

Andrea Rau

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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 am a member of the **Animal Genetics and Integrative Biology** (GABI) research unit (Jouy en Josas, France) in the Genomics, Biodiversity, Bioinformatics, Statistics (GiBBS) team.

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.

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 Director (Directrice de Recherche)

INRAE

2023-present

Jouy-en-Josas, France

Research Scientist (Chargée de Recherche)

INRAE

2011-2022

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
- Honorable mention, Gertrude M. Cox Scholarship 2009
- A.H. Ismail Interdisciplinary Program doctoral research travel award 2009

Professional organizations

F&S	Femmes & Sciences	2022-present
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-Rabuseau, 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. Mollandin, F., Gilbert, H., Croiseau, P., and **Rau, A.** (2022) Accounting for overlapping annotations in genomic prediction models of complex traits. *BMC Bioinformatics*, 23:65. <https://dx.doi.org/10.1186/s12859-022-04914-5>
2. Mazurier, M., Drouaud, J., Bahrman, N., **Rau, A.**, Lejeune-Hénaut, I., Delbreil, B., and Legrand, S. (2022) Integrated sRNA-seq and RNA-seq analyses reveal a microRNA regulation network involved in cold response in *Pisum sativum* L. *Genes*, 13:1119. <https://dx.doi.org/10.3390/genes13071119>
3. **Rau, A.**, Passet, B., Castille, J., Asset, A., Lecardonnel, J., Moroldo, M., Jaffrézic, F., Laloë, D., Moazami-Goudarzi, K., and Vilotte, J.-L. (2022) Potential genetic robustness of Prnp and Sprn double knockout mouse embryos towards ShRNA-lentiviral inoculation. *Veterinary Research*, 53:54. <https://dx.doi.org/10.1186/s13567-022-01075-4>
4. Cazals, A., **Rau, A.**, Estellé, J., Bruneau, N., Coville, J.-L., Menanteau, P., Rossignol, M.-N., Jardet, D., Bevilacqua, C., Bed'Hom, B., Velge, P., and Calenge, F. (2022) Comparative analysis of the caecal tonsil transcriptome in two chicken lines experimentally infected with *Salmonella* Enteritidis. *PLoS ONE*, 17(8): e0270012. <https://dx.doi.org/10.1371/journal.pone.0270012>
5. Cazals, A., Estellé, J., Bruneau, N., Coville, J.-L., Menanteau, P., Rossignol, M.-N., Jardet, D., Bevilacqua, C., **Rau, A.**, Bed'Hom, B., Velge, P., and Calenge, F. (2022) Differences in caecal microbiota composition and *Salmonella* carriage between experimentally infected inbred lines of chickens. *Genetics Selection Evolution*, 54:7. <https://dx.doi.org/10.1186/s12711-022-00699-6>
6. **Rau, A.**, Manansala, R., Flister, M. J., Rui, H., Jaffrézic, F., Laloë, D., and Auer, P. L. (2022) Individualized multi-omic pathway deviation scores using multiple factor analysis. *Biostatistics*, 23(2):362-379. <https://dx.doi.org/10.1093/biostatistics/kxaa029>
7. **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>

8. Mollandin, F., **Rau, A.**, and Croiseau, P. (2021) An evaluation of the predictive performance and mapping power of the BayesR model for genomic prediction. *G3*, jkab225. <https://dx.doi.org/10.1093/g3journal/jkab225>
9. 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*, 14:24. <https://dx.doi.org/10.1186/s13072-021-00397-5>
10. Mach, N., Moroldo, M., **Rau, A.**, Lecardonnell, 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>
11. Devogel, N., Auer, P. L., Manansala, R., **Rau, A.**, and Wang, T. (2021) 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>
12. 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>
13. Sellem, E., Marthey, S., **Rau, A.**, Jouneau, L., Bonnet, A., Perrier, J.-P., Fritz, S., Le Danvic, C. Bousaha, 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/s13072-020-00340-0>
14. 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. <https://dx.doi.org/10.1214/19-AOAS1317>
15. 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>
16. 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. <https://dx.doi.org/10.1186/s12915-019-0726-5>
17. 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>
18. **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>
19. 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>
20. 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>
21. **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>
22. 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. <https://dx.doi.org/10.1080/02664763.2018.1454894>
23. **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>
24. 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. <https://dx.doi.org/10.1186/s12864-018-5048-5>

doi.org/10.1186/s12864-018-4860-1

25. Maroille, 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. <https://dx.doi.org/10.1038/s41598-018-27019-7>
26. 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. <https://dx.doi.org/10.1186/s12864-018-4668-z>
27. 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. <https://dx.doi.org/10.1038/s41598-018-19439-2>
28. 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. <https://dx.doi.org/10.1371/journal.pone.0171142>
29. 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. <https://dx.doi.org/10.1111/tpj.13592>
30. Rigail, 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>
31. 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. <https://dx.doi.org/10.1515/sagmb-2014-0095>
32. 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.
33. **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. <https://dx.doi.org/10.1093/bioinformatics/btu845>
34. **Rau, A.**, Marot, G. and Jaffrézic, F. (2014) Differential meta-analysis of RNA-seq data from multiple studies. *BMC Bioinformatics*, 16:31. <https://dx.doi.org/10.1186/1471-2105-15-91>
35. 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. <https://dx.doi.org/10.1371/journal.pone.0114598>
36. 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. <https://dx.doi.org/10.1080/16843703.2014.11673323>
37. **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. <https://dx.doi.org/10.1186/1752-0509-7-111>
38. 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. <https://dx.doi.org/10.1371/journal.pone.0077503>
39. **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. <https://dx.doi.org/10.1093/bioinformatics/btt350>
40. 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>
41. 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. <https://dx.doi.org/10.1186/1297-9716-45-16>
42. **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. <https://dx.doi.org/10.1007/s11222-011-9309-1>

43. **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. <https://dx.doi.org/10.2202/1544-6115.1513>
44. 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. <https://dx.doi.org/10.1007/s00280-007-0443-6>

Pre-prints, technical reports, & other publications

1. Duran Garzon, C., Chemin, C., **Rau, A.**, Decaux, B., Sellier-Richard, H., Drouaud, J., Soubigou-Taconnat, L., Brunaud, V., Martin, M.-L., Palaffre, C., Rayon, C., Lourgant, K., Guénin, S. Gutierrez, L., Charcosset, A., Coursol, S., and Giauffret, C. (2022) Integrative analysis of genetic and transcriptomic data reveals volatile terpenoids biosynthesis genes linked with chilling tolerance. Submitted.
2. Noël, A., Dumas, C., Rottier, E., Beslay, D., Costagliola, G., Ginies, C., Nicolè, F., **Rau, A.**, Le Conte, Y., and Mondet, F. (2022) Volatolome of the honey bee (*Apis mellifera*) worker brood: from egg to emergence. Submitted.
3. Mollandin, F., Gilbert, H., Croiseau, P., and **Rau, A.** (2022) Capitalizing on complex annotations in Bayesian genomic prediction for a backcross population of growing pigs. *12th World Congress on Genetics Applied to Livestock Production (3-8 July 2022)* Rotterdam, Netherlands.
4. Mazo, G., Karlis, D., and **Rau, A.** (2022) A randomized pairwise likelihood method for complex statistical inferences. Submitted. <https://hal.archives-ouvertes.fr/hal-03126621>
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. **(Invited talk) Leveraging multi-omic data for integrative exploratory and predictive analyses**
Journées Math Bio Santé du GDR MATHSAV @ Besançon (2022-10-06)
2. **(Poster) A hierarchical Bayesian mixture model for predicting phenotypes from genomic data with prior biological information**
Working Group on Model-Based Clustering Summer Session @ virtual (2022-07-26)
3. **(Invited talk) Mixture models as a useful tool for identifying co-expressed genes from RNA-seq data**
MiMo Workshop on mixture models @ virtual (2021-04-08)
4. **(Invited keynote) Integrative and interactive analyses of multi-omics data**
JOBIM 2020 @ virtual (2020-07-02)
5. **(Invited talk) Individualized multi-omic pathway deviation scores using multiple factor analysis**
EuroBioc 2019 @ Brussels, Belgium (2019-12-09)
6. **(Poster) Integrative methods for multi-omic data reveal multi-level gene and pathway regulation**
AgreenSkills+ annual meeting @ Brussels, Belgium (2019-04-12)
7. **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)
8. **(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)

9. **Clustering transformed compositional data using coseq**
useR!2017 @ Brussels, Belgium (2017-07-05)
10. **(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)
11. **(Invited talk) Statistical tools to identify and visualize co-expression clusters from RNA-seq data**
INRA RNA-seq day @ Avignon (2016-11-17)
12. **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)
13. **(Invited talk) Experimental design in 'omics studies**
2nd International Symposium on Microgenomics, Technical Workshop @ Jouy-en-Josas (2016-05-31)
14. **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)
15. **HTSDiff – More sensitive differential analysis of RNA-seq data**
Statistical analysis of RNA-seq data: Advances and challenges @ Paris (2013-11-26)
16. **HTSFilter – Data-based filtering for replicated high-throughput sequencing experiments**
Deuxièmes rencontres R @ Lyon (2013-06-28)
17. **(Invited round table) Statistics applied to RNA-seq**
Journée de la transcriptome végétale de l'URGV-Genopole @ Evry (2013-05-16)
18. **Joint estimation of causal effects from observational and intervention gene expression data**
StatSeq meeting on genetical genomics @ Paris (2013-03-28)
19. **(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)
20. **Clustering high-throughput sequencing data using Poisson mixture models**
Joint Statistical Meetings of the American Statistical Association @ San Diego, California (2012-07-31)
21. **Clustering high-throughput sequencing data using Poisson mixture models**
12th Workshop: Statistical Methods for Post-Genomic Data @ Lyon (2012-01-26)
22. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation**
11th Workshop: Statistical Methods for Post-Genomic Data @ Paris (2011-01-27)
23. **Approximate Bayesian methods for reverse engineering biological networks**
Conference on Applied Statistics in Agriculture @ Manhattan, Kansas (2010-04-26)
24. **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)
25. **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)
26. **(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)
27. **(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)
28. **(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)
29. **(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. **Incorporating multiple annotations in genomic prediction models**
Integration of gene co-expression networks with genomic prediction (IGEN) Workshop, CIRAD @ Montpellier (2022-12-12)
2. **Leveraging multi-omic data for integrative exploratory, predictive, and network analyses**
Séminaire Biogeco @ Bordeaux (2022-09-16)
3. **(Poster) Differential network analysis of mixed-type data with copulae**

Journées Scientifiques du Département de Génétique Animale @ Bordeaux (2022-09-13)

4. **Leveraging multi-omic data for integrative exploratory, predictive, and network analyses**
KIM – Data & Life Sciences seminar (MUSE) @ Montpellier (2022-05-30)
5. **(Invited talk) A randomized pairwise likelihood method for complex statistical inferences**
Séminaire statistique de Paris @ virtual (2022-02-07)
6. **Intégration d'annotations biologiques complexes dans les modèles bayésiens de prédiction génomique – Evaluation et extension du modèle BayesRC**
SAPS seminar @ virtual (2022-01-21)
7. **E pluribus unum – l'intégration de données à GiBBS pour une vision unifiée des données hétérogènes complexes**
Lundi de SAPS seminar @ virtual (2021-12-13)
8. **Leveraging multi-omic data for integrative exploratory, predictive, and network analyses**
NutriNeuro lab seminar @ virtual (2021-11-22)
9. **Multi-omic integration for enhanced interpretability in exploratory analyses**
Grenoble Laboratoire Jean Kuntzmann seminar @ virtual (2021-04-29)
10. **Happy 20th Birthday, R!**
INRAE GiBBS team meeting @ virtual (2020-05-18)
11. **Integrative methods for multi-omic data reveal multi-level gene regulation**
AgroParisTech statistics seminar @ Paris, France (2020-01-20)
12. **Integrative multivariate methods for multi-omic data**
Lundi de GABI seminar @ Jouy en Josas, France (2020-01-13)
13. **Integrative methods for multi-omic data reveal multi-level gene regulation**
INRA MaIAGE research seminar @ Jouy en Josas, France (2019-11-18)
14. **Integrative methods for multi-omic data reveal multi-level gene regulation**
Journée régionale Genotoul @ Toulouse, France (2019-10-04)
15. **Integrative methods for multi-omic data reveal multi-level gene regulation**
EpiFun workshop @ Orléans, France (2019-09-17)
16. **Exploring drivers of gene expression in The Cancer Genome Atlas**
Division of Biostatistics Seminar at MCW @ Milwaukee, Wisconsin (2018-12-04)
17. **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)
18. **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)
19. **Exploring drivers of gene expression in The Cancer Genome Atlas**
Physiology Department Seminar at MCW @ Milwaukee, WI (2018-03-28)
20. **Easy interactivity in R with (gg)plotly and Shiny**
INRA national bioinformatics workshop @ Dijon (2017-06-13)
21. **Challenges in data integration**
SAPS doctoral school – Experimental animal biology and predictive modelisation @ Jouy en Josas, France (2017-03-17)
22. **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)
23. **Transformation, model choice, and visualization for RNA-seq co-expression**
Seminar at the Zilber School of Public Health @ Milwaukee, WI (2016-09-09)
24. **Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression**
Groupe de travail de statistiques du LMRS @ Rouen (2016-05-12)
25. **From genotype to phenotype – what statistical methods to integrate heterogeneous data?**
INRA national bioinformatics workshop @ Toulouse (2016-03-22)
26. **Integration of heterogeneous 'omics data**
SAPS doctoral school: Experimental animal biology and predictive modelisation @ Jouy en Josas, France (2016-03-11)
27. **Poisson mixture models and visualization tools for RNA-seq co-expression**
INRA NGS club @ Jouy en Josas, France (2016-03-08)
28. **Poisson mixtures with slope heuristics and visualization tools for RNA-seq co-expression**
MAP5 seminar at Université Paris-Descartes @ Paris (2016-01-29)

29. **Model selection in mixture model based classification – Applications in biostatistics**
4th Annual SFdS Young Statisticians and Probabilists Day @ Paris (2016-01-22)
30. **Statistical analysis of microarray and RNA-seq data**
Seminar at Toulouse Mathematics Institute (IMT) @ Toulouse (2015-11-17)
31. **Integrative clustering and classification in multiple heterogeneous data**
Statistique seminar @ Paris (2015-11-09)
32. **RNA-seq co-expression analysis using mixture models**
NETBIO working group @ Paris (2015-09-29)
33. **HTScluster, a mixture-based approach for co-expression analyses of RNA-seq data**
Cirad seminar @ Montpellier (2015-09-25)
34. **Slope heuristics – the missing ingredient for identifying co-expressed genes from RNA-seq data**
SELECT seminar @ Orsay (2014-10-16)
35. **HTSFilter – filtering replicated RNA-seq data using a data-driven approach**
Statistics for Systems Biology (SSB) seminar @ Evry (2013-11-12)
36. **Reinforcing the biology-statistics feedback loop with tools for genomic data analysis**
Seminar at INRA-GABI @ Jouy en Josas, France (2013-11-04)
37. **HTSAnalysis – a suite of R/Bioconductor packages for the analysis of RNA-seq data**
Statistics for Integrative Biology (SIB) seminar @ Rennes (2013-10-29)
38. **Joint estimation of causal effects from observational and intervention gene expression data**
NETBIO working group @ Paris (2013-09-20)
39. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistique et Santé working group @ Paris (2013-06-24)
40. **Joint estimation of causal effects from observational and intervention gene expression data**
AppliBUGS Workshop @ Paris (2013-06-20)
41. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistics seminar @ Toulouse (2013-06-18)
42. **Joint estimation of causal effects from observational and intervention gene expression data**
Statistics for Integrative Biology seminar @ Rennes (2013-02-22)
43. **Differential analysis of RNA-seq data by unsupervised classification**
Assemblée générale PEPI IBIS @ Toulouse (2012-12-07)
44. **Independent data-based filtering for replicated high-throughput sequencing experiments**
Statistique seminar @ Lyon (2012-11-27)
45. **Clustering high-throughput sequencing data using Poisson mixture models**
LGC and SAGA seminar at INRA @ Toulouse (2012-06-25)
46. **Clustering high-throughput sequencing data using Poisson mixture models**
SSB working group seminar @ Jouy en Josas, France (2012-06-19)
47. **Inferring gene regulatory networks with hidden variables using state space models**
MIA Biological network inference methodological working group meeting @ Paris (2012-02-09)
48. **Exploring the identifiability of gene regulatory networks with approximate Bayesian computation**
AppliBugs Workshop @ Paris (2011-12-09)
49. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Institut de Recherche Mathématique Avancée @ Strasbourg (2011-05-24)
50. **Reverse Engineering Gene Networks – A Statistician’s Perspective**
Seminar at the Unité de Recherche en Génomique Végétale @ Evry (2011-04-07)
51. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Institut de Mathématiques de Luminy @ Marseille (2011-04-04)
52. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the Laboratoire Statistique et Génome @ Evry (2011-03-22)
53. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Seminar at the équipe Génétique et Génomique Statistique @ Le Kremlin Bicêtre (2011-03-02)
54. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
Rencontre de statistique autour des modèles hiérarchiques @ Strasbourg (2011-01-14)
55. **Reverse Engineering Gene Networks Using Approximate Bayesian Computation (ABC)**
INA P-G, Paris Descartes, and SELECT working group @ Paris (2010-10-18)
56. **Approximate Bayesian methods for reverse engineering biological networks**
Bioinformatics seminar at Purdue University @ West Lafayette, Indiana (2010-04-13)

57. **Inférence sur les réseaux génomiques par des modèles espace-état**
Seminar at the AgroParisTech @ Paris (2009-06-22)
58. **Inférence sur les réseaux génomiques par des modèles espace-état**
Seminar at the UMR GABI-INRA @ Jouy-en-Josas (2009-06-15)
59. **Reverse Engineering Gene Regulatory Networks**
Ph.D. student seminar, INRA Département de Génétique Animale @ Jouy-en-Josas (2009-03-23)
60. **(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. **BayesRCO**: Bayesian genomic prediction models for overlapping annotations, available at GitHub
2. **rpl**: Randomized pairwise likelihood method for complex statistical inferences, available at GitHub
3. **padma**: Pathway deviation scores using multiple factor analysis, available at BioC
4. **Invest Astuces**: An R/Shiny interactive web application for financial and real estate loan simulations, available as a Shiny web app
5. **Regeneration Rosetta**: An R/Shiny interactive web application to explore regeneration-associated gene expression and chromatin accessibility, available as a Shiny web app
6. **maskmeans**: Multi-view aggregation/splitting K-means clustering algorithm, available at GitHub
7. **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
8. **coseq**: Co-expression analysis of sequencing data, available at BioC
9. **ICAL**: Model selection for model based clustering of annotated data, available at GitHub
10. **metaRNASeq**: Meta-analysis of RNA-seq data, available at CRAN
11. **HTSDiff**: Differential analysis for RNA-seq data, available at R-Forge
12. **HTSFilter**: Filter for replicated high-throughput sequencing data, available at BioC
13. **HTSCluster**: Clustering high-throughput sequencing data with Poisson mixture models, available at CRAN
14. **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, GENETICS SELECTION EVOLUTION, GENOME BIOLOGY, GIGASCIENCE, IEEE PROCEEDINGS, JOURNAL OF COMPUTATIONAL BIOLOGY, JOURNAL OF COMPUTATIONAL AND GRAPHICAL STATISTICS, 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

Member	2023
EVALUATION COMMITTEE FOR RESEARCH SCIENTIST (CHARGÉ DE RECHERCHE) POSITION AT INRAE	
Delegate	2022
ANNUAL INRAE – WUR-ASG MEETING (WAGENINGEN, NETHERLANDS; 21-22 NOVEMBER 2022)	
Member	2022
ORGANIZATION COMMITTEE, INRAE DATA SCIENCE WORKSHOP	
Elected member	2022-2024
INRAE GABI CONSEIL D'UNITÉ	
Reviewer	2022
INSTITUT AGRO RENNES-ANGERS INTERNAL PhD FUNDING CALL	
Member	2022
EVALUATION COMMITTEE FOR RESEARCH SCIENTIST (CHARGÉ DE RECHERCHE) POSITION AT INRAE	
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 ROBOTIQUE (MISTI)	
Member	2021-present
INRAE GABI SCIENTIFIC COMMUNICATION AND MEDIATION COMMITTEE	
Reviewer	2021
SACLAY PLANT SCIENCES RESEARCH OPEN CALL	
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	
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

HOLOBIONTS

2022-2027

ANIMAL HOLOBIONTS: A NEW BIOLOGICAL SCALE TO EXPLORE GENETIC DIVERSITY AND REFINE BREEDING STRATEGIES FOR AGROECOLOGY, FRENCH NATIONAL RESEARCH AGENCY (ANR) PEPR AGROÉCOLOGIE ET NUMÉRIQUE

- PI: Jordi Estellé and Sylvie Combes; Role: Partner

AgroDiv

2022-2027

GENOMIC AND FUNCTIONAL CHARACTERIZATION OF DOMESTIC PLANT AND ANIMAL GENETIC DIVERSITY AS A KEYSTONE FOR AGROECOLOGY: LINKING GENOME TO PHENOME, FRENCH NATIONAL RESEARCH AGENCY (ANR) PEPR AGROÉCOLOGIE ET NUMÉRIQUE

- PI: Jérôme Salse, Gwendal Restoux, Matthias Zytynski, Pierre Peterlongo, and François Parcy; Role: WP co-leader

Pixel

2022

PÉNÉTRANCE INCOMPLÈTE ET EXPRESSIVITÉ VARIABLE : ÉTUDES DES MÉCANISMES DANS UN CAS DE PALAIS FENDU, INRAE ANIMAL GENETICS DEPARTMENT INTERNAL GRANT

- PI: Amandine Duchesne; Role: Partner

GEroNIMO

2021-2025

GENOME AND EPIGENOME ENABLED BREEDING IN MONOGASTRICS, EU H2020 RIA GRANT

- PI: Frédérique Pitel and Tatiana Zerjal; Role: Partner

WHAT-SOW

2021-2024

AUTOMATIC RECORDING AND ANALYSIS OF LACTATING SOW POSTURAL ACTIVITY, FRANCE FUTUR ELEVAGE (F2E) GRANT

- PI: Laurianne Canario; Role: Partner

DINAMIC

2021-2023

DIFFERENTIAL NETWORK ANALYSIS OF MIXED-TYPE DATA WITH COPULAE, INRAE DIGIT-BIO METAPROGRAM GRANT

- PI: Andrea Rau

GENE-SWITCH

2019-2023

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

- PI: Elisabetta Giuffra and Herve Acloque; Role: Task leader

MiniSRegress

2019-2021

CHARACTERISATION OF A MINIPIG SPONTANEOUS REGRESSION MODEL WITH NO INVALIDATING ADVERSE EFFECTS, INSERM PLAN CANCER 2014-2019, NEW EXPERIMENTAL MODELS CALL

- PI: Giorgia Egdy-Maskos; Role: Partner

LIPOMECE

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: WP leader

EpiFun

2018-2020

SYSTEMS BIOLOGY FOR GENOMIC SELECTION, INRA SELGEN METAPROGRAM GRANT

- PI: Nathalie Vialaneix and Thomas Faraut; Role: Partner

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: Yulixis Ramayo and Gilles Renand; Role: Partner

<p>CARISTO-PF</p> <p>CHARACTERIZATION AND MANAGEMENT OF HEALTH AND ENVIRONMENTAL RISKS LINKED TO THE DEVELOPMENT OF CIGUATERA IN PHYTOBENTHOS IN FRENCH POLYNESIA, FRENCH POLYNESIA TERRITORY GRANT</p> <ul style="list-style-type: none"> • PI: Gregory Nuel; Role: Partner <p>SalmoCar</p> <p>GENETIC AND MICROBIOTAL CONTROL OF SALMONELLA CARRIAGE IN CHICKEN AND MICE, INSTITUT CARNOT PASTEUR MALADIES INFECTIEUSES (PMI) / INSTITUT CARNOT SANTÉ ANIMALE (ICSA) GRANT</p> <ul style="list-style-type: none"> • PI: Xavier Montagutelli; Role: Partner <p>COSI-net</p> <p>USING COMBINATORIAL GENE SILENCING & INACTIVATION TO INFER GENE NETWORKS, INRA ANIMAL GENETICS DEPARTMENT INTERNAL GRANT</p> <ul style="list-style-type: none"> • PI: Andrea Rau <p>MixStatSeq</p> <p>MIXTURE-BASED PROCEDURES FOR STATISTICAL ANALYSIS OF RNA-SEQ DATA, FRENCH NATIONAL RESEARCH AGENCY (ANR) GRANT (ANR-13-JS01-0001-01)</p> <ul style="list-style-type: none"> • PI: Cathy Maugis-Rabusseau; Role: WP leader <p>Causality</p> <p>CAUSAL NETWORK INFERENCE, INRA ANIMAL GENETICS DEPARTMENT INTERNAL GRANT</p> <ul style="list-style-type: none"> • PI: Florence Jaffrézic; Role: Partner 	<p>2016-2019</p> <p>2015-2017</p> <p>2015-2016</p> <p>2014-2018</p> <p>2014</p>
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Advising

<p>Fanny Mollandin</p> <p>PHD</p> <ul style="list-style-type: none"> • Incorporating known functional annotations into Bayesian genomic prediction models (with Pascal Croiseau, co-funding from EU Horizon 2020 RIA grant GENE-SWitCH) <p>See Hyun Park</p> <p>M2 INTERNSHIP</p> <ul style="list-style-type: none"> • Impact of nutritional supplement intervention on cognitive health networks (with Jean-Christophe Delpech and Charlotte Madore-Delpech) <p>Smahane Chalabi</p> <p>POSTDOC</p> <ul style="list-style-type: none"> • A diet x epigenetics study in pigs, GENE-SWitCH grant (with Elisabetta Giuffra and Sarah Djebali) <p>Maxime Guilleton</p> <p>6-MONTH CDD</p> <ul style="list-style-type: none"> • Bioinformatics research engineer, LIPOMECC grant (with Mylène Delosiere) <p>Alexandre Asset</p> <p>L2 INTERNSHIP</p> <ul style="list-style-type: none"> • Inference of co-expression networks from intervention transcriptomic data (with Florence Jaffrézic and Denis Laloë) <p>Solène Pety</p> <p>M1 INTERNSHIP</p> <ul style="list-style-type: none"> • Knowledge transfer using multivariate gene expression projections onto a large-scale reference database (with Catherine Giauffret) <p>Raphaëlle Momal-Leisenring</p> <p>M2 INTERNSHIP</p> <ul style="list-style-type: none"> • Integrative statistical analysis of multi-omics data <p>Frédéric Jehl</p> <p>M2 INTERNSHIP</p> <ul style="list-style-type: none"> • Impact of heat stress on liver and blood transcriptomes of laying hens (with Tatiana Zerjal) <p>Manuel Revilla Sanchez</p> <p>3-MONTH PHD ERASMUS+ LEARNING MOBILITY</p> <ul style="list-style-type: none"> • An integrative gene network analysis of the genetic determination of pig fatty acid composition (with Jordi Estelle and Yulixis Ramayo Caldas) <p>Babacar Ciss</p> <p>M2 INTERNSHIP</p> <ul style="list-style-type: none"> • Constructing predictive models for ovine production data (with Eli Sellem) 	<p>2019-2022</p> <p>2022</p> <p>2021-2022</p> <p>2021</p> <p>2021</p> <p>2021</p> <p>2017</p> <p>2017</p> <p>2016</p> <p>2016</p>
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Audrey Hulot	2015
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) 	
Meriem Benabbas	2015
M1 INTERNSHIP	
<ul style="list-style-type: none"> Identifying differentially expressed genes from RNA-seq data using mixture models 	
Gilles Monneret	2014-2018
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) 	
Marc Teissier and Chaoyu Dong	2014
M1 STV/EM-ABG INTERNSHIP	
<ul style="list-style-type: none"> Power to detect significantly differential gene expression using RNA-seq data 	
Méline Gallopin	2012-2015
PHD	
<ul style="list-style-type: none"> Clustering and network inference for RNA-seq data (with Gilles Celeux and Florence Jaffrézic) 	
Rémi Bancal	2012
M2 INTERNSHIP	
<ul style="list-style-type: none"> Gene network estimation by adaptive knockout experiments (with Grégory Nuel and Florence Jaffrézic) 	
Méline Gallopin	2012
M2 INTERNSHIP	
<ul style="list-style-type: none"> Gene network inference from RNA sequencing expression data (with Gilles Celeux and Florence Jaffrézic) 	
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Bénédicte Wenden	2023
HDR EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Ousmane Suwareh	2022
PHD EVALUATION COMMITTEE MEMBER (EXAMINATRICE)	
Fotini Panagou	2022
PHD EVALUATION COMMITTEE MEMBER	
Océane Cassan	2022
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Camille Kergal	2022
PHD EVALUATION COMMITTEE MEMBER (EVALUATRICE)	
Baber Ali	2021-2024
PHD ADVISORY COMMITTEE MEMBER	
Ambre Giguelay	2021
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Leila Khajavi	2021
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Thibault Poinignon	2021-2023
PHD ADVISORY COMMITTEE MEMBER	
Nicolas Jouvin	2021
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Lucile Broséus	2021
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	
Wilfried Heyse	2020-2022
PHD ADVISORY COMMITTEE MEMBER	
Antoine Leduc	2019-2022
PHD ADVISORY COMMITTEE MEMBER	
Alyssa Imbert	2018
PHD EVALUATION COMMITTEE MEMBER (RAPPORTRICE)	

Frédéric Jehl

PHD ADVISORY COMMITTEE MEMBER

2017-2020

Valentin Voillet

PHD EVALUATION COMMITTEE MEMBER

2016

Gabriel Guillocheau

PHD ADVISORY COMMITTEE MEMBER

2015-2018

Teaching

Atelier IA: Mes clusters ont-ils un sens ? Quelques indices de la statistique et de la biologie... (1670457600)

INSTRUCTOR @ LYON

- Séminaire métaprogramme DIGIT-BIO

2022

UE Bioinfo, Master Bioinformatique et Biostatistiques Paris-Saclay (November-December)

INSTRUCTOR @ ORSAY

- Co-expression, genomic prediction, and multi-omic analyses

2022

Researcher training session: From gene expression to genomic networks (1-2 March)

INSTRUCTOR (WITH M.-L. MARTIN-MAGNIETTE AND E. DELANNOY) @ INRAE, BioEcoAGRO

- Co-expression and network analysis of RNA-seq data

2022

Agrocampus Researcher School (23 June)

INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES

- Statistical analysis of RNA-seq data

2021

Agrocampus Researcher School (6-7 February)

INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES

- Statistical analysis of RNA-seq data

2020

Researcher training session: From gene expression to genomic networks (2-3 December)

INSTRUCTOR (WITH M.-L. MARTIN-MAGNIETTE AND E. DELANNOY) @ INRAE, BioEcoAGRO

- Differential analysis of RNA-seq data

2019

Analysis of livestock metagenomics datasets (13-17 May)

INSTRUCTOR (WITH J. ESTELLÉ @ INRA URZ, GUADELOUPE

2019

Physiological genomics (10 hours)

INSTRUCTOR @ MEDICAL COLLEGE OF WISCONSIN

- R Bootcamp

2019

Data management and visualization in R (3 course units)

INSTRUCTOR @ UNIVERSITY OF WISCONSIN-MILWAUKEE

2018

PiGutNet Training School (3 hours)

INSTRUCTOR @ INRA, JOUY EN JOSAS

- Differential abundance analysis for microbial marker-gene surveys with metagenomeSeq

2017

Bayesian statistics for genomics course (18 hours)

INSTRUCTOR (COURSEWORK AND LABS) @ UNIVERSITÉ D'EVRY VAL D'ESSONNE

- Mathematics for the Life Sciences: Statistical Engineering and Genomics, M2

2017

Agrocampus Researcher School (1-2 February)

INSTRUCTOR (WITH S. LAGARRIGUE AND Y. BLUM) @ RENNES

- Statistical analysis of RNA-seq data

2017

Genomics course (12 hours)

INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES

- Biostatistics M2

2017

SPS Summer School: From gene expression to genomic networks (17-22 July)

INSTRUCTOR (COURSEWORK AND LABS) @ INSTITUTE OF PLANT SCIENCES PARIS-SACLAY

- Co-expression analysis of RNA-seq data (3 hours)

2016

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	
Training school on rabbit and pig genome analysis (6 hours)	2012
INSTRUCTOR @ COST ACTION RESEARCH SCHOOL, NORWICH, UNITED KINGDOM	
Genomics course (6 hours)	2012
INSTRUCTOR (COURSEWORK AND LABS) @ ENSAI, RENNES	
• Biostatistics M2	
Statistical Methods for Genome Enabled Prediction (2 hours)	2012
INSTRUCTOR @ EUROPEAN GRADUATE SCHOOL IN ANIMAL BREEDING AND GENETICS, PARIS	
• Approximate Bayesian methods: Application to gene regulatory networks	
Next generation sequencing school for INRA researchers (2 hours)	2012
INSTRUCTOR @ INRA RESEARCH SCHOOL, ECULLY	
Computational biostatistics (6 hours)	2012
INSTRUCTOR (COURSEWORK AND LABS) @ UFR DE SCIENCES, UNIVERSITÉ PARIS-SUD 11	
• Bioinformatics and Biostatistics / Mathematical engineering / Probability and Statistics M2	
Statistical modeling (24 hours)	2011
LAB ASSISTANT (R) @ UFR DE SCIENCES, UNIVERSITÉ PARIS-SUD 11	
• Bioinformatics and Biostatistics Master, M1	
Bioinformatics and Biostatistics / Mathematical engineering / Probability and Statistics M2 (12 hours)	2011
INSTRUCTOR (COURSEWORK AND LABS) @ UFR DE SCIENCES, UNIVERSITÉ PARIS-SUD 11	
• Bioinformatics and Biostatistics / Mathematical engineering / Probability and Statistics M2	
Elementary statistical methods (60 hours)	2006
LAB ASSISTANT (SPSS) @ DEPARTMENT OF STATISTICS, PURDUE UNIVERSITY (WEST LAFAYETTE, INDIANA, USA)	
• 1st and 2nd year undergraduate	

Outreach

Member	2023-present
STEERING COMMITTEE, UNIVERSITÉ PARIS-SACLAY WOMEN AND SCIENCE MENTORING PROGRAM	
Organizer	2022
ELEMENTARY SCHOOL ACTIVITY FOR THE FÊTE DE LA SCIENCE: "LA MEILLEURE RECETTE POUR COMPRENDRE LES DONNÉES... LA SCIENCE DES DONNÉES!"	

Creator

VIDEO ABOUT BAYESIAN MODELS AND SIMULATIONS FOR H2020 GENE-SWITCH PROJECT: [HTTPS://YOUTU.BE/VWEBE2WPI60](https://youtu.be/VWEBE2WPI60)

2022

Author

CELEBRATING WOMEN IN STATISTICS AND DATA SCIENCE FEATURED PROFILE FOR THE AMERICAN STATISTICAL ASSOCIATION:
[HTTPS://MAGAZINE.AMSTAT.ORG/BLOG/2022/03/01/ANDREA-RAU](https://magazine.amstat.org/blog/2022/03/01/andrea-rau)

2022

Creator

VIDEO ABOUT DATA SCIENCE FOR H2020 GENE-SWITCH PROJECT: [HTTPS://TWITTER.COM/I/STATUS/1501490287931179012](https://twitter.com/i/status/1501490287931179012)

2022

Facilitator

GERONIMO HACKATHON: A 360° PERSPECTIVE ON NEW GENOMIC SOLUTIONS FOR ADDRESSING THE CHALLENGES IN
SUSTAINABLE LIVESTOCK PRODUCTION

2022

Mentor

UNIVERSITÉ PARIS-SACLAY WOMEN AND SCIENCE MENTORING PROGRAM

2021-2023

Organizer

ELEMENTARY SCHOOL (CE2/CM1/CP2) CLASSROOM ACTIVITY FOR THE FÊTE DE LA SCIENCE: "DATA SCIENCE: FROM DATA TO
DISCOVERY!"

2021