, Marzia Longo, Marta Ponzi, and Elisabetta Pizzi. Studying host-pathogen protein interactions: how malaria parasite rewires the erythrocyte network.
- Simona Catozzi and Christina Kiel. Insights into tissue-specific Ras-effector networks.
- Xiao Wang, Dan Hao, and Haja N. Kadarmideen. GeneDMRs: an R package for Gene-based Differentially Methylated Regions analysis.
- Marcin Choiski Mariusz Bodzioch, and Urszula Fory. SIS discrete model of illness transmission in a homogeneous population.

- Ivan Cimrak and Tibor Postek. Detection of inner space enclosed by triangular mesh for modelling of red blood cells with viscosity ratio.
- Didier Zugaj, Guillaume Bonnefois, Aymen Balti, Cathy Hervouet, Majdi Maiel, Meline Beal, Agnes Paquet, Nicole Bordier, Thomas Maurin, Julie Desrochers, Frederique Fenneteau, Claire Defoin-Platel, Francesca Zolezzi, Claire Wilson, Fahima Nekka, and Pierre-Olivier Tremblay. Implementation of Quantitative System Pharmacology modeling and Whole Slide Imaging tools. Application to personalized medicine in immuno-oncology.

**17:00 – 17:15** Final speech by Elisabetta De Maria

**Saturday December 7, 2019**

**09:30 - 13:00** Excursion

**10:30** Visit of the “Molinard” perfumery in Grasse and "Eau de parfum creation" workshop

