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

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

BRIEF SUMMARY OF ACTIVITIES

Research themes	STATISTICAL AND LEARNING, LIFE SCIENCE, REPRODUCIBLE RESEARCH Sparse Methods and Regularization · Multivariate Analysis · Latent variable models · Optimization and algorithmes · Ecology, Environment · Omics data
production	35 journal papers, 5 book chapters, ≥ 15 maintained R/C++ packages.
students	1 ongoing PhD, 9 alumni
Teaching	STATISTICS, MACHINE LEARNING, COMPUTATIONAL SCIENCE ≈ 1800 hours for undergraduate and Master students in departments of applied mathematics, statistics, biology and computer science
Responsabilities	Head of UMR MIA 518. Chief editor of Computo

PROFESSIONAL EXPERIENCE

since 2020	PART-TIME LECTURER X – École Polytechnique
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	RESEARCH AND TEACHING ASSISTANT, then ASSISTANT PROFESSOR (26ᵉ section) UMR 8071 Statistique & Génome, Université d'Évry
2003 – 2007	PHD STUDENT French Nuclear Agency (CEA) Saclay

EDUCATION

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

2020–2024	**G2WAS – Grape Genes for WAter Scarcity**
Partners	AgroParisTech/INRA, AGAP, LEPSE (INRA)
Support	French National Research Agency (ANR)
Involvement	Team leader, 60,000 € for MIA-Paris

2019–2024	**SingleStatOmics** – http://anr-singlestatomics.pages.math.cnrs.fr
Partners	University of Lyon 1, Mines ParisTech, ENS Lyon, AgroParisTech/INRA
Support	French National Research Agency (ANR)
Involvement	12 month, **co-PI, Team leader**, 210,000 € for MIA-Paris

2019–2023	**EcoNet – Advanced statistical modelling of ecological networks**
Partners	Sorbonne, Lyon 1 and Lille Universities, AgroParisTech/INRA, ISEM, IEES
Support	French National Research Agency (ANR)
Involvement	8 months, collaborator, 136,000 € for MIA-Paris

2018–2022	**Next-Gen. Biomonitoring of change in ecosystems structure and function**
Leader	D. Bohan (DR Inra, Dijon)
Partners	AgroParisTech, INRA (Dijon, Bordeaux, Rennes, Réunion), Imperial College, Cirad
Support	French National Research Agency (ANR)
Involvement	4.8 months, collaborator, 81,000 € for MIA-Paris

Past (selection)

2018–2019	**KineTicks** – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
Partners	INRA (BIPAR, MaIAGE, MIAP)
Support	Metaprogramm MEM (Meta-omics and microbial ecosystems, INRA)

2016–2018	LIONS – Large-scale Integrative approach to unravel the complex relationships between differentiatiON and tumorigenesiS
Partners	IGMM/IBC, MAP5, iSSB Évry, Institut Curie, University of York
Support	Plan Cancer 2015 Inserm

2016–2018	**LearnBioControl : Learning ecological networks from metabarcoding data : application to biological control**
Partners	INRA/UMR BIoGeCo, Imperial College, AgroParisTech/INRA
Support	MP MEM (Inra)

2015–2018	**Hydrogen** – Comparative Metagenomic for Measuring Biodiversity
Partners	AgroParisTech/INRA, CEA-CNS-LABIS, INRIA Rennes/Genscale
Support	French National Research Agency (ANR)

2012–2016	ABS4NGS – Algorithmic, Bioinformatic and Software solutions for the analysis of Next Generation Sequencing data
Partners	Institut Curie, Mines ParisTech, University of Lyon 1, AgroParisTech/INRA,
Support	Investissement d'avenir

2014–2016	AREA – Analyse de la Réponse Evolutive des Arbres forestiers tropicaux dans l'environnement, approche génomique et métabolomique
Partners	AgroParisTech/INRA, UMR EcoFoG, UMR 8638 (CNRS/P5)
Support	Défi CNRS « Enviromics »

2011–2015	**Ploid-Ploid wheat** – Unraveling bases of polyploidy and aneuploidy responses in flowering plants, using the wheat ploid model
Partners	INRA (Rennes, Versailles, Grignon), Génoscope, CNRS
Support	French National Research Agency (ANR)

RESEARCH ENHANCEMENT

since 2022	HEAD OF THE LAB
2020–2021	Co-Head of the lab ; Team leader of team "SOLsTIS" in 2020
	UMR MIA Paris-Saclay, Université Paris-Saclay − AgroParisTech − INRAE
Web	https://www6.inrae.fr/mia-paris

CURRENT WORKGROUPS

since 2021	DIGIT-BIO IA CELL (FUNDING ≈ 7000€/YEAR)
Purpose	The AI animation cell of DIGIT-BIO proposes a cycle of webinars aiming to i) Set up a shared vocabulary on AI methods ii) Raise awareness on AI issues specific to life sciences iii) Identify biological questions for which AI developments deserve to be pursued
Involvement	Co-leader
Web	https://digitbio-ia.github.io/

since 2017	WORKGROUP STATE OF THE R (FUNDING ≈ 5000€/YEAR)
Purpose	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
Format	An annual bootcamp (1 week) + a half-day monthly meeting with 20/30 people
Involvement	Co-founder and Co-leader
Web	https://stateofther.github.io

since 2009	INRA METHODOLOGICAL WORKGROUP NETBIO (FUNDING ≈ 5000€/YEAR)
Purpose	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.
Format	A daylong annual meeting with 50 people
Involvement	Co-leader since 2012
Web	carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseaux_-_réseau_MIA

SCIENTIFIC EVENTS

Conference	ORGANIZING COMMITTEE − LEADER
RencontresR'21	Provide a national forum for the sharing of ideas within the R community. web page
SMPGD	Steering committee since 2019. Annual meeting dedicated to statistical methods for post genomic data analysis. web page
SatRDay'19	SatRDays are community-led, regional conferences with international speakers to support collaboration, networking and innovation in the R community. web page

	SCIENTIFIC COMMITTEES, ORGANIZING COMMITTEE
Conference	JDS 2020, 2021, EcoStat 2021, Rencontres R'18, StatLearn'14, JFRB'14, IWAP 2008, MBN 2007, . . .

Lecturer	RESEARCH SCHOOLS AND TUTORIALS
StatXP'19-20	Life-course epidemiology and Exposome, Imperial College − web page
Surf64'17-18	Advanced OMIC Profiling and Integration, Anglet, London − web page
SPS'16	From gene expression to genomic network, Paris-Saclay − web page
Angers'16	Bioinformatic Summer School in Angers − web page
BigOptim'15	Large-Scale Convex optimization − web page

EDITORIAL ACTIVITIES

	RESPONSABILITIES
since 2021	Chief Editor of *Computo*
since 2019	Associate Editor of the *Journal of Computational and Graphical Statistics*
2018 − 2021	Leader of the publication unit of the French Statistical Society : mission to assist in the renewal of the journals of the society

Reviewer	**PAPER REPORTS**
Journal	JMLR, JSS, JRSS-B, JRSS-C, Scandinavian Jour. Stat., Biometrics, Biometxrika, 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., ...
Conference	ECML22, CAp22, NeurIPS 2012–2017, ICML 2015, 2018, ...

SCIENTIFIC COMMITTEES

	COUNCILS
since 2020	Member of the Steering Committee of Digit-Bio INRAE Metaprogramme
since 2020	Nominated member of the Scientific Council of the INRAE Animal Genetics division
2018–2021	Elected member of the Council of the French Statistical Society
2016–2020	Elected member of the Scientific Council of the INRAE Math-Info division
	BOARD OF RECRUITMENT
Assistant Professor	2022 : INRAE (2 CR, 1 IR) ; 2021 : Paris 1 (26e) ; 2020 : Nancy (26e) ; 2019 : Évry (26e) ; 2016 : Paris Sud (64-65e) ; 2015 : Paris Sud (87e) ; 2013 : Paris 5 (26e) ; 2012 : Rouen (26e) ; 2011 : Picardie (87e) · Paris Sud (67e) · Évry (26e) ; 2010 : Évry (26e)
INRAE	2018 : INRA (4 Researcher), 2012 : INRA (4 Research Engineer)
	HABILITATION REVIEWING
2022	Romain Azaïs ; Matthieu Marbac
	PHD REVIEWING
2022	Florent Bascou ; Eunice Okome Obiang ; Member : Pierre Drouin
2021	Aude Sportisse ; Member : Gabriel Frisch
2020	Yaroslav Averyanov ; Member : Vincent Prost, Nicolas Jouvin
2019	Florian Privé, Arnaud Cougoul, Vivien Goepp ; Perrine Soret Member : Clémence Karmann, Beyrem Khalfaoui
2018	May Taha
2017	Thomas Dias-Alvès ; Member : Pierre-Alexandre Mattéi
2016	Samuel Balmand, Quentin Grimonprez, Rawya Zreik ; Member : Niels Ternes
	PHD FOLLOW-UP
since 2014	14 Students

STUDENTS

PHD AND POST-DOC – ALUMNI

since 2021	**BASTIEN BATARDIÈRE**
PhD	*Statistical Learning for Multivariate Analysis of High Dimensional Count Data*
Supervision	100% supervision, collab. with J. Kwon, CR INRAE
2019 – 2020	**CLAIRE GAYRAL**
PhD	*Single-cell data integration*
Supervision	50% with F. Picard DR CNRS, Lyon
2017–2020	**MARTINA SUNDQVIST**
PhD	*Multi-omic data integration for new classification in triple-negative breast cancer*
Supervision	50% with T. Dubois DR, Institut Curie and G. Rigaill, CR, INRA
2017–2020	**AUDREY HULOT**
PhD	*Analyse de données-omiques : clustering et inférence de réseaux*
Supervision	25% with F. Jaffrezic, DR, Inra (50%) ; H.-J. Garchon, PUPH, Inserm (25%)
2016–2019	**TIMOTHÉE TABOUY**
PhD	*Modeling and inferring sampling design in probabilistic random network models*
Supervision	50% with P. Barbillon, Assoc. Prof., AgroParisTech
2016–2019	**MARIE PERROT-DOCKES**
PhD	*Regularization tools for multivariate analysis : application to multi-omics*
Supervision	50% with Céline Lévy-Leduc, Prof., AgroParisTech

2013-2016 *PhD* *Supervision*	TRUNG HA *Statistical learning and multivariate analysis for robust regulatory network inference* 25% with M.-L. Martin, DR INRA/URGV and G. Rigaill, Assoc. Prof., Évry
2015 *Post-doc* *Supervision*	DAVID BAKER *Regularization methods for genomic selection* 50% with Tristan Mary-Huard, CR INRA/Moulon
2011-2014 *PhD* *Supervision*	SMAHANE CHALABI *Caractérisation de la reprogrammation de l'expression des gènes induite par l'allopo-lyploïdie chez le blé* 25% with Boulos Chaloub, DR INRA/URGV, Évry
2012-2013 *Post-doc* *Supervision*	ÉDITH LE FLOCH *Analysis of NGS data to characterize polyploidy* 50% with Carène Rizzon, Assoc. Prof., Évry
2011-2013 *PhD* *Supervision* *Support*	JONATHAN PLASSAIS *Développement méthodologique pour la méta-analyse appliquée à la caractérisation de signatures chez les patients atteints de maladie auto-immune* 50% with Christophe Ambroise, Prof., Évry CIFRE, société TcLand www.tcland-expression.com
2009–2012 *PhD* *Supervision*	CAMILLE CHARBONNIER *Inference of gene regulatory networks from non-iid transcriptomic data* 50% with Christophe Ambroise, Prof., Évry

MASTERS – ALUMNI

17 MSc. Students (co-)supervized.

TEACHING ACTIVITIES

Approximately 1800 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, HEC Data Science Certificate).

2020-23 *Msc*	STATISTICS IN ACTION WITH R Probabilistic models, data analysis, R programming
2020-21 *Msc* *web*	DATA ANALYSIS AND UNSUPERVISED LEARNING Data and Graph Clustering, Mixture model, Stochastic Block Model https://github.com/jchiquet/CourseUnsupervisedLearningX
2018-19 *Msc* *web*	AN INTRODUCTION TO GRAPH ANALYSIS AND MODELING (36h course/practicals) Descriptive Analysis of networks, Stochastic Block Model, Graphical Lasso https://github.com/jchiquet/CourseStatNetwork
2015-18 *Msc* *web*	INTRODUCTION REGULARIZATION FOR REGRESSION (154h course/practicals) Ridge, Lasso, variable selection, model selection https://github.com/jchiquet/CourseRegLinearRegression
2017 *Msc*	A SHORT INTRODUCTION TO CONVEX OPTIMIZATION (12h course) (sub)-gradient methods, Newton method, Proximal methods
2010,15,16 *undergraduate* *MSc*	LINEAR MODEL AND EXTENSIONS (222h course/practicals) Fisher test, ANOVA, Linear regression, generalized linear model, Smoothing splines Mixed and random effects model, repeated-measurements, application in agronomy
2012, 2015 *undergraduate* *web*	R PROGRAMMING AND STATISTICS (60h course/practicals) Data and control structures, Hypothesis testing, Linear model http://julien.cremeriefamily.info/teachings_L3BI_ISV51.html

2008, 2015 *undergraduate*	INTRODUCTION TO MATRIX ALGEBRA AND DATA ANALYSIS (18h course, 38h practicals) Linear system, Matrix factorization, Spectral decomposition, PCA
2010,12,15 *undergraduate*	SHORT PROJECT IN MATHEMATICS AND STATISTICS (110h course/practicals) Penalized regression, Numerical analysis, Simulation, Optimization
2008–11 *undergraduate*	BASIC MATHEMATICS (148h practicals) Continuity, Differentiation, Integration, Taylor Series, ODE, mechanics, `Maple`
2005–11 *undergraduate*	PROBABILITY AND STATISTIC (39h course, 339h practicals) Random variables, Random Vectors, Independence, Conditioning, Convergence ; Inference, Hypothesis Tesing, Confidence Intervals
2008–10 *undergraduate*	MATHEMATICAL MODELS FOR BIOLOGY (9h course, 35h practicals) dynamic population models, Lokta-Volterra ; sequence analysis, Markov models.
2007–09 *MSc*	NUMERICAL METHODS FOR EDP (66h practicals) Euler, Runge-Kutta and Newton methods, `Scilab`
2003,07 *MSc*	NUMERICAL ANALYSIS (58h practicals) Linear system, Least squares, Numerical integration, Interpolation, ODE
2004,06 *MSc*	OPERATIONAL RESEARCH (50h practicals) Graphs, Combinatorial optimization, Algorithm, Complexity
2005 *postgraduate*	INTRODUCTION TO LaTeX (12h course/practicals) Typography basics, Typesetting math, Bibliography, Index, Style-sheet

Scientific productions

Papers

Preprint

[PP1] B. Bodinier, S. Filippi, T. H. Nost, J. Chiquet, and M. Chadeau-Hyam, *Automated calibration for stability selection in penalised regression and graphical models : a multi-omics network application exploring the molecular response to tobacco smoking*, submitted.

[PP2] H. van Assel, T. Espinasse, J. Chiquet, and F. Picard, *A probabilistic graph coupling view of dimension reduction*, submitted.

[PP3] J. Chiquet, M.-J. Cros, M. Mariadassou, N. Peyrard, and O. Gimenez, *Le modèle poisson lognormal : un cadre générique d'analyse des distributions jointe d'abondance*, 2022.

[PP4] C. Pauvert, T. Fort, A. Calonnec, J. Faivre-d'Arcier, E. Chancerel, M. Massot, J. Chiquet, S. Robin, D. A. Bohan, J. Vallance, and C. Vacher, *Microbial association networks give relevant insights into plant pathobiomes*, 2020, doi :10.1101/2020.02.21.958033.

Journal papers

[JP1] P. Barbillon, J. Chiquet, and T. Tabouy, *misssbm : An r package for handling missing values in the stochastic block model*, Journal of Statistical Software, 101(12) :p. 1–32, 2022, doi :10.18637/jss.v101.i12, URL https://www.jstatsoft.org/index.php/jss/article/view/v101i12.

[JP2] M. Sundqvist, J. Chiquet, and G. Rigaill, *Adjusting the adjusted rand index - a multinomial story*, Computational Statistics, 2022, doi :10.1007/s00180-022-01230-7.

[JP3] C. Brault, A. Doligez, L. Le Cunff, A. Coupel-Ledru, T. Simonneau, J. Chiquet, P. This, and T. Flutre, *Harnessing multivariate, penalized regression methods for genomic prediction and qtl detection to cope with climate change affecting grapevine*, G3 : Genes|Genomes|Genetics, 2021, doi :10.1093/g3journal/jkab248.

[JP4] M. Champion, J. Chiquet, P. Neuvial, M. Elati, F. Radvanyi, and E. Birmelé, *Identification of deregulation mechanisms specific to cancer subtypes*, Journal of Bioinformatics and Computational Biology, 19(01) :p. 2140003, 2021, doi :10.1142/S0219720021400035.

[JP5] J. Chiquet, M. Mariadassou, and S. Robin, *The poisson-lognormal model as a versatile framework for the joint analysis of species abundances*, Frontiers in Ecology and Evolution, 9 :p. 188, 2021, doi :10.3389/fevo.2021.588292.

[JP6] M. Dubart, P. Alonso, D. Barroso-Bergada, N. Becker, K. Bethune, D. A. Bohan, C. Boury, M. Cambon, E. Canard, E. Chancerel, J. Chiquet, P. David, N. de Manincor, S. Donnet, A. Duputié, B. Facon, E. Guichoux, T. Le Minh, S. Ortiz-Martínez, L. Piouceau, A. Sacco-Martret de Préville, M. Plantegenest, C. Poux, V. Ravigné, S. Robin, M. Trillat, C. Vacher, C. Vernière, and F. Massol, *Chapter nine - coupling ecological network analysis with high-throughput sequencing-based surveys : Lessons from the next-generation biomonitoring project*, in D. A. Bohan, A. J. Dumbrell, and A. J. Vanbergen, eds., The Future of Agricultural Landscapes, Part III, vol. 65 of *Advances in Ecological Research*, pp. 367–430, Academic Press, 2021, doi :https://doi.org/10.1016/bs.aecr.2021.10.007, URL https://www.sciencedirect.com/science/article/pii/S0065250421000222.

[JP7] B. Facon, A. Hafsi, M. C. de la Masselière, S. Robin, F. Massol, M. Dubart, J. Chiquet, E. Frago, F. Chiroleu, P.-F. Duyck, and V. Ravigné, *Joint species distributions reveal the combined effects of host plants, abiotic factors and species competition as drivers of species abundances in fruit flies*, Ecological Letters, 2021, doi :10.1111/ele.13825.

[JP8] E. Lejal, J. Chiquet, J. Aubert, S. Robin, A. Estrada-Peña, O. Rue, C. Midoux, M. Mariadassou, X. Bailly, A. Cougoul, P. Gasqui, J. Cosson, K. Chalvet-Monfray, M. Vayssier-Taussat, and T. Pollet, *Temporal patterns in ixodes ricinus microbial communities : an insight into tick-borne microbe interactions*, Microbiome, 9(153), 2021, doi :10.1186/s40168-021-01051-8.

[JP9] F. Guinot, M. Szafranski, J. Chiquet, A. Zancarini, C. Le Signor, C. Mougel, and C. Ambroise, *Fast computation of genome-metagenome interaction effects*, Algorithms for Molecular Biology, 2020, doi :10.1186/s13015-020-00173-2.

[JP10] A. Hulot, J. Chiquet, F. Jaffrezic, and G. Rigaill, *Fast tree aggregation for consensus hierarchical clustering*, BMC Bioinformatics, 2020, doi :10.1186/s12859-020-3453-6.

[JP11] 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.

[JP12] M. Grandclaudon, M. Perrot-Dockès, C. Trichot, O. Mostafa-Abouzid, W. Abou-Jaoudé, F. Berger, P. Hupé, D. Thieffry, L. Sansonnet, J. Chiquet, C. Levy-Leduc, and V. Soumelis, *A quantitative multivariate model of human dendritic cell-t helper cell communication*, Cell, 2019, doi :10.2139/ssrn.3353217.

[JP13] 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.

[JP14] 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.

[JP15] 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, doi :10.1515/sagmb-2017-0077.

[JP16] 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, doi :10.1016/j.jmva.2018.02.006.

[JP17] V. Brault, J. Chiquet, and C. Lévy-Leduc, *Efficient block boundaries estimation in block-wise constant matrices : An application to hic data*, Elec. J. Statist., 11(1) :pp. 1570–1599, 2017, doi : 10.1214/17-EJS1270.

[JP18] J. Chiquet, P. Gutierrez, and G. Rigaill, *Fast tree inference with weighted fusion penalties*, Journal of Computational and Graphical Statistics, pp. 205–216, 2017, doi :10.1080/10618600.2015.1096789.

[JP19] Y. Grandvalet, J. Chiquet, and C. Ambroise, *Sparsity by worst-case penalties*, 2017.

[JP20] J. Chiquet, Y. Grandvalet, and G. Rigaill, *On coding effects in regularized categorical regression*, Statistical Modelling, (3) :pp. 228–237, 2016, doi :10.1177/1471082X16644998.

[JP21] J. Chiquet, T. Mary-Huard, and S. Robin, *Structured regularization for conditional Gaussian graphical models*, Statistics and Computing, (3) :pp. 789–804, 2016, doi :10.1007/s11222-016-9654-1.

[JP22] P. Latouche, P.-A. Mattei, C. Bouveyron, and J. Chiquet, *Combining a relaxed EM algorithm with Occam's razor for Bayesian variable selection in high-dimensional regression*, Journal of Multivariate Analysis, 2016, doi :10.1016/j.jmva.2015.09.004.

[JP23] C. Vacher, A. Tamaddoni-Nezhad, S. Kamenova, N. Peyrard, Y. Moalic, R. Sabbadin, L. Schwaller, J. Chiquet, M. A. Smith, J. Vallance *et al.*, *Learning ecological networks from next-generation sequencing data*, in Advances in Ecological Research, vol. 54, pp. 1–39, Elsevier, 2016, doi :10.1016/bs.aecr.2015.10.004.

[JP24] T. Picchetti, J. Chiquet, M. Elati, P. Neuvial, R. Nicolle, and E. Birmelé, *A model for gene deregulation detection using expression data*, BMC Systems Biology, 2015, doi :10.1186/1752-0509-9-S6-S6.

[JP25] B. Chaloub, F. Denoeud, S. Liu, S. Parkin, H. Tang, W. X., J. Chiquet, and 76 more, *Early allopolyploid evolution in the post-neolithic Brassica napus oilseed genome*, Science, (6199), 2014, doi :10.1126/science.1253435.

[JP26] H. Chelaifa, V. Chagué, S. Chalabi, I. Mestiri, D. Arnaud, D. Deffains, Y. Lu, H. Belcram, V. Huteau, J. Chiquet, O. Coriton, J. Just, J. Jahier, and B. Chalhoub, *Prevalence of gene expression additivity in genetically stable wheat allohexaploids*, New Phytologist, 197(3) :pp. 730–736, 2013, doi :10.1111/nph.12108/full.

[JP27] J. Chiquet, Y. Grandvalet, and C. Charbonnier, *Sparsity in sign-coherent groups of variables via the cooperative-lasso*, The Annals of Applied Statistics, 6(2) :pp. 795–830, 2012, doi :10.1214/11-AOAS520.

[JP28] J. Chiquet, Y. Grandvalet, and C. Ambroise, *Inferring multiple graphical models*, Statistics and Computing, 21(4) :pp. 537–553, 2011, doi :10.1007/s11222-010-9191-2.

[JP29] C. Charbonnier, J. Chiquet, and C. Ambroise, *Weighted-lasso for structured network inference from time course data*, Statistical Applications in Genomics and Molecular Biology, 9, 2010, doi : 1544-6115.1519.

[JP30] C. Ambroise, J. Chiquet, and C. Matias, *Inferring sparse Gaussian graphical models with latent structure*, Electronic Journal of Statistics, 3 :pp. 205–238, 2009, doi :10.1214/08-EJS314.

[JP31] J. Chiquet, N. Limnios, and M. Eid, *Piecewise deterministic Markov processes applied to fatigue crack growth modelling*, Journal of statistical planning and inference, 139(5) :pp. 1657–1667, 2009, doi :10.1016/j.jspi.2008.05.034.

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[JP33] J. Chiquet and N. Limnios, *A method to compute the transition function of a piecewise deterministic Markov process*, Statistics & Probability Letters, 78(12) :pp. 1397–1403, 2008, doi :10.1016/j.spl. 2007.12.016.

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