Predictive Networks: a new framework for inferring robust networks from gene expression data

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ABSTRACT

DNA microarrays and other high-throughput omics technologies provide large datasets that often include hidden patterns of correlation between genes reflecting the complex processes that underlie cellular processes. The challenge in analyzing large-scale expression data has been to extract biologically meaningful inferences regarding these processes – often represented as networks – in an environment where the datasets are complex and noisy. Although many techniques have been developed in an attempt to address these issues, to date their ability to extract meaningful and predictive network relationships has been limited.

In this PQG short course, I will introduce the problem of network inference and I will present a platform developed in John Quackenbus's lab, which enables inference of reliable gene interaction networks from prior biological knowledge, in the form of biomedical literature and structured databases, and gene expression profiling data. The preliminary version of our analytical pipeline is both accessible through the *Predictive Networks* web application and the *predictionet* R package. Using real data, I will show the benefit of using prior biological knowledge to infer networks and how to quantitatively assess the quality of such networks.

An access to *the Predictive Networks* web application and the last version of the *predictionet* package will be provided. The material of this course will consist in a Sweave file including all the R commands you need for inferring networks and analyzing them.

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