SymBioSys from variome to phenome

Postdoctoral scientist – computational systems biology

Network and kernel algorithms for genomic data fusion

Description
SymBioSys is a consortium of computational scientists and molecular biologists at the University of Leuven, Belgium focusing on how individual genomic variation leads to disease through cascading effects across biological networks (in specific types of constitutional disorders and leukemias). We develop innovative computational strategies for next-gen sequencing and biological network analysis, with demonstrated impact on actual biological breakthroughs.

The candidate will be a key player in a workpackage focused on network and kernel algorithms for the integration of heterogeneous biological data towards the identification of disease causing genes. Two research topics are available: (1) advanced kernel methods for the integration of heterogeneous biological data and (2) combining text mining with network analysis to develop a versatile search and discovery engine for disease genes. Those methods will be applied to specific genetic disorders in day-to-day collaboration with the human geneticists of the consortium.

We offer a competitive package and a fun, dynamic environment with a top-notch consortium of young leading scientists in bioinformatics, human genetics, and cancer. Our consortium offers a rare level of interdisciplinarity, from machine learning algorithms to fundamental advances in molecular biology to direct access to the clinic. The University of Leuven is one of Europe’s leading research universities, with English as the working language for research. Leuven is one of Europe’s most beautiful university towns, just outside Brussels, at the heart of Europe.

Profile
The ideal candidate holds a PhD relating to the development and application of machine learning or network analysis algorithms for the integration of biological data or the analysis of biological networks. Expertise in kernel methods or text mining is a plus, as well as strong communication skills and interdisciplinarity. The candidate will collaborate closely with researchers across the consortium and contribute to the reporting of the project. Qualified candidates will be offered the opportunity to work semi-independently under the supervision of a senior investigator, mentor PhD students, and contribute to the acquisition of new funding. A three-year commitment is expected from the candidate.

Related SymBioSys publications
✓ Van Vooren S. et al. Mapping biomedical concepts onto the human genome by mining literature on chromosomal aberrations. Nucleic Acids Res. 2007

Application
Please send in PDF: (1) a CV including education (with Grade Point Average, class rank, honors, etc.), research experience, and bibliography, (2) a one-page research statement, and (3) three references (with phone and email) to Prof. Yves Moreau, c/o Ms. Ida Tassens – ida.tassens@esat.kuleuven.be. Start date is as early as practical.

URL link
http://phd.kuleuven.be/set/postdoc/voorstellen_departement?departement=50000516
SymBioSys from variome to phenome

Postdoctoral scientist – computational biology

Single-cell genomics

Description

SymBioSys is a consortium of computational and molecular biologists and (cyto)geneticists at the University of Leuven (Belgium) focusing on the detection of individual genomic variation, how it arises and leads to specific types of constitutional disorders and cancer. We develop innovative computational strategies for the analysis of next-gen sequencing data and biological networks, with demonstrated impact on actual biological breakthroughs.

The candidate will be a key player in a workpackage focused on the development and application of massive parallel sequencing-based methodology to detect genetic variants in the genome of a single cell, with an initial emphasis on structural variant detection. We have as a consortium established expertise in single cell genomics by combining state-of-the-art microarray-based methods with novel bioinformatic and statistical approaches which led to the discovery of chromosome instability, a hallmark of cancer, in early human embryogenesis as well as to a number of very recent international collaborations with top researchers in the field of embryo-genetics, cancer-genetics and neuro-genetics. Part of these methods is now being evaluated in a clinical trial.

Specifically, the candidate will develop sequencing-based methodology using paired-end mapping and read depth strategies to detect copy number variants (deletions, duplications, amplifications), balanced structural variants (inversions, insertions, translocations) as well as other variants (retrotransposition, SNPs, mutations) in a genome of a single (human) cell and apply this methodology to gain novel insight in genetic stability, the etiology of constitutional and acquired genetic variation, and tumour biology. This involves day-to-day collaboration with other postdocs who develop bioinformatic strategies for genetic variant detection and visualization based on massive parallel sequence analysis of genomic DNA extracted from blood or tumors.

We offer a competitive package and a fun, dynamic environment with a top-notch consortium of young leading scientists in bioinformatics, human genetics, and cancer. Our consortium offers a rare level of interdisciplinarity, from machine learning algorithms to fundamental advances in molecular biology to direct access to the clinic. This research will be performed at the intersection of the Department of Human Genetics, the Department of Electrical Engineering and the Genomics Core Facility. You will be part of the Department of Human Genetics which is a vivid international research centre that studies key issues relevant to human health. The University of Leuven is one of Europe’s leading research universities, with English as the working language for research. Leuven is one of Europe’s most beautiful university towns, just outside Brussels, at the heart of Europe.
Profile
The ideal candidate holds a PhD degree in bioinformatics-genomics with a good understanding of genetics and DNA sequencing technology and has experience in molecular biology. The position necessitates good analytical, algorithmic and mathematical skills. Programming and (statistical) data analysis experience is essential. Prior experience working with (Illumina) sequencing data and/or assembly / alignment of next-generation data as well as a PhD relating to the development and application of methods for genome-wide detection of genetic variation would be a distinct advantage, but is not required. Good communication skills are important for this role.

The candidate will collaborate closely with researchers across the consortium and contribute to the reporting of the project. Qualified candidates will be offered the opportunity to work semi-independently under the supervision of a senior investigator, mentor PhD students, and contribute to the acquisition of new funding. A three-year commitment is expected from the candidate.

Related SymBioSys publications

Application
Please send in PDF: (1) a CV including education (with Grade Point Average, class rank, honors, etc.), research experience, and bibliography, (2) a one-page research statement, and (3) three references (with phone and email) to Thierry.Voet@med.kuleuven.be, Cc Prof. Jan Aerts - Jan.Aerts@gmail.com and Prof. Joris Vermeesch - Joris.Vermeesch@med.kuleuven.be. Start date is as early as practical.
SymBioSys is a consortium of computational scientists and molecular biologists at the University of Leuven, Belgium focusing on how individual genomic variation leads to disease through cascading effects across biological networks (in specific types of constitutional disorders and leukemias). We develop innovative computational strategies for next-generation sequencing and biological network analysis, with demonstrated impact on actual biological breakthroughs. The candidate will be a key player in the workpackage that focuses on genomic variation detection based on next-generation sequencing data and visualization. This will include applying and improving existing algorithms and tools for the detection of SNPs and indels as well as structural variation (insertions, deletions, inversions and translocations) based on read-pairs, read depth and split reads. In addition, the candidate will develop standards and a methodology to visualize structural variation to make the sequencing results comprehensible to the end-user and allow for visual pattern detection. These methods will be applied to specific genetic disorders in day-to-day collaboration with the human geneticists within the consortium.

We offer a competitive package and a fun, dynamic environment with a top-notch consortium of young leading scientists in bioinformatics, human genetics and cancer. Our consortium offers a rare level of interdisciplinarity, from machine learning algorithms to fundamental advances in molecular biology to direct access to the clinic. The University of Leuven is one of Europe’s leading research universities, with English as the working language for research. Leuven is one of Europe’s most beautiful university towns, just east of Brussels, at the heart of Europe.

**Profile**

The ideal candidate holds a PhD degree in bioinformatics/genomics with a good understanding of genetics and DNA sequencing technology. The position requires good analytical, algorithmic and mathematical skills. Programming and (statistical) data analysis experience is essential. Prior experience working with (Illumina) sequencing data, i.e. assembly and alignment of next-generation data, as well as a PhD relating to the development and application of methods for genome-wide detection of genetic variation would be a distinct advantage, but is not required. Experience in data visualization - e.g. within R or using tools like Processing (http://processing.org) - would also be considered a plus. Good communication skills are important for this role.

The candidate will collaborate closely with researchers across the consortium and contribute to the reporting of the project. Qualified candidates will be offered the opportunity to work semi-independently under the supervision of a senior investigator, mentor PhD students, and contribute to the acquisition of new funding. A three-year commitment is expected from the candidate.

**Related publications**


Application
Please send in PDF: (1) a CV including education (with Grade Point Average, class rank, honors, etc.), research experience, and bibliography, (2) a one-page research statement, and (3) three references (with phone and email) to Dr Jan Aerts (jan.aerts@gmail.com), cc Dr Diether Lambrechts (diether.lambrechts@vib-kuleuven.be) and Dr Joris Vermeesch (joris.vermeesch@uz.kuleuven.ac.be). Start date is as early as practical.

URL link
SymBioSys from variome to phenome

Postdoc Bioinformatics: Gene Regulatory Networks in Development and Cancer

Description
SymBioSys is a consortium of computational scientists and molecular biologists at the University of Leuven, Belgium focusing on how individual genomic variation leads to disease through cascading effects across biological networks (in specific types of constitutional disorders and leukemias).

Applications are invited for a postdoctoral position in the Laboratory of Computational Biology at the Center for Human Genetics, University of Leuven, Belgium.

Your research will focus on developing algorithms for the integrated analysis of cis-regulatory and next-generation sequence data, both RNA-Seq and DNA-Seq, with the goal of identifying coding and non-coding variations underlying oncogenesis and developmental diversity. Particular focus will be on integrating genomic variation with transcriptional modules and gene regulatory networks and on the identification of genomic regulatory variations.

The University of Leuven is one of Europe’s leading research universities, with English as the working language for research. Leuven is one of Europe’s most beautiful university towns, just outside Brussels, at the heart of Europe.

What we offer
- You have the opportunity to apply your methods both on patient samples and on mammalian and Drosophila model systems.
- You will work in collaboration with the MPL lab (Molecular Pathogenesis of Leukemia) for next-generation sequencing experiments and functional validations in leukemia cell lines.
- You will have contacts with the Genomics Core Facility, hosting an Illumina HiSEQ2000 and a Roche 454 sequencer.
- You will be part of the Leuven SymBioSys Center of Excellence for Computational Systems Biology, where you will be surrounded by several other postdocs and students in a stimulating environment consisting of four bioinformatics research groups and four genomics labs.

Profile
- We are seeking a motivated and enthusiastic computational biologist, preferably with a proven track record in gene regulatory bioinformatics (e.g., prediction of enhancers, promoters, transcription factor binding sites, gene regulatory networks).
- Experience with transcriptomics and with the analysis of next-generation sequence data is a plus.
- PhD in bioinformatics; PhD in engineering or computer science provided substantial insight in genetics; PhD in biological sciences provided substantial programming experience.
- Skills: genome informatics, statistics, programming.

Links:
- The Laboratory of Computational Biology: http://med.kuleuven.be/bioinformatics/
- University of Leuven: http://www.kuleuven.be/english/

Application
Highly motivated candidates can apply by sending a motivation letter, names and contact information for three references, publication list, and CV to stein.aerts@med.kuleuven.be