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Born: December 5, 1973—Paris, France

Nationality: French

Current Position

Chargé de Recherche Hors Classe (CRHC), Inria Saclay-Île-de-France, EPI Lifeware

Research Interests

Constraint Programming • Model-Checking • Petri nets • Computational Systems Biology
• Structural analysis of ODE-based models.

Experience

- 2024-... Associate Editor for PLoS Computational Biology
- 2020-2024 Co-supervision (50%), with A. Niarakis, of Sahar Aghakhani’s Ph.D. on *Computational modeling of the metabolic reprogramming in Rheumatoid Arthritis synovial fibroblasts and cancer associated fibroblasts*.
- 2023-... President of the Scientific Commission of Inria Saclay (before that, member of said commission since 2017)
- 2020-2021 Giving TDs in the CSE102 course on “Computer Programming” for Polytechnique’s Bachelor program (first year)
- 2019-2020 Teaching INF473L MODAL on “Programming in the Language of Life” for Polytechnique 2nd year students.
- 2019-2021 Teaching CSE301 course on “Logic Programming” in Polytechnique’s Bachelor program (third year).
- 2018-2021 Co-supervision (50%), with F. Fages, of Éléonore Bellot’s Ph.D. on *Model Reduction based on Tropical Equilibration*.
- 2018-2021 Teaching INF555 course on “Constraint-based Modeling & Algorithms for Decision Making” in the AI and Advanced Visual Computing Master, and Polytechnique 3rd year.
- 2018 Supervision of Adrien Baudier for an École Centrale internship leading to a publication in the Journal of Theoretical Biology.

- 2017 Co-supervision (50%), with F. Fages, of Arthur Carcano for an ENS internship, leading to a presentation at the CMSB conference.
- 2010–2015 Co-supervision (50%), with F. Fages, of Steven Gay’s Ph.D. *Subgraph Epimorphisms: Theory and Application to Model Reductions in Systems Biology*
- 2009–2013 Co-supervision (50%), with F. Fages, of Faten Nabli’s Ph.D. *Investigating Petri nets structural properties for biochemical networks analysis*, and of many M.Sc. interns, notably from different IITs (India).
- 2009–2011 Co-supervision of Elisabetta De Maria’s PostDoc. She now has a permanent position at Nice’s University in Computational Systems Biology.
- 2009 Member of the AERES Evaluation Committee of the LIRMM laboratory (Montpellier, France) as Constraint Programming expert
- 2006–... Regular participation in the Program Committees of JFPC and WCB. Punctual participations for other conferences (e.g. CSCLP’07). Article reviewing for TCS, FLOPS, CMSB, PPDP, PLoS One, AMS Math Reviews, BMC Systems Biology, etc. Since 2019, member of the PC of CSBio and in 2019 Chair for the Life-Science track of CP.
- 2005–... Teaching the Constraint Programming course in the MPRI Masters program
- 2005–2008 Secretary of the ERCIM Working Group on Constraints.
- 2004–2006 Co-supervision of Laurence Calzone’s PostDoc. She now has a permanent position at Institut Curie in Systems Biology.
- 2003–... Co-developper of the modelling platform [BIOCHAM](#) and since 2010 of the [Nicotine](#) solver.
- 2003–2004 Teaching assistant for Java at École Polytechnique
- 2001–2002 Ingénieur de l’Armement at DGA’s *Géographie, Imagerie, Perception* lab in Arcueil, France. Responsible for IT Systems’ Security.

Honors & Awards

- 2024–2028 Scientific Excellence award from Inria
- 2014 Co-author with Pauline Traynard of the Best Student Paper Award article at CMSB’14
- 2011–2015 Scientific Excellence award from Inria
- 2007 Selected to be among the six young researchers representing “Advances in Information Sciences”, for a talk at French Academy of Sciences on the use of formal methods of computer science for Systems Biology.
- 2002 Best Graphical Interface Concept award from the UIST Conference, with F.Fages

Education

- 2016 Habilitation à Diriger des Recherches, University Paris Sud *A structural perspective on the dynamics of biochemical systems*
- 1999–2001 Ph.D. in Computer Science, University Paris Diderot. *Programmation concurrente avec contraintes et logique linéaire*, under the supervision of F. Fages.
- 1996–1997 M.Sc. in Computer Science, University Paris Diderot.
- 1993–1996 École Polytechnique.

Publications in the last 5 years

ARTICLES IN PEER-REVIEWED JOURNALS

- [1] Sahar Aghakhani, Anna Niarakis, and Sylvain Soliman. “MetaLo: metabolic analysis of Logical models extracted from molecular interaction maps”. In: *Journal of Integrative Bioinformatics* 21.1 (Feb. 2024), p. 20230048. DOI: [10.1515/jib-2023-0048](https://doi.org/10.1515/jib-2023-0048). URL: <https://hal.science/hal-04439008>.
- [2] Anna Niarakis et al. “Drug-target identification in COVID-19 disease mechanisms using computational systems biology approaches”. In: *Frontiers in Immunology* 14 (Feb. 2024). DOI: [10.3389/fimmu.2023.1282859](https://doi.org/10.3389/fimmu.2023.1282859). URL: <https://hal.science/hal-04454379>.
- [3] Sahar Aghakhani, Sacha E Silva-Saffar, Sylvain Soliman, and Anna Niarakis. “Hybrid computational modeling highlights reverse warburg effect in breast cancer-associated fibroblasts”. In: *Computational and Structural Biotechnology Journal* 21 (Aug. 2023), pp. 4196–4206. DOI: [10.1016/j.csbj.2023.08.015](https://doi.org/10.1016/j.csbj.2023.08.015). URL: <https://hal.science/hal-04192259>.
- [4] Vidisha Singh, Aurélien Naldi, Sylvain Soliman, and Anna Niarakis. “A large-scale Boolean model of the rheumatoid arthritis fibroblast-like synoviocytes predicts drug synergies in the arthritic joint”. In: *npj Systems Biology and Applications* 9.33 (July 2023). DOI: [10.1038/s41540-023-00294-5](https://doi.org/10.1038/s41540-023-00294-5). URL: <https://hal.science/hal-04187223>.
- [5] Van-Giang Trinh, Belaid Benhamou, and Sylvain Soliman. “Trap spaces of Boolean networks are conflict-free siphons of their Petri net encoding”. In: *Theoretical Computer Science* 971 (Sept. 2023), p. 114073. DOI: [10.1016/j.tcs.2023.114073](https://doi.org/10.1016/j.tcs.2023.114073). URL: <https://amu.hal.science/hal-04167028>.
- [6] Sahar Aghakhani, Sylvain Soliman, and Anna Niarakis. “Metabolic Reprogramming in Rheumatoid Arthritis Synovial Fibroblasts: a Hybrid Modeling Approach”. In: *PLoS Computational Biology* 18.12 (Dec. 2022), e1010408. DOI: [10.1371/journal.pcbi.1010408](https://doi.org/10.1371/journal.pcbi.1010408). URL: <https://hal.science/hal-03880870>.
- [7] Anna Niarakis et al. “Addressing barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology”. In: *Briefings in Bioinformatics* 23.4 (June 2022), pp. 1–11. DOI: [10.1093/bib/bbac212](https://doi.org/10.1093/bib/bbac212). URL: <https://hal.science/hal-03690604>.
- [8] Julien Martinelli et al. “Model learning to identify systemic regulators of the peripheral circadian clock”. In: *Bioinformatics* 37.Supplement 1 (July 2021), p. 9. DOI: [10.1093/bioinformatics/btab297](https://doi.org/10.1093/bioinformatics/btab297). URL: <https://hal.science/hal-03183579>.
- [9] Anna Niarakis et al. “Setting the basis of best practices and standards for curation and annotation of logical models in biology—highlights of the [BC]2 2019 CoLo-MoTo/SysMod Workshop”. In: *Briefings in Bioinformatics* 22.2 (2021), pp. 1848–1859. DOI: [10.1093/bib/bbaa046](https://doi.org/10.1093/bib/bbaa046). URL: <https://hal.science/hal-02549796>.

- [10] Marek Ostaszewski et al. “COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms”. In: *Molecular Systems Biology* 17.10 (Oct. 2021), e10387. DOI: [10.15252/msb.202110387](https://doi.org/10.15252/msb.202110387). URL: <https://hal.science/hal-03385317>.
- [11] Sara Sadat Aghamiri et al. “Automated inference of Boolean models from molecular interaction maps using CaSQ”. In: *Bioinformatics* 36.16 (May 2020), pp. 4473–4482. DOI: [10.1093/bioinformatics/btaa484](https://doi.org/10.1093/bioinformatics/btaa484). URL: <https://hal.science/hal-02590714>.
- [12] Sarah Keating et al. “SBML Level 3: an extensible format for the exchange and reuse of biological models”. In: *Molecular Systems Biology* 16.8 (Aug. 2020), pp. 1–21. DOI: [10.15252/msb.20199110](https://doi.org/10.15252/msb.20199110). URL: <https://hal.science/hal-02924909>.

PEER-REVIEWED CONFERENCE PROCEEDINGS

- [13] François Fages, Mathieu Hemery, and Sylvain Soliman. “On BIOCHAM Symbolic Computation Pipeline for Compiling Mathematical Functions into Biochemistry”. In: *ISSAC 2024 - 49th International Symposium on Symbolic and Algebraic Computation*. Raleigh, NC, United States, July 2024. URL: <https://hal.science/hal-04602764>.
- [14] Giang Trinh, Belaid Benhamou, Samuel Pastva, and Sylvain Soliman. “Scalable Enumeration of Trap Spaces in Boolean Networks via Answer Set Programming”. In: *AAAI 2024 - The 38th Annual Conference on Artificial Intelligence*. Vol. 38. 9. Vancouver, Canada, Feb. 2024, pp. 10714–10722. DOI: [10.1609/aaai.v38i9.28943](https://doi.org/10.1609/aaai.v38i9.28943). URL: <https://amu.hal.science/hal-04523118>.
- [15] Van-Giang Trinh, Belaid Benhamou, Sylvain Soliman, and François Fages. “Graphical conditions for the existence, unicity and number of regular models”. In: *ICLP 2024 - 40th International Conference on Logic Programming*. Dallas, United States, Oct. 2024. URL: <https://amu.hal.science/hal-04708861>.
- [16] Van-Giang Trinh, Belaid Benhamou, and Sylvain Soliman. “Efficient Enumeration of Fixed Points in Complex Boolean Networks Using Answer Set Programming”. In: *29th International Conference on Principles and Practice of Constraint Programming (CP 2023)*. Ed. by Roland H. C. Yap. Vol. 280. Toronto, Canada: Schloss Dagstuhl - Leibniz-Zentrum für Informatik, Aug. 2023, 35:1–35:19. DOI: [10.4230/LIPIcs.CP.2023.35](https://doi.org/10.4230/LIPIcs.CP.2023.35). URL: <https://amu.hal.science/hal-04209296>.
- [17] Van-Giang Trinh, Belaid Benhamou, Kunihiro Hiraishi, and Sylvain Soliman. “Minimal trap spaces of Logical models are maximal siphons of their Petri net encoding”. In: *CMSB 2022 - International Conference on Computational Methods in Systems Biology*. Ed. by Ion Petre and Andrei Păun. Vol. 13447. Lecture Notes in Computer Science. Bucarest, Romania: Springer, Sept. 2022, pp. 158–176. DOI: [10.1007/978-3-031-15034-0_8](https://doi.org/10.1007/978-3-031-15034-0_8). URL: <https://hal.science/hal-03721508>.

- [18] Mathieu Hemery, François Fages, and Sylvain Soliman. “A Polynomialization Algorithm for Elementary Functions and ODEs, and their Compilation into Chemical Reaction Networks”. In: *CASC’21 - Computer Algebra in Scientific Computing*. Sochi, Russia, Sept. 2021. URL: <https://hal.science/hal-03271828>.
- [19] Mathieu Hemery, François Fages, and Sylvain Soliman. “Compiling Elementary Mathematical Functions into Finite Chemical Reaction Networks via a Polynomialization Algorithm for ODEs”. In: *CMSB 2021 - 19th International Conference on Computational Methods in Systems Biology*. Bordeaux, France, Sept. 2021. URL: <https://hal.science/hal-03220725>.
- [20] Elisabeth Degrand, François Fages, and Sylvain Soliman. “Graphical Conditions for Rate Independence in Chemical Reaction Networks”. In: *CMSB 2020 - 18th International Conference on Computational Methods in Systems Biology*. Konstanz / Online, Germany, Sept. 2020. URL: <https://hal.science/hal-02900758>.
- [21] Mathieu Hemery, François Fages, and Sylvain Soliman. “On the Complexity of Quadraticization for Polynomial Differential Equations”. In: *CMSB 2020 - 18th International Conference on Computational Methods in Systems Biology*. Konstanz / Online, Germany, Sept. 2020. URL: <https://hal.science/hal-02900798>.
- [22] Julien Martinelli, Jeremy Grignard, Sylvain Soliman, and François Fages. “A Statistical Unsupervised Learning Algorithm for Inferring Reaction Networks from Time Series Data”. In: *ICML 2019 - Workshop on Computational Biology*. Long Beach, CA, United States, June 2019. URL: <https://hal.science/hal-02163862>.
- [23] Julien Martinelli, Jeremy Grignard, Sylvain Soliman, and François Fages. “On Inferring Reactions from Data Time Series by a Statistical Learning Greedy Heuristics”. In: *CMSB 2019 - 17th Computational Methods in Systems Biology*. Ed. by Luca Bortolussi and Guido Sanguinetti. LNCS 11773. Trieste, Italy: Springer-Verlag, Sept. 2019. URL: <https://hal.science/hal-02173721>.

OTHER REFERENCES

- [24] Christoph Lüders, Eléonore Bellot, François Fages, Ovidiu Radulescu, and Sylvain Soliman. *Symbolic Methods for Biological Networks D2.1 Report on Scalable Methods for Tropical Solutions (T1.2)*. Research Report. Inria Saclay, Apr. 2022. URL: <https://hal.science/hal-03648027>.