Komlan Dieu-Donné TOTO

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SKILLS

- **Development in Python, R, and C** : applications in biological data processing, pipeline development, APIs, and Shiny interface creation.
- **Machine and Deep Learning** : training models on Nvidia GPU using PyTorch, knowledge of Scikit learn.
- **Semantic Web** : integrating data into knowledge graphs for modeling and analyzing complex interactions, SPARQL queries.
- **Linux Environment** : advanced bash commands, working on compute clusters, experience with slurm.
- **Development Practices** : version control (Git/GitLab), virtual environments (Conda), bioinformatics workflows (Nextflow), containerization (Singularity).
- **Bioinformatics Analysis of Sequencing Data** : DNA-seq (panels, exomes), RNA-seq.
- **Statistics** : modeling, statistical tests, data visualization (ggplot2).
- **Secure Connection Protocols** : SSH, VNC, and VPN connections to computing servers.
- **Biology** : advanced knowledge in genetics and molecular biology.
- **Technical Writing** : documentation writing using Markdown, LaTeX, and office suite.
- **Bibliographic Management** : Zotero, MeSH method, and alert systems.

LANGUAGES

- **French:** native language
- **English:** level **B2** with professional comprehension and communication skills.

CONFERENCES

- Poster Presentation - PhD Symposium (IGDR - Rennes 2024).
- Participation in the Open Days in Biology, Informatics, and Mathematics (JOBIM - Toulouse 2024).

PERSONAL INTERESTS

Passionate about music, reading, and football.

Bioinformatics Engineer in Data Integration, Analysis, and Interoperability

PROFILE

With two years of experience, mostly as a contractor at CNRS and Inserm units, I have acquired strong skills in bioinformatics applied to research and diagnostics. My adaptability and professional English skills allow me to thrive in international and interdisciplinary environments. Ready to take on new challenges, I am motivated to contribute my expertise to innovative projects.

EXPERIENCE

Research

CNRS: Apprentice Engineer in Bioinformatics (17 months)
Institute of Genetics and Development of Rennes (IGDR)
September 2023 - January 2025: Integration and analysis of multimodal biological data for gene-phenotype association prediction.
Supervisor: **Christophe HÉLIGON**, christophe.heligon@univ-rennes.fr

- **Data Engineering:** Creation of queryable databases (SPARQL endpoint) to integrate heterogeneous, multi-format data into knowledge graphs.
- **Link Prediction:** Using machine learning and deep learning models for knowledge graph embedding to predict gene-phenotype associations.
- **Pipeline Development:** Designing a modular and optimized **Nextflow** pipeline for reproducible analysis.
- **Algorithm Benchmarking:** Evaluating machine learning and deep learning algorithms for graph embedding (ComplEx, TorusE, TransE, ConvKB, RWR).

Diagnostics

INSERM: M1 Bioinformatics Intern (4 months)
Molecular Genetics Laboratory - CHU Rouen
March - July 2023: Evaluation of GATK4, DRAGEN-GATK, DRAGEN, and DeepVariant approaches for genomic data analysis applied to diagnostics.
Supervisor: **Olivier QUENEZ**, olivier.quenez@inserm.fr

- **Bioinformatics Analysis of Sequencing Data:** Alignment using bwa-mem or dragmap, duplicate marking, variant calling, and annotation.
- **Workflow Management and Optimization:** Using **Slurm** for workflow management and optimization.
- **Pipeline Development:** Developing pipelines with **Nextflow**.
- **Tool Benchmarking:** Comparing the performance of GATK4, DRAGEN-GATK, DRAGEN, and DeepVariant tools.

EDUCATION

University of Rouen Normandie, France   **2022 - 2025**
Master in Bioinformatics, Modeling and Statistics (2.5 years, including 17 months of work-study in M2).

Abou Bekr Belkaid University-Tlemcen, Algeria   **2020 - 2022**
Master in Biological Sciences, Specialization in Molecular and Cellular Biology.

Abou Bekr Belkaid University-Tlemcen, Algeria   **2017 - 2020**
Bachelor in Biological Sciences, Specialization in Molecular Biology.