Jobs

e-OMIX has open positions for two collaborators.

Full-stack developper (m/f/x)

Role

- Build bioinformatics pipelines processing single-omics data (mass spectrometry, high-throughput sequencing, etc.)
- Develop solutions for the exchange and interoperability of large sets of biological data (in accordance with HL7 FIHR standards)
- Develop and deploy specific modules to optimize experimental workflow, such as Quality Control or sample tracing.
- Help with implementing automated or semi-automated statistical analyses

Qualifications

- PhD in computer science, engineering, data science or related field, or Master's degree with significant experience (5 years)
- Significant work experience with the following tools:
  - Object-oriented language (R, Python, C++, or similar language)
  - Database queries (PostgreSQL)
  - Development of web-responsives applications (Spring, Vue.js, Bootstrap…)
  - Collaborative research software development (e.g., unit testing, version control, continuous integration, Git, etc.)
  - Cloud architecture
- Interest for biomedical data and topics
- Ability to work both autonomously and within a team
- Good written and oral communication skills, english proficiency

Additional assets

- Experience in biology, bioinformatics, healthcare informatics, or in any position involving biological or medical data
- Experience with Kubernetes or Docker Swarm
- Knowledge with R Bioconductor package
- Familiarity with open-source software distribution
- French proficiency

We offer:

- A collaborative work environment: The project is conjointly led by the Computational Biology (CBIO) and Computer Engineering (INGI) units from UCLouvain and will involve other major academic actors.
- The collaborator will be partly based in the A6K startup incubator in Charleroi, and partly home-based (with occasional travels to UCLouvain's Brussels or Louvain-La-Neuve campuses)
- Flexible workhours
- Reimbursement of travel expenses

Application

Candidates are invited to send their application (resume and cover letter) to the following e-mail address by March 1st 2024.

Bioinformatician (m/f/x)

Role

- Establish bioinformatics pipelines for preprocessing single-omics data (filtering, normalization, control of batch effect, quality control, etc.)
- Adhere to interoperability standards established by the FIHR consortium Ensure compatibility of omics data collected across different platforms and research groups by implanting HL7 FIHR standards.
- Integrate different types of omics data to favor multiomics approach

- Conceive and automate supervised (regression, variable selection, etc.) or unsupervised (network analyses, clustering, PCA, etc.) statistical analyses.

Qualifications

- Master's degree in bioinformatics, statistics, computer sciences, biomedical sciences, bioengineering, or equivalent
- Experience and/or keen interest in one or several of the following:
- One or multiple omics experimental technologies, data processing analysis and/or interpretation
  - interest in developing solutions for the exchange of biomedical data and in multicentric initiatives
  - solid background in statistics, machine learning/artificial intelligence
  - knowledge of one or more programming language (e.g., Rmarkdown, Python, BASH, etc.) and IDE (R, Jupyter notebooks, etc.)
  - open and reproducible research
  - collaborative research software development (e.g., unit testing, version control, continuous integration, Git, etc.)
  - experience in R/Bioconductor data structures, in particular those used for omics data analysis (e.g., *SummarizedExperiment*, *SingleCellExperiment*, *QFeatures*, etc.)
  - contribution to an open and inclusive research environment
  - good written and oral communication skills, english proficiency

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