

# Marwane Bourdim

Université de Paris  
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Webpage : <https://marwanebourdim.github.io> | Interactive CV

MASTER'S IN MATHEMATICS, UNIVERSITÉ DE PARIS AND SORBONNE UNIVERSITÉ

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EDUCATION	<b>Master's degree in Mathematics, Statistics and Machine Learning,</b> <i>Université Paris-Cité, Paris, France</i> <i>Ranked 1st, with Distinction</i>	<i>2021-2022</i>
	<b>Master's degree in Mathematical Modeling</b> <i>Sorbonne Université, Paris, France</i>	<i>2020-2021</i>
	<b>Bachelor's degree in Pure Mathematics</b> <i>Université Paris-Cité, Paris, France</i>	<i>2018-2019</i>
	<b>Classes Préparatoires aux Grandes Écoles, MPSI-MP</b> <i>Lycée Jacques Decour, Paris, France</i>	<i>2016-2018</i>

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INTERESTS	Statistical Learning, Stochastic processes, Data Science, Probabilistic modeling Linguistics, NLP, Computer vision, Personalised medicine, Genomics, Data Ethics
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RESEARCH INTERNSHIPS	<b>Cellular deconvolution algorithms for nanopore bulk methylation data,</b> <i>Institution : European Bioinformatics Institute (EMBL-EBI) in the Cancer Genomics group</i> <i>Supervisor : Dr. Isidro Cortés-Ciriano</i> <i>February 2022 - January 2023</i>  This internship has been made possible by the <i>French Embassy fellowship programme at EMBL-EBI</i>  - <b>Designed a model of methylation reads and developed a supervised cellular deconvolution method</b> based on iteratively reweighted least squares applied to a binomial model, to estimate the proportions of different cell types in a bulk sample from a matrix of methylation profiles  - <b>Developed an unsupervised cellular deconvolution method</b> based on a weighted <b>bounded simplex-structured matrix factorization</b> (a modification of non-negative matrix factorization), to jointly estimate the proportions of the cell types in a reference matrix and the proportion of cell types for which we don't have a methylation profile  - <b>Implemented both algorithms in Python</b> in a self-contained Command-Line Interface software.  <b>Mathematical and computational modeling of the Covid-19 pandemic in France with a spatio-temporal stochastic framework,</b> <i>Institution : French Institute for Research in Computer Science (INRIA) in the SIMBIOTX lab</i> <i>Supervisors : Prof. Dirk Drasdo and Postdoc. Jules Dichamp</i> <i>April 2021 - September 2021</i>  - <b>Applied and extended pre-existent agent-based models</b> that had been used for cellular proliferation to the spread of COVID-19 in France. made use of Markov Processes and Master equations.  - <b>Implemented in Python</b> the Gillespie algorithm for several variations of SIR compartment stochastic models.
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WORK EXPERIENCE	<b>Mathematics Teacher,</b> <i>Institution : École alsacienne</i> <i>February 2022 - June 2022</i> <p>I had four classes to teach, two 4èmes (Year 8) and two 2ndes (Year 10). This gave me the opportunity to improve my communication skills (especially public speaking) through a very rewarding experience.</p>
COMPUTER SKILLS	<b>Languages:</b> C++, Python, R, L <sup>A</sup> T <sub>E</sub> X <b>Packages and libraries:</b> Pytorch, Pandas, TensorFlow
LANGUAGES	French (native), English (fluent)
FELLOWSHIPS	<b>EMBL-EBI / Embassy of France in London Internships Programme</b> <i>January 2022</i> Competitive fellowship for paid internships at EMBL-EBI for computer-science, statistics and bioinformatics students who are working at the Masters level or equivalent at French universities or Grandes Écoles.
ORAL PRESENTATIONS	<b>Graduate School of Translational Bioinformatics Workshop</b> <i>November 2022</i> Presented my methylation cellular deconvolution algorithms at Université Paris-Cité.
EXTRA INTERESTS	Philosophy of science, History of economics, Political theory, Cinema, Drawing, Powerlifting