Jean-Michel Bécu

Education

2012 – 2016	**Phd**, *Université de Technologie de Compiègne*. Thesis in applied mathematics and biostatistics
2009 – 2012	**Master's degree**, *Université de Rouen*. Master's degree in biofinformatic with apprenticeship
2006 – 2009	**Bachelor's degree**, *Université de Rouen*. Bachelor's degree in biochemistry and molecular biology

Thesis (Phd obtained in march 2016)

Titre	*Control of False Discoveries in High-Dimensional Variable Selection*
Thesis supervisor	Yves Grandvalet (Heudiasyc, UTC), Christophe Ambroise (LaMME, UEVE)
Description	Variables selection in bioinformatic handle with the high-dimensional problem. To deal with it, I developed methodologies to test the implication of variables or groups of variables on a biological question with a control of the false positive rate and the false discovery rate. Applications made on GWAS datasets to bring us a better comprehension of the HIV disease.
Keywords	Applied statistics, Variable selection, False discovery rate, Algorithmic
Thesis Comitee	Gérard Govaert (UTC, president),Alain Rakatomamonjy (INSA Rouen, referee), Antoine Cornuéjols (AgroParisTech, referee), Stéphane Robin (AgroParisTech, examiner), Étienne Roquain (UPMC, examiner), , Éric Leclerc (Université de Tokyo, examiner)

Academic experience

Research activity

Since 2016	**Post-doc**, *INRIA - Team Mistis*, Grenoble. Analysis of audio and infrared signal to locate the source (weapon shot) with mobile captor network. This signal processing is made with ABC algorithm approache coupled with the selection of coherent signal events in all events measured to locate an associated source. A data fusion is made on the cluster of coherent events taking account the balistic cinetics.
2012 – 2016	**Thesis**, *Heudiasyc*, CompiÃĺgne. See Thesis section
2010 – 2012	**Master's apprenticeship**, *Laboratoire de Biologie Neurovasculaire et Mitochondriale Intégrée INSERM UME 771 - CNRS UMR 6214*, Angers. Apprenticeship supervised by Marie Chabbert (CR1 CNRS). Study of the evolution of g-protein-coupled receptors by mMDS analysis and clustering on mMDS space.
2010	**Bachelor's internship**, *Laboratoire De Microbiologie du Froid, Signaux et Micro-Environnement (LMDF-SME) UPRES EA4312*, Evreux. Research of targets of the ECF sigma factor in pseudomonas aeruginosa PAO1 and statistical modelisation of their promoters linked to it.

2007 – 2009	**Voluntary internship**, *Laboratoire d'Informatique Traitement de l'Information et des Systèmes (LITIS EA 4108)*, Rouen. Conception and development of PromView, software to detect promoter regions on full genome with variables and discontinuous matrix.

Teaching

2016-2017	Tutor at the University of Grenoble in statistics and probability (Vacation)
2015-2016	Tutor at the IUT of Evry in statistics and probability (ATER)
2013-2014	Tutor at the UTC in algorithmic and programming with C language.

Review of article

2016	Reviewer for *Journal of Multivariate Analysis* (JMVA) (Model Testing)
2015	Reviewer for *BMC bioinformatics* (Variable selection)

French University Qualification

Section 26	Applied mathematics
Section 61	Computer science and signal processing

Publications

Articles

Jean-Michel Becu, Yves Grandvalet, Christophe Ambroise, and Cyril Dalmasso. Beyond support in two-stage variable selection. *Statistics and Computing*, pages 1–11, 2015.

Jean-Michel Becu, Julien Pele, Patrice Rodien, Herve Abdi, and Marie Chabbert. Structural evolution of g-protein-coupled receptors: a sequence space approach. *Methods Enzymol*, 520:49–66, 2013.

Vic Norris, Laurence Menu-Bouaouiche, Jean-Michel Becu, Rachel Legendre, Romain Norman, and Jason A Rosenzweig. Hyperstructure interactions influence the virulence of the type 3 secretion system in yersiniae and other bacteria. *Appl Microbiol Biotechnol*, 96(1):23–36, Oct 2012.

Julien Pele, Jean-Michel Becu, Herve Abdi, and Marie Chabbert. Bios2mds: an r package for comparing orthologous protein families by metric multidimensional scaling. *BMC Bioinformatics*, 13:133, 2012.

Talks in conferences

Conferences with Proceedings

J.-M. Becu, C. Ambroise, Y. Grandvalet, and C. Dalmasso. Significance testing for variable selection in high-dimension. In *Computational Intelligence in Bioinformatics and Computational Biology (CIBCB), 2015 IEEE Conference on*, pages 1–8, Aug 2015.

Conference without proceedings

SMPGD 15 (Munich)	Adaptive ridge regression for variables selection
MAS 14 (Toulouse)	Tests d'hypothèse en régression pénalisée pour la sélection de variables en bioinformatique
NetBio 14 (Paris)	Sélection de variables par la régression ridge adaptative
Jobim 12 (Rennes)	The sequence space of G-protein-coupled receptors: Implications for molecular modeling

Software Development

ridgeAdap	A R package, available in my personal page, dedicated to variables selection in high-dimensional dataset with significance testing based on adaptive-ridge estimates.
Bios2mds	A R package, available in the CRAN repository, dedicated to the analysis of biological sequences by metric MultiDimensional Scaling with projection of supplementary data.