Noël MALOD-DOGNIN: Detailed Curriculum Vitæ

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Citizenship: French

Positions

- Since 2025: **Established Researcher** at Mohamed bin Zayed University of Artificial Intelligence, United Arab Emirates, on the modelling, integration and analysis of large medical and biological networks using XAI for precision medicine.
- Since 2025: **Visiting Research Scientist** at Barcelona Supercomputing Center, Spain, on the modelling, integration and analysis of large medical and biological networks using XAI for precision medicine.
- 2019 to 2025: **Established Researcher** at Barcelona Supercomputing Center, Spain, on the modelling, integration and analysis of large medical and biological networks using XAI for precision medicine.
- 2019 to 2022: **Honorary Senior Research Associate** at University College London, UK, on the modelling, integration and analysis of large medical and biological networks using XAI for precision medicine.
- 2016 to 2018: **Research Fellow** at University College London, UK, on the modelling, integration and analysis of large networks from systems biology and economy.
- 2012 to 2016: **Research Associate, then Research Fellow** at Imperial College London, UK, on the modelling and algorithmic aspects of the analysis of large networks from systems biology and economy.
- 2010 to 2012: **Research Associate** at Inria Sophia Antipolis, France, on the modelling and algorithmic aspects of the protein complex analysis.
- 2006 to 2010: **Ph.D. student** at Inria Rennes, France, on the modelling and algorithmic aspects of the protein structure comparison.

Education

- **Ph.D. in Computer Science** with high Honours, from Rennes 1 University, France, 2010.
  Title: *Protein Structure Comparison: From Contact Map Overlap Maximisation to Distance-based Alignment Search Tool*
  Jury: Pr. D. Lavenier (President), Dr. F. Cazals (Referee), Dr. G.W. Klau (Referee), Dr. J-F. Gibrat (examiner), Dr. M. Molnár (Examiner), Pr. R. Andonov (Advisor).
- **M.Sc. in Computer Science**, Claude Bernard Lyon 1 University, France, 2006.
- **B.Sc. in Computer Science**, Claude Bernard Lyon 1 University, France, 2004.

Publications

I published 44 articles in peer-reviewed journals including high impact factor journals such as Science (IF ≈ 44.7) and Nature Communications (IF ≈ 14.7), and 13 articles in peer-reviewed conferences including in the two main conferences in my field, namely "Intelligent Systems for Molecular Biology" (ISMB) and "European Conference on Computational Biology" (ECCB).

My work is highly cited; according to Google Scholar (accessed in August, 2025), my publications have been cited 3,468 times, with h-index of 22 and i10 index of 33.

Peer-reviewed journals (44)

J-44 Z. Li, S.F.L. Windels, **N. Malod-Dognin**, S.M. Weinberg, M.L. Marazita, S. Walsh, M.D. Shriver, D.W. Fardo, P. Claes, N. Pržulj and K. Van Steen; "Clustering individuals using INMTD: a novel versatile multi-view embedding framework integrating omics and imaging data". *Bioinformatics* btaf122, 2025.

J-43 N. Pržulj and **N. Malod-Dognin**; "Simplicity within biological complexity". *Bioinformatics Advances* 5(1): vbae164, 2025.

J-42 D. Tello Velasco, S.F.L. Windels, M. Rotkevich, **N. Malod-Dognin** and N. Pržulj; "Graphlet-based hyperbolic embeddings capture evolutionary dynamics in genetic network". *Bioinformatics* 40(11): btae650, 2024.

J-41 K. Mihajlović, **N. Malod-Dognin**, C. Ameli, A. Skupin and N. Pržulj; "MONFIT: Multi-omics factorization-based integration of time-series data sheds light on Parkinson's disease". *NAR Molecular Medicine*, ugae012, 2024.

J-40 S. Doria-Belenguer, A. Xenos, G. Ceddia, **N. Malod-Dognin** and N. Pržulj; "The axes of biology: a novel axes-based network embedding paradigm to decipher the functional mechanisms of the cell". *Bioinformatics Advances* 4(1): vbae075, 2024.

J-39 K. Mihajlović, G. Ceddia, **N. Malod-Dognin**, G. Novak, D. Kyriakis, A. Skupin and N. Pržulj; "Multi-omics integration of scRNA-seq time series data predicts new intervention points for Parkinson's disease". *Scientific Reports* 14: 10983, 2024.

J-38 A. Maier, M. Hartung, K. Adamowicz, G.D. Bader, D.B. Blumenthal, J. Chen, M.L. Elkjaer, C.J.G. Hernandez, I. Jurisica, M. Kotlyar, O. Lazareva, H. Levi, M. List, S. Lobentanzer, J. Loscalzo, **N. Malod-Dognin**, Q. Manz, J. Matschinske, M. Oubounyt, A.R. Pico, R.T. Pilllich, D. Pratt, N. Pržulj, S. Sadegh, J. Saez-Rodriguez, S. Sakar, R. Shamir, U. Turhan, R. Wang, O. Zolotareva and J. Baumbach; "Drugst.One - A plug-and-play solution for online systems medicine and network-based drug repurposing". *Nucleic Acids Research*: gkae388, 2024.

J-37 V. Gureghian, H. Herbst, I. Kozar, K. Mihajlovic, **N. Malod-Dognin**, G. Ceddia, C. Angeli, C. Margue, T. Randic, D. Philippidou, M. Tetsi Nomigni, A. Hemedan, L.-C. Tranchevent, J. Longworth, M. Bauer, A. Badkas, A. Gaigneaux, A. Muller, M. Ostaszewski, F. Tolle, N. Pržulj and S. Kreis; "A multi-omics integrative approach unravels novel genes and pathways associated with senescence escape after targeted therapy in NRAS mutant melanoma". *Cancer Gene Therapy*, DOI:10.1038/s41417-023-00640-z, 2023.

J-36 **N. Malod-Dognin**, G. Ceddia, M. Gvozdenov, B. Tomic, S. Dunjic Manevski, V. Djordjevic and N. Pržul; "A phenotype driven integrative framework uncovers molecular mechanisms of a rare hereditary thrombophilia". *PLoS ONE* 18(4): e0284084, 2023.

J-35 S. Doria-Belenguer, A. Xenos, G. Ceddia, **N. Malod-Dognin** and N. Pržul; "A functional analysis of omic network embedding spaces reveals key altered functions in cancer". *Bioinformatics*, btad281, 2023.

J-34 A. Xenos, **N. Malod-Dognin**, C. Zambrana and N. Pržul; "Integrated Data Analysis Uncovers New COVID-19 Related Genes and Potential Drug Re-Purposing Candidates". *International Journal of Molecular Sciences* 24(2): 1431, 2023.

J-33 S.F.L. Windels, **N. Malod-Dognin**, and N. Pržulj; "Identifying cellular cancer mechanisms through pathway-driven data integration". *Bioinformatics* btac493, 2022.

J-32 M.P. Cifuentes, C. Mercedes Suarez, R. Cifuentes, N.J. Doogan, **N. Malod-Dognin**, S.F.L. Windels, J. Valderrama, P.D. Juarez, C. Colen, R. Burciaga Valdez, C. Phillips, A. Ramesh, W. Im, M.Y. Lichtveld, C. Mouton, N. Pržulj, D.B. Hood; "Big Data to Knowledge Analytics reveals the Zika virus epidemic as only one of multiple factors contributing to year-over-year 28-fold increase in microcephaly incidence", *International Journal of Environmental Research and Public Health*, 1731959, 2022.

J-31 S.F.L. Windels, **N. Malod-Dognin**, and N. Pržulj; "Graphlet eigencentralities capture novel central roles of genes in pathways", *PLoS ONE*, to appear, 2022.

J-30 C. Zambrana, A. Xenos, R. Böttcher, **N. Malod-Dognin**, and N. Pržulj; "Network neighbors of viral targets and differentially expressed genes in COVID-19 are drug target candidates", *Scientific Reports* 11, 18985, 2021.

J-29 A. Xenos, **N. Malod-Dognin**, S. Milinkovic, and N. Pržulj; “Linear functional organization of the omic embedding space”, *Bioinformatics* 37(21): 3839–3847, 2021.

J-28 T. Gaudelet, **N. Malod-Dognin**, and N. Pržulj; “Integrative Data Analytic Framework to Enhance Cancer Precision Medicine”, *Network and Systems Medicine* 4(1): 60-73, 2021.

J-27 S. Doria-Belenguer, M.K. Youssef, R. Böttcher, **N. Malod-Dognin**, and N. Pržulj; “Probabilistic Graphlets Capture Biological Function in Probabilistic Molecular Networks”, *Bioinformatics* 36: Issue Supplement 2, i804–i812, 2020. Also Conference paper C13.

J-26 J. Lugo-Martinez, D. Zeiberg, T. Gaudelet, **N. Malod-Dognin**, N. Pržulj and P. Radivojac; “Classification in biological networks with hypergraphlet kernels”, *Bioinformatics* 37(7): 1000–1007, 2020.

J-25 **N. Malod-Dognin**, V. Pancaldi, A. Valencia, and N. Pržulj; “Chromatin network markers of leukemia”, *Bioinformatics* 36: Issue Supplement 1, i455–i463, 2020. Also Conference paper C12.

J-24 T. Gaudelet, **N. Malod-Dognin**, J. Sanchez-Valle, V. Pancaldi, A. Valencia, and N. Pržulj; “Unveiling new disease, pathway, and gene associations via multi-scale neural networks”, *PLoS ONE* 15(4): e0231059, 2020.

J-23 H. Hemingway et al.; “A national initiative in data science for health: an evaluation of the UK Farr Institute”, *International journal of population data science* 5(1), 2020.

J-22 N. Perin, V. Rep, I. Sović, Š. Juričić, D. Selgrad, M. Klobučar; N. Pržulj, C.L. Gupta, **N. Malod-Dognin**, S.K. Pavelić, M. Hranjec; “Antiproliferative activity and mode of action analysis of novel amino and amido substituted phenantrene and naphtho[2,1-b]thiophene derivatives”, *European Journal of Medicinal Chemistry* 185: 111833, 2020.

J-21 S.F.L. Windels, **N. Malod-Dognin**, and N. Pržulj; “Graphlet Laplacians for topology-function and topology-disease relationships”, *Bioinformatics* 35(24): 5226–5234, 2019.

J-20 **N. Malod-Dognin**, J. Petschnigg, S.F.L. Windels, J. Povh, H. Hemingway, R. Ketteler, and N. Pržulj; “Towards a data-integrated cell”, *Nature Communications* 10: 805, 2019.

J-19 **N. Malod-Dognin** and N. Pržulj; “Functional geometry of protein-protein interaction networks”. *Bioinformatics* 35(19): 3727-3734, 2019.

J-18 T. Gaudelet, **N. Malod-Dognin** and N. Pržulj; “Higher order molecular organisation as a source of biological function”, *Bioinformatics* 34(17): i944-i953, 2018. Also conference C11.

J-17 **N. Malod-Dognin**, J. Petschnigg and N. Pržulj; “Precision medicine - a promising, yet challenging road lies ahead”, *Current Opinion in Systems Biology* 7:1-7, 2018.

J-16 **N. Malod-Dognin** and N. Pržulj; “Omics data complementarity underlines functional cross-communication in yeast”, *Journal of Integrative Bioinformatics* 14(2), 2017. Also Conference paper C10.

J-15 **N. Malod-Dognin**, K. Ban and N. Pržulj; “Unified Alignment of Protein-Protein Interaction Networks”, *Scientific Reports* 7:953, 2017.

J-14 O.N. Yaveroğlu, **N. Malod-Dognin**, T. Milenković and N. Pržulj; “Rebuttal to the Letter to the Editor in response to the paper: Proper evaluation of alignment-free network comparison methods”, *Bioinformatics* 33(7):1107-1109, 2017.

J-13 A. Sarajlić, **N. Malod-Dognin**, O.N. Yaveroğlu and N. Pržulj; “Graphlet-based Characterization of Directed Networks”, *Scientific Reports* 6:35098, 2016.

J-12 M. Costanzo, B. VanderSluis, E. N. Koch, A. Baryshnikova, C. Pons, G. Tan, W. Wang, M. Usaj, J. Hanchard, S. D. Lee, V. Pelechano, E. B. Styles, M. Billmann, J. van Leeuwen, N. van Dyk, Z.-Y. Lin, E. Kuzmin, J. Nelson, J. S. Piotrowski, T. Srikumar, S. Bahr, Y. Chen, R. Deshpande, C. F. Kurat, S. C. Li, Z. Li, M. M. Usaj, H. Okada, N. Pascoe, B.-J. San Luis, S. Sharifpoor, E. Shuteriqi, S. W. Simpkins, J. Snider, H. G. Suresh, Y. Tan, H. Zhu, **N. Malod-Dognin**, V. Janjic, N. Pržulj, O. G. Troyanskaya, I. Stagljar, T. Xia, Y. Ohya, A.-C. Gingras, B. Raught, M. Boutros, L. M. Steinmetz, C. L. Moore, A. P. Rosebrock, A. A. Caudy, C. L. Myers, B. Andrews and C. Boone; “A global genetic interaction network maps a wiring diagram of cellular function”, *Science* 353(6306):aaf1420, 2016.

J-11 N. Pržulj and **N. Malod-Dognin**; “Network Analytics in the age of Big Data”, *Science* 353(6295):aah3449, 2016.

J-10 V. Gligorijevic, **N. Malod-Dognin**, and N. Przulj; “Integrative Methods for Analysing Big Data in Precision Medicine”, *Proteomics*16(15):741-758, 2016.

J-9 V. Gligorijevic, **N. Malod-Dognin**, and N. Przulj; “FUSE: Multiple Network Alignment via Data Fusion”, *Bioinformatics* 32(8):1195-1203, 2016.

J-8 **N. Malod-Dognin** and N. Przulj; “L-GRAAL: Lagrangian Graphlet-based Network Aligner”, *Bioinformatics* 31(13):2182-2189, 2015.

J-7 D. Davis, O.N. Yaveroglu, **N. Malod-Dognin**, A. Stojmirovic, and N. Przulj; “Topology-Function Conservation in Protein-Protein Interaction Networks”, *Bioinformatics*31(10):1632-1639, 2015.

J-6 O.N. Yaveroglu, **N. Malod-Dognin**, D.Davis, V. Janjick, Z. Levnajic, R. Karapandza, A. Stojmirovic, and N. Przulj; “Revealing the Hidden Language of Complex Network”, *Scientific Reports*4:4547, 2014.

J-5 **N. Malod-Dognin** and N. Przulj; “GR-Align: Fast and Flexible Alignment of Protein 3D Structures Using Graphlet Degree Similarity”; *Bioinformatics* 30(9):1259-1265, 2014.

J-4 **N. Malod-Dognin**, A. Bansal and F. Cazals; “Characterizing the Morphology of Protein Binding Patches”; *Proteins: structure, function, and bioinformatics* 80(12):2652-2665, 2012.

J-3 I. Wohlers, **N. Malod-Dognin**, R. Andonov, G.W. Klau; “CSA: Comprehensive comparison of pairwise structural protein alignments”; *Nucleic Acids Research* 40(W1):W303-W309, 2012.

J-2 R. Andonov, **N. Malod-Dognin** and N. Yanev; “Maximum Contact Map Overlap Revisited”; *Journal of Computational Biology* 18(1):27-41, 2011.

J-1 **N. Malod-Dognin**, R. Andonov and N. Yanev; “Solving Maximum Clique Problem for Protein Structure Similarity”; *Serdica Journal of Computing* 4(1):93-100, 2010.

Peer-reviewed conference articles (13)

C-13 S. Doria-Belenguer, M.K. Youssef, R. Böttcher, **N. Malod-Dognin** and N. Pržulj; “Probabilistic Graphlets Capture Biological Function in Probabilistic Molecular Networks”, *European Conference on Computational Biology* (ECCB), 2020.

C-12 **N. Malod-Dognin**, V. Pancaldi, A. Valencia and N. Pržulj; “Chromatin network markers of leukemia”, *Intelligent Systems for Molecular Biology* (ISMB), 2020. Also journal publication J24.

C-11 T. Gaudelet, **N. Malod-Dognin** and N. Pržulj; “Higher order molecular organisation as a source of biological function”, *European Conference on Computational Biology* (ECCB), 2018. Also journal publication J18.

C-10 **N. Malod-Dognin** and N. Pržulj; “Omics data complementarity underlines functional cross-communication in yeast”, *Proceedings of the International Symposium on Integrative Bioinformatics*, 2017. Also journal publication J16.

C-9 V. Gligorijevic, **N. Malod-Dognin** and N. Przulj; “Patient-Specific Data Fusion for Cancer Stratification and Personalized Treatment”; *Pacific Symposium on Biocomputing* (PSB), Big Island, Hawaii, January 4-8, 2016.

C-8 I. Wohlers, **N. Malod-Dognin**, R. Andonov, G.W. Klau; “CSA : Comparaison compréhensible d’alignement de paires de structures de protéines”; *Proceedings of JOBIM*, p.201-208, 2012 (in french).

C-7 F. Cazals and **N. Malod-Dognin**; “Shape Matching by Localized Calculations of Quasi-isometric Subsets, with Applications to the Comparison of Protein Binding Patches”; Pattern Recognition in Bioinformatics, Lecture Notes in Computer Science, vol. 7036, p. 272-283, 2011.

C-6 **N. Malod-Dognin**, M. Le Boudic-Jamin, P. Kamath, and R. Andonov; “Using Dominances for Solving the Protein Family Identification Problem”; Algorithms in Bioinformatics, Lecture Notes in Computer Science, vol. 6833, p. 201-212, 2011.

C-5 M. Le Boudic-Jamin, **N. Malod-Dognin**, A. Cornu, J. Nicolas and R. Andonov; "Identification rapide de familles protéiques par dominance"; *Proceedings of ROADEF*, vol. 2, p.791-792, 2011 (in french).

C-4 "SHREC-10 Track: Protein Model Classification"; L. Mavridis, V. Venkatraman, D. W. Ritchie, N. Morikawa, R. Andonov, A. Cornu, **N. Malod-Dognin**, J. Nicolas, M. Temerinac-Ott, M. Reisert, H. Burkhardt, A. Axenopoulos and P. Daras; Eurographics Workshop on 3D Object Retrieval (3DOR), p. 117-124, 2010.

C-3 **N. Malod-Dognin**, R. Andonov and N. Yanev; "Maximum Clique in Protein Structure Comparison"; Experimental Algorithms, Lecture Notes in Computer Science, vol. 6049, p.106-117, 2010.

C-2 R. Andonov, N. Yanev and **N. Malod-Dognin**; "An Efficient Lagrangian Relaxation for the Contact Map Overlap Problem"; Algorithms in Bioinformatics, Lecture Notes in Computer Science, vol. 5251, p. 162-173, 2008.

C-1 **N. Malod-Dognin**, R. Andonov, N. Yanev and J-F. Gibrat; "Modèle de PLNE pour la recherche de cliques de poids maximal"; *Proceedings of ROADEF*, p. 307-308, 25/02/2008 (in french).

Book Chapters (2)

B-02 *N. Malod-Dognin*, S. Windels and N. Pržulj, "Machine Learning for Data Integration in Cancer Precision Medicine: Matrix Factorization Approaches", *Analyzing Network Data in Biology and Medicine*, Cambridge University Press, forthcoming, 2019.

B-01 *N. Malod-Dognin*, S. Windels and N. Pržulj, "Network Alignment", *Analyzing Network Data in Biology and Medicine*, Cambridge University Press, forthcoming, 2019.

Invited and selected talks (18)

T-18 S. Doria-Belenguer, A. Xenos, G. Ceddia, **N. Malod-Dognin** and N. Pržulj ; "The axes of biology: a novel axes-based network embedding approach to decipher the fundamental mechanisms of the cell", ISMB-ECCB, Lyon, France, July 23-27, 2023.

T-17 **N. Malod-Dognin**, A. Xenos, S. Doria Belenguer and N. Pržulj; "Exploiting the linear organization of omics network embedding spaces", The Belgrade Bioinformatics Conference (BelBi2023), Belgrade, Serbia, June 19-23, 2023.

T-16 **N. Malod-Dognin**, J. Petschnigg, S.F.L. Windels, J. Povh, H. Hemingway, R. Ketteler, and N. Pržulj; "Towards a data-integrated cell", UCAncer Symposium, Sophia Antipolis, France, October 25-26, 2021.

T-15 **N. Malod-Dognin**, J. Petschnigg, S.F.L. Windels, J. Povh, H. Hemingway, R. Ketteler, and N. Pržulj; "Towards a data-integrated cell", ISMB-ECCB, Basel, Switzerland, July 21-25, 2019.

T-14 T. Gaudelet, **N. Malod-Dognin**, and N. Pržulj; "Higher order molecular organisation as a source of biological function", ECCB, Athens, Greece, September 8-12, 2018.

T-13 **N. Malod-Dognin**; "Towards higher-order modelling and integration of biological data for precision medicine", 2nd Workshop on Biomedical data fusion and non-negative matrix factorization, Ljubljana, Slovenia, May 23-25, 2018.

T-12 **N. Malod-Dognin**, T. Gaudelet, S. Windels and N. Przulj; "Towards higher-order modelling and integration of biological data for precision medicine", European Conference on Translational Bioinformatics, Barcelona, Spain, April 16-17, 2018.

T-11 V. Gligorijevic, **N. Malod-Dognin** and N. Przulj; "Data-Fusion for Cancer Patient Stratification and Personalised Treatment", International Conference on Complex Networks and Their Applications, Lyon, France, November 29 - December 01, 2017.

T-10 T. Gaudelet, **N. Malod-Dognin**, J. Lugo-Martinez, P. Radivojac and N. Pržulj; "Hypergraphlets Give Insight into Multi-Scale Organisation of Molecular Networks", International Conference on Complex Networks and Their Applications, Lyon, France, November 29 - December 01, 2017.

T-9 V. Gligorijevic, **N. Malod-Dognin** and N. Przulj; "Patient Specific Network Data Integration Enables Precision Medicine in Cancer", Belgrade Bioinformatics Conference, Belgrade, Serbia, 20-24 June 2016.

T-8 **N. Malod-Dognin**; "Network data integration enables precision medicine in cancer", ECCB, Workshop 7, The Hague, Netherlands, September 3, 2016.

T-7 V. Gligorijevic, **N. Malod-Dognin** and N. Przulj; "Network Data Integration Enables Precision Medicine", Summer School: Genomic Medicine, Portoroz, Slovenia, 3-7 May 2016.

T-6 D. Davis, O.N. Yaveroglu, **N. Malod-Dognin**, A Stojmirovic and N Przulj ; "Topology-Function Conservation in Protein-Protein Interaction Networks"; NetSci (International School and Conference on Network Science), Zaragoza, Spain, 1-5 June 2015.

T-5 O. N. Yaveroglu, **N. Malod-Dognin**, D. Davis, Z. Levnajic, V. Janjic, R. Karapandza, A. Stojmirovic, and N. Przulj; "Revealing the Hidden Language of Complex Networks"; NetSci (International School and Conference on Network Science), Berkeley, California, USA, June 2-6, 2014.

T-4 **N. Malod-Dognin** and N. Przulj; "GrAlign: Fast Flexible Alignment of Protein 3D Structures", ISMB - 3DSig, Berlin, Germany, July 19-20, 2013.

T-3 D. Agarwal, **N. Malod-Dognin**, and F. Cazals; "Stoichiometry Determination for Mass-spectrometry Data in Structural Proteomics"; SFBBM-SFB congress, Grenoble, France, November 21-23, 2012.

T-2 **N. Malod-Dognin**, R. Andonov and N. Yanev; "Maximum clique approach to protein structure similarity"; MASSEE International congress on mathematics, Ohrid, Macedonia, September 16-20, 2009.

T-1 **N. Malod-Dognin**, R. Andonov and N. Yanev; "Maximum clique and similarity measures"; MMSC'09 International Workshop on Mathematical modelling and scientific computations, Velingrad, Bulgaria, September 23-26, 2009.

Peer-reviewed posters (30)

Academic Service

Conference program committee / reviewer

- Since 2020, I am a member of the organizing committee for the Network Biology (NetBio) community of special interest at the Intelligent Systems for Molecular Biology (ISMB) conference (chairing NetBio sessions at ISMB conferences; reviewing papers, talks and posters...)
- Since 2017, I'm a reviewer for the Complex Network conference
- Since 2015, I'm a reviewer for the Intelligent Systems for Molecular Biology (ISMB) conference
- Since 2015, I'm a reviewer for the European Conference on Computational Biology (ECCB) conference
- ...

Journal reviewer

- Nature Publishing Group: "Nature Communications", "Scientific Reports"
- Oxford University Press: "Bioinformatics"
- Public Library of Science:"PLOS ONE"
- BioMed Central: "BMC Bioinformatics"
- ...

Teaching

- From 2013 to 2016, I participated each year in the “Introduction to Bioinformatics” courses at Imperial College London, for 3^{rd} and 4^{th} year students. Each year, I gave a two hours lecture on algorithms for protein structures, and one hour of tutorial helping. I was also involved in preparing and marking the corresponding coursework.
- In 2012, was a lecturer at the winter school on “Algorithms in Structural Bio-informatics”, that was organized by Frédéric Cazals (ABS, INRIA Sophia Antipolis - Méditerranée) and Juan Cortés (LAAS, CNRS Toulouse). I gave 1 hour of lecture and 3 hours of tutorial helping to starting Ph.D. students. The outline of the winter school is accessible at `http://www-sop.inria.fr/manifestations/algoSB/`.
- From 2008 to 2010, I participated to the “Operation research” courses at the University of Rennes 1 (IFSIC), in France. I gave a total of 36 hours of tutorial helping for first year Master students in computer sciences and in business informatics.
- From 2008 to 2009, I participated to the “Introduction to algorithmic and programming in Python” courses at the ENSAI engineering school, in Ker Lann, France. I gave a total of 20 hours of tutorial helping for first year students in statistics. I also participated in the marking of the coursework.
- From 2007 to 2008, I participated to the “Introduction to databases” courses at the Agrocampus engineering school, in Rennes, France. I gave a total of 8 hours of tutorial helping for first year students in agronomy.

Student Supervision

Ph.D. Students (10)

- I have tutored six Ph.D. students from the Polytechnic University of Catalonia (UPC) and from the University of Barcelona (UB); S. Doria, D. Tello, A. Xenos, C. Zambrana, M. Rotkevich and K. Mihajlovic, who successfully defended their theses in 2023 $\sim$ 2025.
- I was the honorary supervisor of two Ph.D. Students from the Department of Computer Science, University College London; T. Gaudelet and S.F.L. Windels, who successfully defended their theses in 2021 and 2022, respectively.
- I have tutored two Ph.D. Students from the Department of Computing, Imperial College; Omer Yaveroglu, who successfully denfended his thesis in 2014, and Anida Sarajlic, who successfully defended her thesis in 2015.

Undergraduate students (11)

- In summer 2018, I tutored a master student from Birkbeck College during his master project (L. Quiroga).
- In spring 2018, I co-supervised five 3rd year undergraduate students from University College London (P. Faiz, A. Matineh, R. Puredath, S. Shivam, and A. Mo).
- In spring 2015, I co-supervised three MSc. students from Imperial College London; V. Varun (MSc. Engineering), S. Vasileios (MSc. Bioengineering), and S. Windels (MSc. Computer science).
- In spring 2014, I co-supervised a MSc. students from Imperial College London; J.T. Rodriguez (MSc. Bioinformatics).
- In spring 2011, I supervised a 2^{nd} year student in Computer Science and Engineering, IIT Bombay (D.V. Deepankar Reddy).

Affiliations

I am a member of the International Society of Computational Biology (ISCB).