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Current position

- Research Scientist (*Chargée de Recherche*) at the French National Institute for Agricultural Research (INRA), Jouy en Josas
- AgreenSkills+ Visiting Scholar (October 2017 - May 2019), University of Wisconsin-Milwaukee
- Adjunct Assistant Professor (January 2019 - June 2020), Medical College of Wisconsin

Education

- 2017 **HDR* in Applied Mathematics**, Université d'Évry-Val-d'Essonne (Évry, France) obtained September 26, 2017.
Title : Statistical methods and software for the analysis of transcriptomic data.
*An HDR is the French accreditation to supervise research and represents the highest French academic qualification level based on independent scholarship. It is reviewed by and defended before an academic committee.
- 2007–2010 **Ph.D. in Statistics**, Purdue University (West Lafayette, Indiana, USA) obtained August 6, 2010.
Title : Reverse engineering gene regulatory networks using genomic time-course data.
Advisors : Rebecca W. Doerge, Jean-Louis Foulley, and Florence Jaffrézic
- 2005–2007 **M.S. (Master of Science) in Applied Statistics**, Purdue University (West Lafayette, Indiana, USA).
Internship : Using time series and intervention models to analyze the effect of advertising changes on store sales for the pharmacy chain Walgreens (Deerfield, Illinois, USA)
- 2001–2005 **B.A. (Bachelor of Arts) in French and B.A. in Mathematics**, concentration in Statistics (with distinction), Saint Olaf College (Northfield, Minnesota, USA).
Internship : Application of pharmacokinetic analysis literature to data from a Phase I clinical trial and determination of a limited-sample model, under the direction of Alfred Furth at the Mayo Clinic (Rochester, Minnesota, USA)

Work experience

2017-present	AgreenSkills+ Visiting Scholar (20 months), Zilber School of Public Health, University of Wisconsin-Milwaukee
2016-present	Research Scientist (<i>Chargée de Recherche</i>), INRA (Jouy-en-Josas, France)
2016	Visiting Scholar (6 weeks), Zilber School of Public Health, University of Wisconsin-Milwaukee
2012-2017	Adjunct Assistant Professor , Ensai (Rennes, France)
2011-2016	Junior Research Scientist (<i>Chargée de Recherche</i> 2nd class, CR2), INRA (Jouy-en-Josas, France)
2010-2011	Post-doctoral researcher , Inria - Île-de-France (Orsay, France) <i>Subject</i> : Clustering RNA sequencing data. <i>Advisors</i> : Gilles Celeux and Marie-Laure Martin-Magniette
2008-2010	Research assistant for R. W. Doerge, Department of Statistics at Purdue University (West Lafayette, Indiana, USA)
2007	Consultant in the Statistical Consulting Service, Department of Statistics at Purdue University (West Lafayette, Indiana, USA)

Research subjects

Research themes : Gene regulatory networks, analysis of high-throughput sequencing data (RNA-seq, ATAC-seq), mixture models, supervised classification methods

Areas of application : Genomic and transcriptomic data

Skills

<i>Computing</i>	Operating systems	Linux, Windows
	Languages	C, HTML
	Programs	R, \LaTeX
<i>Languages</i>	English	Maternal language
	French	Fluent (read, written, spoken)

Awards

• Graduate Women in Science Programs travel award	2010
• Student travel award, Conference on Applied Statistics in Agriculture at Kansas State University	2010
• VIGRE Fellowship, Purdue University	2005-2010
• Honorable mention, Gertrude M. Cox Scholarship	2009
• Graduate student scholarship, Gordon Conference on Quantitative Genetics and Genomics	2009
• BioC Conference graduate student scholarship	2009

- A.H. Ismail Interdisciplinary Program doctoral research travel award 2009
- Buntrock academic scholarship, Saint Olaf College 2001
- National Merit Scholar 2001
- Presidential Scholar 2001

Professional organizations

- Société Française de Statistique (SFdS, 2011-present)
- American Statistical Association (ASA, 2005-present)

Books

1. Albert, I., Ancelet, S., David, O., Denis, J.-B., Makowski, D., Parent, É., **Rau, A.**, and Soubeyrand, S. (2015). *Initiation à la statistique bayésienne : Bases théoriques et applications en alimentation, environnmenet, épidémiologie et génétique* : Éditions Ellipses, collection références sciences.

Peer-reviewed articles

Statistical Methods

1. **Rau, A.**, Flister, M. J., Rui, H. and Livermore Auer, P. (2018) Exploring drivers of gene expression in The Cancer Genome Atlas. *Bioinformatics*, doi : <https://doi.org/10.1101/227926>.
2. Godichon-Baggioni, A., Maugis-Rabusseau, C. and **Rau, A.** (2018) Clustering transformed compositional data using K-means, with applications in gene expression and bicycle sharing system data. *Journal of Applied Statistics*, <https://doi.org/10.1080/02664763.2018.1454894>.
3. **Rau, A.** and Maugis-Rabusseau, C. (2018) Transformation and model choice for RNA-seq co-expression analysis. *Briefings in Bioinformatics*, bbw128, <https://doi.org/10.1093/bib/bbw128>.
4. Monneret, G., Jaffrézic, F., **Rau, A.**, Zerjal, T. and Nuel, G. (2017) Identification of marginal causal relationships in gene networks from observational and interventional expression data. *PLoS One* 12(3) : e0171142.
5. Rigai, G., Balzergue, S., Brunaud, V., Blondet, E., **Rau, A.**, Rogier, O., Caius, J., Maugis-Rabusseau, C., Soubigou-Taconnat, L., Aubourg, S., Lurin, C., Martin-Magniette, M.-L., and Delannoy, E. (2016) Synthetic datasets for the identification of key ingredients for RNA-seq differential analysis. *Briefings in Bioinformatics*, doi : <https://doi.org/10.1093/bib/bbw092>.
6. Gallopin, M., Celeux, G., Jaffrézic, F., **Rau, A.** (2015) A model selection criterion for model-based clustering of annotated gene expression data. *Statistical Applications in Genetics and Molecular Biology*, 14(5) : 413-428.
7. Monneret, G., Jaffrézic, F., **Rau, A.**, Nuel, G. (2015). Estimation d'effets causaux dans les réseaux de régulation génique : vers la grande dimension. *Revue d'intelligence artificielle*, 29(2) : 205-227.
8. **Rau, A.**, Maugis-Rabusseau, C., Martin-Magniette, M.-L., Celeux, G. (2015) Co-expression analysis of high-throughput transcriptome sequencing data with Poisson mixture models. *Bioinformatics*, 31(9) : 1420-1427.

9. **Rau, A.**, Marot, G., and Jaffrézic, F. (2014). Differential meta-analysis of RNA-seq data from multiple studies. *BMC Bioinformatics* 15:91.
10. Nuel, G., **Rau, A.**, and Jaffrézic, F. (2014) Using pairwise ordering preferences to estimate causal effects in gene expression from a mixture of observational and intervention experiments. *Quality Technology and Quantitative Management* 11(1):23-37.
11. **Rau, A.**, Jaffrézic, F., and Nuel, G. (2013) Joint estimation of causal effects from observational and intervention gene expression data. *BMC Systems Biology* 7:111.
12. Gallopin, M. **Rau, A.**, and Jaffrézic, F. (2013). A hierarchical Poisson log-normal model for network inference from RNA sequencing data. *PLoS One* 8(10) : e77503.
13. **Rau, A.**, Gallopin, M., Celeux, G., and Jaffrézic, F. (2013). Data-based filtering for replicated high-throughput transcriptome sequencing experiments. *Bioinformatics* 29(17) : 2146-2152.
14. Dillies, M.-A.*, **Rau, A.***, Aubert, J.*, Hennequet-Antier, C.*, Jeanmougin, M.*, Servant, N.*, Keime, C.*, Marot, G., Castel, D., Estelle, J., Guernec, G., Jagla, B., Jouneau, L., Laloë, D., Le Gall, C., Schaëffer, B., Charif, D., Le Crom, S.*, Guedj, M.*, and Jaffrézic, F*. (2013). A comprehensive evaluation of normalization methods for Illumina high-throughput RNA sequencing data analysis. *Briefings in Bioinformatics* 14(6) : 671-683.
* These authors contributed equally to this work.
15. **Rau, A.**, Jaffrézic, F., Foulley, J.-L., and Doerge, R. W. (2012). Reverse engineering gene regulatory networks using approximate Bayesian computation. *Statistics and Computing*, 22 : 1257-1271.
16. **Rau, A.**, Jaffrézic, F., Foulley, J.-L., and Doerge, R. W. (2010). An empirical Bayesian method for estimating biological networks from temporal microarray data. *Statistical Applications in Genetics and Molecular Biology* : Vol. 9 : Iss. 1, Article 9.

Statistical Applications

1. Verrier, E., Genet, C., Laloë, D., Jaffrézic, J., **Rau, A.**, Esquerré, D., Dechamp, N., Ciobartaru, C., Hervet, C., Krieg, F., Quillet, E., Boudinot, P. (2018) Genetic and transcriptomic analyses provide new insights on the early antiviral response to VHSV in resistant and susceptible rainbow trout. *BMC Genomics*, 19 :482.
2. Maroille, T., Berri, M., Lemonnier, G., Esquerré, D., Chevalé, C., Mélo, S., Meurens, F., Coville, J.L., Leplat, J.J, **Rau, A.**, Bedhomme, B., Vincent-Naulleau, S., Mercat, M.J., Billon, Y., Lepage, P., Rogel-Gaillard, C., and Estellé, J. (2018). Immunome differences between porcine ileal and jejunal Peyer's patches revealed by global transcriptome sequencing of gut-associated lymphoid tissues. *Scientific Reports*, 8 :9077.
3. Mondet, F., **Rau, A.**, Klopp, C., Rohmer, M. Severac, D., Le Conte, Y., and Alaux, C. (2018). Transcriptome profiling of the honeybee parasite *Varroa destructor* provides new biological insights into the mite adult life cycle. *BMC Genomics*, 19 :328.
4. He, B., Tjhung, K., Bennett, N., Chou, Y., **Rau, A.**, Huang, J., and Derda, R. (2018). Compositional bias in naïve and chemically-modified phage-displayed libraries uncovered by paired-end deep sequencing. *Scientific Reports*, 8 :1214.
5. Sauvage, C., **Rau, A.**, Aichholz, C., Chadoeuf, J., Sarah, G., Ruiz, M., Santoni, S., Causse, M., David, J., Glémin, S. Domestication rewired gene expression and nucleotide diversity patterns in tomato. *The Plant Journal* 91(4) :631-645..
6. Endale Ahanda, M.-L., Zerjal, T., Dhorne-Pollet, S., **Rau, A.**, Cooksey, A., and Giuffra, E. (2014) Impact of the genetic background on the composition of the chicken plasma miRNome in response to a stress. *PLoS One*, 9(12) : e114598.

7. Brenault, P., Lefevre, L. **Rau, A.**, Laloë, D., Pisoni, G., Moroni, P., Bevilacqua, C. and Martin, P. (2014) Contribution of mammary epithelial cells to the immune response during early stages of a bacterial infection to *Staphylococcus aureus*. *Veterinary Research* 45:16.
8. Furth, A., Mandrekar, S., Tan, A. **Rau, A.**, Felten, S., Ames, M. Adjei, A. Erlichman, C. and Reid, J. (2008). A limited sample model to predict area under the drug concentration curve for 17-(allylamino)-17-demethoxygeldanamycin and its active metabolite 17-(amino)-17-demethoxygeldanamycin. *Cancer Chemotherapy Pharmacology* 61(1) : 39-45.

Peer-reviewed conference proceedings

1. **Rau, A.**, Jaffrézic, F., Foulley, J.-L., and Doerge, R. W. (2010). Approximate Bayesian approaches for reverse engineering biological networks. *Proceedings of the Kansas State University Conference on Applied Statistics in Agriculture*. Manhattan, Kansas.

Book chapters

1. Martin-Magniette, M.-L., Maugis-Rabuseau, C., **Rau, A.** (2016) Clustering of co-expressed genes. In : Choix et agrégation de modèles : Journée d'Etudes Statistiques (to appear).

Pre-prints, technical reports, and submitted articles

1. Foissac, S., Djebali, S., Munyard, K., Villa-Vialaneix, N., **Rau, A.**, Muret, K., Esquerré, D., Zytnicki, M., Derrien, T., Bardou, P., Blanc, F., Cabau, C., Crisci, E., Dhorne-Pollet, S., Drouet, F., Gonzales, I., Goubil, A., Lacroix-Lamande, S., Laurent, F., Marthey, S., Marti-Marimon, M., Momal-Leisenring, R., Mompert, F., Quere, P., Robelin, D., San Cristobal, M., Tosser-Klopp, G., Vincent-Naulleau, S., Fabre, S., Pinard-Van der Laan, M.-H., Klopp, C., Tixier-Boichard, M., Acloque, H., Lagarrigue, S., Giuffra, E. Livestock genome annotation : transcriptome and chromatin structure profiling in cattle, goat, chicken, and pig. *bioRxiv*, doi : <https://doi.org/10.1101/316091>.
2. Nuel, G., **Rau, A.**, and Jaffrézic, F. (2013). Joint likelihood calculation for intervention and observational data from a Gaussian Bayesian network. *arXiv preprint arXiv:1305.0709*.
3. **Rau, A.**, Celeux, G., Martin-Magniette, M.-L., and Maugis-Rabuseau, C. (2011). Clustering high-throughput sequencing data with Poisson mixture models. *Inria Research Report* 7786.

Other publications

1. **Rau, A.** (2008). Success of Volunteer Statistical Consulting Service Leads to Expanded Network. *The Statistical Consultant*, 25(1).
2. **Rau, A.** (2008). STATCOM Network Engages Growing Number of Student Volunteers. *Newsletter for the Section on Statistical Education*, 13(1).
3. **Rau, A.** (2008). Success of Statistical Service Leads to Expanded Network. *Amstat News*, April 2008.

Conference presentations

- Jan. 2018 Plant and Animal Genomes (PAG) XXVI, San Diego, California, USA
coseq : An R/Bioconductor package for co-expression analyses of RNA-seq data
- Jan. 2018 Plant and Animal Genomes (PAG) XXVI, San Diego, California, USA
Invited talk (FAANG workshop) : *An update on the FAANG pilot project FR-AgENCODE*
- July 2017 Working Group on Model-Based Clustering, Perugia, Italy
Invited talk : *Model-based clustering to identify co-expressed genes from high-throughput sequencing data*
- July 2017 useR!2017, Brussels, Belgium
Clustering transformed compositional data using coseq
- July 2016 Joint Statistical Meetings of the American Statistical Association, Chicago
Identifying marginal causal relationships in gene networks from observational and interventional expression data
- May 2016 2nd International Symposium on Microgenomics, Technical Workshop, Jouy-en-Josas
Invited talk : *Experimental design in 'omics studies*
- Feb. 2015 15th Workshop : Statistical Methods for Post-Genomic Data, Munich
HTSCluster : a mixture-based approach for co-expression analyses of RNA-seq data
- Nov. 2013 Statistical analysis of RNA-seq data : Advances and challenges, Paris
HTSDiff : More sensitive differential analysis of RNA-seq data
- June 2013 Deuxièmes rencontres R, Lyon
HTSFilter : Data-based filtering for replicated high-throughput sequencing experiments
- May 2013 Journée de la transcriptome végétale de l'URGV-Genopole, Evry
Invited round table : *Statistics applied to RNA-seq*
- Mar. 2013 StatSeq meeting on genetical genomics, Paris
Joint estimation of causal effects from observational and intervention gene expression data
- Oct. 2012 Journée APLIBIO (Alliance des PLates-formes Île-de-France de BIOinformatique), Paris
Invited talk : *A comprehensive evaluation of normalization methods for high-throughput RNA sequencing data analysis*
- July 2012 Joint Statistical Meetings of the American Statistical Association, San Diego, California
Clustering high-throughput sequencing data using Poisson mixture models
- Jan. 2012 12th Workshop : Statistical Methods for Post-Genomic Data, Lyon
Clustering high-throughput sequencing data using Poisson mixture models
- Apr. 2011 StatSeq Workshop, Toulouse
Invited talk : *Model-based cluster analysis for transcriptomic data* (G. Celeux, speaker)
- Jan. 2011 11th Workshop : Statistical Methods for Post-Genomic Data, Paris
Reverse Engineering Gene Networks Using Approximate Bayesian Computation
- Apr. 2010 Conference on Applied Statistics in Agriculture, Manhattan, Kansas
Approximate Bayesian methods for reverse engineering biological networks
- Sep. 2009 GENESYS Satellite Meeting at the European Conference on Complex Systems, Warwick, UK
Reverse-Engineering Gene Networks from Microarray Data with Dynamic Bayesian Networks
- Aug. 2009 Joint Statistical Meetings of the American Statistical Association, Washington, DC
Using Dynamic Bayesian Networks with Hidden States to Infer Gene Regulatory

Networks

- May 2009 2nd Biennial Workshop on Statistical Bioinformatics and Stochastic Systems Biology, Newcastle, UK
Poster : *Reverse-Engineering Genetic Regulatory Interactions from Transcriptomic Data using Dynamic Bayesian Networks*
- Apr. 2009 Conference on Applied Statistics in Agriculture, Manhattan, Kansas
Poster : *An Empirical Bayes Approach to Inferring Genetic Regulatory Interactions with Dynamic Bayesian Networks*
- Feb. 2009 Gordon Conference on Quantitative Genetics and Genomics, Galveston, Texas
Poster : *An Empirical Bayes Approach to Inferring Genetic Regulatory Interactions with Dynamic Bayesian Networks*
- Aug. 2008 Joint Statistical Meetings of the American Statistical Association, Denver, Colorado
Poster : *Seven Years of StatCom at Purdue : Managing a Growing Number of Student Volunteers*

Seminar and working group presentations

- June 2018 MixStatSeq Workshop on Mixture Models : Theory and Application, Paris
Co-expression analyses of RNA-seq data in practice with the R/Bioconductor package coseq
- March 2018 Physiology Department Seminar at MCW, Milwaukee, Wisconsin
Exploring drivers of gene expression in The Cancer Genome Atlas
- June 2017 INRA national bioinformatics workshop, Dijon
Easy interactivity in R with (gg)plotly and Shiny
- Mar. 2017 SAPS doctoral school : Experimental animal biology and predictive modelisation
Challenges in data integration
- Nov. 2016 INRA RNA-seq day, Avignon
Invited talk : *Statistical tools to identify and visualize co-expression clusters from RNA-seq data*
- Sep 2016 Seminar at the Human and Molecular Genetics Center, Milwaukee College of Medicine
Transformation, model choice, and visualization for RNA-seq co-expression
- Sep 2016 Seminar at the Zilber School of Public Health, Milwaukee, Wisconsin
Transformation, model choice, and visualization for RNA-seq co-expression
- May 2016 Groupe de travail de statistiques du LMRS de Rouen
Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression
- Mar. 2016 INRA national bioinformatics workshop, Toulouse
From genotype to phenotype : what statistical methods to integrate heterogeneous data ?
- Mar. 2016 SAPS doctoral school : Experimental animal biology and predictive modelisation
Integration of heterogeneous 'omics data
- Mar. 2016 INRA NGS club, Jouy-en-Josas
Poisson mixture models and visualization tools for RNA-seq co-expression
- Jan. 2016 MAP5 seminar at Université Paris-Descartes
Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression
- Jan. 2016 4th Annual SFdS Young Statisticians and Probabilists Day, Paris
Model selection in mixture model based classification : Applications in biostatistics
- Nov. 2015 Seminar at Toulouse Mathematics Institute (IMT), Toulouse
Statistical analysis of microarray and RNA-seq data
- Nov. 2015 Statomique seminar, Paris

Integrative clustering and classification in multiple heterogeneous data

- Sep. 2015 NETBIO working group, Paris
RNA-seq co-expression analysis using mixture models
- Sep. 2015 Cirad seminar, Montpellier
HTScluster : a mixture-based approach for co-expression analyses of RNA-seq data
- Oct. 2014 SELECT seminar, Orsay
Slope heuristics : the missing ingredient for identifying co-expressed genes from RNA-seq data
- Nov. 2013 Statistics for Systems Biology (SSB) seminar, Evry
HTSFilter : filtering replicated RNA-seq data using a data-driven approach
- Nov. 2013 Seminar at INRA-GABI, Jouy-en-Josas
Reinforcing the biology-statistics feedback loop with tools for genomic data analysis
- Oct. 2013 Statistics for Integrative Biology (SIB) seminar, Rennes
HTSAnalysis : a suite of R/Bioconductor packages for the analysis of RNA-seq data
- Sep. 2013 NETBIO working group, Paris
Joint estimation of causal effects from observational and intervention gene expression data
- June 2013 Statistique et Santé working group, Paris
Joint estimation of causal effects from observational and intervention gene expression data
- June 2013 AppliBUGS Workshop, Paris
Joint estimation of causal effects from observational and intervention gene expression data
- June 2013 Statistics seminar, Toulouse
Joint estimation of causal effects from observational and intervention gene expression data
- Feb. 2013 Statistics for Integrative Biology seminar, Rennes
Joint estimation of causal effects from observational and intervention gene expression data
- Dec. 2012 Assemblée générale PEPI IBIS, Toulouse
Differential analysis of RNA-seq data by unsupervised classification
- Nov. 2012 Statomique seminar, Lyon
Independent data-based filtering for replicated high-throughput sequencing experiments
- June 2012 LGC and SAGA seminar at INRA, Toulouse
Clustering high-throughput sequencing data using Poisson mixture models
- June 2012 SSB working group seminar, Jouy en Josas
Clustering high-throughput sequencing data using Poisson mixture models
- Feb. 2012 MIA “Biological network inference” methodological working group meeting, Paris
Inferring gene regulatory networks with hidden variables using state space models
- Dec. 2011 AppliBugs Workshop, Paris
Exploring the identifiability of gene regulatory networks with approximate Bayesian computation
- May 2011 Seminar at the Institut de Recherche Mathématique Avancée, Strasbourg
Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)
- Apr. 2011 Seminar at the Unité de Recherche en Génomique Végétale, Évry
Reverse Engineering Gene Networks : A Statistician’s Perspective
- Apr. 2011 Seminar at the Institut de Mathématiques de Luminy, Marseille
Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)
- Mar. 2011 Seminar at the Laboratoire Statistique et Génome, Évry

- Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)*
- Mar. 2011 Seminar at the équipe Génétique et Génomique Statistique, Le Kremlin Bicêtre
Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)
- Jan. 2011 Rencontre de statistique autour des modèles hiérarchiques, Strasbourg
Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)
- Oct. 2010 INA P-G, Paris Descartes, and SELECT working group, Paris
Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)
- Apr. 2010 Bioinformatics seminar at Purdue University, West Lafayette, Indiana
Approximate Bayesian methods for reverse engineering biological networks
- June 2009 Seminar at the AgroParisTech, Paris
Inférence sur les réseaux génomiques par des modèles espace-état
- June 2009 Seminar at the UMR GABI-INRA, Jouy-en-Josas
Inférence sur les réseaux génomiques par des modèles espace-état
- Mar. 2009 Ph.D. student seminar, INRA Département de Génétique Animale, Jouy-en-Josas
Reverse Engineering Gene Regulatory Networks
- Mar. 2008 Ph.D. student seminar, INRA Département de Génétique Animale, Toulouse
Poster : *Inferring Gene Regulatory Network through Linear Feedback State Space Models*

Participation in working groups and seminars

- Statistique working group (quarterly, 2009-present)

Software and R packages

- **maskmeans** : Multi-view aggregation/splitting K-means clustering algorithm
Available on GitHub at <https://github.com/andreamrau/maskmeans>.
- **EDGE in TCGA** : An R/Shiny interactive web application for the exploration of drivers of gene expression in The Cancer Genome Atlas
Available at http://ls-shiny-prod.uwm.edu/edge_in_tcg/.
- **coseq** : Co-expression analysis of sequencing data
Available on Bioconductor at <https://bioconductor.org/packages/coseq/>.
- **ICAL** : Model selection for model based clustering of annotated data
Available on Github at <https://github.com/Gallop/ICAL>.
- **metaRNASeq** : Meta-analysis of RNA-seq data
Available on CRAN at <http://cran.r-project.org/web/packages/metaRNASeq>.
- **HTSFilter** : Filter for replicated high-throughput sequencing data
Available on Bioconductor at www.bioconductor.org/packages/HTSFilter/.
- **HTScluster** : Clustering high throughput sequencing data
Available on CRAN at <http://cran.r-project.org/web/packages/HTScluster>.
- **ebdbNet** : Empirical Bayes estimation for Dynamic Bayesian Networks
Available on CRAN at <http://cran.r-project.org/web/packages/ebdbNet>.

Administrative activities and service

Reviewer *Revue d'Intelligence Artificielle, IEEE Proceedings, Statistical Applications in*

Genetics and Molecular Biology, BMC Bioinformatics, BMC Genomics, RNA, Nucleic Acids Research, Molecular Genetics and Genomics, F1000 Research Bioinformatics, Computational and Structural Biotechnology Journal

- 2010 Chair, Committee on Student Pro Bono Statistics of the ASA
- 2009–2010 Member, Committee on Student Pro Bono Statistics of the American Statistical Association (ASA)
- 2009 Organizer of an invited round table (*The Pros of Pro Bono Statistics*) at the Joint Statistical Meetings of the American Statistical Association (ASA) in Washington, DC, USA
- 2006–2010 Member, Statistics in the Community (StatCom) at Purdue University : StatCom is a volunteer organization of graduate students that provides free professional statistical consulting services to government and nonprofit groups

Funding

Past Research Support

- **MixStatSeq** : Mixture-based procedures for statistical analysis of RNA-seq data
Principal investigator : Cathy Maugis-Rabusseau (IMT, Toulouse)
Role : Co-investigator
Funding period : March 2014 - February 2018
Agency : French National Research Agency (ANR) grant (ANR-13-JS01-0001-01)
- **SalmoCar** : Genetic and microbiotal control of *Salmonella* carriage in chicken and mice
Principal investigator : Xavier Montagutelli (Institut Pasteur, Paris)
Role : Co-investigator
Funding period : January 2015 - December 2017
Agency : Institut Carnot Pasteur Maladies Infectieuses (PMI) / Institut Carnot Santé Animale (ICSA) grant
- **COSI-net** : Using COMbinatorial gene Silencing & Inactivation to infer gene NETworks
Principal investigator : Andrea Rau (INRA, Jouy en Josas)
Funding period : August 2015 - December 2016
Agency : INRA Animal Genetics Department internal grant
- **Causality** : Causal network inference
Principal investigator : Florence Jaffrézic (INRA, Jouy en Josas)
Role : Co-investigator
Funding period : January 2014 - December 2014
Agency : INRA Animal Genetics Department internal grant

Advising

Alumni

- Dr. Gilles Monneret (2014-2017, Ph.D., co-supervision with F. Jaffrézic and G. Nuel)
Estimation of causal effects in gene networks from observational and intervention data
- Raphaëlle Momal-Leisenring (2017, M2 intern)
Integrative statistical analysis of multi-omics data

- Frédéric Jehl (2017, M2 intern, co-supervision with T. Zerjal)
Impact of heat stress on liver and blood transcriptomes of laying hens
- Dr. Manuel Revilla Sanchez (2016 3-month Ph.D. Erasmus+ Learning Mobility, co-supervision with Jordi Estelle and Yulixaxis Ramayo Caldas and Ph.D. manuscript *rapporteur*)
An integrative gene network analysis of the genetic determination of pig fatty acid composition
- Babacar Ciss (2016, M2 intern, co-supervision with E. Sellem)
Constructing predictive models for ovine production data
- Dr. Méline Gallopin (2012-2015, Ph.D., co-supervision with G. Celeux and F. Jaffrézic)
Classification and network inference for RNA-seq data
- Audrey Hulot (2015, M1 intern)
Incorporating a priori biological knowledge into gene network inference from observational and intervention gene expression data
- Meriem Benabbas (2015, M1 intern)
Identifying differentially expressed genes from RNA-seq data using mixtures of generalized linear models
- Marc Teissier and Chaoyu Dong (2014, Master STV/EM-ABG)
Power to detect significantly differential gene expression using RNA-seq data
- Méline Gallopin (2012, M2 intern)
Gene network inference from RNA-seq data
- Rémi Bancal (2012, M2 intern)
Gene network estimation by adaptive knockout experiments

Membership in advisory and evaluation committees

- Dr. Alyssa Imbert (2018, member of Ph.D. evaluation committee)
- Frédéric Jehl (2017-2020, member of Ph.D. advisory committee)
- Gabriel Guillocheau (2016-2018, member of Ph.D. advisory committee)
- Dr. Valentin Voillet (2016, member of Ph.D. evaluation committee)
- Member of evaluation committee for assistant professor position at Université Rennes I, UMR Inserm IRSET 1085 (2016)
- Member of evaluation committee for assistant professor position at Université Rennes I, IGDR (Institute of Genetics and Developmental biology of Rennes), CNRS UMR 6290 (2013)

Teaching

- 2018 **Data management and visualization in R** (3 course units)
Type : Instructor
• University of Wisconsin-Milwaukee
- 2017 **PiGutNet Training School** (3 hours)
Differential abundance analysis for microbial marker-gene surveys with *metagenomeSeq*
Type : Instructor
• Jouy en Josas
- 2017 **Mathematics for the Life Sciences : Statistical Engineering and Genomics, M2**
Bayesian statistics for genomics course (18 hours)
Type : Instructor (coursework and labs)

- Program* : Bayesian statistics for population genetics, numeric methods for Bayesian computation, empirical Bayes, approximate Bayesian computation, Bayesian integrative analysis of multi-omics data
Supervisor : Marie-Luce Taupin
 • Université d'Évry Val d'Essonne
- 2017 **Agrocampus Researcher School** (1-2 February)
 Statistical analysis of RNA-seq data
Type : Instructor (coursework and labs)
 • Rennes
- 2017 **Biostatistics Master, M2** : Genomics course (12 hours)
Type : Instructor (coursework and labs)
Program : Differential analysis for RNA sequencing data, systems biology approaches for gene network inference
Supervisor : Brigitte Gelein
 • Ensai, Rennes
- 2016 **SPS Summer School : From gene expression to genomic networks** (17-22 July)
 Co-expression analysis of RNA-seq data (3 hours)
Type : Instructor (coursework and labs)
Program : Co-expression, K-means, hierarchical clustering, finite mixture models
Supervisor : Marie-Laure Martin-Magniette
 • Institute of Plant Sciences Paris-Saclay
- 2016 **Mathematics for the Life Sciences : Statistical Engineering and Genomics, M2**
 Bayesian statistics for genomics course (18 hours)
Type : Instructor (coursework and labs)
Program : Bayesian statistics for population genetics, numeric methods for Bayesian computation, empirical Bayes, approximate Bayesian computation, Bayesian integrative analysis of multi-omics data
Supervisor : Marie-Luce Taupin
 • Université d'Évry Val d'Essonne
- 2016 **Agrocampus Researcher School** (10-11 February)
 Statistical analysis of RNA-seq data
Type : Instructor (coursework and labs)
 • Rennes
- 2016 **Biostatistics Master, M2** : Genomics course (33 hours)
Type : Instructor (coursework and labs), and genomics project supervision
Program : Differential analysis for RNA sequencing data, systems biology approaches for gene network inference, and analysis of multi-omic TCGA data
Supervisor : Brigitte Gelein
 • Ensai, Rennes
- 2015 **Mathematical Engineering for Life Sciences Master, M1** : Case study (10 hours)
Type : Instructor (coursework and labs)
Program : Differential analysis for RNA sequencing data, systems biology approaches
Supervisor : Etienne Birmelé
 • Université Paris Descartes, Paris
- 2015 **Biostatistics Master, M2** : Genomics course (33 hours)¹

1. The genomics course at Ensai was significantly expanded and re-developed in 2015 by myself and Mickaël

- Type* : Instructor (coursework and labs), and genomics project supervision
Program : Differential analysis for RNA sequencing data, systems biology approaches for gene network inference, and analysis of the Sequencing Quality Control Consortium RNA-seq and qPCR data
Supervisor : Brigitte Gelein
 • Ensai, Rennes
- 2013 **BioBayes Researcher School** (7-11 October)
 Bayesian statistical methods : Introduction to theory and applications in food, environment, epidemiology, and genetics
Type : Scientific committee member and Instructor (coursework and labs)
 • Cannes Mandelieu
- 2013 **Biostatistics Master, M2** : Genomics course (6 hours)
Type : Instructor (coursework and labs) and genomics project jury member
Program : Differential analysis for RNA sequencing data
Supervisor : Brigitte Gelein
 • Ensai, Rennes
- 2012 **Training school on rabbit and pig genome analysis** (6 hours)
Type : Instructor
Program : Differential analysis for microarray and RNA sequencing data
 • COST action research school, Norwich, United Kingdom
- 2012 **Biostatistics Master, M2** : Genomics course (6 hours)
Type : Instructor (coursework and labs)
Program : Differential analysis for RNA sequencing data
Supervisor : Marian Hristache
 • Ensai, Rennes
- 2012 **Statistical Methods for Genome Enabled Prediction** (2 hours)
Type : Intervenante (cours)
Programme : Approximate Bayesian methods : Application to gene regulatory networks
Enseignant principal : Daniel Gianola
 • European Graduate School in Animal Breeding and Genetics, Paris
- 2012 **Next generation sequencing school for INRA researchers** (2 hours)
Type : Instructor
Program : Differential analysis for RNA sequencing data
 • Research school (INRA), Écully
- 2012 **Bioinformatics and Biostatistics / Mathematical engineering / Probability and Statistics Master, M2** : Computational biostatistics (6 hours)
Type : Instructor (coursework and labs)
Program : Differential analysis for RNA sequencing data
Supervisor : Marc Lavielle
 • UFR de Sciences, Université Paris-Sud 11
- 2011 **Bioinformatics and Biostatistics Master, M1** : Statistical modeling (24 hours)
Type : Lab assistant (R)
Program : Maximum likelihood estimation of non-linear models, Wald and likelihood ratio tests, logistic regression, bootstrap

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Supervisor : Marie-Anne Poursat

• UFR de Sciences, Université Paris-Sud 11

2011 **Bioinformatics and Biostatistics / Mathematical engineering / Probability and Statistics Master, M2** : Computational biostatistics (12 hours)

Type : Instructor (coursework and labs)

Program : Introduction to Bayesian analysis for population genetics, introduction to statistical analysis for transcriptome data

Supervisor : Marc Lavielle

• UFR de Sciences, Université Paris-Sud 11

2006 **1st and 2nd year undergraduate** : Elementary statistical methods (60 hours)

Type : Lab assistant (SPSS)

Program : Descriptive statistics, confidence intervals, simple linear regression, probability calculations, test statistics for means and proportions, correlation

Supervisor : Ellen Gundlach

• Department of Statistics, Purdue University (West Lafayette, Indiana, USA)