MAXIME BORRY, PHD. | Curriculum Vitae

✉ maxime.borry@gmail.com • ⌨ maxibor • in/maximeborry • 🔖 maximeborry.com

SUMMARY

Bioinformatician - Life Data Scientist - Postdoctoral researcher at the Max Planck Institute for Evolutionary Anthropology and the Leibniz Institute for Natural Product Research and Infection Biology Hans Knöll Institute - Working on ancient DNA metagenomics

EDUCATION

FRIEDRICH-SCHILLER-UNIVERSITÄT
09/2018-03/2023
Jena, Germany
PhD candidate in Bioinformatics
Software development and statistical data analysis with a focus in ancient DNA metagenomics

UNIVERSITÉ PARIS DIDEROT
2016 - 2018
Paris, France
MSc. Biology-Computer Science/Bioinformatics
Valedictorian
Python programming - R programming - Web programming - Databases - Algorithms - Genomics - Structural Biology - Structural Bioinformatics - Data analysis - Machine learning

UNIVERSITÉ GRENOBLE ALPES
2014 - 2015
Grenoble, France
MSc. Biology, Ecology, Environment
Populations genetic - Evolution - Biostatistics - Metabarcoding

UNIVERSITÉ PARIS DESCARTES
2011 - 2014
Paris, France
BSc. Interdisciplinary approaches to life sciences
Biology - Chemistry - Physics - Dynamic system Modelling - Perl programming - Research oriented projects - Phylosophy of Science - Research ethics - Editor of a scientific journalism publication

EXPERIENCE

POSTDOCTORAL RESEARCHER
Since 04/2023
Jena & Leipzig, Germany
Leibniz Institute for Natural Product Research and Infection Biology
Developing bioinformatics software and analyzing ancient metagenomics sequencing data of ancient fermentation samples.

DOCTORAL RESEARCHER
09/2021-03/2023
Leipzig, Germany
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.

DOCTORAL RESEARCHER
09/2018 - 08/2021
Jena, Germany
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.

GRADUATE RESEARCH INTERN
01/2018 - 07/2018
Paris, France
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.

LAB TECHNICIAN
10/2017 - 05/2018
Paris, France
Learning Planet Institute
Setting up a Lab Inventory Management System (LIMS) - Inventory management, ordering, and supplier contact point - Growing media preparation

GRADUATE RESEARCH INTERN
03/2017 - 05/2017

Institut Pasteur

Paris, France

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

GRADUATE RESEARCH ASSISTANT

06/2016 - 08/2016

Centre for Genomic Regulation

Barcelona, Spain

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

MASTER STUDENT INTERN

12/2015 - 02/2016

Max Planck Institute for Evolutionary Biology

Leipzig, Germany

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

GUEST RESEARCHER

05/2015 - 10/2015

Nature History, University of Oslo

Oslo, Norway

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.

RESEARCH INTERN

02/2014 - 06/2014

University of Gdansk

Gdansk, Poland

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

RESEARCH INTERN

09/2013 - 12/2013

Universitetet i Nordland

Bodø, Norway

Benchmarking de novo assemblers on copepod's transcriptome sequencing data

RESEARCH INTERN

10/2012 - 11/2012

INRA

Jouy en Josas, France

Investigating new recombinase families in Mycobacteriophages

SKILLS

PROGRAMMING LANGUAGE	Experienced: Python, Nextflow Familiar: R	JavaScript
LIBRARIES	pandas	scikit-learn	statsmodels	scikit-bio	pysam	biopython
LANGUAGES	Native: French	Fluent: English (C2)	Conversational: German

HONORS & AWARDS

BEST POSTER PRIZE

01/2019

Société d'Anthropologie de Paris conference

Paris, France

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

VALEDICTORIAN

07/2018

Université Paris Diderot

Paris, France

Valedictorian of the 2018 promotion of the BIB bioinformatics master

BIOINFORMATICS COMPETITION - WINNING TEAM

01/2018

Meet-U

Paris, France

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.

EXTRACURRICULAR ACTIVITIES

PHD REPRESENTATIVE
Max Planck Institute for the Science of Human History

06/2020 - 06/2021

Jena, Germany

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.

BOARD MEMBER
Paris Montagne

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, 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

- Moritz E. Beber, **Maxime Borry**, Sofia Stamouli, James A. Fellows Yates. TAXPASTA: TAXonomic Profile Aggregation and STAndardisation.Journal of Open Source Software, 2023.

- Martin Klapper, Alexander Hübner, Anan Ibrahim, Ina Wasmuth, **Maxime Borry**, Veit G. Haensch, Shuaibing Zhang, Walid K. Al-Jammal, Harikumar Suma, James A. Fellows Yates, Jasmin Frangenberg, Irina M. Velsko, Somak Chowdhury, Rosa Herbst, Evgeni V. Bratovanov, Hans-Martin Dahse, Therese Horch, Christian Hertweck, Manuel Ramon González Morales, Lawrence Guy Straus, Ivan Vilotijevic, Christina Warinner, Pierre Stallforth. Natural Products from Reconstructed Bacterial Genomes of the Middle and Upper Paleolithic. Science, 2023

- **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 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.