UNIVERSITETET
I OSLO

Jobbnorge-ID: 134291
Søknadsfrist: Closed
Nettside:
Omfang:
Varighet:

Postdoctoral Research Fellowship in Bioinformatics

Position as postdoctoral research fellow in Bioinformatics available at the Department of Biosciences, in close collaboration with the Department of Informatics.

The fellowship period is 3 years, with 10 % compulsory work. Within the framework of the position duties may be assigned. Starting date no later than 01.10.2017. No one can be appointed for more than one specified period at the same institution.

The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. Two of the largest departments within the Faculty are the Department of Informatics and the Department of Biosciences. Within the Department of Informatics a Bioinformatics hub has been established, which conducts bioinformatics research and provides bioinformatics support to research groups in biology and biomedicine at the Faculty of Mathematics and Natural Sciences as well as the Medical School and Oslo University Hospital. The Department of Biosciences is host to national centers for next generation sequencing and advanced light microscopy as well as other University of Oslo Core Facilities. To facilitate synergy between research environments in the Department of Informatics and the Department of Biosciences the Faculty of Mathematics and Natural Sciences announces a Postdoctoral Research Fellowship in Bioinformatics. The postdoc will be central to the growing effort of the Faculty to enhance and coordinate bioinformatics research and support. The successful candidate is expected to be able to work independently as well as in teams with both biologists and bioinformaticians. The candidate for the fellowship is expected to be in the upper segment of their class with respect to academic credentials.

Project description: “Novel and robust methodology for integrative epigenomics”
Through next-generation sequencing (NGS) of genomic DNA and RNA, in combination with epigenetic techniques such as ChIP-seq, ATAC-seq, MNase-seq and Hi-C, one can generate genome-wide profiles of a number of features of nuclear DNA, such as histone modifications, chromatin compactness, chromosome conformations and occupancy of DNA-binding proteins. Sequencing can also reveal information on genome variation (SNPs), gene splicing, DNA methylation, and gene expression, to name a few. As most biological processes involve a complex interplay between different types of biological molecules, a natural analytical strategy is to integrate data sets related to such multiple biological features. The integration of data sets enables interrogation of relations between biological molecules and processes in various biological contexts, not least disease. Such data integration is a potent strategy to create novel models that can be tested experimentally, improving our understanding of complex biological/disease mechanisms.
The focus of these efforts will be on the regulatory, non-coding part of the genome. The large majority of human variation associated with disease is located outside protein coding regions of DNA, and it has been speculated that a large part of this variation might have gene regulation effects. Such regulatory effects may be due to modifications to the local chromatin context, through disruption or enhancement of transcription factor binding, or through regional or global DNA conformation changes. Integration of data sets covering the non-coding part of the genome is therefore important to understand basic gene-regulatory mechanisms and how these may be perturbed through human DNA variation and for a range of diseases.
Although the potential gains from integrating multiple types of genomic information is widely appreciated, it is not yet exploited to its full extent. We are seeking a highly motivated candidate to pioneer the development of models, algorithms and software within this area. The aim is to create a generic system that can be used across a broad range of studies (involving various organisms and various genotype/phenotype data) to provide indications or conclusions on underlying biological mechanisms. To ensure a high level of accessibility, interoperability and reproducibility, the developed functionality could be integrated with a system like the open-source Galaxy platform.
The candidate will also have access to computational infrastructure (both HPC hardware and existing genome analysis codebase). The postdoc will collaborate with a team of researchers and software developers to ensure reproducibility, reuse and long-term maintainability.
The candidate will be positioned in the intersection between two strong research environments that will provide a unique opportunity to develop leading solutions in this highly competitive field. The epigenetic environment at the Department of biosciences has both young and senior PIs combining long experience with studies of transcription factors (TF) and epigenetic modifiers with cutting-edge research into chromatin organization in health and disease. This environment has recently been successful in attracting several competitive grants and is employing state-of-the-art genomics, imaging and genome-editing. Epigenetics is currently being further strengthened at the Department through international recruitment of new staff in this field. The HyperBrowser group at the informatics department is a vibrant bioinformatics environment connected to several Norwegian centers of excellence. The group has through the last five years developed a leading system for analysis of genomic data sets (including data sets related to chromatin, TF regulation and genome variation) and has gained a broad experience with software development and statistical inference. Also, the HyperBrowser code base provides around hundred thousand code lines of computational infrastructure for data integration and statistical computations that the candidate can build on to develop a robust and sophisticated system for analyzing regulatory effects of genome variation.

Qualifications:

In line with the strategic ambition of The Faculty of Mathematics and Natural Sciences the candidates for this project are expected to be in the upper segment of their class with respect to academic credentials.

We are looking for an enthusiastic bioinformatician to work closely with an interdisciplinary research team to explore new areas of epigenetic research. Applicants must have a PhD or other corresponding education equivalent to a Norwegian doctoral degree in in computer science or molecular biology or a related field with documented knowledge relevant for the qualifications given above. The balance between system development and modeling of gene regulation can to some degree be tuned to the selected candidate, meaning that a span of expertise ranging from generic software development to transcription factor dynamics could potentially be of relevance.

For the position, the successful candidate should demonstrate the following general abilities:
- Strong quantitative skills, including large-scale modeling, programming and data analysis
- A proven track record in peer-reviewed publications
- Evidence of creativity and capability of independent research
- Active collaborative skills necessary to interact and work within a large interdisciplinary team

In addition to the general requirements given above, the candidate should have documented experience with bioinformatics and preferably with either large-scale software development or with gene regulation and chromatin. Preferably, the candidate should also have strong software development skills, as well as documented experience with bioinformatics or computational biology.

The main purpose of post-doctoral research fellowships is to qualify researchers for work in top academic positions within their disciplines.

Please also refer to the regulations pertaining to the conditions of employment for post-doctoral fellowship positions:

http://www.uio.no/english/about/regulations/personnel/academic/regulations-employment-conditions-postdoc.html

A good command of English is required.

Salary:

Position code 1352, Salary: NOK 486 100 - 567 100 per year, depending on qualifications and seniority.

The application must include:

- Application letter
- CV (summarizing education, positions and academic work)
- Copies of educational certificates, transcript of records and letters of recommendation
- A complete list of publications and up to 5 academic works that the applicant wishes to be considered by the evaluation committee
- Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number)

Please remember that all documents should be in English or a Scandinavian language.

In accordance with the University of Oslo’s equal opportunities policy, we invite applications from all interested individuals regardless of gender or ethnicity.

UiO has an agreement for all employees, aiming to secure rights to research results a.o.

For further information please contact:

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For questions regarding the recruitment system Jobnorge, please contact HR Officer Torunn Standal Guttormsen, e-mail: t.s.guttormsen@mn.uio.no, phone: 22 85 42 72.

Tilleggsinformasjon

Arbeidssted: