

# Pierre Mahé

Research Engineer - Machine Learning for  
Computational Biology

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🌐 <https://pmahe.github.io/>  
Married, 3 children.  
Born on July 8th, 1979.



*Research engineer with a solid expertise in machine learning, I have a broad interest in applying machine learning algorithms to biological data. Over the last decade, I have mainly been involved in clinical microbiology applications, like identifying a bacteria or predicting its antibiotic resistance profile, using various technologies (e.g., mass-spectrometry, imaging and next-generation sequencing). I am currently particularly interested 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.

## Students 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.
- 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

- 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,  $\text{\LaTeX}$ , 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 and bouldering, hiking, mountain biking.

Digital photography.

Graphical novels.

Struggling to learn the guitar.

## Rererences

Available upon request.