



Monday, April 1st

Opening session (chair: D. Kahn)

La Parrachée

- 08:30 **Daniel KAHN**
Course opening
- 08:40 **Eric SIGGIA**
Keynote: *Geometry, Genetics and Gene regulation*

10:00 **Coffee break**

Evolutionary Systems Biology

- 10:30 **Jeff GORE**
The dynamics of biological populations
- 12:15 **Lunch**
Early afternoon free

Parallel blackboard teaching and hands-on sessions

La Scolette

- 16:30 **Jakob RUESS**
Optimally learning dynamical models from data

Le Râteau

- 16:30 **Anne GOELZER**
Resource Balance Analysis

L'Echelle

- 16:30 **François NÉDÉLEC**
Simulation of intracellular mechanics

La Norma

- 16:30 **Wolfram LIEBERMEISTER**
Enzyme economy in metabolic models

19 :00 **Dinner**

Selected short talks (chair: G. Yvert)

La Parrachée

- 20:30 **Emma KEIZER**
Unravelling the dynamics of adaptive immunity in CRISPR-Cas through single-cell histories
- 20:50 **Mona TONN**
Emergence of non-genetic heterogeneity in metabolic reactions

Poster session 1

21:15-22:00 **Even number** poster presenters stand by their posters

Tuesday, April 2nd

Integrated molecular networks (chair: J. Gore)

La Parrachée

- 08:30 **Andrea WEISSE**
Modelling bacterial growth
- 10:00 **Coffee break**
- 10:30 **Mattia ZAMPIERI**
Using metabolic fingerprints to rationally design combination therapies
- 12:15 **Lunch**
Early afternoon free

Parallel blackboard teaching and hands-on sessions

La Scolette

- 16:30 **Jakob RUESS**
Optimally learning dynamical models from data

Le Râteau

- 16:30 **Anne GOELZER**
Resource Balance Analysis

L'Echelle

- 16:30 **François NÉDÉLEC**
Simulation of intracellular mechanics

La Norma

- 16:30 **Wolfram LIEBERMEISTER**
Enzyme economy in metabolic models

19 :00 **Dinner**

Selected short talks (chair: M. Zampieri)

La Parrachée

- 20:30 **Laurens KRAH**
Noise propagation in an integrated model of bacterial gene expression and growth
- 20:50 **Svetlana VOLKOVA**
Towards personalized mechanistic models of red blood cell metabolism

Poster session 2

21:15-22:00 **Odd number** poster presenters stand by their posters

Wednesday, April 3rd

Control Theory in Systems Biology (chair: H. de Jong)

La Parrachée

08:30 **Antonis PAPACHRISTODOULOU**

Control theory tools for the analysis and design of biological networks

10:00 **Coffee break**

10:30 **Irene OTERO-MURAS**

Inferring design principles in systems and synthetic biology through optimization-based methods

12:15 **Lunch**

13:30-16:30

Social program: Guided walking tour of Aussois village, church and fort

Dynamical Systems in Biology (chair: C. Chaouiya)

La Parrachée

17:00 **Felix NAËF**

Organization of temporal gene expression: from promoter cycles to circadian clocks

19 :00 **Dinner**

Selected short talks (chair: D. Jost)

La Parrachée

20:30 **Colas DROIN**

Reconstructing the low-dimensional dynamics of two coupled biological oscillators

20:50 **Sant KUMAR**

Stochastic single-cell feedback provides new insights into biomolecular controller design

Poster session 3

21:15-22:00 Open poster session

Thursday, April 4th

Dynamical Systems in Biology (chair: A. Weisse)

La Parrachée

08:30 **Jana WOLF**
Modeling signalling networks and gene expression involved in cancer

10:00 Coffee break

Evolutionary Systems Biology

10:30 **Orkun SOYER**
Evolution of cell metabolism and metabolic interactions

12:15 Lunch
Early afternoon free

Parallel blackboard teaching and hands-on sessions

La Scolette

16:30 **Mustafa KHAMMASH**
Stochastic modeling, simulation and analysis

Le Râteau

16:30 **Claudine CHAOUIYA**
Qualitative dynamical modelling of (multi-) cellular networks

La Norma

16:30 **Hidde DE JONG**
Dynamic models integrating metabolism and gene expression

19 :00 Dinner

Selected short talks (Chair: M. Ibañes)

La Parrachée

20:30 **Pau CASANOVA**
Modelling of patA and hetF genes function in Anabaena heterocyst formation

20:50 **Anna DENEER**
Mathematical modeling of trichome pattern formation: Explaining complex changes in mutant phenotypes

Poster session 4

21:15-22:00 Open poster session

Friday, April 5th

Spatio-temporal models (Chair: O. Gandrillon)

La Parrachée

- 08:30 **Dagmar IBER**
From Networks to Function – Computational Models of Organogenesis
- 10:00 **Coffee break**
- 10:30 **Marta IBAÑES**
Models for pattern formation in development
- 12:15 **Lunch**
Early afternoon free

Parallel blackboard teaching and hands-on sessions

La Scolette

- 16:30 **Mustafa KHAMMASH**
Stochastic modeling, simulation and analysis

Le Râteau

- 16:30 **Claudine CHAOUIYA**
Qualitative dynamical modelling of (multi-) cellular networks

La Norma

- 16:30 **Hidde DE JONG**
Dynamic models integrating metabolism and gene expression

19:30 **Gala Course Dinner**

21:00 **Closing Course Party**

Posters

- 1 Tunde GAIZER *Role of cell-cell interactions between strains of S. cerevisiae in yeast colony formation*
- 2 Patrick SINCLAIR *Growth-dependent drug susceptibility can prevent or enhance spatial expansion of a bacterial population*
- 3 Stephen WILLIAMS *Colloidal transport in heterogeneous landscapes of micro-swimmer activity*
- 4 Pau CASANOVA *Modelling of patA and hetF genes function in Anabaena heterocyst formation*
- 5 Fabrice DELBARY *3D tension inference of embryo cells*
- 6 Hans KUBITSCHKE *Roadmap to Local Tumor Growth*
- 7 Ernst SCHÄFER *Root Senescence and Soil Nutrient Capture*
- 8 Anna DENEER *Mathematical modeling of trichome pattern formation: Explaining complex changes in mutant phenotypes*
- 9 Ronan DUCHESNE *Identifiability in Mixed Effect Models: the example of in vitro Erythropoiesis*
- 10 Colas DROIN *Exploring circadian liver zonation*
- 11 Masoud HOORE *Multiscale modeling of neuroinflammation in the onset of Alzheimer's disease*
- 12 Hélène ARDUIN *Modelling the differentiation dynamics of monocytes in contact with CLL B cells*
- 13 Micks MORVAN *Communications and processes in complex dynamic biological systems*
- 14 Siras HAKOBYAN *Assessment of somatic mutations impact on the activity of biological pathways in tumours*
- 15 Xavier HERNANDEZ ALIAS *Tissue-specificity of codon usage and tRNAs determines gene expression*
- 16 Daniel JOST *Systems biology of 3D Epigenomics*
- 17 Kapil NEWAR *The epigenetic model of histone modifications to elucidate their diverse distribution around gene*
- 18 Gianluca SELVAGGIO *Logical modelling and analysis of cell adhesion properties along Epithelial to Mesenchymal Transition*
- 19 Dimitrij TSCHODU *Machine Learning mechanical parameters of breast cancer cells and blood cells*
- 20 Pascal GROBECKER *A Bayesian Model for Cell Type Inference from Single-Cell RNAseq Data*
- 21 Alexey KOSHKIN *Infering of B cell gene regulatory networks from the single cell data*
- 22 Flaminia ZANE *Understanding the Gene Regulatory Networks Alterations at the End-Of-Life*
- 23 Debdas PAUL *A rule-based modeling approach for regulation of gene expression*
- 24 Hernan MAKSE *Building blocks of gene regulatory networks*
- 25 Ana FONSECA *Genome-Scale Logical Regulatory Models for S. cerevisiae, C. albicans and C. glabrata*
- 26 Gael YVERT *Standing genetic variation can modify molecular regulations in a probabilistic manner*
- 27 Jiayin HONG *Mathematical modeling reveals the control parameters underlying diverse GAL response in natural yeast isolates*
- 28 Shiny MARTIS BADIADKA *Interplay of local and global regulators in pectin catabolism during plant infection by Dickeya dadantii*
- 29 Irina KALITA *Exploring a mystery of RecBCD regulation in Escherichia coli*
- 30 Luc THOMÈS *Genomic study of oxidative stress response using a multi-species model*
- 31 Fabio MARCHIANO *mitoXplorer 2.0 : A systematic functional analysis of mitochondrial dynamics in health young, aged and sarcopenic muscle*

32	Ousmane	DIOP	<i>Summarizing complex asynchronous Boolean attractors: application to a cell cycle model</i>
33	Rowan	HOWELL	<i>A Boolean model of the Mitotic Exit Network</i>
34	Denise	THIEL	<i>Tracking the metabolic footprints of cancer using network analysis</i>
35	Janina	MÜLLER	<i>High-throughput growth-rate measurements using time-lapse imaging of bacterial colonies</i>
36	Jacques-Alexandre	SEPULCHRE	<i>Modeling the bioconversion of polysaccharides in a continuous reactor: a study case of the recycling of pectin</i>
37	Torkel	LOMAN	<i>Modelling the heterogeneous lysozyme stress response in B. subtilis</i>
38	Chuang	XU	<i>One-dimensional stochastic reaction networks: Classification and dynamics</i>
39	Clarmyra	HAYES	<i>Kinetic and structural requirements for bistability in homotropic allosteric enzyme-mediated substrate cycles</i>
40	Laurens	KRAH	<i>Noise propagation in an integrated model of bacterial gene expression and growth</i>
41	Emma	KEIZER	<i>Unravelling the dynamics of adaptive immunity in CRISPR-Cas through single-cell histories</i>
42	Moritz	BENISCH	<i>Online optogenetic control of protein production in E. Coli</i>
43	Joaquin	GUTIERREZ	<i>Optogenetic feedback stabilization of microbial co-cultures</i>
44	Sant	KUMAR	<i>Stochastic single-cell feedback provides new insights into biomolecular controller design</i>
45	Agustin G.	YABO	<i>Bacterial growth strategies as Optimal Control problems: maximizing metabolite production</i>
46	Bob	VAN SLUIJS	<i>Reverse Engineering in vitro Genetic Networks</i>
47	Lewis	GROZINGER	<i>Investigating the effects of host organism on genetic circuits with interval analysis of context-sensitive model parameters</i>
48	Sarah	CHERKAOUI	<i>Disentangling the relation between metabolite levels and pathway activity</i>
49	Thomas	DIEDEREN	<i>High throughput flux analysis</i>
50	Ohad	GOLAN	<i>Quantitative analysis of the nutrient management: The central metabolism – amino acid module</i>
51	Mona K.	TONN	<i>Emergence of non-genetic heterogeneity in metabolic reactions</i>
52	Antrea	PAVLOU	<i>Experimental and computational analysis of bacterial self-replicators</i>
53	Svetlana	VOLKOVA	<i>Towards personalized mechanistic models of red blood cell metabolism</i>
54	Denis	SHEPELIN	<i>Benchmarking kinetic models of E. coli metabolism.</i>
55	Diane	ADJAVON	<i>Metabolic oscillations as an optimization problem</i>
56	Yu	HUO	<i>Quantification and Modelling of Cellular Decision between Coexisting Maltose and Galactose</i>
57	Soukaina	TIMOUMA	<i>Mining and modeling the genome of yeast industrial hybrids</i>
58	Claudio	TOMI ANDRINO	<i>The use of thermodynamics and biomass assembly to further constrain metabolic flux analysis based methods: toward monitoring bacterial metabolism</i>
59	Hadrien	DELATTRE	<i>Modelling the dynamics of pathway switching in microbial populations</i>
60	Riccardo	MUOLO	<i>Specific Flux Optimization in the Threonine Pathway</i>
61	Rik	VAN ROSMALLEN	<i>Automated Construction and Application of Mathematical Models for Metabolic Systems</i>