Mathilde Sautreuil

Profile

Autonomous and hard-working individual with an interest in development of statistical learning methods and their applications to medical research.

Work

February 2021 -
Study Engineer, *SOLADIS (EFOR Group)*, Consultant as Biomarker Biostatistician - Servier.
In support of Biomarker Biostatistics team: Evaluation of potential biomarkers in immunology, oncology and immuno-oncology projects:
- Benchmark of deconvolution methods on non-standard data
- Updating of deconvolution part of analysis pipeline of RNA-seq and microarrays data
- Data analysis on different projects as (non-exhaustive part):
  - Deconvolution analysis to study the heterogeneity pre- and post-treatment of immune cells
  - Characterization of signatures and indication selection in oncology and immunology (Analysis of RNA-seq, microarrays, and cytokines datasets)
- Use of Machine Learning methods on different projects to classifiy responder and non-responder patients to a treatment

2020-2021
Research Engineer in Biostatistics, *with Dr Guillem Rigaill and Dr Etienne Delannoy*
Stat and Genome team, LaMME - Gnet team, IPS2, Paris-Saclay university.
The subjet concerns the detection of PPR footprints using machine learning methods at Arabidopsis Thaliana.

2017-2020
PhD student in Biostatistics, *supervised by Pr Paul-Henry Cournède and Dr Sarah Lemler*
Biomathematics team - MICS Laboratory, CentraleSupélec.
The subject concerns survival analysis and marker detection in oncology and the main objectives are:
- the study of regularisation and screening methods to detect the biological markers in the case of renal cancer;
- the study and the development of neural networks to predict survival duration in high-dimension.

2015-2017
21 months
Apprentice in Biostatistics, *supervised by Dr Caroline Bérard and Dr Nicolas Vergne*
TIBS Team, LITIS EA 4108 - Statistique Team, LMRS UMR 6085 CNRS, Rouen.
My apprenticeship consisted of the development of:
- a statistical method for RNA-seq data analysis;
- a R package for the Markov and semi-Markov models;
- a Shiny web application for the processing of qRT-PCR data.

Education

2017-2021 **PhD thesis in Applied Mathematics**, *MICS, CentraleSupélec, Paris-Saclay University*, FRANCE.

2014-2017 **Sandwich Master's Degree in Bioinformatics with distinction**, *Normandie University*, *Rouen*, FRANCE.

2011-2014 **Bachelor's Degree in Mathematics**, *Rouen University*, FRANCE.

Tool development for users

R package
survMS: an R package for the simulation of survival data from Cox, AFT and AH models,
disponible sur le cran et sur `https://github.com/mathildesautreuil/survMS`.

Python package
NNsurv: Neural Networks based on a discrete-time model to predict the survival duration,
`https://github.com/mathildesautreuil/nnsurv`.

R Package
SMM: An R Package for Estimation and Simulation of Discrete-time semi-Markov Models,
`https://cran.r-project.org/web/packages/SMM/`.

Application web Shiny
PROqPCR: PROcessing of qRT-PCR data,
`https://qpcrapp.shinyapps.io/proqpcr/`.

Language

English read, written and spoken at an intermediate level – C1 CERCRL

Referees

Pr Paul-Henry Cournède
Professor
MICS Laboratory
CentraleSupélec, Paris-Saclay University
✉ paul-henry.cournede@ecp.fr
📞 +33 1 75 31 67 86

Dr Sarah Lemler
Assistant Professor
MICS Laboratory
CentraleSupélec, Paris-Saclay University
✉ sarah.lemler@ecp.fr
📞 +33 1 75 31 68 85

Dr Caroline Bérard
Assistant Professor
LITIS Laboratory
University of Rouen
✉ caroline.berard@univ-rouen.fr
📞 +33 2 35 14 65 82