

Bioinformatician / Mathematical Biologist

The European ScreeningPort is seeking a dynamic, highly motivated Bioinformatician / Mathematical Biologist to drive the development of our new Drug Discovery and Biomarker facility at the ZMNH, Hamburg.

Job Purpose

The successful candidate will work in close co-operation with colleagues at the European ScreeningPort and partners at the world leading ZMNH Research Institute of the UKE Hamburg. The work will focus initially on Biomarkers linked to Neuro-inflammatory and Neurodegenerative diseases, expanding to other indications in the medium to long term. Utilizing your expertise in the statistical analysis of biological data, your key focus will be on the development of new analysis methods based on mathematical and statistical models of biological systems. This will typically involve collaborative projects alongside experimental scientists, clinicians and partners within the pharmaceutical industry on targeting biomarker discovery and drug development.

Duties

- The successful applicant will specialize in developing innovative computational approaches relating to systems biology and biomarker discovery
- Provide scientific and technical leadership in the area of biomarker informatics, whilst working within a team multi-disciplinary scientists
- Support all aspects of handling and analysis of biomarker data from the ESP Drug Discovery and Biomarker screening platforms
- Provide input into the experimental design, statistical significance, and data analysis strategies used in Biomarker identification and compound screening campaigns
- You will help to define and implement concepts, interfaces, and workflows, especially for data integration, meta-analysis, and result management
- Work closely and flexibly with colleagues within ESP, and external academic partners, to ensure effective and timely project progression and delivery of goals and objectives
- Conduct all work safely, record data in an accurate, timely and GSP-compliant manner and to contribute to the smooth running of ESP
- You will be expected to keep up to date with the latest trends and developments within the bioinformatics & scientific community
- Demonstrate drive and enthusiasm towards the project work

Requirements

- A Ph.D. in Bioinformatics, computational biology or related fields with strong backgrounds in both biological sciences and mathematics
- 3-5 years of postdoctoral training or industry experience in genomics/proteomics data analysis and bioinformatics
- Experience in data analysis of microarray experiments and the experimental design
- Broad knowledge of pathway and network analysis
- Knowledge and experience in statistics and algorithm development
- Capability to learn quickly, handle multitasks, and adjust to constant changes
- Ability to work independently and as part of a team supporting each other
- Strong communication skills, professional appearance, and determination to succeed
- Demonstrable experience working within or supporting one or more of the following research disciplines: Transcriptomics, Proteomics, Pharmacology, Drug-metabolism and Pharmacokinetics, Toxicology or Safety Sciences, High Throughput Screening
- Technical experience with 2 of the following areas or applications
 - Statistical analysis methods and their applications
 - Computer programming skills: .NET, JAVA and Excel VBA
 - Experience in scientific programming, such PERL
 - Lims systems such as A+ Genedata, ActivityBase, Acapella
 - Visualisation programs such as GraphPad Prism, SigmaPlot, Spotfire
 - Statistical packages such as SAS, R, JMP
- Strong technical writing skills and the ability to document requirements and workflow analysis
- Excellent English, spoken and written