



ABSTRACT

"Systems Biology: Network-based data integration"

Prof Kathleen Marchal

VIB, Dept. of Plant Systems Biology

Ghent University

Gent

Dept. of Microbial and Molecular Systems

K.U.Leuven

Leuven

BELGIUM

In current wet-lab practice high-throughput expression profiling techniques are used to find components of response pathways, e.g. mRNA profiling focuses on identifying genes that are differentially expressed following stimuli or ChIP-chip techniques are being used to identify TF-target interactions. With the availability of next-gen sequencing, complete genotyping in combination with expression analysis allows finding genetic loci underlying interesting phenotypic traits. Each of the experiments mentioned above eventually results in a list of candidate genes or loci that all relate to the same phenotype of interest. Computational analysis of such unstructured lists will in most cases be restricted to a simple functional enrichment analysis to elucidate the potential pathways or functions the candidate genes belong to or to identify functionally related gene sets, but the interactions between the identified candidate genes or their role in the global molecular network of the cell remains unknown. To get a more structured insight in these results, we focus our research on developing tools that allow analyzing dedicated in-house experimental expression data and interrogating them with publicly available omics data.