Florian Rohart

PhD in Applied Statistics

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Australian Permanent Resident
French Citizen

Academic Qualifications

2009 – 2012	**PhD**, “Phenotypic prediction and variable selection in high dimensional linear and linear mixed models”, Supervisors: B. Laurent-Bonneau & M. San-Cristobal, Toulouse, France.
2008 – 2009	**Master 2 Research in applied mathematics**, with distinction, Learning of several stochastic tools and statistics tools, Université Paul Sabatier, Toulouse, France.
2006 – 2008	**Master 1 and Licence of fundamental mathematics**, with distinction ($10^{th}/61$ and $9^{th}/76$), Université Paul Sabatier, Toulouse, France.
2003 – 2006	**Two-year highly selective classes to prepare for the competitive exams to the french “Grandes Ecoles", specializing in mathematics and physics (MPSI/MP)**, Lycée Georges Clémenceau, Reims, France.
Juin 2003	**Baccalauréat Scientifique**, with distinction, Lycée Gay-Lussac, Chauny, France.

Professional experience

Research

2017	**Research Fellow - Applied Statistician**, Statistical Genetics, IMB, University of Queensland, Australia.
2016 – 2017	**Research Fellow - Applied Statistician**, Development of multivariate statistical approaches for multi ’omics analyses, UQDI, University of Queensland, Australia.
2013 – 2015	**Postdoctoral Research Fellow**, Development of multivariate statistical approaches for cross platform analyses, AIBN, University of Queensland, Australia.
2012 – 2013	**Research/Teaching Assistant**, INSA Toulouse, France.
March–July 2009	**Internship, Master 2 Research**, “Confidence region & sensitivity analysis”, on failure detection from automotive data, ACTIA-Toulouse, France.

Teaching

2017	**Course coordinator**, Statistical Analysis of Genetic Data (STAT3306/7306), University of Queensland, Australia.
2016	**Substitute - one week**, Applications of Computational Statistics (STAT7174), University of Queensland, Australia.
2015	**Tutor**, ‘Statistics for frightened researchers’, 6 courses, University of Queensland, Australia.
	Tutor, workshop “Methodologies for big data, theory and application using the mixOmics R package and web interface”, 3 days, 40 participants, University of Queensland, Australia.
	Invited tutor, mixOmics workshop, as above, University of Auckland, New Zealand.
2014	**Guest lecturer**, Applications of Computational Statistics (STAT7174), University of Queensland, Australia.
2012	**Tutor**, “Statistiques pour l’analyse de données post-génomiques haut-débit”, Professional training for statistics users that do not possess special skills in mathematics but wish to acquire autonomy to analyze their own datasets, France.
2009–2012	**Teacher of Mathematics from Licence 1 to Licence 3 (first to third year undergraduate students)**, Statistics modelling, Probabilities & Statistics, Differential calculus and Integral calculus,. . . , INSA Toulouse, France.

Accepted manuscripts

2017 **[1] `mixOmics`: an R package for 'omics feature selection and multiple data integration**, F. Rohart, B. Gautier, A. Singh, K-A Lê Cao, *PLOS computational Biology. Available on bioRxiv https://doi.org/10.1101/108597*.

[2] Human Hepatocellular Carcinomas with a Periportal Phenotype Have the Lowest Potential for Early Recurrence after Curative Resection, R. Désert, F. Rohart, F. Canal, M. Sicard, S. Merbarki, M. Desille, S. Renaud, B. Turlin, P. Bellaud, D. Bergeat, L. Sulpice, C. Perret, B. Clément, K-A Lê Cao, O. Musso, *Hepatology. 2017 May 12. doi: 10.1002/hep.29254*.

[3] MINT: A multivariate integrative method to identify reproducible molecular signatures across independent experiments and platforms, F. Rohart, A. Eslami, N. Matigian, S. Bougeard and K-A. Lê Cao, *BMC bioinformatics doi: 10.1186/s12859-017-1553-8*.

2016 **[4] Disease surveillance based on Internet-based linear models: an Australian case study of previously unmodeled infection diseases**, F. Rohart*, G. Milinovich*, S. Avril, K-A. Lê Cao, Sh Tong, W. Hu, *Scientific Reports, doi:10.1038/srep38522*.

[5] Integrating Multi-omics Data to Dissect Mechanisms of DNA repair Dysregulation in Breast Cancer, Ch. Liu, F. Rohart, P. Simpson, K. K. Khanna, M. Ragan and K-A. Lê Cao, *Scientific Reports, doi:10.1038/srep34000*.

[6] Multiple Hypotheses Testing For Variable Selection, F. Rohart, *Australian & New Zealand Journal of Statistics, doi:10.1111/anzs.12157*.

[7] A Molecular Classification of Human Mesenchymal Stromal Cells, F. Rohart, E. Mason, N. Matigian, R. Mosbergen, O. Korn, T. Chen, S. Butcher, J. Patel, K. Atkinson, K. Khosrotehrani, N. Fisk, K-A. Lê Cao and C-A. Wells., *PeerJ, DOI 10.7717/peerj.1845*.

2015 **[8] Exploring transcriptomic diversity in muscle revealed that cellular signaling pathways mainly differentiate five Western porcine breeds**, M. SanCristobal, F. Rohart, C. Lascor, M. Bouffaud, L. Trouilh, P. Martin, Y. Lippi, T. Tribout, T. Faraut, M.J. Mercat, D. Milan and L. Liaubet, *BMC Genomics, 16:1055. DOI: 10.1186/s12864-015-2259-9*.

2014 **[9] YuGene: A simple approach to scale gene expression data derived from different platforms for integrated analyses**, K-A Lê Cao*, F.Rohart*, L. McHugh, O. Korn, C.A. Wells, *Genomics 10.1016/j.ygeno.2014.03.001*.

[10] Fixed Effects Selection in High Dimensional Linear Mixed Models, F. Rohart, B. Laurent and M. SanCristobal, *Computational Statistics and Data Analysis. 10.1016/j.csda.2014.06.022*.

2012 **[11] Phenotypic Prediction Based on Metabolomic Data on the Growing Pig from three main European Breeds.**, F. Rohart, A. Paris, B. Laurent, C. Canlet, J. Molina, M.J. Mercat, T. Tribout, N. Muller, N. Iannucelli, N. Villa-Vialaneix, L. Liaubet, D. Milan and M. SanCristobal, *J Anim Sci. 2012 Dec;90(13):4729-40*.

Manuscripts in progress

[12] DIABLO: a method for multi-omics integration for biomarker discovery, A. Singh, B. Gautier, C. Shannon, M. Vacher, F. Rohart, S. Tebbutt and K-A. Lê Cao, *https://doi.org/10.1101/067611*.

R packages - available on CRAN

bootsPLS **[1] Bootstrap sPLS**, F. Rohart, based on manuscript [7].

mixOmics **[2] Exploration and Integration of 'Omics datasets**, K-A. Le Caô, F. Rohart, I. González, S. Déjean, B. Gautier, F. Bartolo, and others, see `mixomics.org` and manuscript [1].

mht **[3] multiple hypotheses testing**, F. Rohart, based on manuscript [6].

MMS **[4] Mixed Models Selection**, F. Rohart, based on manuscript [10].

YuGene **[5] Normalisation**, F. Rohart, K-A. Le Caô, L. McHugh, O. Korn and C-A Wells, based on ms [9].

Communications

- **Supervised Multivariate Analysis for Biological Data Integration, Dimension Reduction and Feature Selection with `mixOmics`**, *Cinquièmes rencontres R*, Juin 2016, Toulouse, France.
- **MINT: A multivariate integrative method to identify reproducible molecular signatures across independent experiments and platforms**
  - *Open Days in Biology, Computer Science and Mathematics (JOBIM)*, Juin 2016, Lyon, France
  - *CSIRO seminar*, April 2016, QLD, Australia
  - *The International Biometric Society, Biometrics by the canal*, Dec. 2015, Hobart, TAS, Australia.
  - *Collaborative Computational Biology seminar*, Aug. 2015, QLD, Australia
  - *Australian Bioinformatics Conference (ABIC)*, Oct 2014, Melbourne, VIC, Australia.
- **A Molecular Classification of Mesenchymal Stromal Cells (MSCs).**
  - *Genomics of Development and Disease*, May 2014, University of Queensland, Australia
  - *The International Biometric Society, Biometrics by the canal*, Dec. 2013, Mandurah, WA, Australia
  - *The Australasian Microarray and Associated Technologies Association (AMATA) conference*, Oct. 2013, Surfers Paradise, QLD, Australia. Poster
  - *International Society for Stem Cell Research (ISSCR)*, June 2015, Stockholm, Sweden. By C. Wells
- **Multiple Hypotheses Testing For Variable Selection.**
  - *Centre of Statistics Seminar*, Aug. 2014 at University of Queensland, Australia
  - *Statistical Methods for Post-Genomic Data*, Jan. 2012, Lyon, France
  - *Statistiques Mathématiques et Applications*, Sept. 2011, Fréjus, France
  - *Séminaire des Doctorants du Département de Génétique Animale de l'INRA,* April 2011, France.
- **Variable Selection in High Dimensional Linear Mixed Model through ℓ^1 Penalization.** Tenth colloquium of *"Jeunes Probabilistes et Satisticiens"*, April 2012, CIRM Marseille, France.
- **Feature selection in 1H NMR-based metabolomic profiles enables the prediction of growth phenotypes in various pig breeds and highlight few metabolites involved in this complex trait.** *5èmes Journées Scientifiques du Réseau Français de Métabolomique et Fluxomique*, May 2011, Jussieu, France. By A. Paris.
- **Phenotypic prediction based on metabolomic data: lasso vs Bolasso, primary data vs wavelet data.** *9th World Congress on Genetics Applied to Livestock Production*, Aug. 2010, Leipzig, Germany.

Organisations

2015-2016 **Creation and organisation of a weekly meeting**, "**B**iology, **A**pplied **S**tatistics, **I**nformatics and **C**oding" (BASIC) meetings.

2012 **Organising committee**, "Journées Statistiques du Sud", June 20-22th, Toulouse, France.

Organising committee, "quinzième Séminaire des Doctorants du Département de Génétique Animale", March 26-27th, Ile d'Oléron, France.

Supervision

2016 **Co-supervisor of a master's student**, University of Queensland Diamantina Institute, Australia.

2015 **Co-supervisor of a student, winner of a UQ Winter Research Scholarship**, Applying the methodology of the "internet based surveillance system" paper to predict Middle East Respiratory Syndrome (MERS), University of Queensland, Australia.

2011 **Co-supervisor of a 3-months project and a 3-months internship**, *Transcriptomic analysis*, INSA Toulouse, INRA Toulouse, France.

Prize

Travel grant Top 2 best Performers (out of 23 international teams) of the "sbv IMPROVER Systems Toxicology Computational Challenge" in June 2016 that rewarded me with a travel grant to the ISMB 2016 conference in Orlando, USA (8-12 July 2016), and with an oral presentation at the sbv IMPROVER Symposium (11 July 2016).