74 chemins des clotasses, 31400, Toulouse
+33651477290
https://github.com/OwenGriere
owen.griere@gmail.com

OWEN GRIERE BORN ON 06/03/1999

EDUCATION

MASTER DEGREE ERASMUS PROGRAMME – GENETICS AND BIOINFORMATICS

09/2024 – 02/2025 – Università degli studi di Milano

I was lucky enough to be able to attend, as part of an erasmus program, *Neurogenomics and brain disease modelling, Functional biology, Developmental biology, genetics, cellular and molecular biology* and *bioinformatics* courses.

These courses have allowed me to acquire greater knowledge in molecular and cellular biology which is an essential framework for a bioinformatician.

ENGINEERING SCHOOL – BIOINFORMATICS

Sept. 2021 - Jun. 2025 - EIDD University of Paris-Cité

My training at the EIDD Paris gave me a basis of the biological framework necessary to any bioinformatician through courses such as *Molecular and cellular biology, biochemistry* and *biophysics*. My computer training consists of *biostatistics* studied in a theoretical way, *machine learning* with Python and *algorithmic* with an introduction to the language C and Java.

- Group project on creating a C++ algorithm to list the biochemical interactions that occur during the folding of a protein, so only those that constitute the 3D structure of the protein and not the peptide chain. The pipeline then takes as input a PDB file of a protein and outputs a table that lists the probable biochemical interactions and their type.

- individual project using machine learning (dimensionality reduction and clustering) on brain cancer MRI images available on kaggle to identify which type of cancer may be more lethal according to their morphology.

ENGINEERING SCHOOL – MECHANICS AND ENERGY

09/2019 – 06/2020 – INSA Hauts-de-France

In my 6 months (excluding COVID period) in INSA Haut-de-France, I was able to study *Mechanics, Fluid Mechanics* as well as *Design* allowing me to have bases in solid mechanics and in the mathematical equations that govern them. I attended an introduction to *General Thermodynamics* and *Energetics*

CPGE(CLASSE PRÉPARATOIRE AUX GRANDES ECOLES) – MPSI(MATHS PHYSICS INDUSTRIAL SCIENCE)

09/2017 – 06/2019 – HIGH SCHOOL OF Saint-Germain-En-Laye

I took a preparatory class MPSI then PSI which gave me a solid foundation in scientific reasoning through the rigor of mathematics and physics as well as knowledge in solid mechanics, thermal diffusion, particle diffusion, thermodynamics, thermochemistry and linear algebra.

Research Experience

Bioinformatics intern - CRCT, inserm, Toulouse

02/2025 – 08/2025

Current Internship – The objective of this internship is to integrate PDAC spatial data into a PhysiCell model. From the beginning, I had to model a first version of a tumor microenvironment model (TME) thanks to PhysiCell which is an agent based model, by modelling several biological phenomena such as EMT, hypoxia and immunosuppression. I was also able to analyse immunofluorescence data and Imaging mass cytometry via two python packages developed by Alexis Coullomb and Vera Pancaldi, Tysserand and MOSNA. These two tools are specialized in the generation of spatial networks from biological tissue data as well as their statistical analysis.

Bioinformatics intern - institut du thorax, inserm, Nantes

05/2024 – 08/2024

I studied genetic variants in the 5'UTR region as a cause of family dyslipidaemia through the analysis of mutations on the LDLR, APOB, APOE, PCSK9 genes. These genes are responsible for the regulation of cholesterol and especially LDL (bad cholesterol). In familial dyslipidemia, the LDL-C level is too high at birth and can lead to premature heart failure. To be able to curb the effects of hereditary LDL-C, the best solution remains the prevention by studying the genome of each patient and especially of each family member of these patients. The NGS sequencing then allows to generate these genomes, now it is necessary to create bioinformatics tools capable of identifying specific mutations responsible for abnormal levels of LDL-C. The objective was therefore to annotate these variants with the MORFEE pipeline, developed in R language by the team of David-Alexandre Trégouët at INSERM in Bordeaux.

I first set up MORFEE on the BiRD computing cluster in Nantes, I developed a Python and Nextflow pipeline encapsulating MORFEE allowing it to be used on VCF/BCF files of any size and for any gene in the human genome using Nextflow parallelization. In short, my tool was able to be parallelized on 32 threads and to treat mutations of more than 200,000 UKBioBank patients on more than 20,000 genes. Finally, I conducted statistical tests to verify the significance of the results in the outputs of MORFEE, the Manhattan and Forest plots then generated explained the potential impact of certain isolated variants in the increase of LDL-C rate, at birth compared to individuals not showing these mutations.

Communications

O. Griere, M. Bernard and V. Pancaldi. Using PhysiCell modelling to simulate the PDAC tumor microenvironment response to therapies based on patients' spatial omics data.
Poster presentation at JOBIM (French bioinformatics conference) 2025, Bordeaux 8-11th July 2025

Other work Experience

CDI vendeur polyvalent - Les saisonniers, Paris

02/2023 – 08/2023 Part time- restocking the store, checkout, customer reception

Educational territory manager intern - Egalité des Chances, Villiers-le-Bel

06/2020 – 08/2020 Creation of partnerships with the municipal administration and development of free workshops for young people in the priority neighbourhoods of Villiers-le-Bel

Skills

Python, Machine Learning, Linux/Bash, Biostatistics, Mechanics

References

Vera PANCALDI, **Permanent researcher, CRCT, inserm**
vera.pancaldi@inserm.fr

Antoine RIMBERT, **Permanent researcher, institut du thorax, inserm**
antoine.rimbert@univ-nantes.fr

Anne VANET, **Principal professor, EIDD, university paris-cite**
anne.vanet@u-paris.fr