





Amir NAAR

10/08/1988, Bordeaux, France –  LinkedIn •  GitHub
 +33 (0)6.28.94.26.58 •  amir.naar@gmail.com

About Me

I am a Freelance Developer with a foundation in Bioinformatics, specializing in Backend Development and driven by curiosity across various fields. I have over 7 years of experience handling large-scale datasets, mostly through genome sequencing.

I have a deep interest in Web Development, with Django as my framework of choice. I develop websites with HTML, CSS, JavaScript and have strong skills in Python and scripting languages.

Skills

Development.....

Languages: Python, Perl, HTML, CSS, Javascript, PHP, Bash.

Data analysis: Pandas, Numpy, Matplotlib, R.

Frameworks: Django, Ruby on Rails.

Tools: JupyterLab, FastAPI, Git, Snakemake, Heroku.

Database Management System: MySQL, PostgreSQL, MariaDB.

Languages.....

- French: fluent (european level C2).
- English: professional competence (C1).

Education

- Web Development Bootcamp

Le Wagon

2023

Intensive coding bootcamp learning to design, implement and ship web applications from the back-end to the user interface. Responsive design, HTML, CSS, Bootstrap, Javascript, Ruby on Rails, SQL databases, APIs, Git, Github, Heroku.

- Master Degree in Bioinformatic

University of Bordeaux

2013–2015

Programming (Python, Java, C++), Software Engineering, statistics, algorithmics, database, omics, imaging, biomodelisation, datamining, project management.

- Bachelor of Science (Biology)

University of Bordeaux

2009–2012

Genomics, molecular biology, biochemistry, statistics, immunology, animal and vegetal physiology, mathematics applied to biology, informatics: advanced programming and database, neurobiology.

Professional experiences

- Bioinformatician, Data Science & Tertiary Analysis

SOPHiA GENETICS, Bidart.

December 2019 - December 2022

Maintenance, Development & Operations.

- Development of a new API to access data from our internal database with FastAPI.
- Fast-track updates of the release genes panels with regular migrations
- Integration of a reference clinical database (ClinVar) to the genome browser (Alamut Visual).
- Filtration of the gene panels and integration the Matched Annotation from NCBI and EMBL-EBI (MANE) prioritization transcripts for the large panel products.
- Regular update of the variants databases.
- Maintenance of the genome browser backend.
- Internal & External Bio-IT Support.
- Python, FastAPI, PHP, Bash, PostgreSQL, MySQL, SnakeMake, Conda, Docker.

- Bioinformatician, Department of Biology and Medical Pathology

Gustave Roussy, Villejuif.

February 2018 - November 2019

Management of data analysis from high throughput sequencing (NGS) in diagnosis.

- Development and maintenance of pipelines to treat and analyze different types of tumors in somatic and constitutional genetics for diagnosis: lung cancer, colon cancer, melanoma, glioma, hematological malignancies, breast / ovarian cancer.
- Management of NGS data from different types of sequencers: MiSeq, NextSeq, NovaSeq, Vela, S5XL.
- Resolution of routine issues related to the activity of the Department of Biology and Medical Pathology.
- Involvement in accreditation procedures, quality documentation.
- Management, maintenance, development of analyzes in personalized medicine for translational research (MOSCATO, SAFIR, OncoMine, OncoLung ...).
- PHP, MySQL, Perl, HTML, JavaScript.

- Bioinformatician, Biological Oncology Laboratory

Centre Hospitalier et Universitaire (C.H.U.), Poitiers.

September 2015 - February 2018

Development and implementation of NGS technology in routine for the molecular analysis of tumors.

- Management and analysis of NGS data within the lab labeled by DHOS and INCa.
- Pipeline developments to treat and analyze different types of tumors in somatic genetics: lung cancer, colon cancer, melanoma, glioma, hematological malignancies, breast / ovarian cancer in particular.
- Quality control of data, search for variants, annotation of mutations, reporting: PDF (LaTeX), EXCEL and HTML.
- Perl, Python, Bash, Java, Html, JavaScript.

- Software Developer Intern Student, Genome Biology Computational Support Unit

EMBL (European Molecular Biology Laboratory), Heidelberg, Germany.

March–August 2015

Development and integration of analysis tools for high throughput sequencing

- Development and improvement of tools for analysis and management of NGS data.
- Integration on the Galaxy platform of new tools for NGS data analysis. Analysis, workflows and comparison with others NGS tools (MACS, SICER).
- Benchmarking of NGS tools (performance analysis)

- Assistant Developer

INSERM (U862), Neurocentre Magendie, Bordeaux, France.

June 2014

Development of a statistical test of comparison of models of cerebral connectivity.

- Implication in the development of scripts (R, Octave, Lisrel) for making the analysis tests.

- Co-developer of a plugin for a software of image's analysis

Centre d'Etudes Nucléaires de Bordeaux Gradignan, Bordeaux, France.

February–May 2014

Reconstruction and analysis of spectroscopic images.

- Plug-in developed in Java, which allows analysing the acquisition data obtained from a particle accelerator.

Publications

Publications.....

- Portet, S.; Naoufal, R.; Tachon, G.; Simonneau, A.; Chaland, A.; Naar, A.; Milin, S.; Bataille, B.; Karayan-Tapon, L. Histo-Molecular Characterization of Intracranial Meningiomas Developed in Patients Exposed to High-Dose Cyproterone Acetate, An Antiandrogen Treatment. *Neuro-Oncology Advances*, 2019.
- Devès, G.; Daudina, L.; Bessy, A.; Buga, F.; Ghanty, J.; Naar, A.; Sommar, V.; Michelet, C.; Sez nec, H.; Barberet, P. An ImageJ plugin for ion beam imaging and data processing at AIFIRA facility. *Nucl. Instr. Meth. Phys. Res. B*, 2015

Miscellaneous

- Private courses in mathematics : School certificate level. – 2008-2012.
- Journey : Belgium, France, Germany, Morocco, South Africa, Spain, Switzerland.
- Hobbies : Football, Tennis, Footing, Cinema.
- Driving licence.