Bioinformatician Amir NAAR

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Skills

Bioinformatic & Development.

Programming language: Python, Perl, R, Bash, Java, C++, PHP, JavaScript, HTML, CSS.

NGS tools: FastQC, bowtie, bwa, samtools, bedtools, GATK, FreeBayes, MACS, ANNOVAR, snpEff, Galaxy, IGV.

Database Management System: MySQL, PostegreSQL, MariaDB.

Modeling & Datamining: UML, Design patterns, Datawarehouse, parsing, clustering.

Statistics: R, inferential analysis, descriptive analysis.

Imaging: 3D structuring of proteins (Rasmol), programming and scripts (ImageJ).

Integrated development environment & virtualization: Visual Studio, Eclipse, NetBeans, Qt Creator, version control system (git), maven, docker.

Operating system: UNIX/Linux, Mac OS, Microsoft Windows.

Languages.....

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

Spanish: intermediate level (B2).

Professional experiences

- Bioinformatician, Data Science & Tertiary Analysis Team SOPHiA GENETICS, Bidart.

Maintenance, Development & Operations.

December 2019 - Present

SOPHiA GENETICS is a fast-paced growing health-tech company. Combining deep expertise in life sciences, medical disciplines and mathematical modeling, we bring to market data analytics solutions to support healthcare professionals in better diagnosing and treating patients. Today SOPHiA's technologies are being adopted and trusted by over 1000 leading hospitals worldwide, all connected to each other and motivated to provide equal benefits to all patients. Member of the Tertiary analysis team, which is transversal team involved in four business lines: Alamut, Hereditary diseases, Oncology and TrialMatch.

- Complete development of a new API to access data from our internal database with FastAPI.
- O Contribution to the fast-track update in SOPHiA DDM with the migration of the release kit.
- Re-implementation of the ClinVar catalog integration in Alamut Visual: due to formatting changes and the increase
 of the amount of data, the C++ processes were outdated and did not allow to update this catalog anymore,
 complete re-development of the processes from scratch in Python to ensure a regular update of ClinVar in Alamut
 Visual
- O MANE prioritization: The Matched Annotation from NCBI and EMBL-EBI (MANE) project produces a matched set of high-confidence transcripts that are identically annotated between RefSeq and Ensembl/GENCODE. This enhancement provides a more comprehensive annotation by improving transcript mapping on the panel's target regions, without impacting the detection capabilities or accuracy of the SOPHiA Exome Solution.
- O Major contribution to the refinement of gene panels and the integration of MANE prioritization for large panel products. Among these products: CES_v3, Twist_HCExome, WES_v1.
- O Regular update of the catalogs for Alamut products.
- Maintenance of the Alamut backend.
- Internal & External Bio-IT Support.
- O Python, PHP, Bash, PostegreSQL, MySQL, FastAPI, 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.

Gustave Roussy is the first leader cancer-research hospital in Europe and ranked among the top 3 best specialized hospitals in the world. It is a centre for high quality patient care, research and teaching.

- 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.
- Variant calling (GATK, samtools, FreeBayes), variant annotation (ANNOVAR, snpEff), reporting.
- 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 ...).
- O 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.

- O Management and analysis of NGS data within the lab labeled by DHOS and INCa.
- O 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.
- O 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. GlobalQCReport, a program developed in Java, JavaScript, HTML and CSS which allows displaying several types of plots on Web pages.
- O BashGenerateReport, a program developed in Shell in order to generate synthetic summaries, easily manipulated with Excel, from NGS data.
- Integration on the Galaxy platform of new tools for NGS data analysis. Analysis, workflows and comparison with others NGS tools (MACS, SICER).
- O Benchmarking: performance analysis and comparison of several NGS tools, used on the Galaxy platform, on the EMBL LSF cluster.

- 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 codes for making the tests.
- OProcessing of results (languages used: Octave, R, LISREL).

- 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.

- O Plug-in developed in Java, which allows analysing the acquisition data obtained from a particle accelerator.
- Analysis of these data display a spectrum of measured energies.
- O Viewing images of the chemical distribution of an element in a sample.

Education

- Master degree in Bioinformatic

University of Bordeaux

2013-2015

Oriented object programming (Java, C++), software engineering, statistics, algorithmics, database, omics, imaging, biomodelisation, dataming, project management.

- Bachelor of Science (Biology)

University of Bordeaux 2009–2012

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

Additional training.....

- -Advanced Sequence Analysis Centre de Bioinformatique de Bordeaux (CBiB) October 2017.
- -NextSeq System Customer Training Illumina September 2017.
- -Circulating DNA and NGS Laboratoire de Génomique médicale, CHU de Rennes November 2015.

Publications & Working groups

Publications.....

- Portet, S.; Naoufal, R.; Tachon, G.; Simonneau, A.; Chalant, 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.; Seznec, H.; Barberet, P. An ImageJ plugin for ion beam imaging and data processing at AIFIRA facility. *Nucl. Instr. Meth. Phys. Res. B*, 2015

Working groups.....

- INCa (Institut National du Cancer) bioinformatic meetings.
- Club des ingénieurs de Biologie Moléculaire du Grand Ouest meeting.
- Stochastic modeling and statistical analysis of gene expression Futuroscope January 2017.
- Grand Ouest platforms exchanges days AstraZeneca April 2016.

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.