

Fourth CoLoMoTo meeting (Paris, July 17-19 2017)

The fourth CoLoMoTo meeting took place in Paris, from the 17th to the 19th of July, 2017. As usual, the meeting covered a wide range of topics related to logical modelling, from methodological and software developments to biological applications. It was hosted by IBENS in the center of Paris (46 rue d'Ulm).

This meeting was organized by Aurélien Naldi (IBENS, Paris), Claudine Chaouiya (IGC, Lisbon), Denis Thieffry (IBENS, Paris), Gautier Stoll (INSERM, IGR, U. Paris Descartes), and Laurence Calzone (Curie Institute, Paris).

July 17 - Scientific Presentations

Time	Speaker	Title
13:00		Introductory remarks
13:20	Gautier Stoll	Using MaBoSS for modeling heterogeneous cell behavior
13:40	Samuel Collombet	Deciphering the regulatory network of blood cells specification and reprogramming
14:00		<i>Coffee Break</i>
14:30	Loïc Paulevé	Modelling and analysis of transient dynamics of qualitative models (tutorial)
14:50	Enio Gjerga	Efficient modelling of signalling networks derived from mass spectrometry phosphoproteomic data using Integer Linear Programming
15:10	Ping Zhang	Control and Diagnosis of Boolean Networks
15:30		<i>Coffee Break</i>
16:00	Anna Niarakis	Integrative modelling and analysis of molecular pathways involved in Rheumatoid Arthritis
16:20	Arnau Montagud	Conceptual and computational framework for logical modelling of deregulated biological networks
16:40	Claudine Chaouiya	Standards for logical models: current status of SBML qual & SED-ML
17:00		Discussion - planning workgroups

July 18 - Working groups and Presentations

Time	Speaker	Title
09:00		Working group on tooling
•	Aurélien Naldi	Model conversion, modification, and analysis with bioLQM

Time	Speaker	Title
•	Loïc Paulevé	Jupyter Notebook
•	Claudine Chaouiya	Future extensions to SBML qual and SED ML
12:30		<i>Lunch break</i>
13:30		Working group on applications
•	Laurence Calzone	Model composition
•	Gautier Stoll	Modelling the immune system
15:30		Working group on methods
•	Pedro T. Monteiro	On the structure and robustness of gene regulatory network Boolean functions
•	Adrien Fauré	A circuit-preserving mapping from multilevel to Boolean dynamics
•	Aurélien Naldi	Trap-spaces and global reachability mapping
17:30		Wrapping-up

July 19 - Wrapping up and hacking

Time	Title
10:00	MaBoSS Tutorial
10:00	Docker session
12:00	Discussion and Wrapping-up

Participants

- Adrien Fauré (Yamaguchi University)
- Anna Niarakis (Université d'Evry Val d'Essonne)
- Arnau Montagud (Institut Curie)
- Aurélien Naldi (IBENS)
- Célia Biane (UEVE, IBISC Lab)
- Céline Hernandez (IBENS)
- Claudine Chaouiya (Instituto Gulbenkian de Ciência)
- Daniela Ferretti (University of Camerino)
- Delphine Potier (CIML)
- Denis Thieffry (IBENS)
- Élisabeth Remy (CNRS)
- Enio Gjerga (JRC COMBINE, RWTH Aachen University)
- Gautier Stoll (INSERM U1138eq11/Université Paris 5/Gustave Roussy)
- Geoffray Brelurut (IBENS)

- Ghislaine Morvan-Dubois (CNRS)
- Hugues Mandon (INRIA - LSV - LRI)
- Laurence Calzone (Institut Curie)
- Loïc Paulevé (CNRS/LRI)
- Nathalie Lehmann (IBENS)
- Paolo Ballarini (CentraleSupélec)
- Pauline Traynard (Institut Curie)
- Pedro T. Monteiro (INESC-ID/IST - Universidade de Lisboa)
- Ping Zhang (University of Kaiserslautern, Institute of Automatic Control)
- Samuel Collombet (IBENS)
- Samyadeep Basu (IBENS)
- Seraya Maouche (TBI Scientific)
- Swann Flochlay (IBENS)
- Tomas Helikar (University of Nebraska)
- Vidisha Singh (Genhotel, University of Evry val d'essonne)
- Wassim Abou-Jaoude