# JULIEN CHIQUET

# CURRICULUM VITÆ

Last update: October 9, 2018

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# CURRICULUM VITÆ

## JULIEN CHIQUET

Born July 26, 1980 French citizen Married, father of 2 children

**☎** 01.44.08.16.73

julien.chiquet@inra.fr

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 | STATISTICAL LEARNING, COMPUTATIONAL BIOLOGY

themes | Sparse Methods and Regularization  $\cdot$  Gaussian Graphical Models  $\cdot$  Multivariate Anal-

ysis · High Dimensional Data · Applications in Genetics, Genomics and Ecology

production | 20 journal papers, 5 book chapters, 9 maintained R packages, 2 preprint.

students | 4 ongoing PhD (3 x 50%, 1 x 25%), 4 alumni

Teaching | STATISTICS, DATA MINING, NUMERICAL ANALYSIS

 $\approx$  1500 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° 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 | Contributions to sparse methods for complex data analysis

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 | Modeling and Estimating degradation processes with application in reliability

French Nuclear Agency (CEA), Saclay

Supervisor | Nikolaos Limnios (PR Université de Technologie de Compiègne)

2003 M.S. IN COMPUTATIONAL SCIENCE AND STATISTICAL LEARNING, Université de Tech-

nologie de Compiègne

2003 COMPUTER ENGINEERING SCHOOL, Université de Technologie de Compiègne

# SCIENTIFIC ACTIVITIES \_\_\_\_\_

# PARTICIPATION TO RESEARCH GRANTS \_\_\_\_\_

# On going Projects

2019–2022 Leader Partners Support participation	ECONET – ADVANCED STATISTICAL MODELLING OF ECOLOGICAL NETWORKS Catherine Matias (Senior Researcher CNRS, LPMA) MIAP, LPMA, LBBE, ISEM IEES-MNHN, EEP French National Research Agency (ANR) 8 months
2018–2021  Leader Partners  Support participation	NEXT GENERATION BIOMONITORING OF CHANGE IN ECOSYSTEMS STRUCTURE AND FUNCTION David Bohan (Senior Researcher Inra, Dijon) MIAP, UMR AgroÉcologie, UMR EEP, UMR BIoGeCo, Imperial College, Cirad, UMR CEFE, UMR IGEP French National Research Agency (ANR) 4.8 months
2018–2019  Leader  Support participation	KINETICKS – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution Thomas Pollet (CR, BIPAR), <b>Julien Chiquet</b> (CR, MIAP), Béatrice Laroche (Senior Researcher, MaIAGE) Metaprogramm MEM (Meta-omics and microbial ecosystems, Inra) 3.8 months
2017–2019  Leader Support participation	SEARS – STRATÉGIES D'ÉCHANTILLONNAGE ET ANALYSE DES RÉSEAUX D'APPROVISIONNEMENT EN SEMENCES Mathieu Thomas, (CR Cirad, AGAP) MP GloFoods 1 month
2016–2018  Leader Partners Support participation	LEARNBIOCONTROL: LEARNING ECOLOGICAL NETWORKS FROM METABARCODING DATA: APPLICATION TO BIOLOGICAL CONTROL Corinne Vacher (Senior Researcher Inra, Bordeaux) UMR MIAP, UMR BIoGeCo, Imperial College MP MEM (Inra) 1.5 month
2016–2018  Leader  Partners Support participation	BRASSICADIV-PATHO: Microbial diversity and microbial networks associated to Brassica napus and its pathogens Christophe Mougel (Senior Researcher Inra, Rennes), Thierry Candresse (Senior Researcher Inra, Bordeaux) UMR IGEPP, UMR BFP, UMR BioGeCo, UMR EPGV, UMR BioGer Metaprogramm MEM (Meta-omics and microbial ecosystems, Inra) 1.5 month

# Past

2016–2018	LIONS – Large-scale Integrative approach to unravel the complex relationships be-
	tween differentiation and tumorigenesis
Leader	Mohamed ELATI, MCF, Université d'Évry Val-d'Essonne
Partners	IGMM/IBC, MAP5, iSSB Évry, Institut Curie, University of York
Support	Plan Cancer 2015 Inserm
2015-2018	HYDROGEN – Comparative Metagenomic for Measuring Biodiversity, Application to
	Ocean Life Studies
Leader	Dominique Lavenier, DR CNRS, INRIA Rennes
Partners	UMR MIAP, CEA-CNS-LABIS, Inria-Genscale
Support	French National Research Agency (ANR)

2012-2016 ABS4NGS - Algorithmic, Bioinformatic and Software solutions for the analysis of Next Generation Sequencing data LeaderInstitut Curie https://sites.google.com/site/abs4ngs/ webInvestissement d'avenir SupportAREA - Analyse de la Réponse Evolutive des Arbres forestiers tropicaux dans 2014-2016 l'environnement, approche génomique et métabolomique LeaderGrégory Genta-Gouve, Assoc. Prof., Paris 5 Partners UMR MIAP; UMR EcoFoG; UMR 8638 (CNRS/P5) SupportDéfi CNRS "Enviromics" 2015-2016 BEFAST – Deriving Better learning procedures from FASTer algorithms to deal with a huge amount of Data LeaderAlain Célisse, Assoc. Prof., University Lille 1 SupportPEPS CNRS Fascido 2013-2015 REG4SEL - Regularized methods for Genomic Selection LeaderTristan Mary-Huard, CR INRA/AgroParisTech SupportSelGen/French National Institute Agronomic Research (INRA) Partners | UMR MIAP, UMR Le Moulon, GABI 2013-2014 **ENORM** – Enumeration of Near-Optimal Regulation Misbehaviours LeaderÉtienne Birmelé, PR University Paris 5 SupportPEPS CNRS PLOID-PLOID WHEAT – Unraveling bases of polyploidy and aneuploidy responses in 2011-2015 flowering plants, using the wheat ploid model Boulos Chaloub, Senior Researcher INRA LeaderSupportFrench National Research Agency (ANR) 2009–2011 NEMO – Network Motif in Biological Network LeaderStéphane Robin, Senior Researcher INRA/AgroParisTech SupportFrench National Research Agency (ANR) 2005-2008 GD2GS - From Genomic Data to Graph Structure LeaderFlorence d'Alché-Buc, Prof. Évry Support | French National Research Agency (ANR)

#### RESEARCH ENHANCEMENT \_

#### CURRENT WORKGROUPS

since 2017 Purpose	Workgroup State of the R (funding $\approx 4000 \text{€/YEAR}$ ) 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
Format	An annual week of workshops $+$ a half-day monthly meeting
Involvement	Group leader
Web	http://stateofther.github.io
since 2009	INRA METHODOLOGICAL WORKGROUP NETBIO (FUNDING ≈ 5000€/YEAR)
Purpose	This group is meant to evaluate the performance of the reconstruction methods for
1 urpose	networks in the framework of molecular biology
Format	A daylong annual meeting with 50 people
Involvement	, o
	Co-organizer since 2012, regular speaker
Web	carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseauxréseau_MIA
since 2015	GDR "Stat et Santé"
Purpose	This group aims to structure and disseminate the activities of the French community
1	of medical statistics.
Involvement	Co-leader of the research theme "Statistical learning for massive data analysis"
web	http://gdr.statsante.fr/
200	

## SCIENTIFIC EVENTS

Workshop	Organizing committee
StatLearn'14	Challenging problems in Statistical Learning – web page
JFRB'14	Journées Francophones sur les Réseaux Bayésiens – web page
IWAP 2008	International Workshop on Applied Probability 2008 – web pagr
MBN 2007	Mathematics for Biological Networks 2007
Lecturer	Summer School
Surf64'17	Advanced OMIC Profiling and Integration – web page
SPS'16	From gene expression to genomic network – web page
Angers'16	Bioinformatic Summer School in Angers – web page
BigOptim'15	Large-Scale Convex optimization – web page

# OTHER PROFESSIONAL ACTIVITIES \_\_\_\_\_

Committee 2018 2016 2015 2013 2012 2011 2010	BOARD OF RECRUITMENT Researcher INRA (4 postes) Assistant Professor, Paris Sud (64-65°) Assistant Professor, Paris Sud (87°) Assistant Professor, Paris V (26°) Research Engineer INRA · Assistant Professor, Rouen (26°) Assistant Professor, Picardie (87°) · Paris Sud (67°) · Évry (26°) Assistant Professor, Évry (26°)
Committee 2018 2017 2016	PHD DEFENCE COMMITTEE May Taha (Reviewer) Thomas Dias-Alvès (Reviewer), Pierre-Alexandre Mattéi Samuel Balmand (Reviewer), Quentin Grimonprez (Reviewer), Rawya Zreik (Reviewer), Niels Ternes
Committee 2018 2017 2016	PHD FOLLOW-UP Arnaud Cougoul (Inra Theix) May Taha (IGMM Montpellier) Maximilien Grandclaudon (Institut Curie), Arnaud Cougoul (Inra Theix), May Taha (IGMM Montpellier) Mélina Gallopin (Laboratoire de mathématiques d'Orsay)
Reviewer Journal Conference	Paper Reports 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 NIPS 2012–2017, ICML 2015,2018, JdS 2011, JOBIM 2008, ESREL 2007, IWAP 2008
Others <i>2016</i>	VARIOUS RESPONSABILITIES Elected member of the Scientific Council of the INRA Math-Info department

# STUDENTS \_\_\_\_\_

## PHD AND POST-DOC - CURRENT

since 2017	Martina Sundqvist
PhD	Intégration des données protéomiques pour une nouvelle classification des cancers du
	seins triple-négatifs
Supervision	50% with T. Dubois, Institut Curie

since 2017 AUDREY HULOT
PhD Analyse de données-omiques: clustering et inférence de réseaux
Supervision 25% with F. Jaffrezic, Senior Researcher, Inra (50%); H.-J. Garchon, PUPH, Inserm (25%)

since 2016 | TIMOTHÉE TABOUY

PhD | Modeling and inferring Sampling design in probabilistic random network models

Supervision | 50% with P. Barbillon, Assoc. Prof., AgroParisTech

since 2016 | MARIE PERROT-DOCKES

PhD | Regularization tools for multivariate analysis: application to multi-omics

Supervision | 50% with Céline Lévy-Leduc, Prof., AgroParisTech

#### PhD and Post-doc - Alumni

2013-2016 | TRUNG HA

PhD | Statistical learning and multivariate analysis for robust regulatory network inference

Supervision | 25% with M.-L. Martin, DR INRA/URGV and G. Rigaill, Assoc. Prof., Évry

2015 | DAVID BAKER

Post-doc Regularization methods for Genomic Selection Supervision 50% with Tristan Mary-Huard, CR INRA/Moulon

2011-2014 | SMAHANE CHALABI

PhD | Caractérisation de la reprogrammation de l'expression des gènes induite par

l'allopolyploïdie chez le blé

Supervision | 25% with Boulos Chaloub, Senior Researcher INRA/URGV, Évry

2012-2013 | ÉDITH LE FLOCH

Post-doc Analysis of NGS data to characterize polyploidy Supervision 50% with Carène Rizzon, Assoc. Prof., Évry

2011-2013 | JONATHAN PLASSAIS

PhD | Développement méthodologique pour la méta-analyse appliquée à la caractérisation de

signatures chez les patients atteints de maladie auto-immune

Supervision | 50% with Christophe Ambroise, Prof., Évry

Support | CIFRE, société TcLand www.tcland-expression.com

2009–2012 | CAMILLE CHARBONNIER

PhD | Inference of gene regulatory networks from non-iid transcriptomic data

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)

Supervision | with T. Flûtre, CR Inra Montpellier, L. Sansonnet, Assoc. Prof., AgroParisTech; T.

Mary-Huard, CR Inra Moulon

Master 1 | Sélection de variable structurée pour le modèle linéaire général: application aux études

GWAS multi-trait chez la vigne

2017 | MARTINA SUNDQVIST (6 months)

ENS, Paris-Descartes, Institut Curie

Supervision with T. Dubois, L. De Koning, Institut Curie; G. Rigaill, CR Inra/BAP

Master | Clustering for proteomic and transcriptomic analysis of basal breast cancer

### Masters - Alumni

2016 AUDREY HULOT (6 months)

École Nationale de la Statistique et de l'Analyse de l'Information (ENSAI)

Supervision with G. Rigaill, CR and F. Jaffrezic, DR INRA

Master | Clustering convexe à large échelle pour la métagénomique

2016 | TIMOTHÉE TABOUY (6 months)

Master Math et Science du Vivant, Paris-Saclay

Supervision | with P. Barbillon, S. Ouadah, Assoc. Prof., AgroParisTech; S. Donnet, CR Inra
Master | Modeling and inferring Sampling design in probabilistic random network models

2016 | MARGOT BRÉGÈRE (6 months)

Master Math et Science du Vivant, Paris-Saclay

Supervision | 33% with C. Lévy-Leduc, Prof. and L. Sansonnet, Assoc. Prof., AgroParisTech

Master | Variable selection in Multivariate ANOVA for ecological data

2015 | VALENTIN DERVIEUX (6 months)

Télécom Sud Paris

Supervision | 50% with Guillem Rigaill, Assoc. Prof., Évry

Master | Clustering et analyse multivariée de données métagénomique du porc

2012-2013 | PIERRE GUTIERREZ (6 months + 3 months CDD)

École Nationale de la Statistique et de l'Administration (ENSAE)

Supervision | 50% with Guillem Rigaill, Assoc. Prof., Évry Mastère | Multi-class differential analysis with fused-Anova

2011 | GEN YANG (3 months)

École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE)

Supervision | 50% with Christophe Ambroise, Prof., Évry

Master | Hierarchical Lasso and group-Lasso for gene selection

2011 | AURORE MOUTARDE (5 months)

MIGS, Université de Bourgogne

Supervision | 50% with Yves Grandvalet, Senior Researcher, UTC

Master | Développements algorithmiques dans les méthodes de régression pénalisée appliquées

à la sélection de gènes

2010 | CYRILLE LONGIN (6 months)

EGOISt, Université de Rouen

Master | Caractérisation automatique de modules fonctionnels dans les réseaux de régulation

2009 | CAMILLE CHARBONNIER (5 months)

École Nationale de la Statistique et de l'Administration (ENSAE)

Supervision | 50% with Christophe Ambroise, Prof., Évry

Master  $\mid \ell_1 \mid$  penalization and application to the inference of sparse dynamic regulation networks

2008 | ALEXANDER SMITH (6 months)

AgroCampusOuest

Supervision | 50% with Christophe Ambroise, Prof., Évry

Master Développement d'une nouvelle méthode d'estimation de réseaux de régulation

# TEACHING ACTIVITIES \_\_\_\_\_

Approximately 1500 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, Université Paris Dauphine.

$2017-18 \\ M2 \\ web$	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
$2015-18\\M2\\web$	INTRODUCTION REGULARIZATION FOR REGRESSION (154h course/practicals) Ridge, Lasso, variable selection, model selection http://julien.cremeriefamily.info/teachings_M1MINT_Reg.html
$2016 \\ MSc$	LINEAR MIXED MODEL(30h course/practicals) Mixed and random effects model, repeated-measurements, application in agronomy
$2010,15,16\\under graduate$	LINEAR MODEL AND EXTENSION(192h course/practicals) Fisher test, ANOVA, Linear regression, generalized linear model, Smoothing splines
$\begin{array}{c} 2012,2015\\ undergraduate\\ web \end{array}$	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 (112h practicals) Continuity, Differentiation, Integration, Taylor Series, ODE
$2005–11\\undergraduate$	PROBABILITY AND STATISTIC (39h course, 339h practicals) Random variables, Random Vectors, Independence, Conditioning, Convergence; Inference, Hypothesis Tesing, Confidence Intervals
$2008-10 \ gradu ated/undergradua$	MATHEMATICAL MODELS FOR BIOLOGY (9h course, 35h practicals) dynamic population models, Lokta-Volterra; sequence analysis, Markov models.
$2009\\under graduate$	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
$2003,07\\MSc$	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
$\begin{array}{c} 2005 \\ postgraduate \end{array}$	INTRODUCTION TO LATEX (12h course/practicals) Typography basics, Typesetting math, Bibliography, Index, Style-sheet

# SCIENTIFIC PRODUCTIONS

### Papers -

#### **PREPRINT**

- [PP1] J. Chiquet, M. Mariadassous, and S. Robin, Variational inference for sparse network reconstruction from count data.
- [PP2] T. Tabouy, P. Barbillon, and J. Chiquet, Variational inference for stochastic block models from sampled data.

#### JOURNAL PAPERS

- [JP1] J. Chiquet, M. Mariadassous, and S. Robin, Variational inference for probabilistic poisson pca, Annals of Applied Statistics (to appear), 2018.
- [JP2] 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.
- [JP3] 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.
- [JP4] 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.
- [JP5] J. Chiquet, P. Gutierrez, and G. Rigaill, 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.
- [JP6] Y. Grandvalet, J. Chiquet, and C. Ambroise, Sparsity by worst-case penalties, 2017.
- [JP7] J. Chiquet, Y. Grandvalet, and G. Rigaill, On coding effects in regularized categorical regression, Statistical Modelling, (3):pp. 228–237, 2016, URL http://dx.doi.org/10.1177/1471082X16644998.
- [JP8] 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.
- [JP9] 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.
- [JP10] 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://bmcsystbiol.biomedcentral.com/articles/10.1186/1752-0509-9-S6-S6.
- [JP11] 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, URL http://www.sciencemag.org/content/345/6199/950.
- [JP12] 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, URL http://onlinelibrary.wiley.com/doi/10.1111/nph.12108/full.
- [JP13] 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, URL http://projecteuclid.org/euclid.aoas/1339419617.
- [JP14] J. Chiquet, Y. Grandvalet, and C. Ambroise, *Inferring multiple graphical models*, Statistics and Computing, 21(4):pp. 537–553, 2011, URL http://dx.doi.org/10.1007/s11222-010-9191-2.

- [JP15] 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, URL https://doi.org/10.2202/1544-6115.1519.
- [JP16] C. Ambroise, J. Chiquet, and C. Matias, Inferring sparse Gaussian graphical models with latent structure, Electronic Journal of Statistics, 3:pp. 205-238, 2009, URL http://projecteuclid.org/DPubS?service=UI&version=1.0&verb=Display&handle=euclid.ejs/1238078905.
- [JP17] 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, URL http://dx.doi.org/10.1016/j.jspi.2008.05.034.
- [JP18] J. Chiquet, A. Smith, G. Grasseau, C. Matias, and C. Ambroise, SIMoNe: Statistical Inference for MOdular NEtworks, Bioinformatics, 25(3):pp. 417–418, 2009, URL http://dx.doi.org/10.1093/bioinformatics/btn637.
- [JP19] J. Chiquet and N. Limnios, A method to compute the transition function of a piecewise deterministic Markov process, Statistics and Probability Letters, 78(12):pp. 1397–1403, 2008, URL http://dx.doi.org/10.1016/j.spl.2007.12.016.
- [JP20] J. Chiquet, N. Limnios, and M. Eid, Modelling and estimating stochastic dynamical systems with Markovian switching, Reliability Engineering and System Safety, 93(12):pp. 1801–1808, 2008, URL http://dx.doi.org/10.1016/j.ress.2008.03.016.
- [JP21] J. Chiquet and N. Limnios, Estimating stochastic dynamical systems driven by a continuous-time jump Markov process, Methodology and Computing in Applied Probability, 8:pp. 431–447, 2006, URL http://www.springerlink.com/content/e8736480p2027113/.

### **BOOK CHAPTERS**

- [BC1] J. Chiquet, R. Rigaill, and M. Sundqvist, Gene Regulatory Networks: Methods and Protocols (Guido Sanguinetti and Vân Anh Huynh-Thu, eds.)), chap. A multiattribute Gaussian graphical model for inferring multiscale regulatory networks: an application in breast cancer, Springer Science+Business Media, LLC, part of Springer Nature, 2019, URL https://doi.org/10.1007/978-1-4939-8882-2\_6.
- [BC2] A. Vacher, C. Tamaddoni-Nezhad, S. Kamenova, N. Peyrard, L. Schwaller, J. Julien Chiquet, M. Smith, J. Vallance, Y. Moalic, R. Sabbadin, V. Fievet, B. Jakuschkin, and D. Bohan, Advances in Ecological Research, chap. Learning Ecological Networks from Next-Generation Sequencing Data, 2016.
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## TALKS\_

#### CONTRIBUTED TALKS (INTERNATIONAL)

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- [IT1] Fast tree inference with weighted fusion penalties, Computational Intelligence methods for Bioinformatics and Biostatistics (CIBB), Naples, 2015.
- [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.
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- [ST9] J. Chiquet, Statistics and classification for genomic data, Bioinformatics Summer School in Angers, http://summerschools.univ-angers.fr/en/index/about-schools/bioinformatics.html, 2016.
- [ST10] J. Chiquet, Application of sparse convex methods in genomics, Summer School "BigOptim", http://www.gipsa-lab.fr/summerschool/BigOptim, 2015.
- [ST11] J. Chiquet, Introduction to regularization methods in life science, Cours de 3<sup>e</sup> cycle, École doctorale ABIES/AgroParisTech, 2012, 2013, 2014, 2015.

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- [ST1] Séminaire de Probabilité et Statistiques, LMAP, Anglet, 2018.
- [ST2] Pathobiome 2018: Pathogens in microbiota in hosts, Ajaccio, Corsica, 2018.
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- [ST4] Recent Computational Advances in Metagenomics (RCAM'17)", Insitut Pasteur, 2017.
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- [ST6] Recent advances in Segmentation Problems, AgroParisTech, 2017.
- [ST7] MEM INRA metaprogramm: MEM days, Paris, 2017.
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- [ST10] Séminaire MaIAGE, INRA, Jouy, 2016.
- [ST11] Séminaire P-MAG, Paris, 2016.
- [ST12] Séminaire Télécom Paris, Paris, 2016.
- [ST13] Séminaire parisien de statistiques, Paris, 2015, 2011.
- [ST14] Séminaire du groupe SSB (Statistics for Systems Biology), Paris, 2015, 2014, 2012, 2011, 2010.
- [ST15] Séminaire du MAP5, Paris, 2014.
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- [ST18] Modal team workshop, Lille, 2014, 2013.
- [ST19] Séminaire du laboratoire de mathématiques appliquées de Toulouse, Toulouse, 2013.
- [ST20] GDR Modélisation bioinformatique en biologie et médecine, Nice, 2008.
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https://github.com/jchiquet/fusedanova.

- Fused-ANOVA is a penalized method that solves the one-way ANOVA problem by collapsing the coefficients of K conditions. It reconstructs a balanced tree structure between the condition with a homotopy algorithm in  $O(K \log(K))$ .
- [SW4] T. Tabouy, P. Barbillon, and J. Chiquet, missSBM: handling missing data in the Stochastic Bloc Model, 2018.

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Segments a matrix in blocks with constant values. The underlying algorithm is a Lars-type algorithm where all the matrix operation can be computed explicitly.

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Implements a generative model that uses a spike-and-slab like prior distribution obtained by multiplying a deterministic binary vector. Such a model allows an EM algorithm, optimizing a type-II log-likelihood.

[SW9] J. Chiquet, Quadrupen: Sparsity by Worst-Case Quadratic Penalties, 2012.

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This package fits classical sparse regression models with efficient active set algorithms by solving quadratic problems. It also provides a few methods for model selection purposes (cross-validation, stability selection).

[SW10] J. Chiquet, Scoop: Sparse Cooperative Regression, 2011.

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This R package fits coop-Lasso, group-Lasso and tree-group Lasso variants for linear regression and logistic regression. The cooperative-Lasso (in short, coop-Lasso) may be viewed as a modification of the group-Lasso penalty that promotes sign coherence and that allows zeros within groups.

[SW11] J. Chiquet, G. Grasseau, C. Ambroise, and C. Charbonnier, SIMoNe: Statistical Inference for MOdular NEtworks, 2010.

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SIMoNe (Statistical Inference for MOdular NEtworks) is an R package which implements the inference of co-regulated networks based on partial correlation coefficients from either steady-state or time-course transcriptomic data. This package can deal with samples collected in different experimental conditions. In this particular case, multiple related graphs are inferred simultaneously. The underlying statistical tools enter the framework of Gaussian graphical models (GGM). Basically, the algorithm searches for a latent clustering of the network to drive the selection of edges through an adaptive l1-penalization of the model likelihood.