

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

FRIEDRICH-SCHILLER-UNIVERSITÄT

PhD candidate in Bioinformatics

Software development and statistical data analysis with a focus in ancient DNA metagenomics

since 2018

Jena, Germany

UNIVERSITÉ PARIS DIDEROT

MSc. Biology-Computer Science/Bioinformatics

Valedictorian

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

2017 - 2018

Paris, France

UNIVERSITÉ GRENOBLE ALPES

MSc. Biology, Ecology, Environment

Populations genetic - Evolution - Biostatistics - Metabarcoding

2014 - 2015

Grenoble, France

UNIVERSITÉ PARIS DESCARTES

BSc. Interdisciplinary approaches to life sciences

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

2011 - 2014

Paris, France

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

06/2016 - 08/2016

Barcelona, Spain

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

MASTER STUDENT INTERN

Max Planck Institute for Evolutionary Biology

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

12/2015 - 02/2016

Leipzig, Germany

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
pandas | scikit-learn | statsmodels | scikit-bio | pysam | biopython
Native: French | **Fluent:** English (C2) | **Conversational:** German

Familiar: R | JavaScript

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

Mentor for the nexflow bioinformatics mentoring program from the nf-coreorganization/Seqera Labs, with support from the CZI Science fundation.

Since 05/2022

Remote

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

- 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. Luber, 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 Fagnäs, 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.