Pierre Mahé

Research Engineer - Machine Learning for Computational Biology

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Married, 3 children.
Born on July 8th, 1979.

Research engineer with a solid expertise in machine learning, I have extensive experience in applying machine learning algorithms to biological data. Over the last decade, I have mainly been involved in clinical microbiology applications, such as identifying bacteria or predicting their antibiotic resistance profiles using various technologies (e.g. mass-spectrometry, imaging and next-generation sequencing). My current interest lies particularly in analyzing genomics data using k-mer based and/or deep-learning approaches.

Education

2003–2006 **Ecole des Mines de Paris (France)**, *Ph.D.*, Machine Learning and Computational Biology.
Graph kernels and kernel methods for chemoinformatics. Supervised by Jean-Philippe Vert, obtained with honors.

2002–2003 **Ecole Normale Supérieure de Cachan (France)**, *M.Sc.*, Machine Learning and Computer Vision.
Obtained with honors.

1997–2002 **Institut National des Sciences Appliquées (France)**, *French Engineering Degree*, Computer Science.

Experience

2016–present **Associate Professor (part-time)**, *University Grenoble-Alpes (France)*
Teaching statistical machine learning, computational statistics and project management to M.Sc. students.

2008–present **Research Engineer**, *bioMérieux (Grenoble, France)*
Providing machine learning expertise to support R&D projects addressing key *in vitro* diagnostics issues for clinical microbiology, using emerging technologies (e.g. next-generation sequencing, imaging and mass-spectrometry). Mentoring of students and junior employees. Definition, planning and management of R&D projects.

2006–2008 **Post-Doctoral Researcher**, *Xerox Research Center Europe (now Naver Labs, Grenoble, France)*
Statistical learning for machine translation.

Student supervision

2020–present **Teddy Ardouin**, *Ph.D*, Automatic design of PCR primers using deep-generative models.
Co-advised with Adeline Leclercq-Samson (University Grenoble-Alpes) and Laurent Drazek (bioMérieux).

2021 **Thomas Poulain**, *M.Sc*, Taxonomic classification of microbial sequencing reads by deep-learning.

2021 **Lina Khodja**, *M.Sc*, Unsupervised representation learning of bacterial genomes using NLP approaches.

2019 **Sylla Camara**, *M.Sc*, Early prediction of antibiotic resistance from time series of microscopy images.

2018 **Luis Montero**, *M.Sc*, Classification of bacterial 16S genomic sequences by convolutional neural networks.

2017 **Julia Puig**, *M.Sc*, Semantic segmentation of microscopy images by deep-learning.

2017 **Antonin Riffard**, *M.Sc*, Targeted resistance genotyping for *Mycobacterium tuberculosis*.

2015 **Antoine Bonnefoy**, *Ph.D (visiting)*, Sparse multi-task learning for antimicrobial resistance prediction.

2011-2014 **Kévin Vervier**, *Ph.D*, Structured machine learning methods for clinical microbiology.
Co-advised with Jean-Philippe Vert (Ecole des Mines de Paris, now Google Brain).

Selected publications

2022 *Ultra-fast SARS-CoV-2 variant identification from Oxford Nanopore reads using k-mers and local sequencing depth estimation.* Meriem El Azami, Magali Jaillard-Dancette, Aurélien Griffon, Maud Tournoud and Pierre Mahé. Submitted.

2020 *Interpreting k-mer based signatures for antiobiotic resistance prediction.* Magali Jaillard-Dancette, Mattia Palmieri, Alex van Belkum, Pierre Mahé. GigaScience.

2019 *A large scale evaluation of TBProfiler and Mykrobe for antibiotic resistance prediction in M. tuberculosis.* Pierre Mahé, Meriem El Azami, Philippine Barlas, Maud Tournoud. PeerJ.

2018 *Predicting bacterial resistance phenotypes from whole-genome sequences using k-mers and stability selection.* Pierre Mahé, Maud Tournoud. BMC Bioinformatics.

2016 *Large scale machine learning for metagenomics sequence classification.* Kévin Vervier, Pierre Mahé, Maud Tournoud, Jean-Baptiste Veyrieras, Jean-Philippe Vert. Bioinformatics.

2016 *Joint input/output regularization for structured variable selection in a multi-task framework.* Antoine Bonnefoy, Pierre Mahé, Ismael Ouamlil, Jean-Baptiste Veyrieras. Conférence Française d'Apprentissage.

2014 *Automatic identification of mixed bacterial species fingerprints in a MALDI-TOF mass-spectrum.* Pierre Mahé et. al. Bioinformatics.

2009 *Linguistically enriched word-sequence kernels for discriminative language modeling.* Pierre Mahé, Nicola Cancedda. Learning Machine Translation, MIT Press.

2009 *Graph kernels based on tree-patterns for molecules.* Pierre Mahé, Jean-Philippe Vert. Machine Learning

2005 *Graph kernels for molecular structure-activity relationship analysis with support vector machines.* Pierre Mahé, Jean-Philippe Vert. Journal of Chemical Information and Modeling

Full list available at `https://scholar.google.fr/citations?user=3yLMPGgAAAAJ`

Skills

Data Science: R, python, Unix/bash, C/C++, git, LaTeX, keras/tensorflow, scikit-learn.

Machine Learning: broad expertise in supervised and unsupervised learning. Particular interest in deep learning, kernel methods and Lasso penalization for the analysis of structured and high-dimensional data.

Computational Biology: next-generation sequencing, mass spectrometry, image analysis, bioinformatics algorithms, bacterial genomics, clinical microbiology.

Languages: French (native), English (fluent) and Spanish (intermediate).

Personal interests

Rock climbing, hiking, mountain biking.

DIY and renovation work (creation of a 7 person gite - `https://www.aufildelans.com/`) .

Graphical novels.

Struggling to learn the guitar.

Rererences

Available upon request.