

JULIEN CHIQUET

CURRICULUM VITÆ

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CURRICULUM VITÆ

JULIEN CHIQUET

Born July 26, 1980

French citizen

Married, father of 2 children

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<http://julien.cremeriefamily.info>

RESEARCHER in Statistics, INRA

MIA 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 · Gaussian Graphical Models · Multivariate Analysis · High Dimensional Data · Applications in Genetics, Genomics and Ecology
production	18 journal papers, 4 book chapters, 9 maintained R packages, 5 preprint, 5 works in progress.
students	4 ongoing PhD (3 x 50%, 1 x 25%), 4 alumni
Teaching	STATISTICS, DATA MINING, NUMERICAL ANALYSIS ≈ 1465 hours for undergraduate and Master students in biology, mathematics and computer science departments
Schools	Université d'Évry, École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE), Université de Technologie de Compiègne (UTC), École Nationale de la Statistique et de l'Analyse de l'Information (ENSAI), AgroParisTech

PROFESSIONAL EXPERIENCE

since 2016	FIRST CLASS RESEARCHER INRA Department of Applied Mathematics and Informatics (MIA) MIA Paris, UMR 518 INRA/AgroParisTech
2012 – 2015	INVITED RESEARCHER POSITION INRA (3 years) MIA Paris, UMR 518 INRA/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 (DR CNRS, ENS), A. Dalalyan (PR, ENSAE), J.-P. Vert (DR Mines ParisTech/Institut Curie)
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 (PR 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 DEMANDS

2019–2022	G2WAS – GRAPE GENES FOR WATER SCARCITY
<i>Leader</i>	Laurent Torregrosa (Senior Researcher Inra, AGGAP, Montpellier)
<i>Partners</i>	MIAP, AGAP, LEPSE
<i>Support participation</i>	French National Research Agency (ANR) Team leader, MIAP
2019–2022	SINGLESTATOMICS –
<i>Leader</i>	Franck Picard (Senior Researcher CNRS, LBBE, Lyon)
<i>Partners</i>	MIAP, LBBE, MineParisTech
<i>Support participation</i>	French National Research Agency (ANR) Team leader, MIAP
2019–2022	ECONET – ADVANCED STATISTICAL MODELLING OF ECOLOGICAL NETWORKS
<i>Leader</i>	Catherine Matias (Senior Researcher CNRS, LPMA)
<i>Partners</i>	MIAP, LPMA, LBBE, ISEM IEES-MNHN, EEP
<i>Support</i>	French National Research Agency (ANR)
2019–2022	ACCLIMATE – IDENTIFICATION DES RÉPONSES ADAPTATIVES DES PLANTES À L'AUGMENTATION DE LA CONCENTRATION ATMOSPHÉRIQUE EN CO ₂
<i>Leader</i>	Antoine Martin (BPMP, SupAgro)
<i>Partners</i>	MIAP, UMR BPMP/CNRS, UMR Agroécologie,
<i>Support</i>	French National Research Agency (ANR)

ON GOING PROJECTS

2018–2021	NEXT GENERATION BIOMONITORING OF CHANGE IN ECOSYSTEMS STRUCTURE AND FUNCTION
<i>Leader</i>	David Bohan (Senior Researcher Inra, Dijon)
<i>Partners</i>	MIAP, UMR AgroÉcologie, UMR EEP, UMR BIoGeCo, Imperial College, Cirad, UMR CEFE, UMR IGEP
<i>Support participation</i>	French National Research Agency (ANR) 4.8 months
2018–2019	KINETICKS – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
<i>Leader</i>	Thomas Pollet (CR, BIPAR), Julien Chiquet (CR, MIAP), Béatrice Laroche (Senior Researcher, MaIAGE)
<i>Support participation</i>	Metaprogramm MEM (Meta-omics and microbial ecosystems, Inra) 3.8 months
2017–2019	SEARS – STRATÉGIES D'ÉCHANTILLONNAGE ET ANALYSE DES RÉSEAUX D'APPROVISIONNEMENT EN SEMENCES
<i>Leader</i>	Mathieu Thomas, (CR Cirad, AGAP)
<i>Support participation</i>	MP GloFoods 1 month
2016–2018	LEARNBIOCONTROL: LEARNING ECOLOGICAL NETWORKS FROM METABARCODING DATA: APPLICATION TO BIOLOGICAL CONTROL
<i>Leader</i>	Corinne Vacher (Senior Researcher Inra, Bordeaux)
<i>Partners</i>	UMR MIAP, UMR BIoGeCo, Imperial College
<i>Support participation</i>	MP MEM (Inra) 1.5 month

2016–2018	BRASSICADIV-PATHO: Microbial diversity and microbial networks associated to <i>Brassica napus</i> and its pathogens
<i>Leader</i>	Christophe Mougél (Senior Researcher Inra, Rennes), Thierry Candresse (Senior Researcher 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)
<i>participation</i>	1.5 month

PAST

2016–2018	LIONS – Large-scale Integrative approach to unravel the complex relationships between differentiatIOn and tumorigenesiS
<i>Leader</i>	Mohamed ELATI, MCF, Université d'Évry Val-d'Essonne
<i>Partners</i>	IGMM/IBC, MAP5, iSSB Évry, Institut Curie, University of York
<i>Support</i>	Plan Cancer 2015 Inserm
2015–2018	HYDROGEN – Comparative Metagenomic for Measuring Biodiversity, Application to Ocean Life Studies
<i>Leader</i>	Dominique Lavenier, DR CNRS, INRIA Rennes
<i>Partners</i>	UMR MIAP, CEA-CNS-LABIS, Inria-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>Leader</i>	Institut Curie
<i>web</i>	https://sites.google.com/site/abs4ngs/
<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>Leader</i>	Grégory Genta-Gouve, Assoc. Prof., Paris 5
<i>Partners</i>	UMR MIAP; 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>Support</i>	SelGen/French National Institute Agronomic Research (INRA)
<i>Partners</i>	UMR MIAP, UMR Le Moulon, GABI
2013–2014	ENORM – Enumeration of Near-Optimal Regulation Misbehaviours
<i>Leader</i>	Étienne Birmelé, PR University Paris 5
<i>Support</i>	PEPS CNRS
2011–2015	PLOID-PLOID WHEAT – Unraveling bases of polyploidy and aneuploidy responses in flowering plants, using the wheat ploid model
<i>Leader</i>	Boulos Chaloub, Senior Researcher INRA
<i>Support</i>	French National Research Agency (ANR)
2009–2011	NEMO – Network Motif in Biological Network
<i>Leader</i>	Stéphane Robin, Senior Researcher INRA/AgroParisTech
<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)

RESEARCH ENHANCEMENT

CURRENT WORKGROUPS

since 2017	WORKGROUP STATE OF THE R (FUNDING \approx 4000€/YEAR)
<i>Purpose</i>	Group of researchers and engineers meeting to deepen their know-how, improve the dissemination of their statistical methods and exchange around the latest innovations of R and Rstudio
<i>Format</i>	An annual week of workshops + a half-day monthly meeting
<i>Involvement</i>	Group leader
<i>Web</i>	http://stateofther.github.io
since 2009	INRA METHODOLOGICAL WORKGROUP NETBIO (FUNDING \approx 5000€/YEAR)
<i>Purpose</i>	This group is meant to evaluate the performance of the reconstruction methods for networks in the framework of molecular biology
<i>Format</i>	A daylong annual meeting with 50 people
<i>Involvement</i>	Co-organizer since 2012, regular speaker
<i>Web</i>	carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseaux_-_réseau_MIA
since 2015	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

Workshop	ORGANIZING COMMITTEE
<i>StatLearn'14</i>	Challenging problems in Statistical Learning – web page
<i>JFRB'14</i>	Journées Francophones sur les Réseaux Bayésiens – web page
<i>IWAP 2008</i>	International Workshop on Applied Probability 2008 – web page
<i>MBN 2007</i>	Mathematics for Biological Networks 2007
Lecturer	SUMMER SCHOOL
<i>Surf64'17</i>	Advanced OMIC Profiling and Integration – web page
<i>SPS'16</i>	From gene expression to genomic network – 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

Committee	BOARD OF RECRUITMENT
2018	Researcher INRA (4 postes)
2016	Assistant Professor, Paris Sud (64-65 ^e)
2015	Assistant Professor, Paris Sud (87 ^e)
2013	Assistant Professor, Paris V (26 ^e)
2012	Research Engineer INRA · Assistant Professor, Rouen (26 ^e)
2011	Assistant Professor, Picardie (87 ^e) · Paris Sud (67 ^e) · Évreux (26 ^e)
2010	Assistant Professor, Évreux (26 ^e)
Committee	PHD DEFENCE COMMITTEE
2017	Thomas Dias-Alvès (Reviewer), Pierre-Alexandre Mattéi
2016	Samuel Balmand (Reviewer), Quentin Grimonprez (Reviewer), Rawya Zreik (Reviewer), Niels Ternès
Committee	PHD FOLLOW-UP
2018	Arnaud Cougoul (Inra Theix)
2017	May Taha (IGMM Montpellier)
2016	Maximilien Grandclaudon (Institut Curie), Arnaud Cougoul (Inra Theix), May Taha (IGMM Montpellier)
2014	Mélina Gallopin (Laboratoire de mathématiques d'Orsay)

Reviewer	PAPER REPORTS
Journal	Scandinavian Journal Statistics, The International Journal of Biostatistics, IEEE/ACM Transactions on Computational Biology and Bioinformatics Biometrics, Electronic Journal of Statistics, Plos Computational Biology, Computational Statistics and Data Analysis, Biometrika, Bioinformatics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, ESAIM Prob. and Stat., SAGMB, EURASIP Journal on Bioinformatics and Systems Biology, BMC Medical Research Methodology, International Journal of Fatigue, Methodology and Computing in Applied Probability, QTQM, Revue d'Intelligence Artificielle, Revue des Nouvelles Technologies de l'Information
Conference	NIPS 2012–2017, ICML 2015,2018, JdS 2011, JOBIM 2008, ESREL 2007, IWAP 2008
Others	VARIOUS RESPONSABILITIES
2016	Elected member of the Scientific Council of the INRA Math-Info department

STUDENTS

PHD AND POST-DOC – CURRENT

from 2017	MARTINA SUNDQVIST
PhD	<i>Intégration des données protéomiques pour une nouvelle classification des cancers du seins triple-négatifs</i>
Supervision	50% with T. Dubois, Institut Curie
from 2017	AUDREY HULOT
PhD	<i>Analyse de données-omiques: clustering et inférence de réseaux</i>
Supervision	25% with F. Jaffrezic, Senior Researcher, Inra (50%); H.-J. Garchon, PUPH, Inserm (25%)
since 2016	TIMOTHÉE TABOUY
PhD	<i>Modeling and inferring Sampling design in probabilistic random network models</i>
Supervision	50% with P. Barbillon, Assoc. Prof., AgroParisTech
since 2016	MARIE PERROT-DOCKES
PhD	<i>Regularization tools for multivariate analysis: application to multi-omics</i>
Supervision	50% with Céline Lévy-Leduc, Prof., AgroParisTech

PHD AND POST-DOC – ALUMNI

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

MASTERS – CURRENT

2017	RÉMI BERNHARD (2 months) École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE) with T. Flûtre, CR Inra Montpellier, L. Sansonnet, Assoc. Prof., AgroParisTech; T. Mary-Huard, CR Inra Moulon
<i>Supervision</i>	
<i>Master 1</i>	<i>Sélection de variable structurée pour le modèle linéaire général: application aux études GWAS multi-trait chez la vigne</i>
2017	MARTINA SUNDQVIST (6 months) ENS, Paris-Descartes, Institut Curie
<i>Supervision</i>	with T. Dubois, L. De Koning, Institut Curie; G. Rigaille, CR Inra/BAP
<i>Master</i>	<i>Clustering for proteomic and transcriptomic analysis of basal breast cancer</i>

MASTERS – ALUMNI

2016	AUDREY HULOT (6 months) École Nationale de la Statistique et de l'Analyse de l'Information (ENSAI) with G. Rigaille, CR and F. Jaffrezic, DR INRA
<i>Supervision</i>	
<i>Master</i>	<i>Clustering convexe à large échelle pour la métagénomique</i>
2016	TIMOTHÉE TABOUY (6 months) Master Math et Science du Vivant, Paris-Saclay
<i>Supervision</i>	with P. Barbillon, S. Ouadah, Assoc. Prof., AgroParisTech; S. Donnet, CR Inra
<i>Master</i>	<i>Modeling and inferring Sampling design in probabilistic random network models</i>
2016	MARGOT BRÉGÈRE (6 months) Master Math et Science du Vivant, Paris-Saclay
<i>Supervision</i>	33% with C. Lévy-Leduc, Prof. and L. Sansonnet, Assoc. Prof., AgroParisTech
<i>Master</i>	<i>Variable selection in Multivariate ANOVA for ecological data</i>
2015	VALENTIN DERVIEUX (6 months) Télécom Sud Paris
<i>Supervision</i>	50% with Guillem Rigaille, Assoc. Prof., Évry
<i>Master</i>	<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 Rigaille, Assoc. Prof., Évry
<i>Mastère</i>	<i>Multi-class differential analysis with fused-Anova</i>
2011	GEN YANG (3 months) École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE)
<i>Supervision</i>	50% with Christophe Ambroise, Prof., Évry
<i>Master</i>	<i>Hierarchical Lasso and group-Lasso for gene selection</i>
2011	AURORE MOUTARDE (5 months) MIGS, Université de Bourgogne
<i>Supervision</i>	50% with Yves Grandvalet, Senior Researcher, 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) École Nationale de la Statistique et de l'Administration (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 1460 hours of teachings given various schools and universities: Université d'Évry, AgroParis-Tech, 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.

2017 <i>M2</i> <i>web</i>	AN INTRODUCTION TO GRAPH ANALYSIS AND MODELING (18h course/practicals) Descriptive Analysis of networks, Stochastic Bloc Model, Graphical Lasso http://julien.cremeriefamily.info/teachings_ensai_networks.html
2017 <i>M2</i>	A SHORT INTRODUCTION TO CONVEX OPTIMIZATION (9h de cours) (sub)-gradient methods, Newton method, Proximal methods
2015-17 <i>M2</i> <i>web</i>	INTRODUCTION REGULARIZATION FOR REGRESSION (154h course/practicals) Ridge, Lasso, variable selection, model selection http://julien.cremeriefamily.info/teachings_M1MINT_Reg.html
2016 <i>MSc</i>	LINEAR MIXED MODEL(30h course/practicals) Mixed and random effects model, repeated-measurements, application in agronomy
2010,15,16 <i>undergraduate</i>	LINEAR MODEL AND EXTENSION(192h course/practicals) Fisher test, ANOVA, Linear regression, generalized linear model, Smoothing splines
2012, 2015 <i>undergraduate</i> <i>web</i>	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 <i>undergraduate</i>	INTRODUCTION TO MATRIX ALGEBRA AND DATA ANALYSIS (18h course, 38h practicals) Linear system, Matrix factorization, Spectral decomposition, PCA
2010,12,15 <i>undergraduate</i>	SHORT PROJECT IN MATHEMATICS AND STATISTICS (110h course/practicals) Penalized regression, Numerical analysis, Simulation, Optimization
2008–11 <i>undergraduate</i>	BASIC MATHEMATICS (112h practicals) Continuity, Differentiation, Integration, Taylor Series, ODE
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>graduate/undergraduate</i>	MATHEMATICAL MODELS FOR BIOLOGY (9h course, 35h practicals) dynamic population models, Lokta-Volterra; sequence analysis, Markov models.
2009 <i>undergraduate</i>	AN INTRODUCTION TO MAPLE (36h practicals) Calculus, basic mechanics, Maple
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

WORK IN PROGRESS

- [IP1] C. Ambroise, J. Chiquet, F. Guinot, and M. Szafranski, *Fast computation of genome-metagenome interaction effects*, Bioinformatics.
- [IP2] T. Ha, J. Chiquet, M.-L. Martin-Magnette, and G. Rigai, *Enhancing differential analysis with network inference*, chapter in book for GGM inference.
- [IP3] M. Pierrejean, J. Chiquet, H. Bengtsson, and P. Neuvial, *Cancer cell clonality using copy number profiles*, Biostatistics.
- [IP4] G. Rigai and J. Chiquet, *Aricode: an R package for efficient computations of standard clustering comparison measures*, Journal of Statistical Software.

PREPRINT

- [PP1] J. Chiquet, M. Mariadassous, and S. Robin, *Variational inference for probabilistic poisson pca*.
- [PP2] J. Chiquet, R. Rigai, and M. Sundqvist, *A multiattribute gaussian graphical model for inferring multiscale regulatory networks: an application in breast cancer*.
- [PP3] Y. Grandvalet, J. Chiquet, and C. Ambroise, *Sparsity by worst-case penalties*.
- [PP4] M. Perrot, C. Lévy-Leduc, J. Chiquet, L. Sansonnet, M. Brègère, M.-P. Étienne, S. Robin, and G. Genta-Gouve, *A multivariate variable selection approach for analyzing lc-ms metabolomics data*.
- [PP5] T. Tabouy, P. Barbillon, and J. Chiquet, *Variational inference for stochastic block models from sampled data*.

JOURNAL PAPERS

- [JP1] M. Perrot, C. Lévy-Leduc, L. Sansonnet, and J. Chiquet, *Variable selection in multivariate linear models with high-dimensional covariance matrix estimation*, 2018.
- [JP2] 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.
- [JP3] J. Chiquet, P. Gutierrez, and G. Rigai, *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>.
- [JP4] J. Chiquet, Y. Grandvalet, and G. Rigai, *On coding effects in regularized categorical regression*, Statistical Modelling, (3):pp. 228–237, 2016, URL <http://dx.doi.org/10.1177/1471082X16644998>.
- [JP5] J. Chiquet, T. Mary-Huard, and S. Robin, *Structured regularization for conditional Gaussian graphical models*, Statistics and Computing, (3):pp. 789–804, 2016, URL <http://dx.doi.org/10.1007/s11222-016-9654-1>.
- [JP6] 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, URL <http://dx.doi.org/10.1016/j.jmva.2015.09.004>.
- [JP7] 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, URL <http://bmc systbiol.biomedcentral.com/articles/10.1186/1752-0509-9-S6-S6>.
- [JP8] B. Chaloub, F. Denoed, 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, URL <http://www.sciencemag.org/content/345/6199/950>.

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