

# MAXIME BORRY | Curriculum Vitae

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## SUMMARY

Bioinformatician - Life Data Scientist - Doctoral researcher at the Max Planck Institute for Evolutionary Anthropology - Working on ancient DNA metagenomics

## EDUCATION

### UNIVERSITÉ PARIS DIDEROT

MSc. Biology-Computer Science/Bioinformatics  
Valedictorian

2017 - 2018

Paris, France

Python programming - R programming - Web programming - Databases - Algorithms - Genomics - Structural Biology - Structural Bioinformatics - Data analysis - Machine learning

### UNIVERSITÉ GRENOBLE ALPES

MSc. Biology, Ecology, Environment

2014 - 2015

Grenoble, France

Populations genetic - Evolution - Biostatistics - Metabarcoding

### UNIVERSITÉ PARIS DESCARTES

BSc. Interdisciplinary approaches to life sciences

2011 - 2014

Paris, France

Biology - Chemistry - Physics - Dynamic system Modelling - Perl programming - Research oriented projects - Philosophy of Science - Research ethics - Editor of a scientific journalism publication

## EXPERIENCE

### DOCTORAL RESEARCHER

Max Planck Institute for Evolutionary Anthropology

I continue to develop and publish bioinformatics tools and pipelines in Python and Nextflow for ancient DNA metagenomics data, as well as my work on analysing ancient DNA metagenomics data.

Since 09/2021

Leipzig, Germany

### DOCTORAL RESEARCHER

Max Planck Institute for the Science of Human History

I developed and published bioinformatics tools in Python and Nextflow for ancient DNA metagenomics data, as well as performed ancient DNA metagenomics data analysis that led to publications in peer-reviewed journals.

09/2018 - 08/2021

Jena, Germany

### GRADUATE RESEARCH INTERN

Muséum national d'Histoire naturelle

Bioinformatics development and analysis for ancient DNA metagenomics. Nextflow pipeline development for dietary and microbial composition from metagenomics data of bronze-age dental calculus samples.

01/2018 - 07/2018

Paris, France

### LAB TECHNICIAN

Learning Planet Institute

Setting up a Lab Inventory Management System (LIMS) - Inventory management, ordering, and supplier contact point - Growing media preparation

10/2017 - 05/2018

Paris, France

### GRADUATE RESEARCH INTERN

Institut Pasteur

Development of ensemble methods for comparative gene expression analysis, with a R package and an interactive dashboard with Shiny

03/2017 - 05/2017

Paris, France

### GRADUATE RESEARCH ASSISTANT

Centre for Genomic Regulation

Exploration of the oral mycobiome with Gabaldon's comparative genomics research group.

06/2016 - 08/2016

Barcelona, Spain

### MASTER STUDENT INTERN

Max Planck Institute for Evolutionary Biology

12/2015 - 02/2016

Leipzig, Germany

Detection and functional study of gene duplication between Neanderthal and Modern Humans.

### **GUEST RESEARCHER**

**Nature History, University of Oslo**

Development of new markers and metagenomics software for plant identification. De novo and mapping assembly of Illumina data, phylogeny of the *Anacyclus* genus, and metabarcoding visualization software development.

**05/2015 - 10/2015**

Oslo, Norway

### **RESEARCH INTERN**

**University of Gdansk**

Molecular biology internship: Expression of PIK3CA protein in insect cell lines using the BacToBac system.

**02/2014 - 06/2014**

Gdansk, Poland

### **RESEARCH INTERN**

**Universitetet i Nordland**

Benchmarking de novo assemblers on copepod's transcriptome sequencing data

**09/2013 - 12/2013**

Bodø, Norway

### **RESEARCH INTERN**

**INRA**

Investigating new recombinase families in Mycobacteriophages

**10/2012 - 11/2012**

Jouy en Josas, France

## **SKILLS**

### **PROGRAMMING LANGUAGE LIBRARIES LANGUAGES**

**Experienced:** Python, Nextflow

**Familiar:** R | JavaScript

pandas | scikit-learn | statsmodels | scikit-bio | pysam | biopython

**Native:** French | **Fluent:** English (C2) | **Conversational:** German

## **HONORS & AWARDS**

### **BEST POSTER PRIZE**

**Société d'Anthropologie de Paris conference**

"Analysis of the human periodontal microbiome from ancient DNA." Poster based on the research I conducted at the "Musée de l'Homme" in Paris in the Éco-anthropologie et Ethnobiology Lab during my master Thesis.

**01/2019**

Paris, France

### **VALEDICTORIAN**

**Université Paris Diderot**

Valedictorian of the 2018 promotion of the BIB bioinformatics master

**07/2018**

Paris, France

### **BIOINFORMATICS COMPETITION - WINNING TEAM**

**Meet-U**

Structural bioinformatics competition: conceive, design, develop, test and validate a computational program to predict the three-dimensional structure of a protein complex, given the structures of the two monomeric partners.

**01/2018**

Paris, France

## **EXTRACURRICULAR ACTIVITIES**

### **PHD REPRESENTATIVE**

**06/2020 - 06/2021**

PhD representative of the doctoral researchers of the Max Planck Institute for the Science of Human History. I organized social events, and represented them at the instances of the Max Planck society.

**Max Planck Institute for the Science of Human History**

Jena, Germany

### **BOARD MEMBER**

**10/2011 - 11/2012**

Member of the board and volunteer for this scientific popularization NGO offering research lab internship placements to high-school students

**Paris Montagne**

Paris, France

## **TEACHING EXPERIENCE**

### **MENTOR**

**Seqera Labs**

**Since 05/2022**

Remote

Mentor for the nexflow bioinformatics mentoring program from the nf-core/organization/Seqera Labs, with support from the CZI Science foundation.

## LECTURER

### MPI-SHH IMPRS

Teaching a course on microbiome data analysis with a focus on microbial community ecology

08/2021

Remote

## TEACHING ASSISTANT

### Petnica Science Center

Teaching assistant for a molecular biology and ecology workshop for bachelor students.

09/2015

Petnica, Serbia

## TEACHING ASSISTANT

### Université Paris Descartes

Teaching assistant on a workshop about thermodynamics for bachelor students.

04/2015

Paris, France

## PUBLICATIONS

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- Maxime Borry, Alexander Hübner, Christina Warinner. [sam2lca: Lowest Common Ancestor for SAM/BAM/CRAM alignment files](#). Journal of Open Source Software, 2022
- Maxime Borry, Alexander Hübner, Adam B. Rohrlach, Christina Warinner. [PyDamage: automated ancient damage identification and estimation for contigs in ancient DNA de novo assembly](#). PeerJ, 2021
- Marsha C. Wibowo, Zhen Yang, Maxime Borry, Alexander Hübner, Kun D. Huang, Braden T. Tierney, Samuel Zimmerman, Francisco Barajas-Olmos, Cecilia Contreras-Cubas, Humberto García-Ortiz, Angélica Martínez-Hernández, Jacob M. Lubber, Philipp Kirstahler, Tre Blohm, Francis E. Smiley, Richard Arnold, Sonia A. Ballal, Sünje Johanna Pamp, Julia Russ, Frank Maixner, Omar Rota-Stabelli, Nicola Segata, Karl Reinhard, Lorena Orozco, Christina Warinner, Meradeth Snow, Steven LeBlanc, Aleksandar D. Kostic. [Reconstruction of ancient microbial genomes from the human gut](#). Nature, 2021.
- James A. Fellows Yates, Thiseas C. Lamnidis, Maxime Borry, Aida Andrades Valtueña, Zandra Fagernäs, Stephen Clayton, Maxime U. Garcia, Judith Neukamm, Alexander Peltzer. [Reproducible, portable, and efficient ancient genome reconstruction with nf-core/eager](#). PeerJ, 2021.
- James A. Fellows Yates, Aida Andrades Valtueña, Åshild J. Vågene, Becky Cribdon, Irina M. Velsko, Maxime Borry, Miriam J. Bravo-Lopez, Antonio Fernandez-Guerra, Eleanor J. Green, Shreya L. Ramachandran, Peter D. Heintzman, Maria A. Spyrou, Alexander Hübner, Abigail S. Gancz, Jessica Hider, Aurora F. Allshouse, Valentina Zaro, Christina Warinner. [Community-curated and standardised metadata of published ancient metagenomic samples with AncientMetagenomeDir](#). Scientific Data, 2021.
- Maxime Borry et al. [CoproID predicts the source of coprolites and paleofeces using microbiome composition and host DNA content](#). PeerJ, 2020.
- Maxime Borry. [Sourcepredict: Prediction of metagenomic sample sources using dimension reduction followed by machine learning classification](#). Journal of Open Source Software, 2019.