

# 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 algorithms · Ecology, Environment · Omics data
production	39 journal papers, 5 book chapters, $\geq 15$ maintained R/C++ packages.
students	1 ongoing PhD, 9 alumni
Teaching	STATISTICS, MACHINE LEARNING, COMPUTATIONAL SCIENCE $\approx 2000$ hours for undergraduate and Master students in departments of applied mathematics, statistics, biology and computer science
Responsibilities	Head of <a href="#">UMR MIA 518</a> . Chief editor of <a href="#">Computo</a>

## 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 (26 <sup>e</sup> section) UMR 8071 Statistique & Génome, Université d'Évry
2003 – 2007	PHD STUDENT French Nuclear Agency (CEA) Saclay

## EDUCATION

2015	HABILITATION IN MATHEMATICS
Title	<i>Contributions to sparse methods for complex data analysis</i>
Reviewers	A. d'Aspremont (ENS), A. Dalalyan (ENSAE), J.-P. Vert (Mines ParisTech)
2003–2007	PHD IN APPLIED MATHEMATICS
Title	<i>Modeling and Estimating degradation processes with application in reliability</i>
Supervisor	French Nuclear Agency (CEA), Saclay Nikolaos Limnios (Université de Technologie de Compiègne)
2003	M.S. IN COMPUTATIONAL SCIENCE AND STATISTICAL LEARNING, Université de Technologie de Compiègne
2003	COMPUTER ENGINEERING SCHOOL, Université de Technologie de Compiègne

# SCIENTIFIC ACTIVITIES

## PARTICIPATION TO RESEARCH GRANTS

### ON GOING PROJECTS(SELECTION)

2023–2027	DISCERN – DISCOVERING THE CAUSES OF THREE POORLY UNDERSTOOD CANCERS IN EUROPE – <a href="https://discern.iarc.who.int/">https://discern.iarc.who.int/</a>
<i>Partners</i>	20 partners
<i>Support</i>	Horizon Europe
<i>Involvement</i>	Team leader, 250,000 € for MIA Paris-Saclay
2020–2024	G2WAS – GRAPE GENES FOR WATER SCARCITY
<i>Partners</i>	MIA Paris-Saclay, AGAP, LEPSE (INRAE)
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	Team leader, 60,000 € for MIA-Paris
2019–2024	SINGLESTATOMICS – <a href="http://anr-singlestatomics.pages.math.cnrs.fr">http://anr-singlestatomics.pages.math.cnrs.fr</a>
<i>Partners</i>	University of Lyon 1, Mines ParisTech, ENS Lyon, AgroParisTech/INRA
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	12 month, <b>co-PI, Team leader</b> , 210,000 € for MIA-Paris

### PAST (SELECTION)

2019–2023	ECONET – ADVANCED STATISTICAL MODELLING OF ECOLOGICAL NETWORKS
<i>Partners</i>	Sorbonne, Lyon 1 and Lille Universities, AgroParisTech/INRAE, ISEM, IEES
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	8 months, collaborator, 136,000 € for MIA-Paris
2018–2022	NEXT-GEN. BIOMONITORING OF CHANGE IN ECOSYSTEMS STRUCTURE AND FUNCTION
<i>Leader</i>	D. Bohan (DR Inra, Dijon)
<i>Partners</i>	AgroParisTech, INRAE (Dijon, Bordeaux, Rennes, Réunion), Imperial College, Cirad
<i>Support</i>	French National Research Agency (ANR)
<i>Involvement</i>	4.8 months, collaborator, 81,000 € for MIA-Paris
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
<i>Partners</i>	INRAE (GenPhyse, MIA-PS, MaIAGE), Sorbonne U
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2022–2023	PEERSIM – Caractérisation de stress multiple chez les plantes
<i>Partners</i>	INRAE (IPS2, MIA-PS, MIAT), IMT
<i>Support</i>	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
<i>Partners</i>	INRAE (GABI, MIA-PS), UEVE
<i>Support</i>	Metaprogramm DIGIT-BIO (Meta-omics and microbial ecosystems, INRAE)
2021–2022	BOVMovie2PRED – Développement précoce bovin et viabilité : Exploration et Prédiction
<i>Partners</i>	INRAE (MaIAGE, MIA-PS, BREED)
2018–2019	KINETICKS – Network and modelling analyses to describe the dynamics of Ixodes ricinus microbiome and its influence in pathogen evolution
<i>Partners</i>	INRAE (BIPAR, MaIAGE, MIAP)
<i>Support</i>	Metaprogramm MEM (Meta-omics and microbial ecosystems, INRA)
2016–2018	LIONS – Large-scale Integrative approach to unravel the complex relationships between differentiation and tumorigenesis
<i>Partners</i>	IGMM/IBC, MAP5, iSSB Évry, Institut Curie, University of York
<i>Support</i>	Plan Cancer 2015 Inserm

2016–2018	LEARNBIOCONTROL : LEARNING ECOLOGICAL NETWORKS FROM METABARCODING DATA : APPLICATION TO BIOLOGICAL CONTROL
<i>Partners</i>	INRA/UMR BIoGeCo, Imperial College, AgroParisTech/INRA
<i>Support</i>	MP MEM (Inra)
2015–2018	HYDROGEN – Comparative Metagenomic for Measuring Biodiversity
<i>Partners</i>	AgroParisTech/INRA, CEA-CNS-LABIS, INRIA Rennes/Genscale
<i>Support</i>	French National Research Agency (ANR)
2012–2016	ABS4NGS – Algorithmic, Bioinformatic and Software solutions for the analysis of Next Generation Sequencing data
<i>Partners</i>	Institut Curie, Mines ParisTech, University of Lyon 1, AgroParisTech/INRA,
<i>Support</i>	Investissement d’avenir
2014–2016	AREA – Analyse de la Réponse Evolutive des Arbres forestiers tropicaux dans l’environnement, approche génomique et métabolomique
<i>Partners</i>	AgroParisTech/INRA, UMR EcoFoG, UMR 8638 (CNRS/P5)
<i>Support</i>	Défi CNRS « Enviromics »
2011–2015	PLOID-PLOID WHEAT – Unraveling bases of polyploidy and aneuploidy responses in flowering plants, using the wheat ploid model
<i>Partners</i>	INRA (Rennes, Versailles, Grignon), Génoscope, CNRS
<i>Support</i>	French National Research Agency (ANR)

## RESEARCH ENHANCEMENT

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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
<i>Web</i>	<a href="https://www6.inrae.fr/mia-paris">https://www6.inrae.fr/mia-paris</a>

## CURRENT WORKGROUPS

since 2021	DIGIT-BIO IA CELL (FUNDING $\approx$ 7000€/YEAR)
<i>Purpose</i>	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
<i>Involvement</i>	Co-leader
<i>Web</i>	<a href="https://digitbio-ia.github.io/">https://digitbio-ia.github.io/</a>
since 2017	WORKGROUP STATE OF THE R (FUNDING $\approx$ 5000€/YEAR)
<i>Purpose</i>	Group of researchers and engineers meeting to deepen their know-how, improve the dissemination of their methods and exchange around the latest innovations of R
<i>Format</i>	An annual bootcamp (1 week) + a half-day monthly meeting with 20/30 people
<i>Involvement</i>	Co-founder and Co-leader
<i>Web</i>	<a href="https://stateofther.github.io">https://stateofther.github.io</a>
since 2009	INRA METHODOLOGICAL WORKGROUP NETBIO (FUNDING $\approx$ 5000€/YEAR)
<i>Purpose</i>	This group was originally meant to evaluate the performance of the reconstruction methods for networks in the framework of molecular biology. It broadened its activities to every network analyses in biology.
<i>Format</i>	A daylong annual meeting with 50 people
<i>Involvement</i>	Co-leader since 2012
<i>Web</i>	<a href="http://carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseaux_-_réseau_MIA">carlit.toulouse.inra.fr/wikiz/index.php/Inférence_de_réseaux_-_réseau_MIA</a>

## SCIENTIFIC EVENTS

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

<i>Conference</i>	SCIENTIFIC COMMITTEES, ORGANIZING COMMITTEE JDS 2020, 2021, EcoStat 2021, Rencontres R'18, StatLearn'14, JFRB'14, IWAP 2008, MBN 2007, ...
<i>Lecturer</i>	RESEARCH SCHOOLS AND TUTORIALS
<i>StatXP'19-20</i>	Life-course epidemiology and Exposome, Imperial College – <a href="#">web page</a>
<i>Surf64'17-18</i>	Advanced OMIC Profiling and Integration, Anglet, London – <a href="#">web page</a>
<i>SPS'16</i>	From gene expression to genomic network, Paris-Saclay – <a href="#">web page</a>
<i>Angers'16</i>	Bioinformatic Summer School in Angers – <a href="#">web page</a>
<i>BigOptim'15</i>	Large-Scale Convex optimization – <a href="#">web page</a>

## EDITORIAL ACTIVITIES

	RESPONSABILITIES
<i>since 2021</i>	Chief Editor of <i>Computo</i>
<i>2019–2022</i>	Associate Editor of the <i>Journal of Computational and Graphical Statistics</i>
<i>2018 – 2021</i>	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
<i>Journal</i>	JMLR, JSS, JRSS-B, JRSS-C, Scandinavian Jour. Stat., Biometrics, Biometrika, Bioinformatics, EJS, CSDA, Plos Comp. Bio., Inter. Jour. of Biostat., IEEE/ACM Transactions on Comp. Bio. and Bioinf., SAGMB, BMC Medical Research Methodology, EURASIP Journal on Bioinformatics and Systems Biology, ESAIM Prob. and Stat., ...
<i>Conference</i>	ECML22, CAp22, NeurIPS 2012–2017, ICML 2015, 2018, ...

## SCIENTIFIC COMMITTEES

	COUNCILS
<i>since 2022</i>	Member of the <a href="#">FMJH</a> council
<i>since 2020</i>	Member of the Steering Committee of <a href="#">Digit-Bio</a> INRAE Metaprogramme
<i>since 2020</i>	Nominated member of the Scientific Council of the INRAE Animal Genetics division
<i>2018–2021</i>	Elected member of the Council of the French Statistical Society
<i>2016–2020</i>	Elected member of the Scientific Council of the INRAE Math-Info division
	BOARD OF RECRUITMENT
<i>Assistant Professor</i>	2021 : Paris 1 (26 <sup>e</sup> ) ; 2020 : Nancy (26 <sup>e</sup> ) ; 2019 : Évry (26 <sup>e</sup> ) ; 2016 : Paris Sud (64-65 <sup>e</sup> ) ; 2015 : Paris Sud (87 <sup>e</sup> ) ; 2013 : Paris 5 (26 <sup>e</sup> ) ; 2012 : Rouen (26 <sup>e</sup> ) ; 2011 : Picardie (87 <sup>e</sup> ) · Paris Sud (67 <sup>e</sup> ) · Évry (26 <sup>e</sup> ) ; 2010 : Évry (26 <sup>e</sup> )
<i>INRAE</i>	2024 : 3 Researcher ; 2023 : 1 Researcher ; 2022 : 1 Researcher ; 2021 : 2 Researcher, 1 IR ; 2018 : 4 Researcher, 2012 : 4 Research Engineer
	HABILITATION REVIEWING
<i>2022</i>	Romain Azaïs ; Matthieu Marbac
	PHD REVIEWING
<i>2023</i>	Paul Denailly ; Ariane Marandon ; Bastien Chassagnol ; Giulia Marchello Member : Louis Raimbault
<i>2022</i>	Florent Bascou ; Eunice Okome Obiang ; Member : Pierre Drouin
<i>2021</i>	Aude Sportisse ; Member : Gabriel Frisch
<i>2020</i>	Yaroslav Averyanov ; Member : Vincent Prost, Nicolas Jouvin
<i>2019</i>	Florian Privé, Arnaud Cougoul, Vivien Goepp ; Perrine Soret Member : Clémence Karmann, Beyrem Khalfaoui
<i>2018</i>	May Taha
<i>2017</i>	Thomas Dias-Alvès ; Member : Pierre-Alexandre Mattéi
<i>2016</i>	Samuel Balmand, Quentin Grimonprez, Rawya Zreik ; Member : Niels Ternes
	PHD FOLLOW-UP
<i>since 2014</i>	15 Students

## STUDENTS

since 2023	SIHAN XIE
PhD	<i>DeepSelectGene : Apprentissage profond à partir de données de génotypes et application à la sélection génomique</i>
Supervision	supervision (20%) with E. Barrey, DR INRAE and B. Hanczar (PR Évry)
since 2023	JEANNE TOUS
PhD	<i>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</i>
Supervision	supervision (80%) with W. Thuillier (20%), DR CNRS
since 2021	BASTIEN BATARDIÈRE
PhD	<i>Statistical Learning for Multivariate Analysis of High Dimensional Count Data</i>
Supervision	supervision (70%) with J. Kwon (30%), CR INRAE

## PHD AND POST-DOC – ALUMNI

2019 – 2020	CLAIRE GAYRAL
PhD	<i>Single-cell data integration</i>
Supervision	50% with F. Picard DR CNRS, Lyon
2017–2020	MARTINA SUNDQVIST
PhD	<i>Multi-omic data integration for new classification in triple-negative breast cancer</i>
Supervision	50% with T. Dubois DR, Institut Curie and G. Rigai, CR, INRA
2017–2020	AUDREY HULOT
PhD	<i>Analyse de données-omiques : clustering et inférence de réseaux</i>
Supervision	25% with F. Jaffrezic, DR, Inra (50%) ; H.-J. Garchon, PUPH, Inserm (25%)
2016–2019	TIMOTHÉE TABOUY
PhD	<i>Modeling and inferring sampling design in probabilistic random network models</i>
Supervision	50% with P. Barbillon, Assoc. Prof., AgroParisTech
2016–2019	MARIE PERROT-DOCKES
PhD	<i>Regularization tools for multivariate analysis : application to multi-omics</i>
Supervision	50% with Céline Lévy-Leduc, Prof., AgroParisTech
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. Rigai, 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'allopolyploidie chez le blé</i>
Supervision	25% with Boulos Chaloub, DR 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 TcLand <a href="http://www.tcland-expression.com">www.tcland-expression.com</a>
2009–2012	CAMILLE CHARBONNIER
PhD	<i>Inference of gene regulatory networks from non-iid transcriptomic data</i>
Supervision	50% with Christophe Ambroise, Prof., Évry

## TEACHING ACTIVITIES

Approximately 2000 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).

2020-24 <i>Msc</i>	STATISTICS IN ACTION WITH R Probabilistic models, data analysis, R programming
2020-21 <i>Msc</i> <i>web</i>	DATA ANALYSIS AND UNSUPERVISED LEARNING Data and Graph Clustering, Mixture model, Stochastic Block Model <a href="https://github.com/jchiquet/CourseUnsupervisedLearningX">https://github.com/jchiquet/CourseUnsupervisedLearningX</a>
2018-19 <i>Msc</i> <i>web</i>	AN INTRODUCTION TO GRAPH ANALYSIS AND MODELING (36h course/practicals) Descriptive Analysis of networks, Stochastic Block Model, Graphical Lasso <a href="https://github.com/jchiquet/CourseStatNetwork">https://github.com/jchiquet/CourseStatNetwork</a>
2015-18 <i>Msc</i> <i>web</i>	INTRODUCTION REGULARIZATION FOR REGRESSION (154h course/practicals) Ridge, Lasso, variable selection, model selection <a href="https://github.com/jchiquet/CourseRegLinearRegression">https://github.com/jchiquet/CourseRegLinearRegression</a>
2017 <i>Msc</i>	A SHORT INTRODUCTION TO CONVEX OPTIMIZATION (12h course) (sub)-gradient methods, Newton method, Proximal methods
2010,15,16 <i>undergraduate</i> <i>MSc</i>	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 <i>undergraduate</i> <i>web</i>	R PROGRAMMING AND STATISTICS (60h course/practicals) Data and control structures, Hypothesis testing, Linear model <a href="http://julien.cremierfamily.info/teachings_L3BI_ISV51.html">http://julien.cremierfamily.info/teachings_L3BI_ISV51.html</a>
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 (148h practicals) Continuity, Differentiation, Integration, Taylor Series, ODE, mechanics, <b>Maple</b>
2005–11 <i>undergraduate</i>	PROBABILITY AND STATISTIC (39h course, 339h practicals) Random variables, Random Vectors, Independence, Conditioning, Convergence ; Inference, Hypothesis Testing, Confidence Intervals
2008–10 <i>undergraduate</i>	MATHEMATICAL MODELS FOR BIOLOGY (9h course, 35h practicals) dynamic population models, Lotka-Volterra ; sequence analysis, Markov models.
2007–09 <i>MSc</i>	NUMERICAL METHODS FOR EDP (66h practicals) Euler, Runge-Kutta and Newton methods, <b>Scilab</b>
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 $\text{\LaTeX}$ (12h course/practicals) Typography basics, Typesetting math, Bibliography, Index, Style-sheet



## PAPERS

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### PREPRINT

- [PP1] 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*, submitted.
- [PP2] 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. 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/jrssc/qlad058, URL <https://doi.org/10.1093/jrssc/qlad058>.
- [JP2] 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.
- [JP3] E. Delannoy, B. Batardiere, 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.
- [JP4] 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>.
- [JP5] 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>.
- [JP6] M. Sundqvist, J. Chiquet, and G. Rigai, *Adjusting the adjusted rand index - a multinomial story*, Computational Statistics, 2022, doi :10.1007/s00180-022-01230-7.
- [JP7] 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.
- [JP8] 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.
- [JP9] 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.
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## TALKS

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## SOFTWARE

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