

Luc Blassel

PhD Student, interested in Machine learning in Biology

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📍 Paris, France

I am a PhD student in computational biology at the Institut Pasteur in France. I started with biology studies in AgroParisTech, a Parisian "Grande école" but quickly found my way to machine learning. In order to complete my M.Sc, I entered the Institut Pasteur as an intern, and found the fascinating world of academic research.

I have since continued on, entering a PhD program in computational biology, exploring the interface between biology, computer science and machine learning.

This interdisciplinary experience drives me to further explore computational methods to resolve problems of a biological nature.

Experience

Post-Doctoral Researcher, [CNRS](#), Paris, France

2023–

During this postdoc I will work on the [phyhloformer](#) project with [Laurent Jacob](#) and members of the LBBE in Lyon. My work will center around improving the performance of the model, making it's output closer to the real phylogenetic tree. I will also be adding functionality to the model, mainly the ability to take unaligned sequences as input.

PhD Student, [Institut Pasteur](#), Paris, France

2020–2023

PhD in computational biology, focused on improving and learning from sequence alignments. With the ever growing quantity of high quality sequencing data, we are now able to develop methods to take advantage of this data. My PhD project followed 2 different axes: (1) Using machine learning to discover Drug resistance mutations in HIV (Continuation of the M.Sc project) (2) Search of a function space for sequence transformation functions that improve sequence mapping and alignment.

This PhD was supervised by [Rayan Chikhi](#) and funded by the [PRAIRIE](#) institute. The manuscript can be found [here](#)

Research Engineer, [Institut Pasteur](#), Paris, France

2018–2020

Using machine learning and large datasets to explore the drug resistance landscape in HIV. Supervised by [Olivier Gascuel](#). A large dataset of UK HIV sequences associated with patient RT-treatment status was used to train several machine learning algorithms. Examining the important learned features gave us insight in mutations associated to ART failure. This project resulted in a [publication](#).

Project page [here](#), and [M.Sc thesis](#) (in french).

Data Scientist Intern, [CapitalData](#), Paris, France

Mar-Sept 2017

As a data scientist intern at Capital data I was tasked with developing a software pipeline to validate data prior to database integration, and detect anomalies using time series. This was implemented in R and Python. I also, developed reporting-oriented data visualizations of KPIs using BIME and Tableau. Finally statistical AB-testing was also done using python.

Teaching and tutoring, self-employed, Paris, France

2015–2022

Since the beginning of my higher education, I have been tutoring middle school, high school and university students in scientific subjects, mainly mathematics. The aim is to turn the students into independent people, more confident in their abilities and more knowledgeable in order to excel in their respective studies.

Since September 2021, I have been doing oral examination in English for PCSI preparatory class students at the [ENCPB](#) in Paris, France.

Education

Masters of Science (M.Sc.), Dep. MIDO, Dauphine université, France

2017–2018

during the [IASD](#) program, I followed courses in Deep learning, reinforcement learning, statistical modelling, software engineering and data science. This was a double curriculum with the AgroParisTech IODAA program.

Diplôme d'Ingénieur, AgroParisTech, Paris, France

2014–2018

The first two years of this program are focused on biology with courses in molecular biology, ecology, health, epidemiology and statistics.

During the final year, I followed the [IODAA](#) program, which was done as a double curriculum with Dauphine university, studying machine learning, data science and statistical modelling with a focus on biological problems.

BCPST Preparatory class, École Saint-Hilaire, Paris, France

2012–2014

2 year French **preparatory class** to prepare a nationally ranked exam for entry in the "Grande Écoles"
ranked 201/1967 (Veto), ranked 481/2991 (Agro)

Languages

Mother tongue

Other languages¹

German²

Mandarin Chinese³

French & English

Understanding		Speaking		Writing
Listening	Reading	Interaction	Production	
B1 Independent	B1 Independent	B1 Independent	B1 Independent	B1 Independent
A2 Basic	A2 Basic	A2 Basic	A2 Basic	A2 Basic

¹ Common European Framework of Reference for Languages (CEFR)

² 1 month program at **Goethe Institute** in Schwäbisch Hall, Germany

³ 5 month program at **SISU** Shanghai, Chian & 1 month program at UIR, Beijing, CN

Publications (Google scholar, ORCID)

^f co-first authors

Journal articles

Mapping-friendly sequence reductions: Going beyond homopolymer compression

Luc Blassel, Paul Medvedev, Rayan Chikhi

iScience 25.11, p. 105305

DOI: [10.1016/j.isci.2022.105305](https://doi.org/10.1016/j.isci.2022.105305)

Using Machine Learning and Big Data to Explore the Drug Resistance Landscape in HIV

Luc Blassel, Anna Tostevin, Christian Julian Villabona-Arenas, Martine Peeters, Stéphane Hué, Olivier Gascuel

PLOS Computational Biology 17.8, e1008873

DOI: [10.1371/journal.pcbi.1008873](https://doi.org/10.1371/journal.pcbi.1008873)

Drug Resistance Mutations in HIV: New Bioinformatics Approaches and Challenges

Luc Blassel^f, Anna Zhukova^f, Christian J Villabona-Arenas, Katherine E Atkins, Stéphane Hué, Olivier Gascuel

Current Opinion in Virology 51, pp. 56–64

DOI: [10.1016/j.coviro.2021.09.009](https://doi.org/10.1016/j.coviro.2021.09.009)

Origin, Evolution and Global Spread of SARS-CoV-2

Anna Zhukova, **Luc Blassel**, Frédéric Lemoine, Marie Morel, Jakub Voznica, Olivier Gascuel

Comptes Rendus. Biologies 344.1, pp. 57–75

DOI: [10.5802/crbio.29](https://doi.org/10.5802/crbio.29)

COVID-Align: accurate online alignment of hCoV-19 genomes using a profile HMM

Frédéric Lemoine, **Luc Blassel**, Jakub Voznica, Olivier Gascuel

Bioinformatics (btaa871)

DOI: [10.1093/bioinformatics/btaa871](https://doi.org/10.1093/bioinformatics/btaa871)

Conference talks

Mapping-Friendly Sequence Reductions: Going beyond Homopolymer Compression

Luc Blassel, Paul Medvedev, Rayan Chikhi

2022

RECOMB-SEQ 2022