Curriculum Vitae

Nils Giordano, PhD

Research Scientist – Computational Systems Biologist

Data Analysis - Mathematical Modeling - Next-Generation Sequencing (NGS) - Single-cell - Omics

	Skills
Bioinformatics	Scripting (Python/Bash), Version control (Git), Pipeline design (Snakemake, contributor), Cluster usage (SGE/Slurm), Cloud computing (AWS), Metagenomics, scMultiomics (10x Genomics), Genome binning, Genome annotation (EggNOG/KO), Metabolic reconstruction (CarveMe), Metabolic modeling (Cobra)
Biomathematics	Network analysis, Optimal control, Optimization, Metabolic Modeling, Linear/non-linear dynamical systems, Time-series analysis (Kalman filtering/smoothing), Image analysis (commentation/tracking). Sonsitivity analysis
Microbiology	Cloning (molecular design, overlap PCR, Gibson assembly), Chromosome editing (electroporation, lambda-red recombineering), Microplate reader, Fluorescence microscope, Microfluidic
Languages	French (native), English (fluent), Italian (basic)
	Research experience
Since Jan. 2023	Postdoctoral Researcher at INSERM (Nantes, France)
	Mentor: Dr. Éric Letouzé (ICAGEN team, CRCI ² NA, INSERM U1307)
	 Developed, maintained, and deployed pipelines for single-cell multi-omics data analysis of tumor samples
	 Integrated multi-omics datasets at both whole-genome and single-cell resolution Identified features for patient stratification and treatment response prediction Reconstructed the subclonal history of each tumor based on genetic, epigenetic, and functional data
Apr. 2020 - Jun. 2022	Research Scientist at Integrative Phenomics (Paris, France)
	• Developed pipelines for NGS analysis of gut metagenomic data and deployed them on the cloud (AWS)
	• Designed a metabolic modeling platform to predict how metabolites from different dietary options are processed by the microbiote
	 Analyzed blood and stool metabolomics data and compared them to model predictions
	 Produced scientific reports, co-wrote publications, and animated internal/external meetings
	• Participated in grant applications by designing and redacting work packages
Jan. 2018 - Dec. 2019	Postdoctoral Researcher at Université de Nantes (Nantes, France)
	Mentor: Dr. Samuel Chaffron (COMBI team, LS2N, CNRS)
	 Constructed a global network of microbial interactions in the global ocean from Tara expeditions metagenomic and metatranscriptomic data Identified communities of co-active cultivated and non-cultivated microbes

(bacteria/archaea)Uncovered functional traits linked to mutualism, including cross-feeding

interactions derived from metabolic network reconstruction (publication in prep.)

- Developed pipelines for NGS analysis of ocean metatranscriptomic data and deployed them on a cluster
- Co-wrote and obtained a grant application for a 6-month extension of a Postdoc fellowship
- Co-wrote publications and talked at several scientific conferences

Sep. 2012 -Research and Teaching Assistant (PhD Student) at Université Grenoble Alpes - InriaMar. 2017(Grenoble, France)

Supervisors: Dr. Hidde de Jong (Project-team Ibis, Inria) & Pr. Johannes Geiselmann (team BIOP, LIPhy)

- Constructed an abstract mathematical model of nutrient allocation in a microorganism
- Applied Optimal Control to predict the optimal regulation of nutrient allocation during an environmental change
- Showed that such a regulation is reminiscent of known regulatory processes in E. coli (published in Plos Comp. Biol.)
- Engineered bacteria with fluorescent ribosomes and monitored them during an environmental change using a microfluidic device

Internships

Feb.-Jun. 2012 Research Assistant (Intern) at Inria (Grenoble, France)

Supervisors: Dr. Hidde de Jong & Dr. Delphine Ropers (Project-team Ibis, Inria)

- Reviewed and implemented state-of-the-art methods of sensitivity analysis on a complex model of the gene expression machinery in bacterium *E. coli*
- Developed a brand-new dynamical method of global sensitivity analysis
- Helped to identify the key parameters driving the model dynamics and to reduce its complexity

Feb.-Jun. 2011 Research Assistant (Intern) at University of Cambridge – DAMTP (Cambridge, United Kingdom)

Supervisor: Pr. Raymond E. Goldstein (Goldstein lab, University of Cambridge)

- Led a theoretical study about the evolution towards multicellularity in microalgae (Volvocales)
- Developed a general model of phosphate uptake and growth in microalgae
- Explored the role of the extracellular matrix for phosphate storage, especially in changing environments

Jun.-Jul. 2010 Research Assistant (Intern) at École Normale Supérieure (Paris, France)

Supervisor: Dr. Silvia de Monte (Eco-evolutionary Mathematics, IBENS)

- Analyzed time-series fluorescence data of oscillating yeast cells suspensions subject to periodic forcing
- Modified an existing mathematical model based on Hopf bifurcation to recreate the observed dynamics
- Showed that even when an irrational forcing is applied, the biological system does not exhibit any chaotic behavior (published in Journal of Computational Interdisciplinary Sciences)

Publications

2025 Single-cell data reveal heterogeneity of resource allocation across a bacterial population
 Pavlou A, Cinquemani E, Pinel C, Giordano N, Van Melle Gateau M, Mihalcescu I, Geiselmann J, de Jong H
 Nat Commun 16, 285 (2025)
 2024 Genome-scale community modelling reveals conserved metabolic cross-feedings in

	epipelagic bacterioplankton communities
	<u>Giordano N,</u> Gaudin M, Trottier C, Delage E, Nef C, Bowler C, Chaffron S
	Nat Commun 15, 2721 (2024)
2023	Acquired resistance to a GPRC5D-directed T-cell engager in multiple myeloma is
	mediated by genetic or epigenetic target inactivation
	Derrien J, Gastineau S, Frigout A, Giordano N, Cherkaoui M, Gaborit V, Boinon R, Douillard E,
	Devic M, Magrangeas F, Moreau P, Minvielle S, Touzeau C, Letouzé E
	Nat Cancer 4, 1536–1543 (2023)
2022	Characterization of the Gut Microbiota in Individuals with Overweight or Obesity
	during a Real-World Weight Loss Dietary Program: A Focus on the Bacteroides 2
	Enterotype
	Alili R, Belda E, Fabre O, Pelloux V, <u>Giordano N</u> , Legrand R, Bel Lassen P, Swartz TD, Zucker J-
	D, Clément K
	Biomedicines. 2022; 10(1):16.
2017	Mathematical Modeling of Microbes: Metabolism, Gene Expression, and Growth
	de Jong H, Casagranda S, <u>Giordano N</u> , Cinquemani E, Ropers D, Geiselmann J, Gouzé J-L
	Journal of The Royal Society Interface. 14.136 (2017): 20170502.
2016	Dynamical allocation of cellular resources as an optimal control problem: Novel
	insights into microbial growth strategies.
	<u>Giordano N</u> , Mairet F, Gouzé J-L, Geiselmann J, de Jong H.
	PLoS Computational Biology. 2016;12(3):e1004802.
2012	Dynamical responses of oscillating yeast cells suspensions to periodic forcing.
	<u>Giordano N</u> , D'Ovidio F, Danø S, Sørensen PG, De Monte S.
	Journal of Computational Interdisciplinary Sciences. 2012;3(2):77–86.

Other research activities

- Reviewer for mSystems
- Reviewer for European Control Conference 2019 (ECC19)

Teaching experience

Sept. 2024 to Jan. 2025	 Bioinformatics, Université de Nantes, 20 hours <i>Tutorials and pratical exercises</i>. Big Data: introduction to bioanalysis, Université de Nantes, 8 hours <i>Pratical exercises</i>.
July 2018	• Environmental Genomics, Université d'Angers, 3 hours Lecture and practical exercices for PhD students and young scientists at the Angers Bioinformatics Summer School, in collaboration with Dr. Samuel Chaffron.
Sept. 2013 to Aug. 2016	 Teaching assistant; Université Grenoble Alpes (Grenoble, France), 229 hours Bioinformatics: from genome analysis to modeling (BSc) This introductory course was taught to 2nd-year students in collaboration with Dr. Thierry Gautier. I was in charge of the part about modeling, which means I was responsible for choosing the content, designing and teaching the lectures, tutorials, and practical exercices, but also designing the final exam and grading. Population genetics, conservation biology, biodiversity and evolution (BSc and MSc) These different courses were taught from 2nd-year to 4th-year students. I mostly supervized tutorials and helped to design and grade the final exams.
	 Prokaryotic genetics and microbiology (BSc) This course was taught to 2nd-year students. I supervized tutorials and practical exercices at the bench. Modeling and simulation of genetic regulatory networks (MSc) This course was taught to 5th-year students. It was organized for students of École Normale Supérieure, and taught in collaboration with Dr. Hidde de Jong. I helped to choose the content, teach the lectures and supervize the practical exercices. I also helped to design and arad the final exam.

	Education
2017	PhD, Systems Biology – Université Grenoble Alpes (Grenoble, France)
	 Title: Microbial growth control in changing environments: Theoretical and experimental study of resource allocation in Escherichia coli Supervisors: Dr. Hidde de Jong & Pr. Johannes Geiselmann Laboratories: Project-team Ibis (Inria Grenoble – Rhône-Alpes) and team BIOP (Laboratoire Interdisciplinaire de Physique, Université Grenoble Alpes)
2012	MSc, Cell Systems Biology with honours – École Normale Supérieure & Université Pierre et Marie Curie (Paris, France)
	 2nd year: Gene regulatory networks, cell ecosystems, cell machinery, microscopy (quantification, image processing), graph theory, comparative genomics, population genetics, structural bioinformatics, modeling of biopolymers
	 1st year: In silico biology, genes and genomes, from gene to function, ecological systems biology, biophysics, biomathematics
2010	BSc, Life sciences with honours – École Normale Supérieure & Université Pierre et Marie Curie (Paris, France)
	• Experimental practice, ecology, physiology, molecular and cellular biology, genetics and epigenetics, bioinformatics, statistics, biomathematics, statistical and optical physics, weak-bond chemistry, modeling in biology
2009-2013	ENS Diploma – École Normale Supérieure (Paris, France)
	• French leading research school, selected via a national competitive exam
	Misc – Extracurricular activities

- Outdoor and indoor climbing and bouldering (6A/B outdoor, 6B/C indoor, french quotations)
- Advocate for the open-source and libre cultures
- Former contributor on bioinfo-fr.net, a communautary French blog for bioinformaticians. List of articles (French).
- Favorite keyboard layout: BÉPO
- Favorite Linux distribution: Debian Sid
- Favorite hardware brand: AMD (CPU and GPU)