

Sandra Plancade

Researcher at INRAE
(French National Institute for Agriculture and Environmental Research)

INRAE - Unité MIAT
BP 52627
31326 CASTANET TOLOSAN cedex
France
prenom.nom@inrae.fr

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 INRAE

Oct 2017 – April 2019 : Invited researcher at the Catholic University of Louvain-la-Neuve – Belgium
(*Agreenskills+ outgoing fellowship : Survival analysis methods in the current status data framework for plant development analysis.*)

♦ 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

A combined test for feature selection on sparse metaproteomics data - alternative to missing value imputation, Plancade S., Berland M., Blein-Nicolas M., Langella O., Bassignani A., Juste C., *preprint*, bioRxiv 2021.06.22.449387

A stochastic process modelling of maize phyllochron enables to characterize environmental and genetic effects. Plancade S., Marchadier E., Huet S., Ressayre A., Noûs C., Dillmann C., *preprint*, bioRxiv 2021.01.11.426247

New genetic biomarkers to differentiate non-pathogenic from clinically relevant *Bacillus cereus* strains , Kavanaugh DW, Glasset B, Dervyn R, Guérin C, Plancade S, Herbin S, Brisabois A, Nicolas P, Ramarao N., *Clin Microbiol Infect.* 2021 Jun 7:S1198-743X(21)00283-4.

Benefits of Iterative Searches of Large Databases to Interpret Large Human Gut Metaproteomic Data Sets. Bassignani A, Plancade S, Berland M, Blein-Nicolas M, Guillot A, Chevret D, Moritz C, Huet S, Rizkalla S, Clément K, Doré J, Langella O, Juste C, *J Proteome Res.* 2021 Mar 5;20(3):1522-1534.

Unraveling the effects of the gut microbiota composition and function on horse endurance physiology. Plancade S, Clark A, Philippe C, Helbling JC, Moisan MP, Esquerré D, Le Moyec L, Robert C, Barrey E, Mach N, *Sci Rep.* 2019 Jul 3;9(1):9620.

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., Serron, P. (2018). *Scientific Reports*, 8 (1).

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.*

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.

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., Nénot, A., Robert, C., Barrey, E. (2016). *Scientific Reports*.

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.

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)

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

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

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).

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

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

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

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

Student supervision

PhD

Ariane Bassignagni (2016-2019)

Integration and analysis of quantitative shotgun metaproteomics to explore human gut microbiota functionalities in cardiometabolic pathologies.

Supervisors : Catherine Juste, Magali Berland, Sandra Plancade.

Sébastien Raguideau (2013-2016)

Analysis of functional metagenomics data by NMF for modelling of fiber degradation in human gut microbiota.

Supervisors : Béatrice Laroche, Marion Leclerc, Sandra Plancade

Master

Emile Chapuis (avril-juillet 2016)

Analysis of technical variability in metaproteomics data.

Supervisors : Sylvie Huet, Sandra Plancade

Hengjia Xie (mars-septembre 2017)

Analysis of metabolic changes in goat after perturbations

Supervisors : Masoomeh Taghipoor, Sandra Plancade

Oumou Salama Daouda (avril-septembre 2017)

Modelling of maize phyllochron and study of genotypic and environmental effects

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.