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.)
* Implement specific cloud-based storage and computation
* Develop solutions for the exchange and interoperability of large biological datasets (in accordance with HL7 FIHR standards)
* Develop and deploy specific modules to optimize experimental workflow, such as Quality Control or sample tracing.
* Help with designing automated or semi-automated statistical analyses

### *Qualifications*

* PhD in computer science, engineering, or related field, or Master’s degree with significant work experience (5 years)
* Demonstrable experience with the following tools:
  + Object-oriented language (R, Python, C++, or similar language)
  + Database queries (PostgreSQL)
  + Development of web-responsive applications (Spring, Vue.js, Bootstrap…)
  + Collaborative research software development (e.g., unit testing, version control, continuous integration, Git, etc.)
  + Cloud architecture
* Interest for biological or medical research
* 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 of R Bioconductor package
* Familiarity with open-source software distribution

### *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](https://www.a6k.be) 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](mailto:contact@eomix.be) 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 a 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, bio-engineering, 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.)
  + 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.)
  + open and reproducible research
  + contribution to an open and inclusive research environment
  + good written and oral communication skills, english proficiency

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