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Transcriptional module discovery based on heterogeneous information

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Studies of regulatory networks, which control all phenotypic features, critically depend on the ability to characterize transcriptional modules (TMs). A TM can be defined as the set of genes whose transcription is modulated by a common transcription factor (TF). The characterization of TMs raises challenging questions regarding both the choice of the experimental datasets and the bioinformatics methodologies to examine these data. To enhance the reconstruction of TMs different data types have to be used. For instance, transcriptome analyses of mutants, in which the gene coding for a particular TF has been deleted, gives valuable information concerning the genes for which transcription depends on this TF. Additionally, protein/DNA interaction data obtained using ChIP-chip or ChIP-seq technologies allow the identification of the set of genes whose promoter sequences directly bind a particular TF *in vivo*. We present here a general strategy to optimize simultaneously *(i)* the discovery and *(ii)* the cross species comparisons of TMs. Our approach relied on two main points. First, multiple biological data sources are combined using an integrative procedure whose objective is to minimize the risk to select false positive genes. Second, as one TF can control different sets of genes depending on the environmental conditions, we use only data obtained in a specific experimental condition, identical in all the species examined. We applied this rationale to the analysis of the transcriptional programs that drive the chemical stress response in three yeast species: the model yeast *Saccharomyces cerevisiae* and two pathogenic species *Candida glabrata* and *Candida albicans*.

Biography

Gaëlle LELANDAIS is 32 year old. She got a phD in bioinformatics in 2005, working in an experimental laboratory at the Ecole Normale Supérieure in Paris (France). She proved to be an important intermediate between the people who develop mathematical models and the people who produce the experimental data on which these models can be applied. This is attested by her several recent publications using interdisciplinary approaches. As an assistant professor as the University Paris Diderot since 2006, she is used to supervise the work of students in bioinformatics and has published more than 20 papers in repute journals.