Aurélien Naldi

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Méthodes informatiques pour la construction et l'analyse de réseaux de régulation complexes en biologie

Cursus

Assistant de recherche, « Lifeware », Inria Saclay 2020
Propriétés des abstractions de modèles Booléens (F. Fages et S. Soliman).

Visiting scientist, « Mathematics in Life Sciences », FU Berlin, Allemagne 2019-2020
Propriétés des trap-spaces dans une classe topologique de modèles Booléens (A Bockmayr et H. Siebert).

Assistant de recherche, « Computational Systems Biology », IBENS, Paris 2017-2019
Étude de l'hétérogénéité des cellules du système immunitaire (D. Thieffry).

Assistant de recherche, « Theoretical Biophysics and Systems Biology », DIMNP, Montpellier 2015-2016
Étude de la phosphorylation dans le cancer du sein par protéomique à grande échelle (P Coopman).
Approximation probabiliste de modèles continus basée sur leur réduction tropicale (O. Radulescu).

Assistant de recherche, groupe B. Desvergne, CIG, Université de Lausanne, Suisse 2010-2014
Étude du rôle des récepteurs nucléaires dans le métabolisme du foie par génomique à grande échelle.

Doctorat en bioinformatique, TAGC, Marseille 2006-2009
Modélisation logique de la différenciation des Lymphocytes Th (D. Thieffry et C. Chaouiya).

Master bioinformatique (BBSG), Marseille 2006

DESS informatique, Marseille 2004

DEUG Sciences de la Vie, Marseille 1999

Logiciels

GINsim	Outil de référence pour la définition et l'analyse de modèles logiques	depuis 2004
	> 100'000 lines of java code > 200 citations > 30 modèles	
	http://www.ginsim.org	
bioLQM	Conversion et manipulation de modèles logiques	depuis 2012
	> 20'000 lines of java code	
	https://github.com/colomoto/bioLQM	
CoLoMoTo Notebook	Environnement de modélisation orienté vers la reproductibilité	depuis 2018
	17 conda packages, 3 new python API wrappers, 2 docker images	
	http://colomoto.org/notebook	

Responsabilités collectives

SBML qual	Membre du comité de definition du format	depuis 2009
	Définition de la sémantique associée à ce format d'échange de modèles qualitatifs (modèles logiques et réseaux de Petri)	
CoLoMoTo	Membre fondateur du « **Co**nsortium for **Lo**gical **Mo**dels and **To**ols »	depuis 2010
	Organisation de meetings à Lausanne et Paris, animation de réunions, mise en place du site web	
Arbitrage	Revues et conférences internationales : Bioinformatics, PLoS Comp Biol, BMC Neuroscience, Bull Math Biol, J Theor Biol, Theor Biol Med Model, CMSB	

Enseignement

350h d'enseignement en biologie, bioinformatique et programmation
Niveau licence, master et programme doctoral

Participation à l'encadrement de 8 étudiants en stage ou en début de doctorat depuis 2017

Compétences

Langues	Anglais courant, Allemand basique
Programmation	**Java**, **Python**, C, Rust, Prolog, ASP, R, LaTeX, Web
Bioinformatique	Modèles dynamiques, génomique, protéomique
Biologie	Cycle cellulaire, système immunitaire, métabolisme

Séminaires & workshops

Présentations dans 3 conférences internationales et 11 groupes de travail internationaux.

Présentations dans 2 conférences et 6 groupes de travail nationaux.

6 séminaires sur invitation.

Participation à 4 tutoriels ou écoles de modélisation.

Organisation de 3 groupes de travail internationaux.

http://aurelien.naldi.info/seminars/

Publications internationales avec comité de lecture

40 publications   1700 citations   h-index : 20   ResearcherID:B-5401-2008

Journaux internationaux

[1] A Fauré, **A. Naldi**, C Chaouiya, and D Thieffry. Dynamical analysis of a generic Boolean model for the control of the mammalian cell cycle. *Bioinformatics*, 22(14):e124–31, 2006.

[2] A G Gonzalez, **A. Naldi**, L Sánchez, D Thieffry, and C Chaouiya. GINsim: a software suite for the qualitative modelling, simulation and analysis of regulatory networks. *Bio Systems*, 84(2):91–100, 2006.

[3] **A. Naldi**, D Berenguier, A Fauré, F Lopez, D Thieffry, and C Chaouiya. Logical modelling of regulatory networks with GINsim 2.3. *Bio Systems*, 97(2):134–9, 2009.

[4] A Fauré, **A. Naldi**, F Lopez, C Chaouiya, A Ciliberto, and D Thieffry. Modular logical modelling of the budding yeast cell cycle. *Molecular BioSystems*, 5(12):1787–96, 2009.

[5] **A. Naldi**, J Carneiro, C Chaouiya, and D Thieffry. Diversity and plasticity of Th cell types predicted from regulatory network modelling. *PLoS Computational Biology*, 6(9):e1000912, 2010.

[6] **A. Naldi**, E Remy, D Thieffry, and C Chaouiya. Dynamically consistent reduction of logical regulatory graphs. *Theoretical Computer Science*, 412(21):2207–2218, 2011.

[7] C Chaouiya, **A. Naldi**, E Remy, and D Thieffry. Petri net representation of multi-valued logical regulatory graphs. *Natural Computing*, 10(2):727–750, 2011.

[8] C Chaouiya, D Bérenguier, S M Keating, **A. Naldi**, M P van Iersel, N Rodriguez, A Dräger, F Büchel, T Cokelaer, B Kowal, B Wicks, E Gonçalves, J Dorier, M Page, P T Monteiro, A von Kamp, I Xenarios, H de Jong, M Hucka, S Klamt, D Thieffry, N Le Novère, J Saez-Rodriguez, and T Helikar. SBML qualitative models: a model representation format and infrastructure to foster interactions between qualitative modelling formalisms and tools. *BMC Systems Biology*, 7(1):135, 2013.

[9] D Bérenguier, C Chaouiya, P T Monteiro, **A. Naldi**, E Remy, D Thieffry, and L Tichit. Dynamical modeling and analysis of large cellular regulatory networks. *Chaos*, 23(2):025114, 2013.

[10] 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):906–19, 2013.

[11] D Gilardi, E Migliavacca, **A. Naldi**, M Baruchet, D Canella, G Le Martelot, N Guex, and B Desvergne. Genome-wide analysis of SREBP1 activity around the clock reveals its combined dependency on nutrient and circadian signals. *PLoS Genetics*, 10(3):e1004155, 2014.

[12] W Abou-Jaoudé, P T Monteiro, **A. Naldi**, M Grandclaudon, V Soumelis, C Chaouiya, and D Thieffry. Model checking to assess T-helper cell plasticity. *Front. Bioeng. Biotechnol*, 86(2), 2014.

[13] **A. Naldi***, P T Monteiro*, C Müssel*, Consortium for Logical Models, the Tools, H A Kestler, D Thieffry, I Xenarios, J Saez-Rodriguez, T Helikar, and C Chaouiya. Cooperative development of logical modelling standards and tools with CoLoMoTo. *Bioinformatics*, 31(7):1154–1159, 2015.

[14] S S Samal, **A. Naldi**, D Grigoriev, A Weber, N Théret, and O Radulescu. Geometric analysis of pathways dynamics: application to versatility of tgf-beta receptors. *Biosystems*, 149:3–14, 2016.

[15] Eugenio Azpeitia, Stalin Muñoz, Daniel González-Tokman, Mariana Esther Martínez-Sánchez, Nathan Weinstein, **A. Naldi**, Elena R. Álvarez-Buylla, David A. Rosenblueth, and Luis Mendoza. The combination of the functionalities of feedback circuits is determinant for the attractors' number and size in pathway-like Boolean networks. *Scientific Reports*, 7:42023, 2017.

[16] **A. Naldi***, R M Larive*, U Czerwinska, S Urbach, P Montcourrier, C Roy, J Solassol, G Freiss, P J Coopman, and O Radulescu. Reconstruction and signal propagation analysis of the syk signaling network in breat cancer cells. *PLoS Computational Biology*, 13(3):e1005432, 2017.

[17] G Stoll, B Caron, E Viara, A Dugourd, A Zinovyev, **A. Naldi**, G Kroemer, E Barillot, and L Calzone. MaBoSS 2.0: an environment for stochastic Boolean modeling. *Bioinformatics*, 33(14):2226–2228, 2017.

[18] D V Klopfenstein, L Zhang, B S Pedersen, F Ramírez, A Warwick Vesztrocy, **A. Naldi**, C J Mungall, J M Yunes, O Botvinnik, M Weigel, W Dampier, C Dessimoz, P Flick, and H Tang. GOATOOLS: A Python library for Gene Ontology analyses. *Scientific Reports*, 8(1):10872, 2018.

[19] **A. Naldi**. BioLQM: A Java Toolkit for the Manipulation and Conversion of Logical Qualitative Models of Biological Networks. *Frontiers in Physiology*, 9:1605, 2018.

[20] **A. Naldi***, C Hernandez*, W Abou-Jaoudé*, P T Monteiro, C Chaouiya, and D Thieffry. Logical Modeling and Analysis of Cellular Regulatory Networks With GINsim 3.0. *Frontiers in Physiology*, 9:646, 2018.

[21] **A. Naldi***, C Hernandez*, N Levy*, G Stoll, P T Monteiro, C Chaouiya, T Helikar, A Zinovyev, L Calzone, S Cohen-Boulakia, D Thieffry, and L Paulevé. The CoLoMoTo Interactive Notebook: Accessible and Reproducible Computational Analyses for Qualitative Biological Networks. *Frontiers in Physiology*, 9:680, 2018.

[22] N Levy*, **A. Naldi***, C Hernandez*, G Stoll, D Thieffry, A Zinovyev, L Calzone, and L Paulevé. Prediction of Mutations to Control Pathways Enabling Tumor Cell Invasion with the CoLoMoTo Interactive Notebook (Tutorial). *Frontiers in Physiology*, 9:787, 2018.

[23] L Wigger*, C Casals-Casas*, M Baruchet, K B Trang, S Pradervand, **A. Naldi***, and B Desvergne*. System analysis of the functional cross-talk between PPARa, LXR and FXR in human HepaRG liver cells. *PLoS One*, 2019.

[24] M Buffard, **A. Naldi**, O Radulescu, P Coopman, R Larive, and G Freiss. Network Reconstruction and Significant Pathway Extraction Using Phosphoproteomic Data from Cancer Cells. *Proteomics*, 19:1800450, 2019.

[25] J Sánchez-Villanueva, O Rodríguez-Jorge, O Ramírez-Pliego, G Rosas Salgado, W Abou-Jaoudé, C Hernandez, **A. Naldi**, D Thieffry, and M Santana. Contribution of ROS and metabolic status to neonatal and adult CD8+ T cell activation. *PLoS One*, 14:e0226388, 2019.

[26] A Checcoli, J G. Pol, **A. Naldi**, V Noel, E Barillot, G Kroemer, D Thieffry, L Calzone, and G Stoll. Dynamical Boolean Modeling of Immunogenic Cell Death. *Frontiers in Physiology*, 11:590479, 2020.

[27] Mohamed Hamyeh, Florence Bernex, Romain M. Larive, **A. Naldi**, Serge Urbach, Joelle Simony-Lafontaine, Carole Puech, William Bakhache, Jérome Solassol, Peter J. Coopman, Wiljan J.A.J. Hendriks, and Gilles Freiss. PTPN13 induces cell junction stabilization and inhibits mammary tumor invasiveness. *Theranostics*, 10(3):1016–1032, 2020.

[28] S M Keating and the SBML Level 3 Community. SBML Level 3: an extensible format for the exchange and reuse of biological models. *Molecular Systems Biology*, 16(8):e9110, 2020.

[29] C Hernandez, M Thomas-Chollier, **A. Naldi**, and D Thieffry. Computational Verification of Large Logical Models - Application to the Prediction of T Cell Response to Checkpoint Inhibitors. *Frontiers in Physiology*, 11, 2020.

[30] S.S. Aghamiri, V. Singh, **A. Naldi**., T. Helikar, S. Soliman, and A. Niarakis. Automated inference of Boolean models from molecular interaction maps using CaSQ. *Bioinformatics*, 36(16), 2020.

[31] M Hamyeh, F Bernex, R M. Larive, **A. Naldi**, S Urbach, J Simony-Lafontaine, C Puech, W Bakhache, J Solassol, P J. Coopman, W J Hendriks, and G Freiss. PTPN13 induces cell junction stabilization and inhibits mammary tumor invasiveness. *Theranostics*, 10(3):1016–1032, 2020.

[32] L Cantini, P Zakeri, C Hernandez, **A. Naldi**, D Thieffry, E Remy, and A Baudot. Benchmarking joint multi-omics dimensionality reduction approaches for the study of cancer. *Nature Communications*, 12(1):1–12, 2021.

[33] A Niarakis, M Kuiper, M Ostaszewski, R S Malik Sheriff, C Casals-Casas, D Thieffry, T C Freeman, P Thomas, V Touré, V Noël, G Stoll, J Saez-Rodriguez, **A. Naldi**, E Oshurko, I Xenarios, S Soliman, C Chaouiya, T Helikar, and L Calzone. Setting the basis of best practices and standards for curation and annotation of logical models in biology - highlights of the BC2 2019 CoLoMoTo/SysMod Workshop. *Briefings in Bioinformatics*, 22(2):1848–1859, 2021.

[34] M Ostaszewski, A Niarakis, and the COVID-19 Disease Map Community. COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. *Molecular Systems Biology*, 17(10):e10387, 2021.

[35] K J Nuñez-Reza, **A. Naldi**, A Sánchez-Jiménez, A V Leon-Apodaca, M A Santana, M Thomas-Chollier, D Thieffry, and A Medina-Rivera. Logical modelling of in vitro differentiation of human monocytes into dendritic cells unravels novel transcriptional regulatory interactions. *Interface Focus*, 11(4), 2021.

[36] M Schiffrin, C Winkler, L Quignodon, **A. Naldi**, M Trötzmüller, H Köfeler, H Henry, P Parini, B Desvergne, and F Gilardi. Sex Dimorphism of Nonalcoholic Fatty Liver Disease (NAFLD) in Pparg-Null Mice. *International Journal of Molecular Sciences*, 22(18):9969, 2021.

[37] M Buffard, **A. Naldi**, G Freiss, M Deckert, O Radulescu, P J Coopman, and R M Larive. Comparison of SYK Signaling Networks Reveals the Potential Molecular Determinants of Its Tumor-Promoting and Suppressing Functions. *Biomolecules*, 11(2):308, 2021.

[38] K F Corral-Jara, C Chauvin, W Abou-Jaoudé, M Grandclaudon, **A. Naldi**, V Soumelis, and D Thieffry. Interplay between SMAD2 and STAT5A is a critical determinant of IL-17A/IL-17F differential expression. *Molecular Biomedicine*, 2(1):1–16, 2021.

[39] G Stoll, **A. Naldi**, V Noël, E Viara, E Barillot, G Kroemer, D Thieffry, and L Calzone. UPMaBoSS: a novel framework for dynamic cell population modeling. *Frontiers in Physiology*, (accepted).

Actes de conférences internationales

[40] **A. Naldi**, D Thieffry, and C Chaouiya. Decision diagrams for the representation and analysis of logical models of genetic networks. In *Computational Methods in Systems Biology*, volume 4695 of *Lecture Notes in Computer Science*, pages 233–247, 2007.

[41] **A. Naldi**, E Remy, D Thieffry, and C Chaouiya. A reduction of logical regulatory graphs preserving essential dynamical properties. In *Computational Methods in Systems Biology*, volume 5688 of *Lecture Notes in Computer Science*, pages 266–280, 2009.

[42] **A. Naldi**, P T Monteiro, and C Chaouiya. Efficient Handling of Large Signalling-Regulatory Networks by Focusing on Their Core Control. In *Computational Methods in Systems Biology*, Lecture Notes in Computer Science, pages 288–306, 2012.

[43] O Radulescu*, S Swarup Samal*, **A. Naldi**, D Grigoriev, and A Weber. Symbolic dynamics of biochemical pathways as finite states machines. In *Computational Methods in Systems Biology*, volume 9308 of *Lecture Notes in Computer Science*, pages 104–120, 2015.

[44] M Buffard, A Desoeuvres, **A. Naldi**, C Requilé, A Zinovyev, and O Radulescu. LNetReduce: Tool for Reducing Linear Dynamic Networks with Separated Timescales. 12881 LNBI:238–244, 2021.