

Andrea Rau

RESEARCH SCIENTIST • CHARGÉE DE RECHERCHE

INRAE • French National Research Institute for Agriculture, Food and Environment

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About me

My research is focused on developing and writing software for sound statistical methods for genomic and transcriptomic data analysis, including differential expression analyses, co-expression analyses, network inference, and integrative multi-omic analyses.

I currently belong to two INRAE labs:

- **Animal Genetics and Integrative Biology** (GABI) research unit (Jouy en Josas, France) in the Genomics, Biodiversity, Bioinformatics, Statistics (GiBBS) team
- Cross-border **BioEcoAgro** research unit (Estrées-Mons, France)

Keywords: Analysis of high-throughput sequencing data, mixture models, supervised classification methods, multi-omic integration, gene regulatory networks

Languages: English (maternal), French (fluent)

Education

HDR in Applied Mathematics

UNIVERSITÉ D'ÉVRY-VAL-D'ESSONNE

2017

Évry, France

- Title: "Statistical methods and software for the analysis of transcriptomic data"

Note: 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.

Postdoctoral researcher

INRIA - ÎLE-DE-FRANCE

2010-2011

Orsay, France

- Subject: "Clustering RNA sequencing data"

Advisors: Gilles Celeux and Marie-Laure Martin-Magniette

PhD in Statistics

PURDUE UNIVERSITY

2007-2010

West Lafayette, Indiana, USA

- Title: Reverse engineering gene regulatory networks using genomic time-course data

Advisors: Rebecca W. Doerge, Jean-Louis Foulley, and Florence Jaffrézic

MS in Applied Statistics

PURDUE UNIVERSITY

2005-2007

West Lafayette, Indiana, USA

- Internship: Time series modeling of advertising interventions on pharmacy sales (Walgreens; Deerfield, Illinois, USA)

BA in French and Mathematics (concentration in Statistics)

SAINT OLAF COLLEGE

2001-2005

Northfield, Minnesota, USA

- Internship: pharmacokinetic analysis of Phase I clinical trial data using a limited-sample model (Mayo Clinic; Rochester, Minnesota, USA)

Work experience

Research Scientist (Chargée de Recherche)

INRAE

2011-present

Jouy-en-Josas, France

Adjunct Assistant Professor

MEDICAL COLLEGE OF WISCONSIN (4 MONTHS)

2019

Milwaukee, Wisconsin, USA

AgreenSkills+ Visiting Scholar

ZILBER SCHOOL OF PUBLIC HEALTH, UNIVERSITY OF WISCONSIN-MILWAUKEE (20 MONTHS)

2017-2019

Milwaukee, Wisconsin, USA

Visiting Scholar

ZILBER SCHOOL OF PUBLIC HEALTH, UNIVERSITY OF WISCONSIN-MILWAUKEE (6 WEEKS)

2016

Milwaukee, Wisconsin, USA

Adjunct Assistant Professor

ENSAI

2012-2017

Rennes, France

Post-doctoral researcher

INRIA - ÎLE-DE-FRANCE

2010-2011

Orsay, France

Research assistant

DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY (R. W. DOERGE)

2008-2010

West Lafayette, Indiana, USA

Consultant in the Statistical Consulting Service

DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY

2007

West Lafayette, Indiana, USA

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
- Presidential Scholar 2001

Professional organizations

- SFds Société Française de la Statistique 2011-present
- ASA American Statistical Association 2005-present

Dissertations, books & book chapters

1. Duranthon, V., Araújo, S., Palma, M., **Rau, A.**, Matzapetakis, M., and Almeida, A. (2021) Rabbit research in the post-genomic era: transcriptome, proteome, and metabolome analysis. *In: The Genetics and Genomics of the Rabbit*, Ed. L. Fontanesi.
2. **Rau, A.** (2017) Statistical methods and software for the analysis of transcriptomic data. *HDR thesis*, Université d'Évry Val-d'Essonne.
3. Martin-Magniette, M.-L., Maugis-Rabusseau, C. and **Rau, A.** (2017) Clustering of co-expressed genes. *In: Model Choice and Model Aggregation*, Ed. F. Bertrand, J.-J. Dreesbeke, G. Saporta, C. Thomas-Agnan.
4. 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, environnement, épidémiologie et génétique. *Éditions Ellipses*, collection références sciences.
5. **Rau, A.** (2010) Reverse engineering gene networks using genomic time-course data.. *PhD thesis*, Purdue University.

Peer-reviewed publications

1. Sellem, E., Marthey, S., **Rau, A.**, Jouneau, L., Bonnet, A., Le Danvic, C., Kiefer, H., Jammes, H., and Schibler, L. (2021) Dynamics of cattle sperm sncRNAs during maturation, from testis to ejaculated sperm. *Epigenetics and Chromatin*, to appear.
2. Mach, N., Moroldo, M., **Rau, A.**, Lecardonnel, J., Le Moyec, L., Robert, C., and Barrey, E. (2021) Understanding the holobiont: crosstalk between gut microbiota and mitochondria during endurance. *Frontiers Molecular Biosciences*, 8:656204. <https://dx.doi.org/10.3389/fmolb.2021.656204>
3. Devogel, N., Auer, P. L., Manansala, R., **Rau, A.**, and Wang, T. (2020) A unified linear mixed model for familial relatedness and population structure in genetic association studies. *Genetic Epidemiology*, 45(3): 305-315. <https://dx.doi.org/10.1002/gepi.22371>
4. Cho, Y., **Rau, A.**, Reiner, A., Auer, P. L. (2020) Mendelian randomization analysis with survival outcomes. *Genetic Epidemiology*, 45(1): 16-23. <https://dx.doi.org/10.1002/gepi.22354>
5. Sellem, E., Marthey, S., **Rau, A.**, Jouneau, L., Bonnet, A., Perrier, J.-P., Fritz, S., Le Danvic, C. Boussaha, M., Kiefer, H., Jammes, H., Schibler, L. (2020) A comprehensive overview of bull sperm-borne small non-coding RNAs and their diversity in six breeds. *Epigenetics and Chromatin*, 13:19. <https://dx.doi.org/10.1186/>

6. **Rau, A.**, Manansala, R., Flister, M. J., Rui, H., Jaffrézic, F., Laloë, D., and Auer, P. L. (2020) Individualized multi-omic pathway deviation scores using multiple factor analysis. *Biostatistics*, kxaa029. <https://dx.doi.org/10.1101/827022>
7. Godichon-Baggioni, A., Maugis-Rabusseau, C. and **Rau, A.** (2020) Multi-view cluster aggregation and splitting, with an application to multi-omic breast cancer data. *Annals of Applied Statistics*, 14:2, 752-767.
8. Jehl, F., Désert, C., Klopp, C., Brenet, M., **Rau, A.**, Leroux, S., Boutin, M., Muret, K., Blum, Y., Esquerré, D., Gourichon, D., Burlot, T., Collin, A., Pitel, F., Benani, A., Zerjal, T., Lagarrigue, S. (2019) Chicken adaptive response to low energy diet: main role of the hypothalamic lipid metabolism revealed by a phenotypic and multi-tissue transcriptomic approach. *BMC Genomics*, 20. <https://dx.doi.org/10.1186/s12864-019-6384-8>
9. Foissac, S., Djebali, S., Munyard, K., Villa-Vialaneix, N., **Rau, A.**, Muret, K., Esquerre, 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. (2019) Multi-species annotation of transcriptome and chromatin structure in domesticated animals. *BMC Biology*, 18:48.
10. Dhara, S., **Rau, A.**, Flister, M., Recka, N., Laiosa, M., Auer, P., and Udvadia, A. (2019) Cellular reprogramming for successful CNS axon regeneration is driven by a temporally changing cast of transcription factors. *Scientific Reports*, 9:14198. <https://dx.doi.org/10.1038/s41598-019-50485-6>
11. **Rau, A.**, Dhara, S., Udvadia, A., and Auer, P. (2019) Regeneration Rosetta: An interactive web application to explore regeneration-associated gene expression and chromatin accessibility. *G3: Genes|Genomes|Genetics*, 9(12): 3953-3959. <https://dx.doi.org/10.1534/g3.119.400729>
12. Plasterer, C., Tsaih, S.-W., Lemke, A., Schilling, R., Dwinell, M., **Rau, A.**, Auer, P., Rui, H., Flister, M.J. (2019) Identification of a rat mammary tumor risk locus that is syntenic with the commonly amplified 8q12.1 and 8q22.1 regions in human breast cancer patients. *G3: Genes|Genomes|Genetics*, 9(5): 1739-1743. <https://dx.doi.org/10.1534/g3.118.200873>
13. Ramayo-Caldas, Y., Zingaretti, L., Bernard, A., Estellé, J. Popova, M., Pons, N., Bellot, P., Mach, N., **Rau, A.**, Roume, H., Perez-Encisco, M., Faverdin, P., Edouard, N., Dusko, S., Morgavi, D.P. and Renand, G. (2019) Identification of rumen microbial biomarkers linked to methane emission in Holstein dairy cows. *Journal of Animal Breeding and Genetics*, 137:49-59. <https://dx.doi.org/10.1111/jbg.12427>
14. **Rau, A.**, Flister, M. J., Rui, H. and Livermore Auer, P. (2019) Exploring drivers of gene expression in The Cancer Genome Atlas. *Bioinformatics*, 35(1): 62-68. <https://dx.doi.org/10.1093/bioinformatics/bty551>
15. 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*, 46(1):47-65.
16. **Rau, A.** and Maugis-Rabusseau, C. (2018) Transformation and model choice for RNA-seq co-expression analysis. *Briefings in Bioinformatics*, bbw128. <https://dx.doi.org/10.1093/bib/bbw128>
17. Verrier, E., Genet, C., Laloë, D., Jaffrézic, J., **Rau, A.**, Esquerre, D., Dechamp, N., Ciobataru, 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.
18. Maroilley, T., Berri, M., Lemonnier, G., Esquerré, D., Chevaleyre, C., Mélo, S., Meurens, F., Coville, J.L., Leplat, J.J., **Rau, A.**, Bed'hom, 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.
19. 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.
20. 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.
21. 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.
22. Sauvage, C., **Rau, A.**, Aichholz, C., Chadoeuf, J., Sarah, G., Ruiz, M., Santoni, S., Causse, M., David, J., Glémin, S. (2017) Domestication rewired gene expression and nucleotide diversity patterns in tomato. *The Plant Journal*, 91(4):631-645.
23. 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*, 19(1):65-76. <https://dx.doi.org/10.1093/bib/bbw092>
24. 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.
 25. 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.
 26. **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.
 27. **Rau, A.**, Marot, G. and Jaffrézic, F. (2014) Differential meta-analysis of RNA-seq data from multiple studies. *BMC Bioinformatics*, 16:31.
 28. 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.
 29. Nuel, G., **Rau, A.**, and Jaffrézic, F. (2013) 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.
 30. **Rau, A.**, Jaffrézic, F., and Nuel, G. (2013) Joint estimation of causal effects from observational and intervention gene expression data. *BMC Systems Biology*, 8:51.
 31. 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.
 32. **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.
 33. 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. <https://dx.doi.org/10.1093/bib/bbs046>
 34. Brenault, P., Lefevre, L. **Rau, A.**, Laloë, D., Pisoni, G., Moroni, P., Bevilacqua, C. and Martin, P. (2013) Contribution of mammary epithelial cells to the immune response during early stages of a bacterial infection to *Staphylococcus aureus*. *Veterinary Research*, 45:16.
 35. **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.
 36. **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*, 9(1): 9.
 37. 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.

Pre-prints, technical reports, & other publications

1. **Rau, A.** (2021) Cooking up knowledge from big data using data science. *Frontiers in Young Minds* 9:632923. <https://dx.doi.org/10.3389/frym.2021.632923>
2. Mollandin, F., **Rau, A.**, and Croiseau, P. (2021) An evaluation of the interpretability and predictive performance of the BayesR model for genomic prediction. Submitted. <https://www.biorxiv.org/content/10.1101/2020.10.23.351700v1>
3. Mazo, G., Karlis, D., and **Rau, A.** (2021) A randomized pairwise likelihood method for complex statistical inferences. Submitted. <https://hal.archives-ouvertes.fr/hal-03126621>
4. Cazals, A., Estellé, J., Bruneau, N., Coville, J.-L., Menanteau, P., Rossignol, M.-N., Jarret, D., Bevilacqua, C., **Rau, A.**, Bed'Hom, B., Velge, P., and Calenge, F. (2020) Impact of host genetics on caecal microbiota composition and on *Salmonella* carriage in chicken. Submitted. <https://www.researchsquare.com/article/rs-76645/v1>
5. Bruford, M., Leroy, G., Orozco-terWengel, P., **Rau, A.**, and Simianer H. (2015) Section B: Molecular tools for exploring genetic diversity. *The Second Report on the State of the World's Animal Genetic Resources for Food and Agriculture* FAO Commission on Genetic Resources for Food and Agriculture.

6. Nuel, G., **Rau, A.**, and Jaffrézic, F. (2013) Joint likelihood calculation for intervention and observational data from a Gaussian Bayesian network. *arXiv* 1305.0709.
7. **Rau, A.**, Celeux, G., Martin-Magniette, M.-L., and Maugis-Rabusseau, C. (2011) Clustering high-throughput sequencing data with Poisson mixture models. *Inria Research Report* 7786.
8. **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.
9. **Rau, A.** (2008) Success of Volunteer Statistical Consulting Service Leads to Expanded Network. *The Statistical Consultant* 25(1).
10. **Rau, A.** (2008) STATCOM Network Engages Growing Number of Student Volunteers. *Newsletter for the Section on Statistical Education* 13(1).
11. **Rau, A.** (2008) Success of Statistical Service Leads to Expanded Network. *Amstat News* April 2008.

Conference presentations

1. **Mixture models as a useful tool for identifying co-expressed genes from RNA-seq data**
MiMo Workshop on mixture models @ virtual (2021-04-08)
2. **Invited keynote: Integrative and interactive analyses of multi-omics data**
JOBIM 2020 @ virtual (2020-07-02)
3. **Invited talk: Individualized multi-omic pathway deviation scores using multiple factor analysis**
EuroBioc 2019 @ Brussels, Belgium (2019-12-09)
4. **Poster: Integrative methods for multi-omic data reveal multi-level gene and pathway regulation**
AgreenSkills+ annual meeting @ Brussels, Belgium (2019-04-12)
5. **coseq: An R/Bioconductor package for co-expression analyses of RNA-seq data**
Plant and Animal Genomes (PAG) XXVI @ San Diego, California, USA (2018-01-15)
6. **Invited talk: Model-based clustering to identify co-expressed genes from high-throughput sequencing data**
Working Group on Model-Based Clustering @ Perugia, Italy (2017-07-20)
7. **Clustering transformed compositional data using coseq**
user!2017 @ Brussels, Belgium (2017-07-05)
8. **Invited talk (FAANG workshop): An update on the FAANG pilot project FR-AgENCODE**
Plant and Animal Genomes (PAG) XXVI @ San Diego, California, USA (2017-01-12)
9. **Invited talk: Statistical tools to identify and visualize co-expression clusters from RNA-seq data**
INRA RNA-seq day @ Avignon (2016-11-17)
10. **Identifying marginal causal relationships in gene networks from observational and interventional expression data**
Joint Statistical Meetings of the American Statistical Association @ Chicago (2016-07-31)
11. **Invited talk: Experimental design in 'omics studies**
2nd International Symposium on Microgenomics, Technical Workshop @ Jouy-en-Josas (2016-05-31)
12. **HTScluster: a mixture-based approach for co-expression analyses of RNA-seq data**
15th Workshop: Statistical Methods for Post-Genomic Data @ Munich (2015-02-13)
13. **HTSDiff: More sensitive differential analysis of RNA-seq data**
Statistical analysis of RNA-seq data: Advances and challenges @ Paris (2013-11-26)
14. **HTSFilter: Data-based filtering for replicated high-throughput sequencing experiments**
Deuxièmes rencontres R @ Lyon (2013-06-28)
15. **Invited round table: Statistics applied to RNA-seq**
Journée de la transcriptome végétale de l'URGV-Genopole @ Evry (2013-05-16)
16. **Joint estimation of causal effects from observational and intervention gene expression data**
StatSeq meeting on genetical genomics @ Paris (2013-03-28)
17. **Invited talk: A comprehensive evaluation of normalization methods for high-throughput RNA sequencing data analysis**
Journée APLIBIO (Alliance des PLates-formes Île-de-France de BIOinformatique) @ Paris (2012-10-11)
18. **Clustering high-throughput sequencing data using Poisson mixture models**
Joint Statistical Meetings of the American Statistical Association @ San Diego, California (2012-07-31)
19. **Clustering high-throughput sequencing data using Poisson mixture models**
12th Workshop: Statistical Methods for Post-Genomic Data @ Lyon (2012-01-26)
20. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation**

- 11th Workshop: Statistical Methods for Post-Genomic Data @ Paris (2011-01-27)
21. **Approximate Bayesian methods for reverse engineering biological networks**
Conference on Applied Statistics in Agriculture @ Manhattan, Kansas (2010-04-26)
 22. **Reverse-Engineering Gene Networks from Microarray Data with Dynamic Bayesian Networks**
GENESYS Satellite Meeting at the European Conference on Complex Systems @ Warwick, UK (2009-09-22)
 23. **Using Dynamic Bayesian Networks with Hidden States to Infer Gene Regulatory Networks**
Joint Statistical Meetings of the American Statistical Association @ Washington, DC (2009-08-05)
 24. **Poster: Reverse-Engineering Genetic Regulatory Interactions from Transcriptomic Data using Dynamic Bayesian Networks**
2nd Biennial Workshop on Statistical Bioinformatics and Stochastic Systems Biology @ Newcastle, UK (2009-05-18)
 25. **Poster: An Empirical Bayes Approach to Inferring Genetic Regulatory Interactions with Dynamic Bayesian Networks**
Conference on Applied Statistics in Agriculture @ Manhattan, Kansas (2009-04-19)
 26. **Poster: An Empirical Bayes Approach to Inferring Genetic Regulatory Interactions with Dynamic Bayesian Networks**
Gordon Conference on Quantitative Genetics and Genomics @ Galveston, Texas (2009-02-22)
 27. **Poster: Seven Years of StatCom at Purdue: Managing a Growing Number of Student Volunteers**
Joint Statistical Meetings of the American Statistical Association @ Denver, Colorado (2008-08-04)

Seminar & working group presentations

1. **Multi-omic integration for enhanced interpretability in exploratory analyses**
Grenoble Laboratoire Jean Kuntzmann seminar @ virtual (2021-04-29)
2. **Happy 20th Birthday, R!**
INRAE GiBBS team meeting @ virtual (2020-05-18)
3. **Integrative methods for multi-omic data reveal multi-level gene regulation**
AgroParisTech statistics seminar @ Paris, France (2020-01-20)
4. **Integrative multivariate methods for multi-omic data**
Lundi de GABI seminar @ Jouy en Josas, France (2020-01-13)
5. **Integrative methods for multi-omic data reveal multi-level gene regulation**
INRA MalAGE research seminar @ Jouy en Josas, France (2019-11-18)
6. **Integrative methods for multi-omic data reveal multi-level gene regulation**
Journée régionale Genotoul @ Toulouse, France (2019-10-04)
7. **Integrative methods for multi-omic data reveal multi-level gene regulation**
EpiFun workshop @ Orléans, France (2019-09-17)
8. **Exploring drivers of gene expression in The Cancer Genome Atlas**
Division of Biostatistics Seminar at MCW @ Milwaukee, Wisconsin (2018-12-04)
9. **Co-expression analyses of RNA-seq data in practice with the R/Bioconductor package coseq**
MixStatSeq Workshop on Mixture Models: Theory and Application @ Paris (2018-06-22)
10. **Exploring drivers of gene expression in The Cancer Genome Atlas**
Research seminar series, Joseph J. Zilber School of Public Health @ Milwaukee, WI (2018-04-09)
11. **Exploring drivers of gene expression in The Cancer Genome Atlas**
Physiology Department Seminar at MCW @ Milwaukee, WI (2018-03-28)
12. **Easy interactivity in R with (gg)plotly and Shiny**
INRA national bioinformatics workshop @ Dijon (2017-06-13)
13. **Challenges in data integration**
SAPS doctoral school: Experimental animal biology and predictive modelisation @ Jouy en Josas, France (2017-03-17)
14. **Transformation, model choice, and visualization for RNA-seq co-expression**
Seminar at the Human and Molecular Genetics Center, Milwaukee College of Medicine @ Milwaukee, WI (2016-09-10)
15. **Transformation, model choice, and visualization for RNA-seq co-expression**
Seminar at the Zilber School of Public Health @ Milwaukee, WI (2016-09-09)
16. **Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression**
Groupe de travail de statistiques du LMRS @ Rouen (2016-05-12)
17. **From genotype to phenotype: what statistical methods to integrate heterogeneous data?**

INRA national bioinformatics workshop @ Toulouse (2016-03-22)

18. **Integration of heterogeneous 'omics data**
SAPS doctoral school: Experimental animal biology and predictive modelisation @ Jouy en Josas, France (2016-03-11)
19. **Poisson mixture models and visualization tools for RNA-seq co-expression**
INRA NGS club @ Jouy en Josas, France (2016-03-08)
20. **Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression**
MAP5 seminar at Université Paris-Descartes @ Paris (2016-01-29)
21. **Model selection in mixture model based classification: Applications in biostatistics**
4th Annual SFdS Young Statisticians and Probabilists Day @ Paris (2016-01-22)
22. **Statistical analysis of microarray and RNA-seq data**
Seminar at Toulouse Mathematics Institute (IMT) @ Toulouse (2015-11-17)
23. **Integrative clustering and classification in multiple heterogeneous data**
Statistique seminar @ Paris (2015-11-09)
24. **RNA-seq co-expression analysis using mixture models**
NETBIO working group @ Paris (2015-09-29)
25. **HTScluster: a mixture-based approach for co-expression analyses of RNA-seq data**
Cirad seminar @ Montpellier (2015-09-25)
26. **Slope heuristics: the missing ingredient for identifying co-expressed genes from RNA-seq data**
SELECT seminar @ Orsay (2014-10-16)
27. **HTSFilter: filtering replicated RNA-seq data using a data-driven approach**
Statistics for Systems Biology (SSB) seminar @ Evry (2013-11-12)
28. **Reinforcing the biology-statistics feedback loop with tools for genomic data analysis**
Seminar at INRA-GABI @ Jouy en Josas, France (2013-11-04)
29. **HTSAnalysis: a suite of R/Bioconductor packages for the analysis of RNA-seq data**
Statistics for Integrative Biology (SIB) seminar @ Rennes (2013-10-29)
30. **Joint estimation of causal effects from observational and intervention gene expression data**
NETBIO working group @ Paris (2013-09-20)
31. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistique et Santé working group @ Paris (2013-06-24)
32. **Joint estimation of causal effects from observational and intervention gene expression data**
AppliBUGS Workshop @ Paris (2013-06-20)
33. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistics seminar @ Toulouse (2013-06-18)
34. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistics for Integrative Biology seminar @ Rennes (2013-02-22)
35. **Differential analysis of RNA-seq data by unsupervised classification**
Assemblée générale PEPI IBIS @ Toulouse (2012-12-07)
36. **Independent data-based filtering for replicated high-throughput sequencing experiments**
Statistique seminar @ Lyon (2012-11-27)
37. **Clustering high-throughput sequencing data using Poisson mixture models**
LGC and SAGA seminar at INRA @ Toulouse (2012-06-25)
38. **Clustering high-throughput sequencing data using Poisson mixture models**
SSB working group seminar @ Jouy en Josas, France (2012-06-19)
39. **Inferring gene regulatory networks with hidden variables using state space models**
MIA Biological network inference methodological working group meeting @ Paris (2012-02-09)
40. **Exploring the identifiability of gene regulatory networks with approximate Bayesian computation**
AppliBugs Workshop @ Paris (2011-12-09)
41. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Institut de Recherche Mathématique Avancée @ Strasbourg (2011-05-24)
42. **Reverse Engineering Gene Networks: A Statistician's Perspective**
Seminar at the Unité de Recherche en Génomique Végétale @ Evry (2011-04-07)
43. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Institut de Mathématiques de Luminy @ Marseille (2011-04-04)
44. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Laboratoire Statistique et Génome @ Evry (2011-03-22)

45. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the équipe Génétique et Génomique Statistique @ Le Kremlin Bicêtre (2011-03-02)
46. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Rencontre de statistique autour des modèles hiérarchiques @ Strasbourg (2011-01-14)
47. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
INA P-G, Paris Descartes, and SELECT working group @ Paris (2010-10-18)
48. **Approximate Bayesian methods for reverse engineering biological networks**
Bioinformatics seminar at Purdue University @ West Lafayette, Indiana (2010-04-13)
49. **Inférence sur les réseaux génomiques par des modèles espace-état**
Seminar at the AgroParisTech @ Paris (2009-06-22)
50. **Inférence sur les réseaux génomiques par des modèles espace-état**
Seminar at the UMR GABI-INRA @ Jouy-en-Josas (2009-06-15)
51. **Reverse Engineering Gene Regulatory Networks**
Ph.D. student seminar, INRA Département de Génétique Animale @ Jouy-en-Josas (2009-03-23)
52. **Poster: Inferring Gene Regulatory Network through Linear Feedback State Space Models**
Ph.D. student seminar, INRA Département de Génétique Animale @ Toulouse (2008-03-20)

Participation in working groups

- Statomique (2009-present)
- Netbio (2014-present)

Software

1. **padma**: Pathway deviation scores using multiple factor analysis, available at BioC
2. **Invest Astuces**: An R/Shiny interactive web application for financial and real estate loan simulations, available as a Shiny web app
3. **Regeneration Rosetta**: An R/Shiny interactive web application to explore regeneration-associated gene expression and chromatin accessibility, available as a Shiny web app
4. **maskmeans**: Multi-view aggregation/splitting K-means clustering algorithm, available at GitHub
5. **Edge in TCGA**: An R/Shiny interactive web application for the exploration of drivers of gene expression in The Cancer Genome Atlas, available as a Shiny web app
6. **coseq**: Co-expression analysis of sequencing data, available at BioC
7. **ICAL**: Model selection for model based clustering of annotated data, available at GitHub
8. **metaRNASeq**: Meta-analysis of RNA-seq data, available at CRAN
9. **HTSDiff**: Differential analysis for RNA-seq data, available at R-Forge
10. **HTSFilter**: Filter for replicated high-throughput sequencing data, available at BioC
11. **HTScluster**: Clustering high-throughput sequencing data with Poisson mixture models, available at CRAN
12. **ebdbNet**: Empirical Bayes estimation for dynamic Bayesian networks, available at CRAN

Administrative activities

Reviewer	2010-present
ANNALS OF APPLIED STATISTICS, BIOINFORMATICS, BMC BIOINFORMATICS, BMC GENOMICS, BMC MEDICAL GENETICS, BRIEFINGS IN BIOINFORMATICS, COMPUTATIONAL AND STRUCTURAL BIOTECHNOLOGY JOURNAL, F1000 RESEARCH, G3, GENOME BIOLOGY, GIGA SCIENCE, IEEE PROCEEDINGS, JOURNAL OF COMPUTATIONAL BIOLOGY, JRSS-C, MOLECULAR GENETICS AND GENOMICS, NATURE COMPUTATIONAL SCIENCE, NUCLEIC ACIDS RESEARCH, REVUE D'INTELLIGENCE ARTIFICIELLE, RNA, STATISTICAL APPLICATIONS IN GENETICS AND MOLECULAR BIOLOGY, THE PLANT JOURNAL	
Elected member (substitute)	2021-2024
INRAE ANIMAL GENETICS DEPARTMENT CONSEIL SCIENTIFIQUE	
Appointed member	2021-2024
INRAE COMMISSION SCIENTIFIQUE SPÉCIALISÉE (CSS) MATHÉMATIQUES, INFORMATIQUE, SCIENCES ET TECHNOLOGIES DU NUMÉRIQUE, INTELLIGENCE ARTIFICIELLE ET ROBOTOLOGIE (MISTI)	
Member	2021
EVALUATION COMMITTEE FOR ASSISTANT PROFESSOR POSITION AT UNIVERSITÉ LE MANS	
Member	2021
EVALUATION COMMITTEE FOR RESEARCH SCIENTIST (CHARGÉ DE RECHERCHE) POSITION AT INRAE	
Associate Editor	2021
BMC GENOMICS	
Review Editor	2021
EDITORIAL BOARD OF STATISTICAL GENETICS AND METHODOLOGY, FRONTIERS IN GENETICS	
Mentor	2021
UNIVERSITÉ PARIS-SACLAY, WOMEN AND SCIENCE MENTORING PROGRAM	
Reviewer	2020
ANR MRSEI GRANT CALL	
Scientific committee member	2019
USER!2019 INTERNATIONAL CONFERENCE	
Reviewer	2017
UNIVERSITY OF WISCONSIN-MILWAUKEE RESEARCH GROWTH INITIATIVE GRANT CALL	
Reviewer	2017
INRA SELGEN METAPROGRAMME GRANT CALL	
Reviewer	2017
NANTES EXCELLENCE TRAJECTORY (NEXT) HEALTH AND ENGINEERING INITIATIVE "INTERNAL INTERDISCIPLINARY PROJECT" CALL	
Member	2016
EVALUATION COMMITTEE FOR ASSISTANT PROFESSOR POSITION AT UNIVERSITÉ RENNES I, UMR INSERM IRSET 1085	
Member	2016
EVALUATION COMMITTEE FOR ASSISTANT PROFESSOR POSITION AT UNIVERSITÉ RENNES I, IGDR (INSTITUTE OF GENETICS AND DEVELOPMENTAL BIOLOGY OF RENNES), CNRS UMR 6290	
Scientific committee president	2016
RENCONTRES R NATIONAL CONFERENCE	
Member	2015-2019
CONSEIL SCIENTIFIQUE DES UTILISATEURS (CSU) OF THE MIGALE BIOINFORMATICS PLATFORM (INRA, JOUY EN JOSAS)	
Chair	2010
COMMITTEE ON STUDENT PRO BONO STATISTICS OF THE ASA	
Member	2009-2010
COMMITTEE ON STUDENT PRO BONO STATISTICS OF THE AMERICAN STATISTICAL ASSOCIATION (ASA)	
Organizer	2009
INVITED ROUND TABLE (THE PROS OF PRO BONO STATISTICS) AT THE ASA JOINT STATISTICAL MEETINGS (WASHINGTON, DC, USA)	
Member	2006-2010
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

GENE-SWitCH

2019-2023

THE REGULATORY GENOME OF SWINE AND CHICKEN: FUNCTIONAL ANNOTATION DURING DEVELOPMENT, H2020 RIA GRANT

- PI: Elisabetta Giuffra and Herve Acloque; Role: Co-investigator and task leader

LIPOMECH

2018-2022

TOWARDS A BETTER UNDERSTANDING OF RUMINANT MILK LIPOLYSIS THROUGH AN INTEGRATIVE BIOLOGY APPROACH IN MILK

AND MAMMARY EPITHELIAL CELLS, FRENCH NATIONAL RESEARCH AGENCY (ANR) GRANT

- PI: Christelle Cebo; Role: Co-investigator

EpiFun

2018-2020

SYSTEMS BIOLOGY FOR GENOMIC SELECTION, INRA SELGEN METAPROGRAM GRANT

- PI: Nathalie Vialaneix and Thomas Faraut; Role: Co-investigator

AgreenSkills+

2017-2019

INTEGRATIVE ANALYSIS OF MULTI-OMICS DATA FOR IMPROVED DETECTION POWER OF FUNCTIONAL GENETIC VARIANTS,

AGREENSKILLS+ MOBILITY GRANT (UNIVERSITY OF WISCONSIN-MILWAUKEE)

- PI: Andrea Rau

Microficient

2016-2019

RELATIONSHIPS BETWEEN DIGESTIVE MICROBIOTA AND FEED EFFICIENCY IN CATTLE, AP-2016-007

- PI: Yuliaxis Ramayo and Gilles Renand; Role: Co-investigator

CARISTO-PF

2016-2019

CHARACTERIZATION AND MANAGEMENT OF HEALTH AND ENVIRONMENTAL RISKS LINKED TO THE DEVELOPMENT OF CIGUATERA

IN PHYTOBENTHOS IN FRENCH POLYNESIA, FRENCH POLYNESIA TERRITORY GRANT

- PI: Gregory Nuel; Role: Co-investigator

SalmoCar

2015-2017

GENETIC AND MICROBIOTAL CONTROL OF SALMONELLA CARRIAGE IN CHICKEN AND MICE, INSTITUT CARNOT PASTEUR MALADIES

INFECTIEUSES (PMI) / INSTITUT CARNOT SANTÉ ANIMALE (ICSA) GRANT

- PI: Xavier Montagutelli; Role: Co-investigator

COSI-net

2015-2016

USING COMBINATORIAL GENE SILENCING & INACTIVATION TO INFER GENE NETWORKS, INRA ANIMAL GENETICS DEPARTMENT

INTERNAL GRANT

- PI: Andrea Rau

MixStatSeq

2014-2018

MIXTURE-BASED PROCEDURES FOR STATISTICAL ANALYSIS OF RNA-SEQ DATA, FRENCH NATIONAL RESEARCH AGENCY (ANR)

GRANT (ANR-13-JS01-0001-01)

- PI: Cathy Maugis-Rabousseau; Role: Co-investigator

Causality

2014

CAUSAL NETWORK INFERENCE, INRA ANIMAL GENETICS DEPARTMENT INTERNAL GRANT

- PI: Florence Jaffrézic; Role: Co-investigator

Advising

Alexandre Asset

2021

L2 INTERNSHIP

- Inference of co-expression networks from intervention transcriptomic data (with Florence Jaffrézic and Denis Laloë)

Solène Pety

2021

M1 INTERNSHIP

- Knowledge transfer using multivariate gene expression projections onto a large-scale reference database (with Catherine Giauffret)

Fanny Mollandin

2019-2022

PHD

- Incorporating known functional annotations into Bayesian genomic prediction models (with Pascal Croiseau, co-funding from EU Horizon 2020 RIA grant GENE-SWitCH)

Raphaëlle Momal-Leisenring M2 INTERNSHIP <ul style="list-style-type: none"> Integrative statistical analysis of multi-omics data 	2017
Frédéric Jehl M2 INTERNSHIP <ul style="list-style-type: none"> Impact of heat stress on liver and blood transcriptomes of laying hens (with Tatiana Zerjal) 	2017
Dr. Manuel Revilla Sanchez 3-MONTH PHD ERASMUS+ LEARNING MOBILITY <ul style="list-style-type: none"> An integrative gene network analysis of the genetic determination of pig fatty acid composition (with Jordi Estelle and Yulixaxis Ramayo Caldas) 	2016
Babacar Ciss M2 INTERNSHIP <ul style="list-style-type: none"> Constructing predictive models for ovine production data (with Eli Sellem, Allice) 	2016
Audrey Hulot M1 INTERNSHIP <ul style="list-style-type: none"> Incorporating a priori biological knowledge into gene network inference from observational and intervention gene expression data (with Florence Jaffrézic) 	2015
Meriem Benabbas M1 INTERNSHIP <ul style="list-style-type: none"> Identifying differentially expressed genes from RNA-seq data using mixture models 	2015
Gilles Monneret PHD <ul style="list-style-type: none"> Estimation of causal effects in gene networks from observational and intervention data (with Grégory Nuel and Florence Jaffrézic) 	2014-2018
Marc Teissier and Chaoyu Dong M1 STV/EM-ABG INTERNSHIP <ul style="list-style-type: none"> Power to detect significantly differential gene expression using RNA-seq data 	2014
Mélina Gallopin PHD <ul style="list-style-type: none"> Clustering and network inference for RNA-seq data (with Gilles Celeux and Florence Jaffrézic) 	2012-2015
Rémi Bancal M2 INTERNSHIP <ul style="list-style-type: none"> Gene network estimation by adaptive knockout experiments (with Grégory Nuel and Florence Jaffrézic) 	2012
Mélina Gallopin M2 INTERNSHIP <ul style="list-style-type: none"> Gene network inference from RNA sequencing expression data (with Gilles Celeux and Florence Jaffrézic) 	2012
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Thibault Poinsignon PHD ADVISORY COMMITTEE MEMBER	2021-2023
Nicolas Jouvin PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	2021
Lucile Broséus PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	2021
Wilfried Heyse PHD ADVISORY COMMITTEE MEMBER	2020-2022
Antoine Leduc PHD ADVISORY COMMITTEE MEMBER	2019-2022
Alyssa Imbert PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	2018
Frédéric Jehl PHD ADVISORY COMMITTEE MEMBER	2017-2020
Valentin Voillet PHD EVALUATION COMMITTEE MEMBER	2016

Teaching

Agrocampus Researcher School (6-7 February)	2020
INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES	
• Statistical analysis of RNA-seq data	
Researcher training session: From gene expression to genomic networks (17-22 July)	2019
INSTRUCTOR (WITH M.-L. MARTIN-MAGNIETTE AND E. DELANNOY) @ INRAE, AGROIMPACT	
• Differential analysis of RNA-seq data	
Analysis of livestock metagenomics datasets (13-17 May)	2019
INSTRUCTOR (WITH J. ESTELLÉ @ INRA URZ, GUADELOUPE	
Physiological genomics (10 hours)	2019
INSTRUCTOR @ MEDICAL COLLEGE OF WISCONSIN	
• R Bootcamp	
Data management and visualization in R (3 course units)	2018
INSTRUCTOR @ UNIVERSITY OF WISCONSIN-MILWAUKEE	
PiGutNet Training School (3 hours)	2017
INSTRUCTOR @ INRA, JOUY EN JOSAS	
• Differential abundance analysis for microbial marker-gene surveys with metagenomeSeq	
Bayesian statistics for genomics course (18 hours)	2017
INSTRUCTOR (COURSEWORK AND LABS) @ UNIVERSITÉ D'EVRY VAL D'ESSONNE	
• Mathematics for the Life Sciences: Statistical Engineering and Genomics, M2	
Agrocampus Researcher School (1-2 February)	2017
INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES	
• Statistical analysis of RNA-seq data	
Genomics course (12 hours)	2017
INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES	
• Biostatistics M2	
SPS Summer School: From gene expression to genomic networks (17-22 July)	2016
INSTRUCTOR (COURSEWORK AND LABS) @ INSTITUTE OF PLANT SCIENCES PARIS-SACLAY	
• Co-expression analysis of RNA-seq data (3 hours)	
Bayesian statistics for genomics course (18 hours)	2016
INSTRUCTOR (COURSEWORK AND LABS) @ UNIVERSITÉ D'EVRY VAL D'ESSONNE	
• Mathematics for the Life Sciences: Statistical Engineering and Genomics, M2	
Agrocampus Researcher School (10-11 February)	2016
INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES	
• Statistical analysis of RNA-seq data	
Genomics course (33 hours)	2016
INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES	
• Biostatistics M2	
Mathematical Engineering for Life Sciences Master, M1: Case study (10 hours)	2015
INSTRUCTOR (COURSEWORK AND LABS) @ UNIVERSITÉ PARIS DESCARTES	
Genomics course (33 hours)	2015
INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES	
• Biostatistics M2. Note: The genomics course at Ensaï was significantly expanded and re-developed in 2015 by myself and Mickaël Guedj.	
BioBayes Researcher School (7-11 October)	2013
SCIENTIFIC COMMITTEE MEMBER AND INSTRUCTOR (COURSEWORK AND LABS) @ CANNES MANDELIEU	
• Bayesian statistical methods: Introduction to theory and applications in food, environment, epidemiology, and genetics	
Genomics course (6 hours)	2013
INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES	
• Biostatistics M2	

2012

2012

2012

2012

- 2012

2011

2011

- 2006

13

- 1st and 2nd year undergraduate