

Date of birth : October 24th, 1968
 Grade : Full Professor, 1st class, 27th section of CNU
 Assignment establishment: Université Côte d’Azur
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Education / Degrees :

2006 **Habilitation to supervise research (HDR)** from *Université d’Évry-Val d’Essonne*. Title: *From textual bioinformatics to a formal approach of systems biology* (in French).
1999-2000 **Post-doc in bioinformatics** at *Whitehead Institute/MIT Center for Genome Research*, Cambridge (MA) USA.
1995-1998 **PhD in Computer science** at Université de Technologie de Compiègne, host laboratory: INRIA Rocquencourt. *Dynamics Programming and biological sequence alignments* (in French).

Academic Professional Career:

- Since January 2019: deputy director of SPARKS team (Scalable and Pervasive softwARe and Knowledge Systems) of I3S lab., Head: A. TETTAMANZI, deputised by M. WINCKLER and J.-P. COMET.
- Since 2012: in charge of *bioinfo* group which became *formal bioinfo*.
- Since sept. 2007: Full Professor in Computer science at Université de Nice-Sophia-Antipolis / Université Côte d’Azur. Promoted to first class full professor in 2014, PEDR obtained in 2006, 2010, 2014 and 2019.
- 2000–2007: Assistant Professor (PEDR 2006, obtained in 2004 but renouncement because of the sabbatical leave for research (délégation CNRS). Host laboratory: IBISC F.R.E. 2873 CNRS. Teams: *bioinfo* from 2000 to 2005, *Networks and Formal Methods* from 2006 to 2007.
- 2004–2006: "Délégation CNRS" (sabbatical leave for research) at Programme d’Épigénomique d’Évry
- 1999: Post-doc at Whitehead Institute/MIT Center for Genome Research, Cambridge (MA) USA.
- 1995–1998: PhD in Computer Science at UTC (France). Host laboratory: INRIA Rocquencourt.

I. Scientific activities

Search topics: Modeling of biological systems, Extensions and applications of formal methods for formal modelling of biological regulation networks, Machine learning and evolutionary methods for biology.

Systems biology aims at giving meaning to all the information generated by genome sequencing and by all transcriptomic and proteomic techniques. It focuses on the dynamical functioning of the genome taken as a system in its own right. Thus we focus on the modelling of the dynamics of biological systems and develop formal methods for the study of these systems, one of the goals being ultimately the identification of the parameters of the models guided by biological knowledge and hypotheses.

We were the first in 2004 to give a formal framework to the modelling of genetic networks introduced by R. Thomas in the 1970s. This formalization allowed us to propose several extensions (bipartite, stochastic, hybrid modelling), making possible to study biological systems whose fine functioning relies heavily on temporal aspects, as is the case for the cell cycle and the circadian cycle (alternating sleep / wake). The associated models are controlled by parameters whose identification is difficult since the domains of the parameters are intervals in \mathbb{R} , which makes their enumeration impossible.

To cope with this difficulty, we therefore developed a Hoare logic dedicated to gene networks as well as its weakest precondition calculus, first in the discrete framework; this logic is proven correct and complete [ij-3]. This approach has also been developed for hybrid models taking into account a continuous time: the Hoare logic dedicated to hybrid automata is proven correct [ic-5]. We have also developed the first formal modelling framework dedicated to toxicology: the system is described by rules, and the sequence of these rules is controlled by constraints expressed in a temporal logic. This more abstract level of description favours the detection of toxicity pathways [ic-6,ic-7].

Finally, the study of the toxicity of molecules carries enormous societal challenges and the prediction of these toxic effects is a major subject on the economic level for a good number of companies. We are therefore also interested in the evaluation of the predictive potential of *machine learning* tools to predict the adverse effects induced by chemicals [ij-1,ij-2,ij-4,ic-3]. Industrial applications are numerous, ranging from the simple use of these predictors to prioritize the molecules to be developed first, to the search for the most significant *in vitro* tests of a particular toxicity. This work is continued with the PhD of F. Camillery in collaboration with Bayer.

1. Publications

The complete list of my publications is available at: <http://www.i3s.unice.fr/~comet/publications.php>

Summary	Total	since sept 2007 ^(*)
Editions	2	
Book Chapters	16	10
Peer Reviewed Articles in international journals	27	15
Peer Reviewed Articles in national journals	2	
International Conferences (with proceedings)	24	16

(*) this date corresponds to my arrival at Université Côte d'Azur as a full professor.

Here are the 5 publications that I consider the most significant (starting from the most significant) for the presented research proposal (Modelling Biological Systems with AI and Formal Methods).

- [1] G. Bernot, J.-P. Comet, Z. Khalis, A. Richard, and O. F. Roux. A genetically modified Hoare logic. *Theoretical Computer Science*, 765:145-157, 2019. <https://doi.org/10.1016/j.tcs.2018.02.003>.

We modify in this article the Hoare logic initially dedicated to the verification of imperative programs, to build the weakest precondition on the parameters of a genetic regulation network so that it exhibits the observed traces. We show that this Hoare logic is correct and complete. The method is extremely efficient for finding the parameters of a discrete model. The main idea lies in the coding in the form of logic of the semantics of the modelling of genetic regulation networks.

- [2] J. Behaegel, J.-P. Comet, and F. Folschette. Constraint identification using modified Hoare logic on hybrid models of gene networks. In *Proceedings of the 24th International Symposium on Temporal Representation and Reasoning (TIME)*, pages 5:1–5:21, 2017.

For the study of biological networks in which time plays an important role, the discrete modelling framework is not enough. Hybrid models are then useful, but determining parameters is the limiting step in the modelling process. We have adapted the Hoare logic of [1] to the hybrid setting, making it possible to build the constraints on the parameters so that the model exhibits an observed trace. This logic is correct.

- [3] M. Miraglio, G. Bernot, J.-P. Comet, and C. Risso-De Faverney. Detecting toxicity pathways with a formal framework based on equilibrium changes. In *Proceedings of the 15th conference on Computational Methods for Systems Biology (CMSB)*, 2017.

We introduce in this article the first formal modelling framework dedicated to the study of toxicity pathways. The states of equilibrium between the different chemical species constitute the states to be considered and the pathways of toxicity are paths passing from one state of equilibrium to another. Our rules describe qualitatively changes in equilibrium. We illustrate this modelling framework on endocrine disruption of the thyroid hormone system.

- [4] I. Grenet, Y. Yin, J.-P. Comet. G-networks to predict the outcome of sensing of toxicity. *Sensors*, 2018. DOI 10.3390/s18103483,

We present a use of the random neural network for the detection of the potential of toxic chemical compounds *via* the prediction of their bioactivity from the physico-chemical structure of these compounds, and propose to automate it using machine learning (ML) techniques. Random neural networks are proving to be an effective analytical tool for this task. The approach is illustrated and compared to several ML techniques.

- [5] I. Grenet, K. Merlo, J.-P. Comet, R. Tertiaux, D. Rouquié, and F. Dayan. Stacked generalization with applicability domain outperforms simple qsar on in vitro toxicological data. *J. Chemical Information and Modeling*, 59(4):1486–1496, 2019.

A large scale analysis on the entire database ToxCast has been performed to build models to predict bioactivities measured in *in vitro* assays. We prove that the use of an ensemble method named "Stacked generalization" could improve the model performance on this type of data (compared with classical ML technics). Moreover, the combination of this ensemble method with an applicability domain filter allows one to assess the reliability of the predictions for further compound prioritization.

List of my publications by categories [2017–2021].

1.1 Book chapters

1.2 Peer Reviewed Articles in international journals

- [ij-1] L. Gibart, R. Khoodeeram, G. Bernot, J.-P. Comet, and J.-Y. Trosset. Regulation of eukaryote metabolism: An abstract model explaining the warburg/crabtree effect. *Processes*, 9:1496, 2021.
- [ij-2] I. Grenet, J.-P. Comet, F. Schorsch, N. Ryan, J. Wichard, and D. Rouquié. Chemical in vitro bioactivity profiles are not informative about the long-term in vivo endocrine mediated toxicity. *Computational Toxicology*, 12:100098, nov. 2019.
- [ij-3] I. Grenet, K. Merlo, J.-P. Comet, R. Tertiaux, D. Rouquié, and F. Dayan. Stacked generalization with applicability domain outperforms simple qsar on in vitro toxicological data. *J. Chemical Information and Modeling*, 59(4):1486–1496, 2019.

- [ij-4] G. Bernot, J.-P. Comet, Z. Khalis, A. Richard, and O. F. Roux. A genetically modified Hoare logic. *Theoretical Computer Science*, 765:145–157, 2019. <https://doi.org/10.1016/j.tcs.2018.02.003>.
- [ij-5] I. Grenet, Y. Yin, and J.-P. Comet. G-networks to predict the outcome of sensing of toxicity. *Sensors*, 18:3483, 2018.

1.3 International Conferences (with proceedings)

- [ic-1] L. Gibart, H. Collavizza, and J.-P. Comet. Greening R. Thomas' framework with environment variables: a divide and conquer approach. In *Proceedings of the 19th International Conference on Computational Methods in Systems Biology (CMSB)*, LNBI, pages 36–56, September 22-24 2021.
- [ic-2] L. Gibart, G. Bernot, H. Collavizza, and J.-P. Comet. Totembionet enrichment methodology: Application to the qualitative regulatory network of the cell metabolism. In *Proceedings of the 14th International Joint Conference on Biomedical Engineering Systems and Technologies, Volume 3: BIOINFORMATICS*, volume 3, pages 85–92, 2021.
- [ic-3] D. Boyenval, G. Bernot, H. Collavizza, and J.-P. Comet. What is a cell cycle checkpoint? the totembionet answer. In *Proceedings of the 18th International Conference on Computational Methods in Systems Biology (CMSB)*, volume 12314 of *LNCS*, pages 362–372, online, September 23-25 2020.
- [ic-4] I. Grenet, Y. Yin, J.-P. Comet, and E. Gelenbe. Machine learning to predict toxicity of compounds. In *Proceedings of the 27th International Conference on Artificial Neural Networks (ICANN)*, volume 11139 of *LNCS*, pages 335–345, 2018.
- [ic-5] J. Behaegel, J.-P. Comet, and M. Pelleau. Identification of dynamic parameters for gene networks. In *Proceedings of the 30th IEEE International Conference on Tools with Artificial Intelligence (ICTAI)*, Volos, Greece., November 5-7 2018.
- [ic-6] J. Behaegel, J.-P. Comet, and F. Folschette. Constraint identification using modified Hoare logic on hybrid models of gene networks. In *Proceedings of the 24th International Symposium on Temporal Representation and Reasoning (TIME)*, pages 5:1–5:21, 2017.
- [ic-7] M. Miraglio, G. Bernot, J.-P. Comet, and C. Risso-De Faverney. Detecting toxicity pathways with a formal framework based on equilibrium changes. In *Proceedings of the 15th conference on Computational Methods for Systems Biology (CMSB)*, 2017.
- [ic-8] M. Miraglio, G. Bernot, J.-P. Comet, and C. Risso-De Faverney. A qualitative framework dedicated to toxicology. In *Proceedings of the 8th International Conference on Bioinformatics Models, Methods and Algorithms*, 2017.

2. Dissemination (outreach and popularization)

Invitation to foreign universities: university of Concepcion in Chile in 2011 (3 weeks).

National or international expertise:

- AERES / HCERES evaluation committees for the LIRIS laboratory (2014) and for the LIX (2018).
- 2011, 2012, 2013: evaluation committee for the ANR "SIMI 2 Computer Science and Application"
- 2010: expertise for the self-assessment of the university in view of the four-year plan by evaluating the bachelor's degree "life and health sciences".
- 2009, 2012 and 2013: Scientific excellence bonus (PEDR) national commission for section 27 of the CNU.

Participation in PhD and habilitation juries:

summary	as associate professor (MCF) PhDs	as full professor	
		PhDs	Habilitations
as president of the jury		2	
as reviewer		11	1
as an examiner	1	2	
as PhD supervisor	1	9	

It should be noted that I was rapporteur for a German thesis, a thesis carried out in Pakistan and two theses in joint supervision with foreign universities.

I was rapporteur for PhDs of

- Philippe Veber, Université de Rennes 1, defended on 17/12/2007.
- Marco Montalva Medel, Univ. Grenoble & Univ. of Concepcion (Chili), defended on 18/08/2011 in Chile.
- Joëlle Compaore, Univ. d'Evry & Univ. Ouagadougou (Burkina Faso), defended on 7/03/2012 in France.
- Shahradd Jamshidi, Freie Universität Berlin (Germany), defended on 15/04/2013 in Germany.
- Maxime Folschette, École Centrale de Nantes, defended on 8/10/2014.
- Babar Aslam, National University of Sciences and Technology, Islamabad, Pakistan, 2015.
- Bassam Alkindy, (PhD written in english supported by the minister of higher education and scientific researches in Iraq), Université de Franche-Comté, defended on 17/12/2015.
- Karim El Soufi, Université de Strasbourg, defended on 24/02/2017.
- Jean Coquet, Université de Rennes, defended on 20/12/2017.

- Hugues Mandon, Université Paris-Saclay (ENS Paris-Saclay), defended on 19/11/2019.
- Samuel Buchet, Ecole Centrale de Nantes, will be defended on 14/03/2021.

I was rapporteur for the habilitation of

- Jean-François Couchot, Université de Franche-Comté, defended on 30/01/2017.

I was examiner of the PhD of

- Olivier Bastien, Univ. Joseph Fourier, Grenoble, defended on 21/04/2006.
- Adrien Elena, Université Joseph Fourier, Grenoble, defended on 12/05/2009.
- Eleni Firippi, Université Côte-d’Azur, Nice, defended on 16/12/2020.

I was the president of the jury for PhDs of

- Sofia Figueiredo Almeida, Université Côte-d’Azur, Nice, defended on 17/12/2018.
- Fabien Vilar, Université Aix-Marseille, dfended on 21/12/2018.

For the record, I was also part of the PhD juries of my students: Adrien Richard (2006), Mathieu Poudret (2009), Sylvie Troncale (2008), Jonathan Fromentin (2009), Zohra Khalis (2010), Aparna Das (2012), Emilien Cornillon (2017), Benjamin Miraglio (2018), Jonathan Behaegel (2018) and Ingrid Grenet (2019).

Animation: Organization of scientific events

- Scientific and organizational chair or co-chair of four thematic schools (in IT) *Formal modelling of regulatory biological networks*, 2019, 2016, 2013 and 2010. This thematic school has the CNRS label (and support). <http://www.i3s.unice.fr/bioregul/>

Program committees

- *ICBPE’2009*, International Conference on Biomedical and Pharmaceutical Engineering (Singapore); *CS-Bio’2010*, *CSBio’2011*, *CSBio’2012* et de *CSBio’2014*, International Conferences on Computational Systems-Biology (Bangkok); LMBS’2015 1st International Workshop on Logical Modeling of Biological Systems; International Conference on Bioinformatics, Biocomputational Systems and Biotechnologies BIOTECHNO’2018, BIOTECHNO’2018; Bioinformatics’20.
- Membre du *Scientific Program Committee* de la *Conference on Modelling Methods in Computer Systems, Networks and Bioinformatics*. <https://confs.iitis.pl//iscis2019>.

Economic partners: establishment of a long-term collaboration with Bayer CropScience, having already led to two CIFRE PhDs (Ingrid Grenet, 2019 and F. Camilleri, on-going). A collaboration project has recently been planned with Altran.

3. Students supervision

Post-docs	students	dates	supervision
	Gaëlle Rossignol	2008–2009	G. Bernot (50%), A. Richard (25%) and my-self (25%)
	Mathilde Noual	2012–2014	A. Richard (50%), G. Bernot (25%) and my-self (25%)
	Maxime Folschette	2015–2016	100% supervision
PhD students	students	dates	supervision
	A. Richard	2003–2006	G. Bernot (10%) and my-self (90%)
	M. Poudret (*)	2005–2009	P. Le Gall (20%), A. Arnould (50%) and my-self (30%)
	D. Mateus	2004–2006	P. Le Gall (50%) and my-self (50%)
	S. Troncale (*)	2005–2008	G. Bernot (50%) and my-self (50%)
	J. Fromentin (*)	2006–2009	O. Roux (60%), P. Le Gall (20%) and my-self (20%)
	Z. Khalis (*)	2006–2010	G. Bernot (50%) and my-self (50%)
	A. Das (*)	2009–2012	F. Diener (50%), G. Bernot (25%) and my-self (25%)
	E. Cornillon (*)	2013–2017	G. Bernot (50%) and my-self (50%)
	B. Miraglio (*)	2014–2018	G. Bernot (40%), C. Risso (20%) and my-self (40%)
	J. Behaegel (*)	2015–2018	F. Delaunay (45%), P. Pelleau (10%) and my-self (45%)
	I. Grenet (*)	2016–2019	convention CIFRE, Bayer Crop Science
	D. Boyenval	2018–2021	F. Delaunay (35%), G. Bernot (25%), H. Collavizza (20%), my-self (20%)
	L. Gibart	2019–2022	G. Bernot (35%), H. Collavizza (30%) and my-self (35%)
	R. Michelucci	2021–2024	D. Pallez (50%) and my-self (50%)
	F. Camilleri	2021–2024	convention CIFRE, Bayer Crop Science
Master-2 students	students	dates	supervision
	M. Van de Voorde	2001	100% supervision
	S. Pérès	2002	G. Bernot (25%) et and my-self (75%)
	C. Auliac	2003	V. Frouin (50%) du CEA/SGF and my-self (50%)
	C. Müller	2003	F. Delaplace (50%) and my-self (50%)
	A. Richard	2003	Encadrement à 100%
	X. Goffin	2004	P. Le Gall (33%), G. Bernot (33%) and my-self (33%)
	H. Hanen	2004	F. Delaplace (50%) and my-self (50%)
	D. Girin	2005	100% supervision
	C. Damon	2005	d’Alché-Buc (50%) and my-self (50%)
	J. Fromentin	2006	P. Le Gall (33%), O. Roux (33%) and my-self (33%)
	J. Laville	2011	G. Bernot (50%) and my-self (50%)
	V. Barghavi	2012	G. Bernot (40%), E. de Maria (30%) and my-self (30%)
	E. Cornillon	2013	G. Bernot (50%) and my-self (50%)
	J. Behaegel	2015	G. Bernot (50%) and my-self (50%)
	L. Gibart	2019	G. Bernot (25%), H. Collavizza (50%) and my-self (25%)

4. Scientific responsibilities

4.1 Responsibilities oriented by the theme of research

Research contracts / collected budgets

- Participation to ANR HyClock project, local project leader, 2014–2018. Local budget: 138 k€.
- 2 CIFRE contracts with Bayer CropScience. Laboratory budget: 30 k€ for each contract (2016-2019 and 2021-2024)
- Co-chair of a pluridisciplinary project of UCA (2019). Laboratory Budget: 12 k€.
- Participation to a pluridisciplinary project PAIR-Pancreas (2018-2021). Laboratory Budget: 32 k€.
- organization of a summer school (2019: 25000 €; 2016: 21000 €; 2013: 18000 €).

4.2 Research administration

Piloting a school for young researchers. I'm part of the school steering committee (in computer science) on *formal modelling of biological regulation networks*. The school takes place every 3 years (2010, 2013, 2016, 2019).

Responsibilities of a research team. Since 2012, I have been responsible for the I3S *bioinfo* team which includes now (8 people). The themes of this team are as follows: Logical approaches for genetic network modelling, Theory of Boolean interaction networks, Hybrid modelling, Parameter identification, Application to concrete biological problems, Machine learning methods for toxicity prediction, Functional analysis of ecological systems (this is also a possible application domain for the deposited research proposal).

This diversity of modelling frameworks allows us to approach new biological systems with more flexibility, and to be able to choose the framework best suited to the case studies, taking into account both the biological questions posed and the experimental capacities.

Deputy director of SPARKS (39 permanents and 34 non-permanents) **Team** since january 2020.

4.3 Teaching

My teaching load has been in the order of 200 hours per year for more than 20 years. During my career, I have taught in many fields. Here are the different courses for which I have been responsible since my arrival on Sophia-Antipolis: Mathematical tools for biology (EPU GB3), Python programming (Master SVS, Nice), Algorithmics for bioinformatics (EPU GB4), Discrete modelling of gene networks (EPU GB5), Techniques of simulation and modelling of biological networks (EPU GB4), Introduction to relational databases (EPU GB4), Software engineering & UML (EPU GB5), *Introduction to AI for Biology* (EPU GB5).

4.4 Other activities and responsibilities (educational, administrative, etc.)

Responsibilities of teaching tracks

- Since 2008: Responsibility for the BIMB option of the Biological Engineering department of Polytech "Bioinformatics and Modelling for Biology" (BIMB). Definition of the scientific content of the curriculum (more than 400 hours of annual teaching), looking for the teachers, modification of the RCC, ...
- 2000-2003: responsible for the computer science teaching at the IUP Biological and computer engineering of Evry (450 hours of computer science education).
- 2001-2003: responsible for computer science education at the DESS "Biological and computer engineering" of Evry (350 hours of computer science education).
- 2003–2005: in charge of the Miage license from Evry, 2 groups of 30 students, one of whom was an apprenticeship training.

National Council of Universities (CNU): I have been elected to the CNU in 2015 and 2019 (until 2023).

Collective responsibilities

- Since February 2016: member of the scientific council of the "Complexity and diversity of living systems" academy of "Université Côte-d'Azur". This academy is responsible for promoting transdisciplinarity (around the life sciences) and the development of new research funding tools (around 500 k€ per year).
- Since 2018: member of the animation committee of the structuring axis "Modelife" of Université Côte-d'Azur since 2018. Scientific animation around modelling for the living (annual budget of 45 k€).
- 2008–2021: elected member of the I3S laboratory council.
- 2008–2018: elected member of the school council of Polytech'Nice-Sophia.

4.5 Awards

- 2006–2009: Scientific excellence bonus (PEDR)
- 2010: Best paper award at CSBio’10.
- 2010–2013: Scientific excellence bonus (PEDR)
- 2014–2017: Scientific excellence bonus (PEDR)
- 2019–2022: Scientific excellence bonus (PEDR)

II. Exhaustive bibliography

Editions

- [e1] P. Amar, J.-P. Comet, F. Képès, and V. Norris, editors. *Modelling and simulation of biological processes in the context of genomics*. Publisher Frontier group (ISBN : 2-84704-0374), June 2004.
- [e2] J.-P. Comet and M. Kaufman, editors. *Modélisation et simulation pour la post-génomique*. TSI, numéro spécial, Mars 2007.

Book chapters

- [c1] J.-J. Codani, J.-P. Comet, J.-C. Aude, E. Glémet, A. Wozniak, J.-L. Risler, A. Hénaut, and P.P. Slonimski. *Automation, Genomic and Functional Analyses*, volume 28, chapter Automatic analysis of large scale pairwise alignments of protein sequences, pages 229–244. Academic Press, ISBN : 0-12-521527-4, 1999.
- [c2] J. Mary, G. Mercier, J.-P. Comet, A. Cornuéjols, C. Froidevaux, and M. Dutreix. *Proc. of the Dieppe Spring school on Modelling and simulation of biological processes in the context of genomics*, chapter Using an attribute estimation technique for the analysis of microarray data, pages 69–77. Publisher Frontier group, ISBN : 2-84704-036, 2003.
- [c3] G. Bernot, J. Guespin-Michel, J.-P. Comet, P. Amar, A. Zemirline, F. Delaplace, P. Ballet, and A. Richard. *Proc. of the Dieppe Spring school on Modelling and simulation of biological processes in the context of genomics*, chapter Modelling, observability and experiment: a case study, pages 49–55. Publisher Frontier group, ISBN : 2-84704-036, 2003.
- [c4] J. Mary, G. Mercier, J.-P. Comet, A. Cornuéjols, C. Froidevaux, and M. Dutreix. *Informatique pour l’analyse du transcriptome*, chapter Utilisation d’une méthode de sélection d’attributs pour l’analyse du transcriptome de cellules de levure exposées à de faibles doses de radiation, pages 189–205. Hermes, ISBN : 2-7462-0850-4, 2004.
- [c5] A. Richard, J.-P. Comet, and G. Bernot. *Modern Formal Methods and Applications*, chapter Formal Methods for Modeling Biological Regulatory Networks, pages 83–122. Springer, ISBN: 1-4020-4222-1, 2006.
- [c6] D. Mateus, J.-P. Comet, J.-P. Gallois, and P. Le Gall. *Proc. of the Evry Spring school on Modelling complex biological systems in the context of genomics*, chapter Inferring parameters of genetic regulatory networks with symbolic formal methods, pages 51–70. EDP Science, ISBN : 978-2-7598-0019-3, 2007.
- [c7] M. Poudret, J.-P. Comet, P. Le Gall, F. Képès, A. Arnould, P. Meseure, J.-M. Verbavatz, and A. Rambourg. *Proc. of the Lille Spring school on Modelling complex biological systems in the context of genomics*, chapter Toward a computer-aided methodology for topology-based simulation of the Golgi apparatus, pages 89–104. EDP Science, ISBN : 978-2-7598-0075-9, 2008.
- [c8] Z. Khalis, G. Bernot, and J.-P. Comet. *Proc. of the Nice Spring school on Modelling complex biological systems in the context of genomics*, chapter Gene Regulatory Networks: Introduction of multiplexes into R. Thomas’ modelling, pages 139–151. EDP Science, ISBN : 978-2-7598-0437-5, 2009.
- [c9] J.-P. Comet and G. Bernot. *Proc. of the Evry Spring school on Modelling complex biological systems in the context of genomics*, chapter Introducing continuous time in discrete models of gene regulatory networks, pages 61–94. EDP Sciences, ISBN : 978-2-7598-0545-7, 2010.
- [c10] J.-P. Comet, G. Bernot, A. Das, F. Diener, Massot C., and A. Cessieux. *Proc. of the Evry Spring school on Modelling complex biological systems in the context of genomics*, chapter Simplified models for the mammalian circadian clock, pages 85–106. EDP Sciences, 2012.
- [c11] G. Bernot, J.-P. Comet, A. Richard, M. Chaves, J.-L. Gouzé, and F. Dayan. *Modeling in Computational Biology and Biomedicine, A Multidisciplinary Endeavor*, chapter Modeling and analysis of gene regulatory networks, pages 47–80. Springer, ISBN : 978-3-642-31208-3, 2013.
- [c12] G. Bernot, J.-P. Comet, and C. Risso-de Faverney. *Computational Toxicology*, volume II, chapter Regulatory networks, pages 215–234. Humana Press, ISBN 978-1-62703-058-8, USA, 2013.
- [c13] El Houssine Snoussi Gilles Bernot, Jean-Paul Comet. *Logical Modeling of Biological Systems*, chapter Formal methods applied to gene network modelling, pages 77–90. 2014.
- [c14] K.J.E. Carpio, G. Bernot, J.-P. Comet, and F. Diener. *Proc. of the Thematic Research School on Advances in Systems and Synthetic Biology, Modelling Complex Biological Systems in the Context of Genomics*, chapter Probabilistic Gene Network, pages 77–90. EDP Sciences, ISBN 978-2-7598-1764-1, 2015.
- [c15] B. Miraglio, B. Bernot, J.-P. Comet, and C. Risso-de Faverney. *Proc. of the Thematic Research School on Advances in Systems and Synthetic Biology, Modelling Complex Biological Systems in the Context of Genomics*, chapter Towards a Computer Aided Toxicology, pages 85–101. EDP Sciences, ISBN : ISBN : 978-2-7598-1971-3, 2016.

- [c16] E. Cornillon, J.-P. Comet, G. Bernot, and G. Enée. *Proc. of the Thematic Research School on Advances in Systems and Synthetic Biology, Modelling Complex Biological Systems in the Context of Genomics*, chapter Hybrid Gene Networks: a new Framework and a Software Environment, pages 57–84. EDP Sciences, ISBN: 978-2-7598-1971-3, 2016.

The volumes in which the references [c2, c3, c6] [c7, c8, c9, c10, c14, c15, c16] appear, combine both proceedings of the thematic schools and book chapters. The references above correspond to chapters.

International journals

- [ij1] J.-P. Comet, J.-C. Aude, E. Glémet, A. Hénaut, J.-L. Risler, P.P. Slonimski, and J.-J. Codani. Significance of Z-value statistic of Smith-Waterman scores for protein alignments. *Computers and Chemistry*, 23(3-4):317–331, 1999.
- [ij2] J.-N. Bacro and J.-P. Comet. Sequence alignment: an approximation law for the Z-value with applications to databank scanning. *Computers and Chemistry*, 25:401–410, 2000.
- [ij3] J.-P. Comet and J. Henry. Pairwise sequence alignment using a PROSITE pattern-derived similarity score. *Computers and Chemistry*, 26(5):421–436, 2002.
- [ij4] J.-P. Comet. Application of max-plus algebra to biological sequence comparisons. *Theoretical Computer Science*, 293:189–217, 2003.
- [ij5] G. Mercier, N. Berthault, J. Mary, J. Peyre, A. Antoniadis, J.-P. Comet, A. Cornuéjols, C. Froidevaux, and M. Dutreix. Biological detection of low radiation by combining results of two microarray analysis methods. *Nucleic Acids Research*, 32(1):e12, 2004.
- [ij6] G. Bernot, J.-P. Comet, A. Richard, and J. Guespin. Application of formal methods to biological regulatory networks: Extending Thomas’ asynchronous logical approach with temporal logic. *Journal of Theoretical Biology*, 229(3):339–347, 2004.
- [ij7] J. Guespin-Michel, G. Bernot, J.-P. Comet, A. Mérieau, A. Richard, C. Hulen, and B. Polack. Epigenesis and dynamic similarity in two regulatory networks in *pseudomonas aeruginosa*. *Acta Biotheoretica*, 52(4):379–390, 2004.
- [ij8] A. Richard, J.-P. Comet, and G. Bernot. R. Thomas’ modeling of biological regulatory networks: introduction of singular states in the qualitative dynamics. *Fundamenta Informaticae*, 65(4):373–392, 2005.
- [ij9] D. Filopon, A. Merieau, G. Bernot, J.-P. Comet, R. Leberre, B. Guery, B. Polack, and J. Guespin-Michel. Epigenetic acquisition of inducibility of type III cytotoxicity in *p. aeruginosa*. *BMC Bioinformatics*, 7:272, 2006.
- [ij10] D. Mateus, J.-P. Gallois, J.-P. Comet, and P. Le Gall. Symbolic modeling of genetic regulatory networks. *Journal of Bioinformatics and Computational Biology*, 5(2B):627–640, 2007.
- [ij11] A. Richard and J.-P. Comet. Necessary conditions for multistationarity in discrete dynamical systems. *Discrete Applied Mathematics*, 155(18):2403–2413, 2007.
- [ij12] S. Troncale, R. Thuret, C. Ben, N. Pollet, J.-P. Comet, and G. Bernot. Modelling of the TH-dependent regulation of tadpole tail resorption. *Journal of Biological Physics and Chemistry*, 7(2):45–50, 2007.
- [ij13] J. Ahmad, G. Bernot, J.-P. Comet, D. Lime, and O. Roux. Hybrid modelling and dynamical analysis of gene regulatory networks with delays. *ComplexUs*, 3(4):231–251, 2006 (Cover Date: November 2007).
- [ij14] J. Ahmad, O. Roux, G. Bernot, J.-P. Comet, and A. Richard. Analysing formal models of genetic regulatory networks with delays: Applications to lambda phage and T-cell activation systems. *Int. J. Bioinformatics Research and Applications*, 4(3):240–262, 2008.
- [ij15] M. Poudret, J.-P. Comet, P. Le Gall, F. Képès, A. Arnould, and P. Meseure. Topology-based abstraction of complex biological systems: Application to the Golgi apparatus. *Theory in Biosciences*, 127:79–88, 2008.
- [ij16] S. Troncale, J.-P. Comet, and G. Bernot. Enzymatic competition: Modeling and verification with timed hybrid Petri nets. *Pattern Recognition*, 42(4):562–566, 2009.
- [ij17] Z. Khalis, J.-P. Comet, A. Richard, and G. Bernot. The SMBioNet method for discovering models of gene regulatory networks. *Genes, Genomes and Genomics*, 3(special issue 1):15–22, 2009.
- [ij18] A. Richard and J.-P. Comet. Stable periodicity and negative circuits in differential systems. *Journal of Mathematical Biology*, 63(3):593–600, 2011 [online, december 1st, 2010].
- [ij19] M. Mabrouki, M. Aiguier, J.-P. Comet, P. Le Gall, and A. Richard. Embedding of biological regulatory networks and properties preservation. *Mathematics in Computer Science*, 5(3):263–288, 2011.
- [ij20] S. Taati, E. Formenti, J.-P. Comet, and G. Bernot. On the impact of the distance between two genes on their interaction curve. *Journal of Mathematical Biology*, 64(1):131–147, 2012.
- [ij21] A. Richard, G. Rossignol, J.-P. Comet, G. Bernot, J. Guespin-Michel, and A. Mérieau. Boolean models of biosurfactants production in *pseudomonas fluorescens*. *PlosOne*, 7(1):e24651, 2012.
- [ij22] J.-P. Comet, M. Noual, A. Richard, J. Aracena, L. Calzone, J. Demongeot, M. Kaufman, A. Naldi, E.H. Snoussi, and D. Thieffry. On circuit functionality in boolean networks. *Bulletin of Mathematical Biology*, 75(6):906–919, 2013.
- [ij23] J. Behaegel, J.-P. Comet, G. Bernot, E. Cornillon, and F. Delaunay. A hybrid model of cell cycle in mammals. *J. Bioinformatics and Comput. Biol.*, 14(1):1640001 [17 pp.], 2016.
- [ij24] I. Grenet, Y. Yin, and J.-P. Comet. G-networks to predict the outcome of sensing of toxicity. *Sensors*, 18:3483, 2018.

- [ij25] I. Grenet, K. Merlo, J.-P. Comet, R. Tertiaux, D. Rouquié, and F. Dayan. Stacked generalization with applicability domain outperforms simple qsar on in vitro toxicological data. *J. Chemical Information and Modeling*, 59(4):1486–1496, 2019.
- [ij26] I. Grenet, J.-P. Comet, F. Schorsch, N. Ryan, J. Wichard, and D. Rouquié. Chemical in vitro bioactivity profiles are not informative about the long-term in vivo endocrine mediated toxicity. *Computational Toxicology*, 12:100098, nov. 2019.
- [ij27] L. Gibart, R. Khoodeeram, G. Bernot, J.-P. Comet, and J.-Y. Trosset. Regulation of eukaryote metabolism: An abstract model explaining the warburg/crabtree effect. *Processes*, 9:1496, 2021.

National journals

- [nj1] J. Guespin, J.-P. Comet, and G. Bernot. Les réseaux de régulation biologique : rencontre entre biologie et informatique. *T.S.I.*, 23(7):939–945, 2004.
- [nj2] G. Bernot, J.-P. Comet, and J. Guespin. Elucider le fonctionnement d’un réseau de régulation biologique par l’informatique. *Biofutur (Mensuel de vulgarisation), numéro spécial sur la biologie intégrative*, 275:22–25, 2007.

International Conferences and workshops with proceedings

- [ic1] S. Pérès and J.-P. Comet. Contribution of computational tree logic to biological regulatory networks: example from *Pseudomonas aeruginosa*. In *International workshop on Computational Methods in Systems Biology*, volume 2602 of *LNCS*, pages 47–56, February 24–26, 2003, taux d’acceptation : 28%.
- [ic2] G. Bernot, F. Cassez, J.-P. Comet, F. Delaplace, C. Müller, O. Roux, and O.H. Roux. Semantics of biological regulatory networks. In *Proceedings of the Workshop on Concurrent Models in Molecular Biology (BioConcur’2003)*, 2003.
- [ic3] A. Richard, J.-P. Comet, and G. Bernot. Graph-based modeling of biological regulatory networks : Introduction of singular states. In *Proceedings of the second International workshop on Computational Methods in Systems Biology (CMSB)*, volume 3082 of *LNBI*, pages 58–72, 2004.
- [ic4] J.-P. Comet, H. Klaudel, and S. Liauzu. Modeling multi-valued genetic regulatory networks using high-level Petri nets. In *ICATPN 2005*, volume 3536 of *LNCS*, pages 208–227, 2005.
- [ic5] J. Ahmad, A. Richard, G. Bernot, J.-P. Comet, and O. Roux. Delays in biological regulatory networks. In *Proceedings of IWBRA06*, volume 3992 of *LNCS*, pages 887–894, 2006, taux d’acceptation : 37%.
- [ic6] M. Poudret, J.-P. Comet, P. Le Gall, A. Arnould, and Ph. Meseure. Topology-based geometric modelling for biological cellular processes. In *first International Conference on Language and Automata Theory and Applications, LATA’07*, See the proceedings on the website of the conference, pages 497–508, 2007, taux d’acceptation : 28%.
- [ic7] J. Fromentin, J.-P. Comet, P. Le Gall, and O. Roux. Analysing gene regulatory networks by both constraint programming and model-checking. In *EMBC’07, 29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pages 4595–4598, Lyon, France, 2007, August 23–26.
- [ic8] S. Troncale, J.-P. Comet, and G. Bernot. Validation of biological models with temporal logic and timed hybrid Petri nets. In *EMBC’07, 29th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, pages 4603–4608, Lyon, France, 2007, August 23–26.
- [ic9] S. Troncale, J.-P. Comet, and G. Bernot. Verification of biological models with timed hybrid Petri nets. In Xiaobo Pham, Tuan D.; Zhou, editor, *Proc. of the 2007 Intl Symp. on Computational Models for Life Sciences (CMLS07), American Institute of Physics Conference Proc. Series (AIP), ISBN 978-0-7354-0466-3*, volume 952, pages 287–296, Gold Coast, Queensland, Australia, 2007, December 17–19.
- [ic10] M. Mabrouki, M. Aiguier, J.-P. Comet, and P. Le Gall. Property preservation along embedding of biological regulatory networks. In *Algebraic Biology*, volume 5147 of *LNCS*, pages 125–138, Austria, July 31st–August 2d 2008.
- [ic11] M. Poudret, A. Arnould, J.-P. Comet, and P. Le Gall. Graph transformation for topology modelling. In H. Ehrig et al., editor, *Proceedings of the ICGT 2008*, volume 5214 of *LNCS*, pages 147–161, Leicester, United Kingdom, September 7 - 13 2008. Springer-Verlag Berlin Heidelberg.
- [ic12] G. Bernot, J.-P. Comet, and Z. Khalis. Gene regulatory networks with multiplexes. In *European Simulation and Modelling Conference Proceedings*, ISBN: 978-90-77381-44-1, pages 423–432, France, October 27st–29th 2008.
- [ic13] G. Bernot, J.-P. Comet, E. Formenti, and S. Taati. Gene regulatory networks: the impact of distance between genes. In *19th International Symposium in Mathematical Theory of Networks and Systems (MTNS’10)*, Budapest (Hungary), July 5–9 2010.
- [ic14] J.-P. Comet, J. Fromentin, G. Bernot, and O. Roux. A formal model for gene regulatory networks with time delays. In J.H. Chan, Ong Y.-S., and Cho S.-B., editors, *1st International Conference on Computational Systems-Biology and Bioinformatics (CSBio’2010)*, volume 115 of *Communications in Computer and Information Science (CCIS)*, pages 1–13, Bangkok (Thailand), November 3–5 2010. Springer.
- [ic15] J.-P. Comet, G. Bernot, A. Das, F. Diener, C. Massot, and A. Cessieux. Simplified models for the mammalian circadian clock. In *3rd International Conference on Computational Systems-Biology and Bioinformatics (CSBio’2012)*, volume 11 of *Procedia Computer Science*, pages 127–138, Bangkok (Thailand), October 3–5 2012.
- [ic16] J. Behaegel, J.-P. Comet, G. Bernot, E. Cornillon, and F. Delaunay. A hybrid model of cell cycle in mammals. In *6th International Conference on Computational Systems-Biology and Bioinformatics (CSBio’2015)*, Bangkok (Thailand), November 22–25 2015.

- [ic17] M. Miraglio, G. Bernot, J.-P. Comet, and C. Risso-De Faverney. A qualitative framework dedicated to toxicology. In *Proceedings of the 8th International Conference on Bioinformatics Models, Methods and Algorithms*, 2017.
- [ic18] M. Miraglio, G. Bernot, J.-P. Comet, and C. Risso-De Faverney. Detecting toxicity pathways with a formal framework based on equilibrium changes. In *Proceedings of the 15th conference on Computational Methods for Systems Biology (CMSB)*, 2017.
- [ic19] J. Behaegel, J.-P. Comet, and F. Folschette. Constraint identification using modified Hoare logic on hybrid models of gene networks. In *Proceedings of the 24th International Symposium on Temporal Representation and Reasoning (TIME)*, pages 5:1–5:21, 2017.
- [ic20] I. Grenet, Y. Yin, J.-P. Comet, and E. Gelenbe. Machine learning to predict toxicity of compounds. In *Proceedings of the 27th International Conference on Artificial Neural Networks (ICANN)*, volume 11139 of *LNCS*, pages 335–345, 2018.
- [ic21] J. Behaegel, J.-P. Comet, and M. Pelleau. Identification of dynamic parameters for gene networks. In *Proceedings of the 30th IEEE International Conference on Tools with Artificial Intelligence (ICTAI)*, Volos, Greece., November 5-7 2018.
- [ic22] D. Boyenval, G. Bernot, H. Collavizza, and J.-P. Comet. What is a cell cycle checkpoint? the totembionet answer. In *Proceedings of the 18th International Conference on Computational Methods in Systems Biology (CMSB)*, volume 12314 of *LNCS*, pages 362–372, online, September 23-25 2020.
- [ic23] L. Gibart, H. Collavizza, and J.-P. Comet. Greening R. Thomas’ framework with environment variables: a divide and conquer approach. In *Proceedings of the 19th International Conference on Computational Methods in Systems Biology (CMSB)*, LNBI, pages 36–56, September 22-24 2021.
- [ic24] L. Gibart, G. Bernot, H. Collavizza, and J.-P. Comet. Totembionet enrichment methodology: Application to the qualitative regulatory network of the cell metabolism. In *Proceedings of the 14th International Joint Conference on Biomedical Engineering Systems and Technologies, Volume 3: BIOINFORMATICS*, volume 3, pages 85–92, 2021.

International conferences and workshops without proceedings

- [ic-wp1] J.-C. Aude and J.-P. Comet. Construction of protein sequences families. In *24th Aharon Katzir-Katchalsky conference BIOINFORMATICS-STRUCTURE*, Jerusalem, Israel, November 1996.
- [ic-wp2] S. Pérès and J.-P. Comet. A formal approach to modelize biological regulatory networks. Workshop theoretical biophysics, Hiddensee, Germany, April 02-05, 2003.
- [ic-wp3] G. Bernot, O. Roux, C. Auberger, V. Bassano, F. Cassez, J.-P. Comet, F. Delaplace, A. Richard, O.H. Roux, and F. Tahi. Temporal logics and biological regulatory networks. ECCB Satellite Meeting on Modeling and Simulation of Biological Regulatory Processes, Paris, October 2003.
- [ic-wp4] J.-P. Comet, H. Klaudel, and S. Liauzu. Qualitative modelling of genetic networks using high-level Petri nets. IPG’2004, Lyon, France, October 14-15, 2004.
- [ic-wp5] D. Mateus, J.-P. Comet, J.-P. Galois, and P. Le Gall. Modeling genetic regulatory networks from specified behaviors. IPG’2006, Lyon, France, November 29th- December 1st, 2006.
- [ic-wp6] D. Mateus, J.-P. Comet, J.-P. Galois, and P. Le Gall. Modeling genetic regulatory networks from specified behaviors. BioSysBio’2007 (Systems Biology, Bioinformatics, synthetic biology), Manchester, UK, Jan. 11th- Jan. 13th , 2007 [abstract will be published in BMC Systems Biology – feb. 2007].

Invited international conferences

- [iic1] P.P. Slonimski, J.-L. Risler, M.-O. Mossé, A. Hénaut, Y. Diaz, J.-P. Comet, and J.-C. Aude. What can we learn about proteins from complete sequences of microbial genome. In *Protein Science*, volume 6(1), 1997.
- [iic2] P.P. Slonimski, M.-O. Mossé, P. Golik, A. Hénaut, Y. Diaz, J.-L. Risler, J.-P. Comet, J.-C. Aude, A. Wozniak, E. Glémet, and J.-J. Codani. The first laws of genomics. In *Microbial and Comparative Genomics in Microbial Genomes II: Sequencing, Functional Analysis and Comparative Genomics*, volume 46(3), Jan 1998.
- [iic3] M. Dutreix, J.-P. Comet, A. Cornuéjols, and C. Froidevaux. Determination of cellular drug targets: Searching for functional informations in the jungle of microarrays data. International Conference on Current Trends in Drug Discovery Research, Abstract will be published in a special issue of journal "Medicinal Chemistry Research", India, Feb. 17–20. 2004.
- [iic4] G. Bernot, J.-P. Comet, and J. Guespin. Formal methods from computer science to treat temporal properties of biological regulatory networks, applied to mucus production in pseudomonas aeruginosa. Symposium Modeling approaches in Systems Biology, Physiology, and Pathophysiology, Poitiers (Futuroscope), France, October 7–12 2005.
- [iic5] G. Bernot, J.-P. Comet, and J. Guespin. Using formal temporal logic to model biological regulatory networks and to propose new wet experiments. abstract in Proc. of SGF annual meeting, Genetics meets Systems Biology: Theory and Practice, p.17.
- [iic6] G. Bernot, J.-P. Comet, and J. Guespin. A discrete approach to model biological gene regulatory networks and the use of temporal logic to propose wet experiments. Gene regulatory networks: Dynamics, spatial organization and inference: Gennetec International Conference, Torino, Italy, April 23th-2th 2008.
- [iic7] G. Bernot and J.-P. Comet. On the use of temporal formal logic to model gene regulatory networks. In F. Masulli, L. Peterson, and R. Tagliaferri, editors, *6th International Meeting on Computational Intelligence Methods for Bioinformatics and biostatistics, CIBB’2009*, volume 6160 of *LNBI/LNCS*, pages 112–138, Genova (Italy), 15-17 October 2009 2010. Springer.

- [iic8] J.-P. Comet and G. Bernot. A Hoare logic for gene regulatory networks. In *2nd Workshop on Computational Structural Biology: Integrative Approaches for Modeling Biomolecular Complexes 2013*, Nice (France), 29-31 May 2013 2013.
- [iic9] G. Bernot, J.-P. Comet, and O. Roux. A genetically modified Hoare logic that identifies the parameters of a gene networks. In O. Roux and J. Bourdon, editors, *Proceedings of the 13th International Conference on Computational Methods in Systems Biology (CMSB)*, volume 9308 of *LNBI*, pages 8–12, Nantes, France, Sept. 16–18 2015.

Invited national conferences

- [inc1] J.-P. Comet and F. Tahi. Structuration et analyse des données d'expression de gènes. Journées Peri-Bio à l'université d'Evry, Avril 2000.
- [inc2] G. Bernot, J. Michel-Guespin, A. Zermiline, J.-P. Comet, F. Delaplace, P. Ballet, and P. Amar. Modélisation, observabilité et expérimentation : étude d'un cas, boucle de rétroaction positive dans un réseau de régulation génétique. In *Séminaire d'Autrans « Modélisation et simulation des processus biologiques dans le contexte de la génomique »*, Mars 2002.
- [inc3] J. Michel-Guespin, J.-P. Comet, and G. Bernot. Comment valider un modèle mathématique en biologie? AFADL'03, Rennes (France), 15-17 janvier 2003.
- [inc4] G. Bernot and J.-P. Comet. Logique temporelle et model-checking pour les réseaux de régulation biologiques. 3èmes Journées de Post-Génomique de la Doua (JPGD'03), Lyon (France), 14-16 mai 2003.
- [inc5] G. Bernot, J.-P. Comet, and Z. Khalis. Une extension de la logique de Hoare pour les réseaux génétique. Rencontre scientifique « Formalisme logique, apports et défis pour la modélisation de réseaux de régulation biologique », Rabat, Maroc, 12-15 avril 2011.
- [inc6] F. Diener, A. Das, G. Bernot, J.-P. Comet, and F. Eyssette. Correspondence between discrete and piecewise linear models of gene regulatory networks. Actes du colloque à la mémoire d'Emmanuel Isambert, Philosophie, méthodologie et applications de l'analyse non standard, 21-22 décembre 2007, Univ. Paris 7, A. Fruchard, V. Gautheron & T. Sari Eds., Publications de l'Université de Paris 13, p.185-194, 14 février , 2012.
- [inc7] G. Bernot, J.-P. Comet, Z. Khalis, A. Richard, and O. Roux. An extension of Hoare logic to identify the parameters of gene regulatory networks. Invited talk, Modélisation Mathématique des Systèmes Complexes, SMAI & SMF, Ecole Centrale Paris (France), 11-13 dec 2013.
- [inc8] J.-P. Comet, A. Richard, and A. Muzy. Plasticité des réseaux de neurones: Un modèle de réseaux booléens avec règle de Hebb. Workshop sur la Théorie des réseaux booléens et ses applications en biologie, Nice (France).
- [inc9] J.-P. Comet. Automata, logics and biology. Workshop on "Le Monde des Mathématiques Industrielles" (MO-MI'2020), Sophia Antipolis, France, 9-10 march 2020.
- [inc10] G. Bernot and J.-P. Comet. Towards a qualitative understanding of cancer metabolism. Symposium Multidisciplinary Approaches in Cancer Research, Sophia Antipolis (France).

National conferences with proceedings

- [nc1] J. Behaegel, J.-P. Comet, and M. Pelleau. Identification de paramètres dynamiques de réseaux de gènes. In *Quatorzièmes Journées Francophones de Programmation par Contraintes*, 2018.

PhD and Habilitation

- [th1] J.-P. Comet. *Programmation dynamique et comparaison de séquences biologiques*. PhD thesis, Université de Technologie de Compiègne, Novembre 1998.
- [th2] J.-P. Comet. *De la bio-informatique textuelle à une approche formelle de la biologie des systèmes*. H.D.R. spécialité informatique, Université d'Evry-Val d'Essonne, Novembre 2006.