

The BioStat research group of Ghent University offers the following PhD position.

## Statistical Analysis of Microbiome Studies

This project is in collaboration with Janssen Pharmaceuticals.

The candidate will conduct research in the field of statistical genomics, particularly on data analysis of microbiome data with applications in drug and biomarker development (see further down for more details). The candidate should hold a master degree in statistics and/or life sciences, or show at least a strong interest in life sciences applications (e.g biology, biomedical sciences, biotechnology, bio-engineering sciences, biochemistry, ...), but **students currently enrolled in a master program are also welcome to apply**.

Applicants should submit a cover letter (including a brief but detailed statement of interest) and cv to [Olivier.Thas@UGent.be](mailto:Olivier.Thas@UGent.be). Applications will be received until the position is filled.

For more information, please contact

Prof. O. Thas  
[Olivier.Thas@UGent.be](mailto:Olivier.Thas@UGent.be)

Project details:

Massive parallel sequencing (MPS) technologies nowadays allow for detailed assessment of microbial communities (microbiome) in e.g. human samples (e.g. gut, stool, ...). The scientific community expects that knowledge of the microbiome will allow for new therapeutic targets and for new diagnostic tools. For example, microbiome research might help (1) to identify high risk populations, (2) to develop diagnostic tests to replace invasive physical investigations as a diagnostic tool and (3) to develop novel therapeutic interventions to intercept disease progression.

Microbiome data are starting to get massively produced, but appropriate and efficient data analysis methods are only slowly being developed. On the one hand several methods for MPS data analysis are available (e.g. for RNAseq or viral variant detection), and on the other hand statistical methods for the analysis of classical ecological abundance studies are well developed. Bringing the two together would be a great step forward for microbiome data analysis. Also experience with microarray gene expression studies can be useful; both microbiome and microarray data are high dimensional. The major differences, however, are: the data-generation technology and the type of correlations (in microbiome data, correlations between abundances come from a multinomial type of distribution and are subject to e.g. competition between micro-organisms).

The objective of this PhD project is to

- explore and evaluate existing methods for microbiome data exploration and analysis
- evaluate bio-informatics MPS pipelines and R packages
- develop methods for data exploration and data visualisation.
- understand the sources of variability in microbiome data.
- develop targeted statistical methods for specific microbiome research questions in the oncology projects (e.g. testing for differential microbiomes, developing data-driven methods that select the right taxonomic or resolution level, ...)

All methods developed in the PhD project will be evaluated on data from Janssen Pharmaceuticals.