Sandra Plancade

Researcher at INRA (French National Institute for Agriculture Research)

INRA
Unité MaIAGE\I
Domaine de Vilvert\I
78352 JOUY-EN-JOSAS CEDEX\I
France
prenom.nom@inra.fr

ISBA
Université catholique de Louvain
Voie du Roman Pays 20, bte L1.04.01
B-1348 Louvain-la-Neuve
Belgique

Education

2007- 2010: PhD at University Paris Descartes, Department of mathematics, supervised by Professor Fabienne Comte
Subject: Estimation by pointwise and global model selection from partially observed data.

2005/2007: Master's degree in Probability and Statistics, University Paris-Sud.

2006 : Agrégation de mathématiques (ability for higher education teaching)

2003/2006: Bachelor degree at Ecole Normale Supérieure (Lyon, France).

Working experiences

♦ 2013 - : Researcher at the department of Applied Mathematics and Informatics of INRA (French National Institute for Agriculture Research)

Oct 2017 – April 2019 : Invited researcher at the Catholic University of Louvain-la-Neuve – Belgium
(Agreenskills outgoing fellowship)

♦ 2010-13: Post-doctoral position - Department of Community Medicine at the University of Tromsø (Norway)

April-May 2011 : Invited researcher at Technion (Israel)
Sept 2012-July 2013 : Invited researcher at Curie Institute (Paris)

Publications

Nonparametric estimation of the density of the regression noise, S.Plancade, *C. R. Acad. Sci.* (2008).

Estimation of the density of regression errors by pointwise model selection, S. Plancade, *Math. Methods Statist.* (2009).

Nonparametric estimation of hazard rate in presence of censoring, S. Plancade, *Metrika* (2010).

Guidelines for controlled trials of drugs in migraine: Third edition (International Headache Society Clinical Trials Subcommittee), *Cephalalgia* (2011).

Transcriptional output in a prospective design conditionallly on follow-up and exposure – the multistage model of cancer, E. Lund, S. Plancade, *Int J Mol Epidemiol Genet (2012).*

Generalization of the normal-exponential model: exploration of a more accurate parametrisation for the signal distribution on Illumina BeadArrays, S. Plancade, Y. Rozenholc and E. Lund, *BMC Bioinfo* (2012).

Estimation of cumulative distribution function from current status data, S. Plancade, *J. Statist. Plann. Inference* (2013).

A processual model for functional analyses of carcinogenesis in the prospective cohort design, E. Lund*, S. Plancade*, G. Nuel, H. Bovelstad and J.C. Thalabard, *Medical hypotheses* (2015)

A generic methodological framework for studying single cell motility in high-throughput time-lapse data, A. Schoenauer Sebag, S. Plancade, C. Raulet-Tomkiewicz, R. Barouki, J.P. Vert. and T. Walter (2015) BioInfo, i320-i328.

Integrated mRNA and miRNA expression profiling in blood reveals candidate biomarkers associated with endurance exercise in the horse, Mach, N., Plancade, S., Pacholewska, A., Lecardonnel, J., Rivière, J., Moroldo, M., Vaiman, A., Morgenthaler, C., Beinat, M., Névot, A., Robert, C., Barrey, E. (2016). Scientific Reports.

A new statistical method for curve group analysis of longitudinal gene expression data illustrated for breast cancer in the NOWAC postgenome cohort as a proof of principle. Lund, E., Holden, L., Bøvelstad, H., Plancade, S., Mode, N., Günther, C.-C., Nuel, G., Thalabard, J.-C., Holden, M. (2016). BMC Medical Research Methodology, 16.

Inferring Aggregated Functional Traits from Metagenomic Data Using Constrained Non-Negative Matrix Factorization: Application to Fiber Degradation in the Human Gut Microbiota, Raguideau, S, Plancade, S, Pons, N., Leclerc, M. Laroche, B. (2016) *PLOS Comput. Bio.*

Lactobacillus paracasei CNCM I-3689 reduces vancomycin-resistant Enterococcus persistence and promotes Bacteroidetes resilience in the gut following antibiotic challenge. Crouzet, L., Derrien, M., Cherbuy, C., Plancade, S., Foulon, M., Chalin, B., van Hylckama Vlieg, J. E. T., Grompone, G., Rigottier-Gois, L., Serror, P. (2018). *Scientific Reports, 8* (1)*.*

Student supervision

PhD

Ariane Bassignagni (octobre 2016-)
Integration et analyse de données de méta-protéomique quantitative en shotgun pour explorer les fonctionnalités du microbiote intestinal humain dans le cadre des maladies cardiométaboliques.

Supervisors : Catherine Juste, Magali Berland, Sandra Plancade.

Sébastien Raguideau (octobre 2013-décembre 2016)
Analyse de données de métagénomique fonctionnelle par NMF pour la modélisation de la dégradation des fibres par le microbiote intestinal humain
Supervisors : Béatrice Laroche, Marion Leclerc, Sandra Plancade

Master

Emile Chapuis (avril-juillet 2016)
Analyse de la variabilité technique dans des variables méta-protéomiques.
Supervisors : Sylvie Huet, Sandra Plancade

Hengjia Xie (mars-septembre 2017)
Analyse statistique des changements métaboliques suite à une perturbation chez la chèvre
Supervisors : Masoomeh Taghipoor, Sandra Plancade

Oumou Salama Daouda (avril-septembre 2017)
Modélisation et estimation du phyllochrone du maïs. Etude des e#ets du génotype et de l'environnement.
Supervisors : Sylvie Huet, Sandra Plancade

Teaching

2014-2017: Introduction to nonparametric statistics, Master, Université Paris-Saclay/ENSIIE.
2014-2015: "Case study", Université Paris-Descartes, Master.
2015-2016: Practical session in mathematics, undergraduate, Université Pierre et Marie Curie
2012-2013: Analysis of Variance -course and practical sessions, undergraduate, IUT Paris-Descartes.
2006-2010: Practical session in mathematics, undergraduate, Université Paris-Descartes.
2006-2009: Practical session in statistics, undergraduate, Université Paris-Descartes.

Software

NormalGamma: R package for the normal-gamma convolution model.