

JULIEN CHIQUET

CURRICULUM VITÆ

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CURRICULUM VITÆ

JULIEN CHIQUET, RESEARCHER IN STATISTICS, HABILITATION

Statistical Learning, Life Science, Reproducible Research

Sparse methods and regularization · Multivariate analysis · Latent variable models · Optimization and algorithms · Ecology, environment · Omics data



Born July 26, 1980

Married, father of 3 children

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🌐 <https://jchiquet.github.io>

🌐 <https://github.com/jchiquet>

Professional address

UMR MIA Paris-Saclay
Campus Agro Paris Saclay
22, place de l'agronomie
91120 Palaiseau, France

MAIN RESPONSIBILITIES

- Head of UMR MIA Paris-Saclay (since 2022)
- Creator and Chief Editor of *Computo* (since 2022).

SUMMARY OF ACTIVITIES

<i>Production</i>	48 journal papers, 5 preprints, 21 book chapters, 18 maintained software packages.
<i>Students</i>	4 ongoing PhD, 11 alumni, 24 Master.
<i>Grants</i>	3 ongoing, 23 past.
<i>Juries</i>	26 PhD + 5 HDR as reviewer, 12 PhD + 2 HDR as examiner.
<i>Teaching</i>	1824 undergraduate/MSc hours + ≈ 100 hours for continuing education courses.

PROFESSIONAL EXPERIENCE

since 2020	SENIOR RESEARCHER INRAE UMR MIA Paris-Saclay, AgroParisTech/INRAE Applied Mathematics and Computer Science
2020 – 2024	PART-TIME LECTURER X – École Polytechnique
2016–2019	FIRST CLASS RESEARCHER INRA UMR 518 MIA Paris, AgroParisTech/INRAE
2008 – 2015	RESEARCH AND TEACHING ASSISTANT, then ASSISTANT PROFESSOR (26 ^e section) UMR 8071 Statistique & Génome, Université d'Évry
2003 – 2007	PHD STUDENT French Nuclear Agency (CEA) Saclay

EDUCATION

2015	HABILITATION IN MATHEMATICS
<i>Title</i>	<i>Contributions to sparse methods for complex data analysis</i>
<i>Reviewers</i>	A. d'Aspremont (ENS), A. Dalalyan (ENSAE), J.-P. Vert (Mines ParisTech)
2003–2007	PHD IN APPLIED MATHEMATICS
<i>Title</i>	<i>Modeling and Estimating degradation processes with application in reliability</i>
	French Nuclear Agency (CEA), Saclay
<i>Supervisor</i>	Nikolaos Limnios (Université de Technologie de Compiègne)
2003	M.S. IN COMPUTATIONAL SCIENCE AND STATISTICAL LEARNING, Université de Technologie de Compiègne
2003	COMPUTER ENGINEERING SCHOOL, Université de Technologie de Compiègne

SCIENTIFIC ACTIVITIES

RESEARCH ENHANCEMENT

TEAM MANAGEMENT

	JOINT RESEARCH UNIT MIA PARIS-SACLAY , AGROPARISTECH/INRAE
<i>Since 2022</i>	Director of the lab
<i>2020–2021</i>	Deputy Director of the lab ; Team leader of team “SOLsTIS”

SCIENTIFIC COMMITTEES

	COUNCILS
<i>since 2020</i>	Member of the Steering Committee of Digit-Bio INRAE Metaprogramme
<i>since 2020</i>	Nominated member of the Scientific Council of the INRAE Animal Genetics division
<i>2016–2021</i>	Elected member of the Council of the French Statistical Society (2018–2021) and of the Scientific Council of the INRAE Math-Info division (2016–2020)
	BOARD OF RECRUITMENT
<i>Status</i>	1 Prof., 11 Assoc. Prof., 9 Junior Researchers, 6 Research Engineers
	PHD & HDR JURIES
<i>PhD</i>	26 jurys as Reviewer, 12 as Examiner.
<i>HDR</i>	5 jurys as Reviewer, 2 as Examiner.
	PHD FOLLOW-UP
<i>since 2014</i>	19 PhD students

EDITORIAL ACTIVITIES

	RESPONSIBILITIES
<i>since 2021</i>	Creator and Chief Editor of <i>Computo</i>
<i>2019 – 2022</i>	Associate Editor of the <i>Journal of Computational and Graphical Statistics</i>
<i>2018 – 2021</i>	Leader of the publication unit of the French Statistical Society
<i>Reviewer</i>	PAPER REPORTS
<i>Journal</i>	JMLR, JSS, JRSS-B, JRSS-C, Scandinavian, Biometrics, Biometrika, EJS, CSDA, JCGS, Stat. & Comp., Bioinformatics, BMC Bioinformatics, Plos Comp. Bio., ...
<i>Conference</i>	ECCB 2026, NIPS 2012–2017, ICML 2015, 2018, CAp 2025, ...

SCIENTIFIC EVENTS

	LEADER OF ORGANIZING COMMITTEES
<i>Conference</i>	RencontresR’21 , SMPGD (2019–2022), SatRDay’19
	PARTICIPATION IN SCIENTIFIC OR ORGANIZING COMMITTEES
<i>Conference</i>	RR 18/21/26, JDS 20/21, EcoStat 21, StatLearn’14, JFRB’14, IWAP 2008, ...
	RESEARCH SCHOOLS AND TUTORIALS
<i>Lecturer</i>	StatXP’19/20, Surf64’17/18, SPS’16, BigOptim’15, ... (see §3.2.2)

IMPORTANT WORKGROUPS

<i>since 2021</i>	DIGIT-BIO IA CELL
<i>Involvement</i>	Co-leader: webinar cycle to build a shared AI vocabulary, raise awareness of AI issues in life sciences, and identify biological questions for AI development.
<i>2017 – 2022</i>	WORKGROUP STATE OF THE R (FUNDING ≈ 5000€/YEAR)
<i>Involvement</i>	Co-founder and Co-leader, deepening know-how and exchanging around the latest innovations of R (annual bootcamp + monthly meeting, 20/30 people).
<i>2009 – 2022</i>	INRAE METHODOLOGICAL WORKGROUP NETBIO (FUNDING ≈ 5000€/YEAR)
<i>Involvement</i>	Co-leader between 2012 and 2022, network reconstruction methods in biology (annual meeting, 50 people; funded internships).

ONGOING PROJECTS

2023–2027	DISCERN – DISCOVERING THE CAUSES OF THREE POORLY UNDERSTOOD CANCERS IN EUROPE – https://discern.iarc.who.int/
<i>Partners</i>	20 partners
<i>Involvement</i>	Team leader, 250,000 € for MIA Paris-Saclay
<i>Description</i>	DISCERN investigates the causes of three poorly understood cancers (renal, pancreatic, colorectal) and the geographical disparities in their incidence across Europe, notably the higher rates observed in Central and Eastern Europe. The 20-institution consortium, coordinated by IARC, combines epidemiological, exposomic and multi-omics approaches within the Horizon Europe Mission on Cancer. I co-lead the methodological work package with Imperial College.
<i>Support</i>	Horizon Europe
2024–2027	COBREEDING – https://www.pepr-agroecinum.fr/les-projets-finances/socio-ecosysteme/projets-cibles/cobreeding
<i>Partners</i>	GQE Le Moulon, HeuDiaSyC (UTC)
<i>Description</i>	CoBreeding develops statistical and deep learning methods to predict the performance of maize hybrids from pools of parental lines, combining mixed models from quantitative genetics with neural network architectures, and transferring information between US and European maize line populations. Funds the PhD of François Victor.
<i>Support</i>	PEPR Agroécologie Numérique
2024–2027	HEPATOTWIN – https://digitbio.hub.inrae.fr/rubriques-verticales2/nos-actions/projets-phares/projet-phare-hepato-twin-2024-2028
<i>Partners</i>	INRAE (Toxalim, MIA-PS, NumeCan, UNH, TBI)
<i>Description</i>	HEPATOTWIN gathers INRAE units in toxicology, applied mathematics and nutrition to develop modelling approaches for liver toxicology.
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)

PAST

2020–2025	EXPANSE: EXPOSOME POWERED TOOLS FOR HEALTHY LIVING IN URBAN SETTINGS – https://expanseproject.eu/
<i>Partners</i>	Imperial College, Utrecht, Columbia, Inserm, IARC + 15 others
<i>Description</i>	EXPANSE studies how the urban exposome – environmental exposures specific to city living – affects cardiometabolic and pulmonary disease, Europe’s leading disease burden. It combines exposome and health data from over 55 million Europeans, multi-omics data from 2 million individuals, and personalized exposure assessment for 5,000 participants across five urban regions.
<i>Support</i>	Horizon H2020
2020–2024	G2WAS – GRAPE GENES FOR WATER SCARCITY – https://anr.fr/Project-ANR-19-CE20-0024
<i>Partners</i>	MIA Paris-Saclay, AGAP, LEPSE (INRAE)
<i>Involvement</i>	Team leader, 60,000 € for MIA-Paris
<i>Description</i>	G2WAS aims to identify the genetic regulators of grapevine adaptation to water deficit through genome-wide association studies (GWAS), to support the breeding of drought-tolerant varieties in the context of climate change.
<i>Support</i>	French National Research Agency (ANR)
2019–2024	SINGLESTATOMICS – http://anr-singlestatomics.pages.math.cnrs.fr
<i>Partners</i>	University of Lyon 1, Mines ParisTech, ENS Lyon, AgroParisTech/INRA
<i>Involvement</i>	12 month, co-PI, Team leader , 210,000 € for MIA-Paris
<i>Description</i>	SingleStatOmics develops statistical and machine learning methods for single-cell genomics, to study cell identity, cell differentiation dynamics, gene regulation and single-cell epigenomics, combining expertise in statistics, machine learning and optimal transport.
<i>Support</i>	French National Research Agency (ANR)

2023–2024	BEHIND THE COUNT'HER – Estimation de paramètres génétiques pour des données de comptage en grande dimension à l'aide du modèle Poisson-lognormal
<i>Partners</i>	INRAE (GenPhyse, MIA-PS, MaIAGE), Sorbonne U
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2019–2023	ECONET – ADVANCED STATISTICAL MODELLING OF ECOLOGICAL NETWORKS – https://cmatias.perso.math.cnrs.fr/ANR_EcoNet.html
<i>Partners</i>	Sorbonne, Lyon 1 and Lille Universities, AgroParisTech/INRAE, ISEM, IEES
<i>Description</i>	EcoNet develops statistical methods for the analysis of ecological networks (trophic, mutualistic, competitive, host-parasite), integrating space and time, multiple interaction types, covariate information and sampling effects, to predict how ecosystems respond to environmental change.
<i>Support</i>	French National Research Agency (ANR)
2022–2023	PEERSIM – Caractérisation de stress multiple chez les plantes
<i>Partners</i>	INRAE (IPS2, MIA-PS, MIAT), IMT
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2022–2023	GENIALEARN – Intérêts et limites de l'apprentissage statistique et de l'apprentissage profond appliqués à la sélection génomique multi-caractères
<i>Partners</i>	INRAE (GABI, MIA-PS), UEVE
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2022–2023	BOVMovie2Pred – Développement précoce bovin et viabilité: Exploration et Prédiction
<i>Partners</i>	INRAE (MaIAGE, MIA-PS, BREED)
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2018–2022	NEXT-GEN. BIOMONITORING OF CHANGE IN ECOSYSTEMS STRUCTURE AND FUNCTION
<i>Partners</i>	AgroParisTech, INRAE (Dijon, Bordeaux, Rennes, Réunion), Imperial College, Cirad
<i>Description</i>	Next Generation Biomonitoring combines high-throughput sequencing with statistical network reconstruction to detect ecosystem change across six ecosystems (microbial to macro-invertebrate), covering drivers such as invasion, disease, conservation and climate change.
<i>Support</i>	French National Research Agency (ANR)
2018–2019	KINETICKS – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
<i>Partners</i>	INRAE (BIPAR, MaIAGE, MIAP)
<i>Support</i>	Metaprogramm MEM (Meta-omics and microbial ecosystems, INRA)
2017–2019	SEARS – STRATÉGIES D'ÉCHANTILLONNAGE ET ANALYSE DES RÉSEAUX D'APPROVISIONNEMENT EN SEMENCES
<i>Leader</i>	Mathieu Thomas, (CR Cirad, AGAP)
<i>Involvement</i>	1 month
<i>Support</i>	MP GloFoods
2016–2018	BRASSICADIV-PATHO: Microbial diversity and microbial networks associated to Brassica napus and its pathogens
<i>Leader</i>	Christophe Mougél (DR Inra, Rennes), Thierry Candresse (DR Inra, Bordeaux)
<i>Partners</i>	UMR IGEPP, UMR BFP, UMR BioGeCo, UMR EPGV, UMR BioGer
<i>Support</i>	Metaprogramm MEM (Meta-omics and microbial ecosystems, Inra)
2016–2018	LIONS – Large-scale Integrative approach to unravel the complex relationships between differentiation and tumorigenesis
<i>Partners</i>	IGMM/IBC, MAP5, iSSB Évry, Institut Curie, University of York
<i>Support</i>	Plan Cancer 2015 Inserm
2016–2018	LEARNBIOCONTROL: LEARNING ECOLOGICAL NETWORKS FROM METABARCODING DATA: APPLICATION TO BIOLOGICAL CONTROL
<i>Partners</i>	INRA/UMR BioGeCo, Imperial College, AgroParisTech/INRA
<i>Support</i>	MP MEM (Inra)
2015–2018	HYDROGEN – Comparative Metagenomic for Measuring Biodiversity
<i>Partners</i>	AgroParisTech/INRA, CEA-CNS-LABIS, INRIA Rennes/Genscale
<i>Support</i>	French National Research Agency (ANR)

2012–2016	ABS4NGS – Algorithmic, Bioinformatic and Software solutions for the analysis of Next Generation Sequencing data
<i>Partners</i>	Institut Curie, Mines ParisTech, University of Lyon 1, AgroParisTech/INRA
<i>Support</i>	Investissement d’avenir
2014–2016	AREA – Analyse de la Réponse Evolutive des Arbres forestiers tropicaux dans l’environnement, approche génomique et métabolomique
<i>Partners</i>	AgroParisTech/INRA, UMR EcoFoG, UMR 8638 (CNRS/P5)
<i>Support</i>	Défi CNRS “Enviromics”
2015–2016	BEFAST – Deriving Better learning procedures from FASTer algorithms to deal with a huge amount of Data
<i>Leader</i>	Alain Célisse, Assoc. Prof., University Lille 1
<i>Support</i>	PEPS CNRS Fascido
2013–2015	REG4SEL – Regularized methods for Genomic Selection
<i>Leader</i>	Tristan Mary-Huard, CR INRA/AgroParisTech
<i>Partners</i>	UMR MIAP, UMR Le Moulon, GABI
<i>Support</i>	SelGen/French National Institute for Agricultural Research (INRAE)
2011–2015	PLOID-PLOID WHEAT – Unraveling bases of polyploidy and aneuploidy responses in flowering plants, using the wheat ploid model
<i>Partners</i>	INRA (Rennes, Versailles, Grignon), Génoscope, CNRS
<i>Support</i>	French National Research Agency (ANR)
2013–2014	ENORM – Enumeration of Near-Optimal Regulation Misbehaviours
<i>Leader</i>	Étienne Birmelé, PR University Paris 5
<i>Support</i>	PEPS CNRS
2009–2011	NEMO – Network Motif in Biological Network
<i>Partners</i>	AgroParisTech/INRA, University of Lyon 1, University of Évry
<i>Support</i>	French National Research Agency (ANR)
2005–2008	GD2GS – From Genomic Data to Graph Structure
<i>Leader</i>	Florence d’Alché-Buc, Prof. Évry
<i>Support</i>	French National Research Agency (ANR)

STUDENTS

PHD AND POST-DOC - CURRENT

from 2024	BLANCHE FRANCHETERRE
<i>PhD</i>	<i>Interpretable Methods in Unsupervised and Supervised Learning for Multisource analysis of Exposome Data and Prediction of cancer outcomes</i>
<i>Supervision</i>	supervision (50%) with M. Chadeau, Senior Researcher, Imperial College
<i>Support</i>	Horizon Europe (DISCERN)
<i>Summary</i>	Blanche’s PhD develops high-dimensional variable selection and network inference methods for proteomic cancer data, as part of Work Package 5 of the European DISCERN project. Her first paper, from her Master’s research, applied high-dimensional variable selection to plasma proteomic data to identify biomarkers distinguishing stages of human papillomavirus (HPV)-related cervical carcinoma. Building on this applied work, her thesis now focuses on comparing molecular networks across conditions rather than single biomarkers: she introduced Data Shared Neighborhood Selection (DSNS), a joint graphical model that decomposes each condition’s network into a shared component and condition-specific perturbations, extending the Data Shared Lasso to neighborhood selection. She is currently pursuing the development of additional models that attempt to disentangle adverse effects, in the form of latent factors, from variables directly associated with a specific cancer subtype.

from 2024	FRANÇOIS VICTOR
PhD	<i>Développement de méthodes d'apprentissage statistique et d'apprentissage par transfert pour la caractérisation du potentiel agro-écologique et le screening des ressources génétiques</i>
Supervision	supervision (33%) with T. Mary-Huard, DR INRAE and J.B. Léger (MCU Compiègne)
Support	PEPR Agroécologie Numérique (CoBreeding)
Summary	François's PhD develops statistical and deep learning methods to predict the performance of maize hybrids that can be formed from pools of parental lines, as part of the CoBreeding project (PEPR Agroécologie Numérique). Because only a small, unbalanced fraction of possible hybrid combinations is ever observed in the field, the work combines state-of-the-art mixed models from quantitative genetics with neural network architectures (variational autoencoders) to scale inference to large genomic and phenotypic datasets while preserving interpretability. The thesis addresses three complementary questions: predicting the stability of a hybrid's performance across environments from a generalized mixed model with genotype-dependent residual variance, predicting hybrid performance directly in target environments by reformulating factor-analytic and AMMI genotype-by-environment models in a variational framework, and transferring information learned from a data-rich reference population (US maize lines, from the Genomes To Fields initiative) to a more limited population of European lines through transfer learning and domain adaptation.
2023 – 2026	SIHAN XIE
PhD	<i>DeepSelectGene: Apprentissage profond à partir de données de géotypes et application à la sélection génomique</i>
Supervision	supervision (33%) with E. Barrey, DR INRAE and B. Hanczar (PR Évry)
Support	Metaprogramme DigitBio (INRAE)
Summary	Deep learning models are increasingly used to predict phenotypes from genotypes, for human diseases as well as production traits in genomic selection, but training them requires many genotype-phenotype pairs – rarely available for species genotyped on only a few thousand animals. Sihan's PhD works around this limit by chaining two deep learning models: a first, generative model (e.g. generative adversarial networks) trained on scarce but representative real data to simulate additional, realistic genotype data (50–800K SNPs); this augmented dataset then trains a second, simpler model dedicated to phenotype prediction, building on exploratory work from the GenIALearn project on bovine genomic selection (Metaprogramme DIGIT-BIO, 2022–2024). His first paper compared several generative models (VAEs, diffusion models, GANs) for simulating discrete genotype data, unconditioned or phenotype-conditioned, showing they capture genetic patterns and preserve genotype-phenotype associations – opening the way to privacy-preserving data sharing and to this augmentation strategy for phenotype prediction from only a few thousand genotype-phenotype pairs.
2023 - 2026	JEANNE TOUS
PhD	<i>Graphical and latent variable models for species community modelling in ecology.</i>
Supervision	100%
Support	PFI (IPEF)
Summary	Deciphering the processes that govern the distribution of species has long been a major goal of ecology. It is also critical to predict biodiversity responses to future changes and devise reliable conservation strategies. These processes (dispersal, abiotic factors, biotic conditions) can usually not be directly observed and must instead be inferred from observational data, mainly species community distribution data and environmental descriptors, but their complexity and their intermingled influences make them hard to decipher. Among the most recent community ecology methods designed to study this question, Joint Species Distribution Models (JSDMs) are a statistical approach, usually based on multivariate latent variable models, that simultaneously model the distributions of all the species in a community, in relationship with the effects of environmental covariates, and infer a network of inter-species residual (marginal or partial) correlations. In this thesis, we develop original models that mix graphical models (for association networks) with multivariate latent variable models (to figure distribution data) while integrating different types of variables clustering. We show that the modelling of zero-inflation in community data can be critical to the JSDM-based analysis of species association networks, and we study the relationship between species competition/facilitation interactions and JSDM-inferred correlations.

PHD AND POST-DOC - ALUMNI

2021 – 2024	BASTIEN BATARDIÈRE
<i>PhD</i>	<i>Machine learning for multivariate analysis of high-dimensional count data</i>
<i>Supervision</i>	supervision (50%) with J. Kwon (50%), CR INRAE
<i>Support</i>	ANR SingleStatOmics
2017–2020	MARTINA SUNDQVIST
<i>PhD</i>	<i>Multi-omic data integration for new classification in triple-negative breast cancer</i>
<i>Supervision</i>	50% with T. Dubois DR, Institut Curie and G. Rigai, CR, INRA
<i>Support</i>	DIM Île-de-France
2017–2020	AUDREY HULOT
<i>PhD</i>	<i>Analyse de données-omiques: clustering et inférence de réseaux</i>
<i>Supervision</i>	33% with F. Jaffrezic, DR, Inra (33%); H.-J. Garchon, PUPH, Inserm (33%)
<i>Support</i>	Co-financement MathNum-INRAE / Inserm
2016–2019	TIMOTHÉE TABOUY
<i>PhD</i>	<i>Modeling and inferring sampling design in probabilistic random network models</i>
<i>Supervision</i>	50% with P. Barbillon, Assoc. Prof., AgroParisTech
<i>Support</i>	FMJH IDI
2016–2019	MARIE PERROT-DOCKES
<i>PhD</i>	<i>Regularization tools for multivariate analysis: application to multi-omics</i>
<i>Supervision</i>	50% with Céline Lévy-Leduc, Prof., AgroParisTech
<i>Support</i>	FMJH
2013-2016	TRUNG HA
<i>PhD</i>	<i>Statistical learning and multivariate analysis for robust regulatory network inference</i>
<i>Supervision</i>	25% with M.-L. Martin, DR INRA/URGV and G. Rigai, Assoc. Prof., Évry
2015	DAVID BAKER
<i>Post-doc</i>	<i>Regularization methods for genomic selection</i>
<i>Supervision</i>	50% with Tristan Mary-Huard, CR INRA/Moulon
<i>Support</i>	SelGen (Reg4Sel)
2011-2014	SMAHANE CHALABI
<i>PhD</i>	<i>Caractérisation de la reprogrammation de l'expression des gènes induite par l'alloploïdie chez le blé</i>
<i>Supervision</i>	25% with Boulos Chaloub, DR INRA/URGV, Évry
<i>Support</i>	ANR Ploid-Ploid wheat
2012-2013	ÉDITH LE FLOCH
<i>Post-doc</i>	<i>Analysis of NGS data to characterize polyploidy</i>
<i>Supervision</i>	50% with Carène Rizzon, Assoc. Prof., Évry
2011-2013	JONATHAN PLASSAIS
<i>PhD</i>	<i>Développement méthodologique pour la méta-analyse appliquée à la caractérisation de signatures chez les patients atteints de maladie auto-immune</i>
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Support</i>	CIFRE, société TcLand www.tcland-expression.com
2009–2012	CAMILLE CHARBONNIER
<i>PhD</i>	<i>Inference of gene regulatory networks from non-iid transcriptomic data</i>
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Support</i>	EDGO Évry

MASTERS - ALUMNI

24 MSc. Students (co-)supervised.

TEACHING ACTIVITIES

Approximately 2000 hours of undergraduate and Master's teaching in applied mathematics, statistics, biology and computer science at Université d'Évry, AgroParisTech, École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE), École Nationale de la Statistique et de l'Analyse de l'Information

(ENSAI), Université de Technologie de Compiègne, Université Paris-Sud, Université Paris Dauphine and X – École Polytechnique, including as lecturer and teaching supervisor at École Polytechnique (2020–2024) and ENSAI (2015–2018).

Also teach continuing education courses in data science and machine learning for industry professionals (X-Executive Education, Dauphine Executive Education, HEC Data Science Certificate).

I mention here only a few lessons that I consider noteworthy, as they correspond to the production of support material and responsibility for a course.

2020-24	STATISTICS IN ACTION WITH R
<i>Msc</i>	Probabilistic models, data analysis, R programming
<i>web</i>	https://jchiquet.github.io/map566
2020-21	DATA ANALYSIS AND UNSUPERVISED LEARNING
<i>Msc</i>	Data and Graph Clustering, Mixture model, Stochastic Block Model
<i>web</i>	https://jchiquet.github.io/map573
2018-19	AN INTRODUCTION TO GRAPH ANALYSIS AND MODELING (36h course/practicals)
<i>Msc</i>	Descriptive Analysis of networks, Stochastic Block Model, Graphical Lasso
<i>web</i>	https://github.com/jchiquet/CourseStatNetwork
2015-18	INTRODUCTION TO REGULARIZATION FOR REGRESSION (154h course/practicals)
<i>Msc</i>	Ridge, Lasso, variable selection, model selection
<i>web</i>	https://github.com/jchiquet/CourseRegLinearRegression

PAPERS

PREPRINTS

- [PP1] D. Agyapong, J. Chiquet, J. Marks, and T. D. Hocking. *Understanding When Poisson Log-Normal Models Outperform Penalized Poisson Regression for Microbiome Count Data*. 2026. DOI: [10.48550/arXiv.2604.03853](https://doi.org/10.48550/arXiv.2604.03853).
- [PP2] J. Tous and J. Chiquet. *Catching the effects of biotic interactions on community data: partial correlations outperform marginal ones with proper abiotic modelling*. 2026. DOI: [10.64898/2026.05.20.726512](https://doi.org/10.64898/2026.05.20.726512).
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- [IT1] J. Chiquet. *Computo: Redefining Academic Publishing through Native Computational Reproducibility*. In: Zurich, Switzerland, 2026.
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- [IT4] J. Chiquet. *The Poisson-Lognormal Model as a Versatile Framework for the Joint Analysis of Species Abundances*. In: Cergy-Pontoise, 2021.
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- [IT6] J. Chiquet. *Sparse Gaussian graphical models for biological network inference*. In: Hong-Kong, 2013.
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SOFTWARE

Most of the public codes in which I participate are accessible via my github page <https://github.com/jchiquet>.

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