Position: PhD student at Ghent University, Faculty of Bioscience Engineering

At the Faculty of Bioscience Engineering, Ghent University (Belgium), the **BIOBIX lab** of Bioinformatics and Computational Genomics (Prof. Tim De Meyer, promoter) and the **Thomas Van Leeuwen research group** (Dr. Wannes Dermauw, copromoter) have joined forces to develop a novel methodology to identify **heritable variation in gene expression** (expression quantitative trait loci; eQTLs), using **herbivore adaptation** as highly relevant case study. We are therefore looking for a highly motivated **PhD student**, starting as soon as possible.

Background

The identification of heritable variation in gene expression, linked to a phenotype of interest (e.g. crop yield, resistance ...) is of major importance in the field of applied biological research. However, the identification of such loci, i.e. eQTLs, currently requires laborious breeding schemes and/or the combination of transcriptomics and DNA genotyping data, leading to a very high cost for comprehensive analyses. As a solution, the group of Prof. De Meyer is currently developing a far cheaper and more robust **eQTL scanning** methodology through statistical modelling of (solely) RNA-seq data. The applicant will further develop and apply this methodology to identify eQTLs in the **spider mite** *T. urticae* genome. *T. urticae* is a world champion in feeding on different plant species (over 1,100 different hosts) and pesticide resistance. As its small genome has been sequenced, it provides the ideal model organism to study rapid genetic adaptation, the field of expertise of Dr. Dermauw and Prof. Van Leeuwen. By bringing the expertise of both research groups together, the applicant will validate the novel eQTL scanning methodology by showing that it is able to identify eQTLs explaining fast spider mite adaptation. Relevance will be further demonstrated by linking obtained results with already available spider mite omics datasets at the copromoter's lab through bioinformatics analysis.

As a candidate, you have/are:
- well acquainted with molecular biology, biostatistics and scripting
- a drive to answer biological questions by analyzing omics data sets
- an analytical, critical and independent attitude
- an MSc degree in **Bioinformatics, Bioscience Engineering, Biochemistry and Biotechnology** or equivalent (or will have this degree at the beginning of the project); related degrees may be considered but only when sufficient background in molecular biology, biostatistics ánd scripting can be clearly demonstrated
- 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 and apply expert statistical methods** is sufficient to apply.

We provide an open and stimulating working environment in a top 100 ranking university, 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 **April 1st 2020** the latest.

Relevant publications of the promoters:

Goovaerts et al. A comprehensive overview of genomic imprinting in breast and its deregulation in cancer. *Nature Communications* 2018. (Introduces methodologically relevant concepts).

Wybouw et al. Long-term population studies uncover the genome structure and genetic basis of xenobiotic and host plant adaptation in the herbivore *Tetranychus urticae. Genetics* 2019.

Dermauw et al. A link between host plant adaptation and pesticide resistance in the polyphagous spider mite *Tetranychus urticae*. *PNAS* 2013. (Plant adaptation and pesticide resistance are intertwined)

Grbic et al. The genome of *Tetranychus urticae* reveals herbivorous pest adaptations. *Nature* 2011. (Genome paper spider mite)