

JULIEN CHIQUET

CURRICULUM VITÆ

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CURRICULUM VITÆ

JULIEN CHIQUET

Born July 26, 1980

French citizen

Married, father of 3 children

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🌐 <https://jchiquet.github.io>

🌐 <https://github.com/jchiquet>

RESEARCHER in Statistics, Habilitation

MIA-NUMM Paris

UMR 518 AgroParistech/INRA

16, rue Claude Bernard

75231 Paris Cedex 05, France

BRIEF SUMMARY OF ACTIVITIES

Research themes	STATISTICAL LEARNING, COMPUTATIONAL BIOLOGY Sparse Methods and Regularization · Multivariate Analysis · Latent variable models · Graphical Models · Biological Networks · Applications in Genetics, Genomics and Ecology
production	26 journal papers, 5 book chapters, ≥ 11 maintained R/C++ packages.
students	3 ongoing PhD (2 x 50%, 1 x 25%), 6 alumni
Teaching	STATISTICS, MACHINE LEARNING, COMPUTATIONAL SCIENCE ≈ 1660 hours for undergraduate and Master students in departments of mathematics, statistics, biology and computer science
Schools	Université d'Évry, École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE), Université de Technologie de Compiègne (UTC), X – École Polytechnique, École Nationale de la Statistique et de l'Analyse de l'Information (ENSAI), AgroParisTech

PROFESSIONAL EXPERIENCE

since 2020	SENIOR RESEARCHER INRAE NUMM – Department Mathematics, Informatics and AI MIA Paris, UMR 518 INRAE/AgroParisTech
2016–2019	FIRST CLASS RESEARCHER INRA Department of Applied Mathematics and Informatics MIA Paris, UMR 518 INRAE/AgroParisTech
2008 – 2015	ASSISTANT PROFESSOR (26 ^e section) UMR 8071 Statistique & Génome, Université d'Évry
2006 – 2008	RESEARCH AND TEACHING ASSISTANT Université de Technologie de Compiègne, Université d'Évry
2003 – 2006	PHD STUDENT French Nuclear Agency (CEA) Saclay

EDUCATION

2015	HABILITATION IN MATHEMATICS
Title	<i>Contributions to sparse methods for complex data analysis</i>
Reviewers	A. d'Aspremont (ENS), A. Dalalyan (ENSAE), J.-P. Vert (Mines ParisTech)
2003–2007	PHD IN APPLIED MATHEMATICS
Title	<i>Modeling and Estimating degradation processes with application in reliability</i>
Supervisor	French Nuclear Agency (CEA), Saclay 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

PARTICIPATION TO RESEARCH GRANTS

ON GOING PROJECTS

2020–2025	EXPANSE : EXPOSOME POWERED TOOLS FOR HEALTHY LIVING IN URBAN SETTINGS
<i>Partners</i>	Imperial College, Utrecht, Columbia, Inserm, IARC + 15 others
<i>Support</i>	Horizon H2020
2020–2023	G2WAS – GRAPE GENES FOR WATER SCARCITY
<i>Partners</i>	AgroParisTech/INRA, AGAP, LEPSE (INRA)
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	Team leader, 60,000 € for MIA-Paris
2019–2022	SINGLESTATOMICS – http://anr-singlestatomics.pages.math.cnrs.fr
<i>Partners</i>	University of Lyon 1, Mines ParisTech, ENS Lyon, AgroParisTech/INRA
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	12 month, co-PI, Team leader , 210,000 € for MIA-Paris
2019–2022	ECONET – ADVANCED STATISTICAL MODELLING OF ECOLOGICAL NETWORKS
<i>Partners</i>	Sorbonne, Lyon 1 and Lille Universities, AgroParisTech/INRA, ISEM, IEES
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	8 months, collaborator, 136,000 € for MIA-Paris
2018–2021	NEXT-GEN. BIOMONITORING OF CHANGE IN ECOSYSTEMS STRUCTURE AND FUNCTION
<i>Leader</i>	D. Bohan (DR Inra, Dijon)
<i>Partners</i>	AgroParisTech, INRA (Dijon, Bordeaux, Rennes, Réunion), Imperial College, Cirad
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	4.8 months, collaborator, 81,000 € for MIA-Paris

PAST

2018–2019	KINETICKS – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
<i>Partners</i>	INRA (BIPAR, MaIAGE, MIAP)
<i>Support</i>	Metaprogramm MEM (Meta-omics and microbial ecosystems, INRA)
2016–2018	BRASSICADIV-PATHO : Microbial diversity and microbial networks associated to Brassica napus and its pathogens
<i>Leader</i>	Christophe Mougel (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 »
2013–2015	REG4SEL – Regularized methods for Genomic Selection
<i>Leader</i>	Tristan Mary-Huard, CR INRA/AgroParisTech
<i>Support</i>	SelGen/French National Institute Agronomic Research (INRAE)
<i>Partners</i>	UMR MIAP, UMR Le Moulon, GABI
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)
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)

RESEARCH ENHANCEMENT

since 2020	TEAM LEADER OF “STATISTIQUE & GÉNOME” UMR 518 Université Paris-Saclay – AgroParisTech – INRAE
<i>Web</i>	https://www6.inrae.fr/mia-paris

CURRENT WORKGROUPS

since 2017	WORKGROUP STATE OF THE R (FUNDING ≈ 5000€/YEAR)
<i>Purpose</i>	Group of researchers and engineers meeting to deepen their know-how, improve the dissemination of their methods and exchange around the latest innovations of R
<i>Format</i>	An annual bootcamp (1 week) + a half-day monthly meeting with 20/30 people
<i>Involvement</i>	Group leader
<i>Web</i>	http://stateofther.github.io
since 2009	INRA METHODOLOGICAL WORKGROUP NETBIO (FUNDING ≈ 5000€/YEAR)
<i>Purpose</i>	This group was originally meant to evaluate the performance of the reconstruction methods for networks in the framework of molecular biology. It broadened its activities to every network analyses in biology.
<i>Format</i>	A daylong annual meeting with 50 people
<i>Involvement</i>	Co-leader since 2012
<i>Web</i>	carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseaux_-_réseau_MIA
2015–2019	GDR “STAT ET SANTÉ”
<i>Purpose</i>	This group aims to structure and disseminate the activities of the French community of medical statistics.
<i>Involvement</i>	Co-leader of the research theme « Statistical learning for massive data analysis »
<i>web</i>	http://gdr.statsante.fr/

SCIENTIFIC EVENTS

Conference	ORGANIZING COMMITTEE – LEADER
<i>RencontresR’20</i>	Provide a national forum for the sharing of ideas within the R community.
<i>SatRDay’19</i>	SatRDays are community-led, regional conferences with international speakers to support collaboration, networking and innovation in the R community. – web page
Conference	SCIENTIFIC COMMITTEES, ORGANIZING COMMITTEE – PARTICIPATION
	JDS 2020, Rencontres R’18, StatLearn’14, JFRB’14, IWAP 2008, MBN 2007, ...
Lecturer	RESEARCH SCHOOLS AND TUTORIALS
<i>StatXP’19-20</i>	Life-course epidemiology and Exposome, Imperial College – web page
<i>Surf64’17-18</i>	AdvancedOMIC Profiling and Integration, Anglet, London – web page
<i>SPS’16</i>	From gene expression to genomic network, Paris-Saclay – web page
<i>Angers’16</i>	Bioinformatic Summer School in Angers – web page
<i>BigOptim’15</i>	Large-Scale Convex optimization – web page

OTHER PROFESSIONAL ACTIVITIES

SCIENTIFIC COMMITTEES

	COUNCILS
<i>since 2018</i>	Elected member of the Council of the French Statistical Society
<i>since 2016</i>	Elected member of the Scientific Council of the INRA Math-Info department
	BOARD OF RECRUITMENT
<i>Assistant Professor</i>	2020 : Nancy (26 ^e) ; 2019 : Évry (26 ^e) ; 2016 : Paris Sud (64-65 ^e) ; 2015 : Paris Sud (87 ^e) ; 2013 : Paris 5 (26 ^e) ; 2012 : Rouen (26 ^e) ; 2011 : Picardie (87 ^e) · Paris Sud (67 ^e) · Évry (26 ^e) ; 2010 : Évry (26 ^e)
<i>INRA</i>	2018 : INRA (4 Researcher), 2012 : INRA (4 Research Engineer)
	PHD REVIEWING
<i>2019</i>	Florian Privé, Arnaud Cougoul, Vivien Goepp ; Perrine Soret Member : Clémence Karmann, Beyrem Khalfaoui
<i>2018</i>	May Taha
<i>2017</i>	Thomas Dias-Alvès ; Member : Pierre-Alexandre Mattéi
<i>2016</i>	Samuel Balmand, Quentin Grimonprez, Rawya Zreik ; Member : Niels Ternes
	PHD FOLLOW-UP
<i>2019</i>	Charlotte Brault (Inra Montpellier)
<i>2018</i>	Arnaud Cougoul (Inra Theix)
<i>2017</i>	May Taha (IGMM Montpellier)
<i>2016</i>	Maximilien Grandclaoudon (Institut Curie), Arnaud Cougoul (Inra Theix), May Taha (IGMM Montpellier)
<i>2014</i>	Mélina Gallopin (Laboratoire de mathématiques d'Orsay)

EDITORIAL ACTIVITIES

	RESPONSABILITIES
<i>since 2019</i>	Associate Editor of the <i>Journal of Computational and Graphical Statistics</i>
<i>since 2018</i>	Leader of the publication unit of the French Statistical Society : mission to assist in the renewal of the journals of the society
<i>Reviewer Journal</i>	PAPER REPORTS
	JMLR, JRSS-B, JRSS-C, Scandinavian Jour. Stat., Biometrics, Biometrika, Bioinformatics, EJS, CSDA, Plos Comp. Bio., Inter. Jour. of Biostat., IEEE/ACM Transactions on Comp. Bio. and Bioinf., SAGMB, BMC Medical Research Methodology, EURASIP Journal on Bioinformatics and Systems Biology, ESAIM Prob. and Stat., ...
<i>Conference</i>	NIPS 2012–2017, ICML 2015, 2018, ...

STUDENTS

PHD AND POST-DOC – CURRENT

<i>from 2019</i>	CLAIRE GAYRAL
<i>PhD</i>	<i>Single-cell data integration</i>
<i>Supervision</i>	50% with F. Picard DR CNRS, Lyon
<i>since 2017</i>	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. Rigall, CR, INRA
<i>since 2017</i>	AUDREY HULOT
<i>PhD</i>	<i>Analyse de données-omiques : clustering et inférence de réseaux</i>
<i>Supervision</i>	25% with F. Jaffrezic, DR, Inra (50%) ; H.-J. Garchon, PUPH, Inserm (25%)

PHD AND POST-DOC – ALUMNI

since 2016 <i>PhD</i> <i>Supervision</i>	TIMOTHÉE TABOUY <i>Modeling and inferring sampling design in probabilistic random network models</i> 50% with P. Barbillon, Assoc. Prof., AgroParisTech
since 2016 <i>PhD</i> <i>Supervision</i>	MARIE PERROT-DOCKES <i>Regularization tools for multivariate analysis : application to multi-omics</i> 50% with Céline Lévy-Leduc, Prof., AgroParisTech
2013-2016 <i>PhD</i> <i>Supervision</i>	TRUNG HA <i>Statistical learning and multivariate analysis for robust regulatory network inference</i> 25% with M.-L. Martin, DR INRA/URGV and G. Rigaiïl, Assoc. Prof., Évry
2015 <i>Post-doc</i> <i>Supervision</i>	DAVID BAKER <i>Regularization methods for genomic selection</i> 50% with Tristan Mary-Huard, CR INRA/Moulon
2011-2014 <i>PhD</i> <i>Supervision</i>	SMAHANE CHALABI <i>Caractérisation de la reprogrammation de l'expression des gènes induite par l'allopolyploidie chez le blé</i> 25% with Boulos Chaloub, DR INRA/URGV, Évry
2012-2013 <i>Post-doc</i> <i>Supervision</i>	ÉDITH LE FLOCH <i>Analysis of NGS data to characterize polyploidy</i> 50% with Carène Rizzon, Assoc. Prof., Évry
2011-2013 <i>PhD</i> <i>Supervision</i> <i>Support</i>	JONATHAN PLASSAIS <i>Développement méthodologique pour la méta-analyse appliquée à la caractérisation de signatures chez les patients atteints de maladie auto-immune</i> 50% with Christophe Ambroise, Prof., Évry CIFRE, société TeLand www.tcland-expression.com
2009–2012 <i>PhD</i> <i>Supervision</i>	CAMILLE CHARBONNIER <i>Inference of gene regulatory networks from non-iid transcriptomic data</i> 50% with Christophe Ambroise, Prof., Évry

MASTERS – ALUMNI

2019 <i>Supervision</i> <i>Master</i>	CLAIRE GAYRAL (6 months), University of Lyon 1 with F. Picard (DR CNRS, LBBE, Lyon) <i>Integrating epigenetic and expression data for subclone discrimination in single-cell</i>
2017 <i>Supervision</i> <i>Master 1</i>	RÉMI BERNHARD (2 months), ENSIIE with T. Flûtre, T. Mary-Huard CR INRA, L. Sansonnet, AgroParisTech <i>Structured variable selection for multi-trait GWAS in grapevine</i>
2017 <i>Supervision</i> <i>Master</i>	MARTINA SUNDQVIST (6 months), ENS, Paris-Descartes with T. Dubois, L. De Koning, Institut Curie ; G. Rigaiïl, CR Inra/BAP <i>Clustering for proteomic and transcriptomic analysis of basal breast cancer</i>
2016 <i>Supervision</i> <i>Master</i>	AUDREY HULOT (6 months), ENSAI with G. Rigaiïl, CR and F. Jaffrezic, DR INRA <i>Clustering convexe à large échelle pour la métagénomique</i>
2016 <i>Supervision</i> <i>Master</i>	TIMOTHÉE TABOUY (6 months), Master Math et Science du Vivant, Paris-Saclay with P. Barbillon, S. Ouadah, Assoc. Prof., AgroParisTech ; S. Donnet, CR Inra <i>Modeling and inferring sampling design in probabilistic random network models</i>
2016 <i>Supervision</i> <i>Master</i>	MARGOT BRÉGÈRE (6 months), Master Math et Science du Vivant, Paris-Saclay 33% with C. Lévy-Leduc, Prof. and L. Sansonnet, Assoc. Prof., AgroParisTech <i>Variable selection in Multivariate ANOVA for ecological data</i>
2015 <i>Supervision</i> <i>Master</i>	VALENTIN DERVIEUX (6 months), Télécom Sud Paris 50% with Guillem Rigaiïl, Assoc. Prof., Évry <i>Clustering et analyse multivariée de données métagénomique du porc</i>

2012-2013	PIERRE GUTIERREZ (6 months + 3 months CDD), École Nationale de la Statistique et de l'Administration (ENSAE)
<i>Supervision</i>	50% with Guillem Rigail, Assoc. Prof., Évry
<i>Mastère</i>	<i>Multi-class differential analysis with fused-Anova</i>
2011	GEN YANG (3 months), ENSIIE
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Master</i>	<i>Hierarchical Lasso and group-Lasso for gene selection</i>
2011	AUORE MOUTARDE (5 months), MIGS, Université de Bourgogne
<i>Supervision</i>	50% with Yves Grandvalet, DR, UTC
<i>Master</i>	<i>Développements algorithmiques dans les méthodes de régression pénalisée appliquées à la sélection de gènes</i>
2010	CYRILLE LONGIN (6 months), EGOISt, Université de Rouen
<i>Master</i>	<i>Caractérisation automatique de modules fonctionnels dans les réseaux de régulation</i>
2009	CAMILLE CHARBONNIER (5 months), ENSAE
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Master</i>	<i>ℓ_1 penalization and application to the inference of sparse dynamic regulation networks</i>
2008	ALEXANDER SMITH (6 months), AgroCampusOuest
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Master</i>	<i>Développement d'une nouvelle méthode d'estimation de réseaux de régulation</i>

TEACHING ACTIVITIES

Approximately 1660 hours of teachings given various schools and universities : Université d'Évry, Agro-ParisTech, 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, X – École Polytechnique.

I also participate in continuing education courses in data science and machine learning for software engineers and developers in private companies (X-Executive Education, Dauphine Executive Education).

2020	DATA ANALYSIS AND UNSUPERVISED LEARNING
<i>Msc</i>	Data and Graph Clustering, Mixture model, Stochastic Block Model
<i>web</i>	https://github.com/jchiquet/CourseUnsupervisedLearningX
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 REGULARIZATION FOR REGRESSION (154h course/practicals)
<i>Msc</i>	Ridge, Lasso, variable selection, model selection
<i>web</i>	https://github.com/jchiquet/CourseRegLinearRegression
2017	A SHORT INTRODUCTION TO CONVEX OPTIMIZATION (12h course)
<i>Msc</i>	(sub)-gradient methods, Newton method, Proximal methods
2010,15,16	LINEAR MODEL AND EXTENSIONS (222h course/practicals)
<i>undergraduate</i>	Fisher test, ANOVA, Linear regression, generalized linear model, Smoothing splines
<i>MSc</i>	Mixed and random effects model, repeated-measurements, application in agronomy
2012, 2015	R PROGRAMMING AND STATISTICS (60h course/practicals)
<i>undergraduate</i>	Data and control structures, Hypothesis testing, Linear model
<i>web</i>	http://julien.cremierfamily.info/teachings_L3BI_ISV51.html
2008, 2015	INTRODUCTION TO MATRIX ALGEBRA AND DATA ANALYSIS (18h course, 38h practicals)
<i>undergraduate</i>	Linear system, Matrix factorization, Spectral decomposition, PCA
2010,12,15	SHORT PROJECT IN MATHEMATICS AND STATISTICS (110h course/practicals)
<i>undergraduate</i>	Penalized regression, Numerical analysis, Simulation, Optimization
2008–11	BASIC MATHEMATICS (148h practicals)
<i>undergraduate</i>	Continuity, Differentiation, Integration, Taylor Series, ODE, mechanics, Maple

2005–11 <i>undergraduate</i>	PROBABILITY AND STATISTIC (39h course, 339h practicals) Random variables, Random Vectors, Independence, Conditioning, Convergence ; Inference, Hypothesis Testing, Confidence Intervals
2008–10 <i>undergraduate</i>	MATHEMATICAL MODELS FOR BIOLOGY (9h course, 35h practicals) dynamic population models, Lotka-Volterra ; sequence analysis, Markov models.
2007–09 <i>MSc</i>	NUMERICAL METHODS FOR EDP (66h practicals) Euler, Runge-Kutta and Newton methods, Scilab
2003,07 <i>MSc</i>	NUMERICAL ANALYSIS (58h practicals) Linear system, Least squares, Numerical integration, Interpolation, ODE
2004,06 <i>MSc</i>	OPERATIONAL RESEARCH (50h practicals) Graphs, Combinatorial optimization, Algorithm, Complexity
2005 <i>postgraduate</i>	INTRODUCTION TO L ^A T _E X (12h course/practicals) Typography basics, Typesetting math, Bibliography, Index, Style-sheet

PAPERS

PREPRINT

- [PP1] T. Tabouy, P. Barbillon, and J. Chiquet, *misssbm : An r package for handling missing values in the stochastic block model*, 2019, URL <https://arxiv.org/abs/1906.12201>.
- [PP2] C. Ambroise, J. C. F. Guinot, and M. Szafranski, *Fast Computation of Genome-Metagenome interaction effects*, URL <https://arxiv.org/abs/1810.12169>.

JOURNAL PAPERS

- [JP1] A. Huot, J. Chiquet, F. Jaffrezic, and G. Rigaiil, *Fast tree aggregation for consensus hierarchical clustering*, BMC Bioinformatics, 2020, URL [toappear](https://doi.org/10.1186/s12859-020-02000-0).
- [JP2] J. Chiquet, S. Robin, and M. Mariadassou, *Variational inference for sparse network reconstruction from count data*, in K. Chaudhuri and R. Salakhutdinov, eds., Proceedings of the 36th International Conference on Machine Learning, vol. 97 of *Proceedings of Machine Learning Research*, pp. 1162–1171, PMLR, Long Beach, California, USA, 2019, URL <http://proceedings.mlr.press/v97/chiquet19a.html>.
- [JP3] M. Grandclaudon, M. Perrot-Dockès, C. Trichot, O. Mostafa-Abouzid, W. Abou-Jaoudé, F. Berger, P. Hupé, D. Thieffry, L. Sansonnet, J. Chiquet, C. Lévy-Leduc, and V. Soumelis, *A Quantitative Multivariate Model of Human Dendritic Cell-T Helper Cell Communication*, Cell, 2019, URL <http://dx.doi.org/10.2139/ssrn.3353217>.
- [JP4] T. Tabouy, P. Barbillon, and J. Chiquet, *Variational inference for stochastic block models from sampled data*, Journal of the American Statistical Association, 0(ja) :pp. 1–20, 2019, doi :10.1080/01621459.2018.1562934, URL <https://doi.org/10.1080/01621459.2018.1562934>.
- [JP5] J. Chiquet, M. Mariadassou, and S. Robin, *Variational inference for probabilistic poisson pca*, Ann. Appl. Statist., 12(4) :pp. 2674–2698, 2018, doi :10.1214/18-AOAS1177, URL <http://dx.doi.org/10.1214/18-AOAS1177>.
- [JP6] M. Perrot, C. Lévy-Leduc, J. Chiquet, L. Sansonnet, M. Brégère, M.-P. Étienne, S. Robin, and G. Genta-Gouve, *A multivariate variable selection approach for analyzing lc-ms metabolomics data*, SAGMB, 2018, URL <https://doi.org/10.1515/sagmb-2017-0077>.
- [JP7] M. Perrot, C. Lévy-Leduc, L. Sansonnet, and J. Chiquet, *Variable selection in multivariate linear models with high-dimensional covariance matrix estimation*, J. Multivar. Anal., 166 :pp. 78–97, 2018, URL <https://doi.org/10.1016/j.jmva.2018.02.006>.
- [JP8] V. Brault, J. Chiquet, and C. Lévy-Leduc, *Efficient block boundaries estimation in block-wise constant matrices : An application to hic data*, Electron. J. Statist., 11(1) :pp. 1570–1599, 2017, doi :10.1214/17-EJS1270.
- [JP9] J. Chiquet, P. Gutierrez, and G. Rigaiil, *Fast tree inference with weighted fusion penalties*, Journal of Computational and Graphical Statistics, pp. 205–216, 2017, URL <http://dx.doi.org/10.1080/10618600.2015.1096789>.
- [JP10] Y. Grandvalet, J. Chiquet, and C. Ambroise, *Sparsity by worst-case penalties*, 2017.
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- [IT2] *Sparse Gaussian graphical models for biological network inference*, ISI World Statistics Congress, Hong-Kong, 2013.
- [IT3] *Sparse Gaussian graphical models for biological network inference*, StatLearn'13, Bordeaux, 2013.
- [IT4] *Sparsity with sign-coherent groups of variables via the cooperative-lasso*, Statistics and Modeling for Complex Data, Marne-la-Vallée, 2011.
- [IT5] *Learning the structure of Bayesian networks with application in post-genomics*, International Workshop on Bayesian Networks and Applications in Post-genomics, Paris, 2010.
- [IT6] *Penalized maximum likelihood approach for sparse Gaussian graphical models with hidden structure*, International Workshop on Applied Probability, Compiègne, 2008.
- [IT7] *Reliability evaluation of a dynamical system in semi-Markovian environment*, International Workshop on Applied Probability, Compiègne, 2008.
- [IT8] *Modelling degradation processes through a piecewise deterministic Markov process*, Mathematical Methodologies for Operational Risk, Eindhoven, 2007.
- [IT9] *Modelling degradation processes through a piecewise deterministic Markov process with applications to fatigue crack growth*, Recent Advances in Stochastic Operations Research II, Nagoya, 2007.

RESEARCH SCHOOLS AND TUTORIALS

- [ST1] J. Chiquet, S. Donnet, M. Mariadassou, S. Ouadah, and S. Robin, *Introduction à l'analyse de réseau et l'analyse multivariée pour les données de comptage en écologique*, 2 jours d'ateliers de formation pour l'ANR NG, 2019.
- [ST2] J. Chiquet, *Network inference and penalisation : lectures*, Surf 64 : Advanced OMIC Profiling and Integration, <http://www.imperial.ac.uk/school-public-health/study/short-courses/surf-64/>, London, 2018,2019.
- [ST3] J. Chiquet, *Network inference and penalisation : tutorial*, Surf 64 : Advanced OMIC Profiling and Integration, https://github.com/benoit-liquet/XP_Practice_SURF64, Anglet, 2018.
- [ST4] J. Chiquet, *Perspective for network inference for microbiological data*, PathoBiome MEM subgroup meeting, INRA, Rennes, 2017.
- [ST5] J. Chiquet, *Tutorial on network inference*, STRATEGe : MIA Methodological Network for omic data in Ecology, AgroParisTech, Paris, 2017.
- [ST6] J. Chiquet, *Tutorial on network inference*, Conference CARTABLE, INRA Toulouse, 2016.
- [ST7] J. Chiquet, *From gene expression to genomic network*, "Saclay Plant Science" Summer School , https://www6.inra.fr/saclay-plant-sciences_eng/Teaching-and-training/Summer-schools/Summer-School-2016, 2016.
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- [ST9] J. Chiquet, *Perspective for network inference for microbiological data*, MEM methodological network, Paris, 2016.
- [ST10] J. Chiquet, *Statistics and classification for genomic data*, Bioinformatics Summer School in Angers, <http://summerschools.univ-angers.fr/en/index/about-schools/schools/bioinformatics.html>, 2016.
- [ST11] J. Chiquet, *Application of sparse convex methods in genomics*, Summer School "BigOptim", <http://www.gipsa-lab.fr/summerschool/BigOptim>, 2015.
- [ST12] J. Chiquet, *Introduction to regularization methods in life science*, Cours de 3^e cycle, École doctorale ABIES/AgroParisTech, 2012, 2013, 2014, 2015.

SEMINARS AND ORAL COMMUNICATIONS

- [ST1] Séminaire de l'équipe de statistique, IMT, Toulouse, 2019.
- [ST2] Assemblée général du département MIA, MaIAGE, Jouy-en-Josas, 2019.
- [ST3] Séminaire du groupe de travail Pasadena, Université Paris Saclay, 2019.
- [ST4] Séminaire du Centre de Bioinformatique de Bordeaux, Centre de Génomique Fonctionnelle de Bordeaux, 2019.

- [ST5] Séminaire de Probabilité et Statistiques, LMAP, Anglet, 2018.
- [ST6] Pathobiome 2018 : Pathogens in microbiota in hosts, Ajaccio, Corsica, 2018.
- [ST7] Séminaire de Probabilité et Statistiques, Institut Élie Cartan de Lorraine, 2018.
- [ST8] Recent Computational Advances in Metagenomics (RCAM'17)", Insitut Pasteur, 2017.
- [ST9] Séminaire joint AgroParisTech, Paris, 2017, 2015, 2014, 2013a, 2013b.
- [ST10] Recent advances in Segmentation Problems, AgroParisTech, 2017.
- [ST11] MEM INRA metaprogramm : MEM days, Paris, 2017.
- [ST12] SMPGD : Statistical Methods for Post-Genomic Data, Paris, 2017a, 2017b.
- [ST13] Séminaire LMAC, UTC, Compiègne, 2016.
- [ST14] Séminaire MaIAGE, INRA, Jouy, 2016.
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- [ST16] Séminaire Télécom Paris, Paris, 2016.
- [ST17] Séminaire parisien de statistiques, Paris, 2015, 2011.
- [ST18] Séminaire du groupe SSB (Statistics for Systems Biology), Paris, 2015, 2014, 2012, 2011, 2010.
- [ST19] Séminaire du MAP5, Paris, 2014.
- [ST20] Séminaire du SAMM, Paris 1, Paris, 2014.
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- [ST22] Modal team workshop, Lille, 2014, 2013.
- [ST23] Séminaire du laboratoire de mathématiques appliquées de Toulouse, Toulouse, 2013.
- [ST24] GDR Modélisation bioinformatique en biologie et médecine, Nice, 2008.
- [ST25] Groupe de travail en statistique du laboratoire Raphaël Salem, Rouen, 2007,2016.
- [ST26] Séminaire du Laboratoire Statistique et Génome, Évry, 2007.
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SOFTWARE

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

- [SW1] F. Guinot, M. Szafranski, J. Chiquet, and C. Ambroise, **SIComORe : Selection of Interaction effects in Compressed Multiple Omics REpresentation**, 2020.
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