Job Title

Data Scientist

Job Summary

Kinomica is a precision medicine company developing next-generation diagnostic tests to help clinicians prescribe the right drug, for the right patient, at the right time. We acquire large, high-quality phosphoproteomics datasets from clinical samples using our state of the art KScan® platform; through which, we were the first to demonstrate that phosphoprotein signatures can be predictive of drug response in a clinical setting (see our profile in Nature: https://www.nature.com/articles/d43747-022-00013-9).

We are seeking an exceptional Data Scientist to drive the development of innovative AI and ML solutions for biomarker discovery, drug response prediction and clinical decision making support. This is an excellent opportunity to utilise AI/ML technologies for improving cancer patient outcomes.

Using your programming and data science expertise to lead on aspects of both the development and clinical implementation of phosphoproteomics-derived predictive biomarkers will require solid foundations in traditional statistical approaches, as well as expert knowledge of ML methodologies to analyse complex LC-MS/MS derived phosphoproteomic datasets.

Working closely with the wet lab and bioinformatics teams you will be responsible for delivering a new precision medicine paradigm of one test, predictive of a patient's response to multiple therapies. You will also be expected to promote your work through high impact publications and talks at national/international conferences.

Responsibilities and Duties

Prototyping ML/AI solutions

- Build upon our existing ML module, by integrating novel solutions and methodologies to facilitate the generation of biologically relevant insights.
- Run consultations with colleagues and clinicians to identify aspects of the platform could be improved by ML solutions.
- Provide support to colleagues in AI/ML best-practice.

Bioinformatics pipeline development

- Develop innovative and fit for purpose statistical and predictive modelling methods for the analysis of high dimensional biological data.
- Support the development and maintenance of Kinomica's suite of computational tools for the analysis large (phospho)proteomics datasets. Work with the bioinformatics team to develop high-quality, maintainable code in compliance with regulatory requirements.
- Contribute to local and global data management processes and solutions for capturing and exploiting proteomics data.

Prototyping tools necessary for the clinical deployment of KScan®-derived predictive signatures

- Identify emerging technologies and approaches, leading practices, and/or changes in industry trends.
- Help to streamline/automate current bioinformatics workflows.
- Review cloud computing solutions suitable for end-user engagement.

Promote the technology

- Attend conferences to present data, network, gain knowledge and represent Kinomica.
- Contribute to marketing materials (e.g., website, tech/application notes, white papers) by finding ways to clearly communicate the advantages of KScan®, so that clinicians trust the technology and start to use it for clinical decision making.

Qualifications and Skills

Essential:

- Highly educated to at least a Masters level standard in a relevant or STEM based subject.
- ≥5 years of experience in roles applying ML and Deep-Learning (DL) methods.
- Experience in applying a range of ML approaches to large and complex molecular and clinical data, for biomarker discovery.
- A strong track record of problem solving by employing an analytical and structured approach within an interdisciplinary environment.
- Expertise in at least one cloud platform (e.g., GCP, AWS or Azure).
- Experienced with source control and software lifecycle management.
- Knowledge and understanding of fundamental principles of biochemical and molecular biological systems.
- Passion for mentoring and supporting colleagues (particularly in ML best-practice).
- Excellent communication skills.
- Excellent organisational skills.

Non-essential but added advantage:

- PhD qualification or equivalent experience in Bioinformatics, Computational Biology, or relevant discipline.
- Fluent in R, Python or C++.
- Experience in applying Bayesian statistical methods.
- Experience using bioinformatics pipelines to analyse proteomics data.
- Experience working in a regulated environment.