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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Researcher in Statistics, Habilitation

UMR MIA Paris-Saclay
UPsay, AgroParisTech, INRAE
Campus Agro Paris Saclay
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91120 Palaiseau, France

Brief summary of activities

Research	Statistical and Learning, Life Science, Reproducible Research
themes	Sparse Methods and Regularization · Multivariate Analysis · Latent variable models · Optimization and algorithms · Ecology, Environment · Omics data
production	43 journal papers, 5 book chapters, ≥ 15 maintained `R/C++` packages.
students	4 ongoing PhD, 11 alumni
Teaching	Statistics, Machine learning, Computational Science ≈ 2000 hours for undergraduate and Master students in departments of applied mathematics, statistics, biology and computer science
Responsabilities	Head of UMR MIA Paris-Saclay. Chief editor of Computo

Professional experience

since 2020	Senior Researcher INRAE UMR MIA Paris-Saclay, AgroParisTech/INRAE Applied Mathematics and Computer Science
2020 – 2024	Part-Time Lecturer X – École Polytechnique
2016–2019	First class Researcher INRA UMR 518 MIA Paris, AgroParisTech/INRAE
2008 – 2015	Research and Teaching Assistant, then Assistant Professor (26^{e} section) UMR 8071 Statistique & Génome, Université d'Évry
2003 – 2007	PhD student French Nuclear Agency (CEA) Saclay

Education

2015	Habilitation in Mathematics
Title	*Contributions to sparse methods for complex data analysis*
Reviewers	A. d'Aspremont (ENS), A. Dalalyan (ENSAE), J.-P. Vert (Mines ParisTech)
2003–2007	PhD in Applied Mathematics
Title	*Modeling and Estimating degradation processes with application in reliability* French Nuclear Agency (CEA), Saclay
Supervisor	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

2023–2027	DISCERN – Discovering the causes of three poorly understood cancers in Europe – `https://discern.iarc.who.int/`
Partners	20 partners
Support	Horizon Europe
Involvement	Team leader, 250,000 € for MIA Paris-Saclay
2020–2025	EXPANSE : EXposome Powered tools for healthy living in urbAN SEttings
Partners	Imperial College, Utrecht, Columbia, Inserm, IARC + 15 others
Support	Horizon H2020

Past (selection)

2020–2024	G2WAS – Grape Genes for WAter Scarcity
Partners	MIA Paris-Saclay, AGAP, LEPSE (INRAE)
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/INRAE, ISEM, IEES
Support	French National Research Agency (ANR)
2018–2022	Next-Gen. Biomonitoring of change in ecosystems structure and function
Partners	AgroParisTech, INRAE (Dijon, Bordeaux, Rennes, Réunion), Imperial College, Cirad
Support	French National Research Agency (ANR)
2022–2023	Behind the Count´her – Estimation de paramètres génétiques pour des données de comptage en grande dimension à l'aide du modèle Poisson-lognormal
Partners	INRAE (GenPhyse, MIA-PS, MaIAGE), Sorobnne U
Support	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2022–2023	PEERSIM – Caractérisation de stress multiple chez les plantes
Partners	INRAE (IPS2, MIA-PS, MIAT), IMT
Support	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2022–2023	GENIALEARN – Intérêts et limites de l'apprentissage statistique et de l'apprentissage profond appliqués à la sélection génomique multi-caractères
Partners	INRAE (GABI, MIA-PS), UEVE
Support	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2021–2022	BovMovie2Pred – Développement précoce bovin et viabilité : Exploration et Prédiction
Partners	INRAE (MaIAGE, MIA-PS, BREED)
Support	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2018–2019	KineTicks – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
Partners	INRAE (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 »

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://mia-ps.inrae.fr

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/

2017 – 2022	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

2009 – 2022	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 between 2019 and 2022. 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

Students

from 2024	Blanche Francheterre
PhD	*Interpretable Methods in Unsupervised and Supervised Learning for Multisource analysis of Exposome Data and Prediction of cancer outcomes*
Supervision	supervision (50%) with M. Chadeau, Senior Researcher, Imperial College
from 2024	François Victor
PhD	*Développement de méthodes d'apprentissage statistique et d'apprentissage par transfert pour la caractérisation du potentiel agro-écologique et le screening des ressources génétiques*
Supervision	supervision (25%) with T. Mary-Huard (DR INRAE), J.-B. Léger (MCU Compiègne), A. Charcosset DR INRAE)
since 2023	Sihan Xie
PhD	*DeepSelectGene : Apprentissage profond à partir de données de génotypes et application à la sélection génomique*
Supervision	supervision (33%) with E. Barrey, DR INRAE and B. Hanczar (PR Évry)
since 2023	Jeanne Tous
PhD	*Detection of changes in group structure within species association networks as a function of changing environmental parameters, and assessment of the causes of these changes*
Supervision	supervision (100%)

PhD and Post-doc – Alumni

2021–2024	Bastien Batardière
PhD	*Statistical Learning for Multivariate Analysis of High Dimensional Count Data*
Supervision	supervision (50%) with J. Kwon (50%), CR INRAE
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	33% with F. Jaffrezic, DR, Inra (33%) ; H.-J. Garchon, PUPH, Inserm (33%)
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	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, DR 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 – Alumni

22 MSc. Students (co-)supervized.

Teaching activities

Approximately 2000 hours of teachings given various schools and universities : Université d'Évry, AgroParisTech, École Nationale Supérieure d'Informatique pour l'Industrie et l'Entreprise (ENSIIE), École Nationale de la Statistique et de l'Analyse de l'Information (ENSAI), Université de Technologie de Compiègne, Université Paris-Sud, Université Paris Dauphine, X – École Polytechnique. In particular, I was a lecturer and teaching supervisor at École Polytechnique (64h/year) from 2020 to 2024, and at ENSAI (around 40h/year) from 2015 to 2018.

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).

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

2020-24	Statistics in Action with R
Msc	Probabilistic models, data analysis, R programming
web	https://jchiquet.github.io/map566

2020-21	Data Analysis and Unsupervised Learning
Msc	Data and Graph Clustering, Mixture model, Stochastic Block Model
web	https://jchiquet.github.io/map573

2018-19	An introduction to graph analysis and modeling (36h course/practicals)
Msc	Descriptive Analysis of networks, Stochastic Block Model, Graphical Lasso
web	https://github.com/jchiquet/CourseStatNetwork

2015-18	Introduction regularization for regression (154h course/practicals)
Msc	Ridge, Lasso, variable selection, model selection
web	https://github.com/jchiquet/CourseRegLinearRegression

Scientific productions

Papers

Preprint

[PP1] J. Tous and J. Chiquet, *An integrated method for clustering and association network inference*, 2025, doi :10.48550/arXiv.2503.2246.

[PP2] B. Batardière, J. Chiquet, F. Gindraud, and M. Mariadassou, *Zero-inflation in the multivariate poisson lognormal family*, 2024, doi :10.48550/arXiv.14711.

[PP3] B. Batardière, J. Chiquet, and M. Mariadassou, *Evaluating parameter uncertainty in the poisson lognormal model with corrected variational estimators*, 2024, doi :10.48550/arXiv.2411.08524.

[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] B. Batardière, J. Chiquet, J. Kwon, and J. Stoehr, *Importance sampling-based gradient method for dimension reduction in poisson log-normal model*, Electronic Journal of Statistics, 19(1), 2025, doi :10.1214/25-EJS2384.

[JP2] B. Bodinier, S. Rodrigues, M. Karimi, S. Filippi, J. Chiquet, and M. Chadeau-Hyam, *Stability selection and consensus clustering in r : The r package sharp*, Journal of Statistical Software, 112(5), 2025, doi :10.18637/jss.v112.i05, URL `https://www.jstatsoft.org/index.php/jss/article/view/v112i05`.

[JP3] B. Batardiere, J. Kwon, and J. Chiquet, *pyplnmodels : A python package to analyze multivariate high-dimensional count data*, Journal of Open Source Software, 9(104) :p. 6969, 2024, doi :10.21105/joss.06969, URL `https://doi.org/10.21105/joss.06969`.

[JP4] R. Wada, F.-J. Peng, C.-A. Lin, R. Vermeulen, A. Iglesias-González, P. Palazzi, B. Bodinier, S. Streel, M. Guillaume, D. Vuckovic *et al.*, *Hair-derived exposome exploration of cardiometabolic health : Piloting a bayesian multitrait variable selection approach*, Environmental Science & Technology, 2024, doi :https://doi.org/10.1021/acs.est.3c08739.

[JP5] B. Bodinier, S. Filippi, T. H. Nøst, J. Chiquet, and M. Chadeau-Hyam, *Automated calibration for stability selection in penalised regression and graphical models*, Journal of the Royal Statistical Society Series C : Applied Statistics, 2023, doi :10.1093/jrsssc/qlad058, URL `https://doi.org/10.1093/jrsssc/qlad058`.

[JP6] B. Bodinier, S. Rodrigues, M. Karimi, S. Filippi, J. Chiquet, and M. Chadeau-Hyam, *Automated calibration of consensus weighted distance-based clustering approaches using sharp*, Bioinformatics, 2023, doi :https://doi.org/10.1093/bioinformatics/btad635.

[JP7] E. Delannoy, B. Batardière, S. Pateyron, L. Soubigou-Taconnat, J. Chiquet, J. Colcombet, and J. Lang, *Cell specialization and coordination in arabidopsis leaves upon pathogenic attack revealed by scrna-seq*, Plant Communications, 4(5) :p. 100676, 2023, doi :https://doi.org/10.1016/j.xplc.2023.100676, URL `https://www.sciencedirect.com/science/article/pii/S2590346223002043`, focus Issue on Plant Single-Cell Biology.

[JP8] H. V. Assel, T. Espinasse, J. Chiquet, and F. Picard, *A probabilistic graph coupling view of dimension reduction*, in A. H. Oh, A. Agarwal, D. Belgrave, and K. Cho, eds., Advances in Neural Information Processing Systems, 2022, URL `https://openreview.net/forum?id=tNXumks8yHv`.

[JP9] 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`.

[JP10] 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.

[JP11] 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.

[JP12] 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.

[JP13] 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.

[JP14] 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`.

[JP15] 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.

[JP16] 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.

[JP17] 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.

[JP18] 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.

[JP19] 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.

[JP20] 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.

[JP21] 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.

[JP22] 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.

[JP23] 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.

[JP24] 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.

[JP25] 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.

[JP26] 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.

[JP27] Y. Grandvalet, J. Chiquet, and C. Ambroise, *Sparsity by worst-case penalties*, 2017.

[JP28] 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.

[JP29] 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.

[JP30] 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.

[JP31] 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.

[JP32] 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.

[JP33] 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.

[JP34] 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.

[JP35] 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.

[JP36] 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.

[JP37] 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.

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