
Preface

A gene changes the activity of the genes it interacts with. The entirety of these effects in a set of genes represents the dynamical behavior of a gene network. The analysis of this behavior can reveal how a network stabilizes the expression level of its components against perturbations, how it specifies the range of signaling intensity and frequency that can be efficiently transmitted in a pathway, or how it induces gene expression to oscillate. Regulation of gene expression – a major determinant of gene activity – occupies a central place in molecular biology. A detailed mechanistic description of the processes involved, methods for highly quantitative measurements, and an array of biotechnological tools are available to understand, to measure and to control gene expression. These favorable conditions explain why yeast genetic networks attracted the attention of many scientists in the nascent field of molecular systems biology. The book *Yeast Genetic Networks: Methods and Protocols* covers approaches to the systems biological analysis of small-scale gene networks in yeast.

Gene expression is primarily determined by how activators and repressors bound to promoters set the level of mRNA production and how quickly the produced mRNA decays. Part I of the book discusses the methods to analyze gene expression quantitatively: identification of promoter regulatory functions, measurement of mRNA production rates, inference of mRNA decay rates based on mRNA production rates, and detection of oscillatory patterns in gene expression. Furthermore, approaches are presented how to control and analyze signaling in genetic networks by implementing self-regulatory synthetic networks and by using microfluidics to dynamically modulate the intensity of external signals.

Part II is a collection of mathematical and computational tools to analyze stochasticity, adaptation, sensitivity in signal transmission, and oscillations in gene expression.

Control of genetic circuits by synthetic elements and dynamical external stimulation are carefully designed for specific purposes. On the other hand, natural genetic variations in a species provide a gratuitous form of control of genetic networks. While the potential to explore the behavior of networks by natural mutations is more restricted, they offer the advantage of identifying the naturally occurring gene variants that shape the behavior of networks. In Part III, methods are presented how to use the tools of quantitative genetics to identify genes that regulate stochasticity and oscillations in gene expression.

Genetic variations are even larger among related fungal species and evolution can shed a different light on network behavior. Thus, Part IV outlines the analysis of conserved gene expression systems and networks in different fungal species: the galactose network in *Kluyveromyces lactis*, and transcriptional silencing is described in *Candida glabrata*. While the former two species are close relatives of the baker's yeast, more diverged pathogenic fungi, *Candida albicans* and *Cryptococcus neoformans* were also included, to emphasize the medical aspects of fungal systems biology.

In summary, *Yeast Genetic Networks: Methods and Protocols* contains a broad range of resources of significant value to both novices and experienced researchers.

Zurich, Switzerland

Attila Becskei



<http://www.springer.com/978-1-61779-085-0>

Yeast Genetic Networks

Methods and Protocols

Becskei, A. (Ed.)

2011, XI, 344 p., Hardcover

ISBN: 978-1-61779-085-0

A product of Humana Press