

## **Strategic approach to determine the Yeast Genetic Regulatory network with microarray data**

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The whole DNA sequences of many organisms are being determined by international collaborations. *Saccharomyces cerevisiae* is the first eukaryotic organism whose whole DNA sequences have been determined. The completion of the sequencing project was announced in 1996 with 16 DNA sequences of the chromosomes whose total amount is about 12M base pairs. Currently, it is considered that these DNA sequences encode 6,200 genes. A hot research topic on *Saccharomyces cerevisiae* is to analyze the interactions between genes by systematic experiments and logical analysis.

Our research group has installed a systematic experimental method which observes the changes of expression level of genes on microarray by gene disruptions and gene overexpressions. By using this method, we have launched a project whose purpose is to reveal the gene regulatory networks between the 6,200 genes of *Saccharomyces cerevisiae* while many laboratories have also started similar projects. This project consists of two different tasks in addition to the task of experiments. One is to develop algorithms for constructing gene regulatory networks from experimental data and testing the consistency of data with already known gene regulatory networks. The second is to construct a knowledge base of gene regulatory networks which have been already known for various organisms. By combining the results of these tasks, our project will determine a rough figure of the gene regulatory network of *Saccharomyces cerevisiae*.