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Education

- 2013–*** : Postdoctoral fellow, French National Institute for Agricultural Research (INRA), France. Work in collaboration with Researcher Brigitte Mangin. Research on genomic selection and high-dimensional statistics.
- 2010–2013** : Postdoctoral fellow, Statistics department, University of Wisconsin-Madison. Work in collaboration with Professor Cécile Ané. Research on random trees, phylogenetics, gene trees/species trees reconciliation, whole genome duplications.
- 2006–2010** : PhD, Mathematical Statistics, University Paul Sabatier, Toulouse 3, France. Advisors J-M. Azaïs (Professor of applied mathematics at university Paul Sabatier), J-M. Elsen (Senior Researcher in genetics at INRA). Dissertation title : "Statistical methods for the detection of Quantitative Trait Loci".
- 2005-2006** : Master's Degree, "Probability and Statistics", University Paul Sabatier, Toulouse 3, France, with honours.
- 2004-2005** : Autumn semester at the University of Montreal, Canada. Graduate courses in applied mathematics.
- 2002-2005** : Engineering degree diploma specialized in Mathematics, Probability and Statistics in a french "Grande Ecole" : INSA in Toulouse, France.
- 2000-2002** : Bachelor of Sciences in "Mathematics, Computer science applied to sciences", University of Poitiers, France, with honours.
- 2000** : French High school diploma specialized in mathematics, Lycée C.Guérin, Poitiers, France, with honours.

Professional Experiences

- 2013–2014** : Teaching Assistant, INSA, National Institute of Applied Sciences, Toulouse, France.
- 2009–2010** : Teaching Assistant, INSA, Toulouse, France.
- 2008–2009** : Teaching Assistant, University Paul Sabatier, Toulouse 3, France.
- 2006 (5 months)** : Internship (Master level) at INRA, "Shuffling methods for selective genotyping experiments".
- 2005 (5 months)** : Internship (5th year INSA) at INRA, "Dynamic reserve site selection under contagion risk of deforestation".
- Summer 2004** : Internship (4th year INSA) at University College Dublin, Ireland. Statistical consulting in the "Summer Statistics Support Unit" (SSSU), service proposed by the university to enterprises and searchers.
- Summer 2003** : Internship (3th year INSA) at "Laboratoire de Métallurgie Physique", University of Poitiers, France, "Delamination of a covered material".

Research and Skills

- Research Interest** : Asymptotic Statistics, Mixture models, Statistical Genetics, Gaussian Processes, Chi-Square Processes, Computational Biology, Phylogenetics, Random Trees, Reconciliation between Gene Trees and Species Trees.
- Programming** : Matlab, R, SAS, Splus, SPSS, C, C++, Java, Fortran 90, Maple, Ada 95, Turbo Pascal, SPIMAP, SPIMAPWGD, Bucky.
- Languages** : French(native), English(fluent), German(basic).

Publications and Presentations

Publications :

1. **R Sabbadin, D Spring, C-E Rabier (2007)**. Dynamic reserve site selection under contagion risk of deforestation. *Ecological Modelling*, Vol 201, Issue 1, pp. 75-81.
2. **J-M Azaïs, C Delmas, C-E Rabier (published by alphabetical order) (2014)**. Likelihood Ratio Test process for Quantitative Trait Locus detection, *Statistics*, Vol 48, Issue 4, pp. 787-801 (accepted in December 2012).
3. **C-E Rabier, A Genz (2014)**. The supremum of Chi-Square processes, *Methodology and Computing in Applied Probability*, Vol 16, Issue 3, pp. 715-729 (accepted in March 2013).
4. **C-E Rabier (2013)**. On Quantitative Trait Locus mapping with an interference phenomenon, *TEST*, Vol 23, Issue 2, pp. 311-329 (accepted in November 2013).

5. **C-E Rabier (2014)**. On statistical inference for selective genotyping, *Journal of Statistical Planning and Inference*, Vol 147, pp. 24-52 (accepted in November 2013).
6. **C-E Rabier, T Ta, C Ané (2014)**. Detecting and Locating Whole Genome Duplications on a phylogeny : a probabilistic approach, *Molecular Biology and Evolution*, DOI :10.1093/molbev/mst263.
7. **C-E Rabier (2014)**. On empirical processes for Quantitative Trait Locus mapping under the presence of a selective genotyping and an interference phenomenon, *Journal of Statistical Planning and Inference*, Vol 153, pp. 42-55.
8. **C-E Rabier (2014)**. An asymptotic test for Quantitative Trait Locus detection in presence of missing genotypes, *Annales de la Faculté des Sciences de Toulouse*, Sér 6, Vol 23(4), p755-778.
9. **C-E Rabier (2014)**. On the asymptotic robustness of the Likelihood Ratio Test in Quantitative Trait Locus detection, *Electronic Journal of Statistics*, Vol 8(2), p2138-2157.
10. **C-E Rabier (2015)**. On stochastic processes for Quantitative Trait Locus mapping under selective genotyping, *Statistics*, Vol 49(1), p19-34

Work Under Revision :

- **C-E Rabier, P Barre, T Asp, G Charmet, Mangin B.** On the accuracy of Genomic Selection. Under revision for Plos One.

Work in Progress :

- **C-E Rabier, J-M Azaïs, J-M Elsen, C Delmas.** Chi square processes for gene mapping in a population with family structure, submitted.
- **C-E Rabier, Delmas C.** On gene mapping with the mixture model in preparation.

Invited Conferences (speaker underlined)

- **C Ané, T Ta, C-E Rabier (2014)**. "Probabilistic approaches for detecting and locating whole genome duplications". *Statistical Methods for Post-Genomic Data*, Paris, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus mapping under selective genotyping, *International Indian Statistical Association Conference*, Riverside, California, USA

Oral Presentations (speaker underlined)

- **R Sabbadin, D Spring, C-E Rabier (2005)**. Dynamic reserve site selection under contagion risk of deforestation, *International Congress on Modelling and Simulation*, Melbourne, Australia.
- **C-E Rabier, J-M Elsen, C Delmas (2007)**. Rejection thresholds in Quantitative Trait Loci detection, *11th QTL-MAS Workshop*, Toulouse, France.
- **C-E Rabier, J-M Azaïs (2007)**. Selective Genotyping for Quantitative Trait Locus detection, *Meeting of the MAFIA team of Laboratoire de Statistiques et Probabilités de Toulouse*, Nissan lez Enserunes, France.
- **C-E Rabier, J-M Azaïs (2008)**. Selective Genotyping for Quantitative Trait Locus detection, *Statistical Meeting, Santander-Toulouse-Valladolid*, Valladolid, Spain.
- **C-E Rabier, J-M Elsen, C Delmas (2008)**. On the theory of Quantitative Trait Locus detection, *24th International Biometric Conference*, Dublin, Ireland.

- **C-E Rabier, J-M Elsen, C Delmas (2008)**. Rejection thresholds in Quantitative Trait Locus detection, *Meeting of the European Association for Animal Production*, Vilnius, Poland.
- **C-E Rabier, J-M Azaïs (2008)**. Selective Genotyping for Quantitative Trait Locus detection, *Meeting Statistics and its applications*, Frejus, France.
- **C-E Rabier, J-M Azaïs (2009)**. Selective Genotyping for Quantitative Trait Locus detection, *Meeting of the French Statistical society*, Bordeaux, France.
- **C-E Rabier, J-M Azaïs, C Delmas (2010)**. Likelihood Ratio Test process for the detection of Quantitative Trait Locus, *Meeting of the French Statistical society*, Marseille, France.
- **C-E Rabier (2011)**. My research in QTL detection, *Stat/Math Phylogenetics group*, University of Wisconsin-Madison, USA.
- **C-E Rabier, C Delmas(2011)**. Likelihood Ratio Test process for Quantitative Trait Loci detection, *Joint Statistical Meetings*, Miami Beach, USA.
- **C-E Rabier, C Ané (2012)**. Testing Whole Genome Duplications, *Stat/Math Phylogenetics group*, University of Wisconsin-Madison, USA.
- **C-E Rabier, T Ta, C Ané (2013)**. Testing Whole Genome Duplications, *Evolution Seminar Series*, University of Wisconsin-Madison, USA.
- **C-E Rabier, T Ta, C Ané (2013)**. Testing Whole Genome Duplications, *Evolution*, Snowbird.
- **C-E Rabier, T Ta, C Ané (2014)**. Probabilistic approaches for detecting and locating whole genome duplications, *Seminar of the laboratory of Biometry and Evolutionary Biology*, University Lyon 1.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics Seminar*, Mathematics Research Institute of Rennes, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics and Probability Seminar*, University of Nice, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics Seminar*, University Joseph Fourier, Grenoble, France.
- **C-E Rabier (2014)**. Gaussian processes and Phylogenetic trees for the genome, *Statistics Seminar, Statistics and Genome*, University of Evry, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics and Probability Seminar*, University of Angers, France.
- **C-E Rabier (2014)**. Gaussian processes and Phylogenetic trees for the genome, *Mathematics, Evolution and Genomic Seminar*, University Aix-Marseille, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics and Probability Seminar*, University of Pau, France.
- **C-E Rabier (2014)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection. *Statistics Seminar*, University Lyon 1, France.
- **C-E Rabier, Ta T, Ané C (2014)**. Testing Whole Genome Duplications. *MIAT Unit Seminar*, INRA Toulouse, France.
- **C-E Rabier (2015)**. Gaussian and Chi-Square processes for Quantitative Trait Locus detection, *Statistics Seminar, TEAM MODAL*, INRIA Lille, France.
- **C-E Rabier, T Ta, C Ané (2015)**. “Probabilistic approaches for detecting and locating whole genome duplications”. *Mathematical Biology Seminar*, GenPhySE Unit, INRA Toulouse, France.
- **C-E Rabier, T Ta, C Ané (2015)**. “Probabilistic approaches for detecting and locating whole genome duplications”. *Seminar of the Team Methods and Algorithms in bioinformatics*, LIRMM, Montpellier, France.

- **C-E Rabier (2015)**. “Gaussian and Chi-Square processes for Quantitative Trait Locus detection”, *Math Seminar*, University of South Brittany, France.
- **C-E Rabier (2015)**. “Gaussian and Chi-Square processes for Quantitative Trait Locus detection”, *Statistics and Probability Seminar*, University Bordeaux 1, France.
- **C-E Rabier (2015)**. “Gaussian processes and phylogenetic trees in genomics”, *Statistics Seminar*, ENSAI, Rennes, France.
- **C-E Rabier, P Barre, G Charmet, B Mangin (2015)**. “On the accuracy of genomic selection”, *IMS-China International Conference on Statistics and Probability*, Kunming, China.
- **C-E Rabier, P Barre, G Charmet, B Mangin (2015)**. “On the accuracy of genomic selection”, *MIAT Unit Seminar*, INRA Toulouse, France.
- **C-E Rabier (2015)**. “Gaussian processes for gene mapping”, *Statistics Seminar*, University of Strasbourg, France.

Softwares

- IMAPPING (Rabier) : package with a graphical interface implementing the method for computing critical values, and presented in the article "Likelihood Ratio Test Process for Quantitative Trait Locus Detection"
- IMAPPINGFAMILY (Rabier) : package with a graphical interface regrouping the different methods presented in the article submitted "Chi square processes for gene mapping in a population with family structure".
- SPIMAPWGD (Rabier, Ané) : version of the software SPIMAP of Matthew Rasmussen and Manolis Kellis, using sequence data, and which incorporates Whole Genome Detection (WGD) events.
- GENE COUNT SOFTWARE (Ta, Rabier, Ané) : R package in order to detect WGD events. It uses gene count data across species, i.e. the number of gene copies in each species for each family.