Marie Curie Industry-Academia Partnerships SARM

Postdoctoral scientist – computational biology

Single-cell genomics and transcriptomics : 2 positions open

SymbioSys is a consortium of computational biologists, 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. The candidates will be key players in managing single-cell array and sequencing work and will actively engage in the SARM project, a Marie Curie Industry-Academia Partnership between researchers from the University of Leuven (Belgium), the University of Tartu (Estonia), The Karolinska Institute (Sweden) and Iviomics (Spain). The project aims on the development and application of massive parallel sequencing-based methodology to detect genetic variants in single-cell genomes as well as to capture transcriptomes derived from individual cells of human preimplantation stage embryos to unravel the mechanisms of genomic instability during the first cell cycles of human life. Technology will be developed to combine time-laps microscopy of human preimplantation embryo development with state-of-the-art single-cell analyses. Additionally, the candidates will be involved in the development of novel approaches for preimplantation genetic diagnosis guided by single-cell genomics assays, genome-wide single-cell haplotyping in particular. We are embedded in the Center for Human genetics with a strong background in cytogenetics and embryo preimplantation genetic research.

The candidates will develop both array and sequencing based single-cell methods and will be involved in developing the algorithms applying paired-end mapping and read depth strategies to detect copy number variants, balanced structural variants as well as other variants (retrotransposition, SNPs, mutations) in single cell genomes. Furthermore, they will implement and further develop the methods for single-cell transcriptome analysis, and integrate single-cell transcriptome with genome data. We have multiple second and third generation sequencing platforms in our facility: one Illumina HiSeq2000, one Illumina HiSeq2500, one Roche 454 pyrosequencer, one MiSeq and one PacBio single-molecule sequencer. Novel approaches to analyse the genomes and transcriptomes of single cells using long read lengths are planned on the latter instrument. The candidates will be pioneering this single molecule sequencer and develop novel analysis pipelines for its data interpretation. This involves day-to-day collaboration with other postdoctoral and doctoral researchers who develop bioinformatics strategies for genetic variant detection and visualization based on massive parallel sequence analysis of genomic DNA extracted from blood as well as with molecular biologists who perform follow-up experiments.

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 with direct access to the clinic. This research will be performed at the intersection of the Department of Human Genetics, the Department of Electrical Engineering, the Genomics Core Facility and the Leuven University Fertility Clinic (LUFC). 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.

The postdocs will have the opportunity to interact with a single-cell research team at the Wellcome Trust Sanger Institute (Hinxton – Cambridge, UK).

Profile

Importantly, at the time of recruitment the newly recruited researcher must not have resided or carried out his/her main activity in the country of the beneficiary (Belgium), for more than 12 months in the 3 years immediately prior to his/her recruitment. Compulsory national service and/or short stays such as holidays are not taken into account.

Postdoc position 1 under supervision of Prof. Joris Vermeesch

The ideal candidate holds a PhD degree in genomics/biology with a good understanding of genetics and DNA sequencing technology and has vast experience in molecular biology with an interest in bioinformatics. The position necessitates good laboratory skills. Programming experience is an asset. 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.

Postdoc position 2 under supervision of Prof. Thierry Voet

The ideal candidate holds a PhD degree in genomics / bioinformatics / computational biology with a good understanding of genetics and DNA sequencing technology and has vast experience in computational biology with a good understanding of wet-lab procedures (with/without hands-on experience). Analytical, algorithmic and mathematical skills are essential, as well as programming and statistical data analysis expertise is a requirement. Prior experience working with second generation (Illumina) and/or third generation (single-molecule) sequencing data as well as a PhD relating to the development and application of methods for genome-wide detection of genetic variation and/or transcriptomics data analysis would be a distinct advantage, but is not required. Good communication skills are important for this role.

Both candidates will collaborate closely with each other as well as with other 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 two-year commitment is expected from the candidate.

Websites:

http://sarm.edicy.co/project
http://med.kuleuven.be/cme/
http://www.kuleuven.be/symbiosys/
http://www.sanger.ac.uk/research/faculty/tvoet/
http://www.sanger.ac.uk/research/projects/singlecellgenomics/
http://www.sanger.ac.uk/research/projects/singlecellcentre/

Related publications

- **Voet T**, Kumar P, Van Loo P, Cooke SL, Marshall J, Lin ML, Zamani Esteki M, Van der Aa N, Mateiu L, McBride DJ, Bignell GR, McLaren S, Teague J, Butler A, Raine K, Stebbings LA, Quail MA, D'Hooghe T, Moreau Y, Futreal PA, Stratton MR, **Vermeesch JR, Campbell PJ**. Single-cell paired-end genome sequencing reveals structural variation per cell cycle. ***Nucleic Acids Res***. 2013 Apr 29. [Epub ahead of print] PubMed PMID: 23630320.

- Robberecht C, **Voet T**, Esteki MZ, Nowakowska BA, **Vermeesch JR**. Nonallelic homologous recombination between retrotransposable elements is a driver of de novo unbalanced translocations. ***Genome Res***. 2013 Mar;23(3):411-8

- Van der Aa N, Cheng J, Mateiu L, Esteki MZ, Kumar P, Dimitriadou E, Vanneste E, Moreau Y, **Vermeesch JR, Voet T.** Genome-wide copy number profiling of single cells in S-phase reveals DNA-replication domains. ***Nucleic Acids Res.*** 2013 Apr 1;41(6):e66. doi: 10.1093/nar/gks1352. Epub 2013 Jan 7. PubMed PMID: 23295674.

- Pavlopoulos GA, Kumar P, Sifrim A, Sakai R, Lin ML, **Voet T**, Moreau Y, Aerts J. Meander: visually exploring the structural variome using space-filling curves. ***Nucleic Acids Res***. 2013 Jun 1;41(11):e118. PubMed PMID: 23605045.

- Konings P, Vanneste E, Jackmaert S, Ampe M, Verbeke G, Moreau Y, **Vermeesch JR, Voet T.** Microarray analysis of copy number variation in single cells. ***Nature Protocols***. 2012 Jan 19;7(2):281-310. PubMed PMID: 22262009.

- Desmedt C, **Voet T**, Sotiriou C, Campbell PJ. Next-generation sequencing in breast cancer: first take home messages. ***Curr Opin Oncol***. 2012 Nov;24(6):597-604. PubMed PMID: 23014189.

- Van Houdt, J., Nowakowska, B., Sousa, S., van Schaik, B., Seuntjens, E., Avonce, N., Sifrim, A., Abdul-Rahman,O., van den Boogaard, M., Bottani, A., Castori, M., Cormier-Daire, V., Deardorff, M., Filges, I., Fryer, A., Fryns, J., Gana, S., Garavelli, L., Gillessen-Kaesbach, G., Hall, B., Horn, D., Huylebroeck, D., Klapecki, J., Krajewska-Walasek, M., Kuechler, A., Lines, M., Maas, S., Macdermot, K., McKee, S., Magee, A., de Man, S., Moreau, Y., Morice-Picard, F., Obersztyn, E., Pilch, J., Rosser, E., Shannon, N., Stolte-Dijkstra, I., Van Dijck, P., Vilain, C., Vogels, A., Wakeling, E., Wieczorek, D., Wilson, L., Zuffardi, O., van Kampen, A., Devriendt, K., Hennekam, R., **Vermeesch, J**. (2012). Heterozygous missense mutations in SMARCA2 cause Nicolaides-Baraitser syndrome. ***Nature Genetics*** 2012 Feb 26;44(4):445-9

- Vanneste, E.*, **Voet, T.***, Le Caignec, C., Ampe, M., Konings, P., Melotte, C., Debrock, S., Amyere, M., Vikkula,M., Schuit, F., Fryns, J., Verbeke, G., D'Hooghe, T., Moreau, Y., **Vermeesch, J.** (2009).

Chromosome instability is common in human cleavage-stage embryos. ***Nature Medicine**, 15*(5), 577-583. *** joint first**

Application procedures

For post 1:

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. Joris.Vermeesch@med.kuleuven.be, Cc Prof. Thierry.Voet@med.kuleuven.be

For post 2:

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. Thierry.Voet@med.kuleuven.be, Cc Prof. Joris.Vermeesch@med.kuleuven.be

Start date is as early as practical.