

Integration, analysis and presentation of yeast phenomics data

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ABSTRACT

Understanding the mechanistic connections between genotype and phenotype is fundamental to biomedical research and has far-reaching implications for treatment of diseases. A major challenge in the post-genomic era is the functional characterization of genes, and in that process analysis of mutant phenotypes is vital. The field of phenomics - the large-scale analysis of gene function by quantitative analysis of phenotypes on a genome-wide scale - is evolving rapidly, leading to increasing demand for novel data analysis, integration, mining and visualization tools. In an attempt to further advance our understanding about the functional role of yeast genes the PROPHECY (PROfiling of PHENotypic Characteristics in Yeast) project was initiated. PROPHECY is a high-resolution experimental system aimed at the precise quantification of growth alterations, during various physiological states, recorded by measuring changes in population density (OD) over time, as a consequence of the genetic alteration (e.g. gene deletion, overexpression or point mutation) in the yeast genome. In this thesis I describe a computational framework for phenomic research. This framework integrates, manages, analyzes and presents yeast phenotypic data. The project functions as an example of how to model and exploit experimental data obtained from phenotypic profiling. It also demonstrates the potential of the integration of yeast phenomics data with other experimental resources, while illustrating a pragmatic approach to data integration. The system proved that new knowledge can be gained by mining integrated data sources. Finally, the project contributes to the phenomics effort not only by releasing the results of the phenotypic screens but also establishing a phenomics database where researchers can visualize and analyse this data in a user-oriented manner. PROPHECY is available at <http://prophecy.lundberg.gu.se>

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