Marie Curie Industry-Academia Partnerships SARM

Postdoctoral scientist – computational biology

Embryonic genomics to improve assisted reproduction

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. The candidate will be a key player 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 and the Universities of Tartu, Estonia, The Karolinska Institute in Stockholm and Iviomics in Spain. The researcher will develop array and sequencing assays as well as technology to combine time-laps microscopy with single cell analysis. The project aims on the development and application of massive parallel sequencing-based methodology to detect genetic variants in single cell genomes derived from polar bodies, blastomeres or blastocystsWe are embedded in the Center for Human genetics with a strong background in cytogenetics and preimplantation genetic research.

The candidate will develop both array and sequencing based single cell methods and will be involved in developing the algorithms 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 single cell genomes. Most recently we acquired the Pacific Biosciences instrumentation. Novel approaches to analyse single cell analysis using long read lengths as well as methylome analysis are planned on this instrument. The candidate will be pioneering this new revolutionary 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 bioinformatic strategies for genetic variant detection and visualization based on massive parallel sequence analysis of genomic DNA extracted from blood as well as with molecular biologist 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 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 or holds a Ph.D degree in a biological area with strong interest in bioinformatics. The position necessitates good laboratory skills as well as analytical, algorithmic and mathematical skills. Programming and (statistical) data analysis 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.

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 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.

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 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 Genetics2012 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

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 Joris.Vermeesch@med.kuleuven.be, Cc Prof. Thierry.Voet@med.kuleuven.be -. Start date is as early as practical.