Simon CROUZET

LOOKING FOR ML RESEARCH ENGINEER POSITIONS IN DRUG DISCOVERY





Contact & Info

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Programming: Languages:

Main: Julia, Python Others: R, Java, C, C++, SQL, Matlab, PHP, HTML/CSS,

Fields of Interest:

Artificial Intelligence, Machine Learning, Deep Learning, Neural Networks. Computational **Biology, Drug Discovery, Protein** Precision Medicine, Design, Genomics, Systems Modelling, **Problem Solving**

OS: Windows, GNU/Linux

Tools:

Git, Unit Testing, Object Oriented Programming, Parallel Programming, HPC Cluster, **PowerBI**

Libraries:

PvTorch, PvTorch-Geometric, TensorFlow, JAX, Rosetta, Rfdiffusion, ProteinMPNN, AlphaFold, ColabDesign, ...

Transversal: **Project Management**



English:



Work Experiences

2023 - 2025 **Research Scientist** - EPFL (Switzerland)

Development of a conditional diffusion model based on RFdiffusion to sample antibody backbone decoys. Conception of a sequence-structure guided codesign pipeline for antibody discovery based on AlphaFold and ProteinMPNN, using cryoEM density maps. Deployment of diverse tools to build and refine protein structures from cryoEM data and to evaluate protein-protein binding conformations based on Rosetta. Deployment of MD simulations using GROMACS to study viral capsid variants.

2022 Computational Biologist Intern - Roche (Switzerland)

Design and development of a knowledge graph neural network (GNN) method, called G-PLIP, for protein ligand bioactivity prediction. Analysis of data generated by phenotypic screens and identification of putative high-potential targets for novel drug discovery programmes using explainable AI.

2022 **Research Assistant** - ETH Zurich (Switzerland)

Design, implementation, and evaluation of a recurrent neural network (RNN) to predict HIV evolutionary pathways, induced drug resistance and designing optimal treatment combinations.

2021 **Research Assistant** - Wellcome Sanger Institute (England)

Pangenomics exploration of Anopheles Funestus (mosquito, major vector of malaria). Development of a SnakeMake pipeline for the characterization and analysis of short and long-range structural variation events from high-quality assemblies of specimens.

2020 **Research Intern** - University of Glasgow (Scotland)

Development and improvement of a viral host prediction model in Julia through genomic feature, phylogenetic neighbourhoods (using BLAST search) and protein characteristics.

2018 **Research Intern** - Aix-Marseille University (France)

Development in C of an automaton network solver using data-flow algorithms to model genetic regulatory networks as the control of floral morphogenesis in Arabidopsis Thaliana.

Qualifications

L - 2022	M.Sc. in Systems biology, Genomics and Bioinformatics - with First Class Honours Ecole Normale Supérieure (ENS-PSL) - <i>Paris (France)</i>
) - 2021	M.Sc. in Bioinformatics and Modelling - with High Honours Sorbonne University - <i>Paris (France)</i>
2019	Semester Abroad during B.Sc. in Computer Science Linnaeaus University - Växjö (Sweden)
7 - 2020	B.Sc. in Computer Sciences - with First Class Honours Aix-Marseille University - <i>Marseille (France)</i>
5 - 2017	Interruption of studies due to health issues
8 - 2016	B.Sc. in Chemistry Grenoble Alpes University - <i>Grenoble (France)</i>
	Achievements & Awards

Publications available on Google Scholar

- 2024 "AI For Good" Hackathon Winner Entrepreneur First
- 2022 IP2TIS "Think Tank in Innovation & Sustainability" Fellow Roche Holding Ltd.
- 2021 **Qlife Institute Scholarship** - École Normale Supérieure (ENS-PSL)
- **2018** FIP « Incubateur de Jeunes Talents » Scholarship Aix-Marseille University



2021

2020

2017

2016