**Position:** PhD student @BIOBIX to mine the genome for allele-specific effects

The **BIOBIX** lab of Bioinformatics and Computational Genomics at the Faculty of Bioscience Engineering of Ghent University (Belgium) has a vacancy for a PhD student in bioinformatics/omics data analysis. BIOBIX has major expertise in the analysis of omics data, and is currently innovating the study of **allele-specific expression (ASE)**. We are looking for a highly motivated PhD student to join our forces, from **October 1st 2019** onwards.

ASE is the generic term for the phenomenon where one of both alleles (in diploid organisms) is expressed to a higher extent than the other one. In health, ASE can be caused by several molecular phenomena, including genomic imprinting and random monoallelic expression. Moreover, loci featuring recurrent ASE in disease are likely to be causally involved, independent of the fact whether the ASE observed is due to copy number variation, allele-specific (epi) mutations, … Despite major relevance in health and disease, common methods to study ASE are typically very expensive, prone to artefacts, and blind to the type of ASE. At the BIOBIX lab, we are currently developing the MAGE suite (Modeller of Allelic Gene Expression) which circumvents these problems by **explicit allele-specific statistical modelling of RNA-seq data** (or similar) **at the population level**. The candidate will introduce novel functionality in MAGE and apply this innovative methodological framework in different settings (e.g. oncology, aging, agriculture…).

**As a candidate**, you have/are:

- sufficiently acquainted with molecular biology to understand the above
- a drive to answer biological questions by mining huge omics data sets
- an analytical, critical and independent attitude
- an MSc degree in Bioinformatics, Bioscience Engineering, Biochemistry and Biotechnology, Statistical Data Analysis, Biomedical Sciences or similar (or will have this degree at the beginning of the project)
- proficient in basic biostatistics and scripting
- proficient in English, both written and oral

Ideally, you are acquainted with the statistical analysis of next generation sequencing or other biological big data. However, note that we focus on answering biological questions, and that the **ambition to learn expert statistical methods** whenever necessary is sufficient to apply.

We provide an open and stimulating working environment, in which teamwork, initiative, a critical mindset and originality are highly appreciated. We offer a position for 1 year, which will normally be extended to **4 years** in case of a positive evaluation. Note that the latter may require application for a FWO/BOF doctoral fellowship.

**How to apply?**

Candidates should send their CV, a motivation letter (approx. 1 page) and the email addresses of two potential referees to prof. Tim De Meyer (tim.demeyer@ugent.be), by **August 15th 2019** the latest.

For more information on BIOBIX: www.biobix.be

To learn more on our methodological approach (in the context of imprinting), see e.g. Goovaerts et al., *Nature Communications* 2018 (https://www.nature.com/articles/s41467-018-06566-7).