

# METHODS IN MOLECULAR BIOLOGY™

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# Plant Systems Biology

Edited by

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*Dedicated in memory of Dmitry Belostotsky, who passed away just before the publication of the volume. Special thanks are extended to Julia Chekanova for her gracious help during the book's final weeks.*

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## Foreword

Systems biology has been called many things by many people. Rather than making another attempt at an all-encompassing definition, it may be better to take a historical perspective. Back at the dawn of time there was molecular biology, whose goal was to identify individual genes. With a gene in hand, one then searched upstream and downstream for other genes that acted on it or that it targeted. This led to the description of linear pathways with little arrows between each of the genes. Then came genomics with its high-throughput technologies to determine the expression of all genes, proteins, metabolites, etc. The output was usually a long list of cellular components ordered by expression level or some other metric. These were parsed for meaning based on where something was found on the list.

What systems biology has brought that is new and different is an emphasis on finding the connections among the parts. From these connections, the hope is that new properties will be identified that were not apparent from just staring at the list of parts. These are called “emergent properties.” But systems biology does not stop there. After the connections are found and networks begin to emerge, the next step is to characterize the dynamic properties of these networks. Accomplishing this requires perturbing the system and then determining how the system responds. In biology, perturbations can take the form of external stimuli such as sunlight or withholding a nutrient. They can also be at the level of mutations that alter gene function or expression.

A distinguishing feature of systems biology is the integration of quantitative analytical and modeling approaches. In the days of molecular biology, the view of quantitative analysis was, “If you have to use statistics, it means you need to do another experiment.” With the advent of genomics, most scientists realized that they needed help to make sense of the masses of data. Nevertheless, the general approach was that of a “hand-off” – the experimental biologist would find someone with quantitative expertise to “analyze my data.” When the analysis was completed it would be handed back to the biologist and that was the end of the interaction. The complexity of dynamic systems has convinced most biologists that the human brain needs mathematical formalisms to make any sense of the processes being studied. This means that systems biology is by and large practiced by collaborative teams, which comprise experimentalists and theorists, with equal weighting between them.

In this book you will find chapters that describe how to identify cellular components as well as the interactions among these components. You will also find chapters that describe methods for perturbing biological systems such as the use of small molecules in chemical genomics. Fittingly, a large portion of the book is devoted to quantitative approaches to analyze and model the interactions, emergent properties, and dynamics of the networks identified.

This work focuses on systems biology applied to plants. For many of the approaches described here there is no distinction between plants and animals. However, it is

appropriate to focus an entire book on plant systems biology as plants have been in the vanguard of this field. The sequencing of the *Arabidopsis* genome opened the way for a host of new and innovative approaches to understanding plant biology. From live imaging of protein dynamics in floral meristems to the ability to follow chromosome dynamics in individual cells, plant biologists are among the pioneers in this area. No matter how you choose to define systems biology, it is likely to play an increasingly important role in elucidating the mysteries of plant biology.

*Philip N. Benfey*

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# Preface

## Plant Systems Biology: Shooting a Moving Target

Plant systems biology is a fairly new art form. Unsurprisingly, its practitioners come in a variety of different flavors, and accordingly, there exist a great many conflicting definitions of what this art form really is (although this probably is true of any art form). Researchers have been entering this field from all walks of scientific life – there are classical plant physiologists by training, wet bench gene expression biologists like myself, cell biologists, mathematicians, statisticians, bioinformaticians, software engineers, and other more esoteric types ranging all the way to astrophysicists, etc.

The eclectic nature of this proverbial melting pot is also reflected in the content of this volume, which contains sections covering topics from systems biology of plant gene expression to analysis of networks, pathways, specific statistical issues and novel computational tools, imaging-based tools as well as chemical genetic, metabolomic, and integrative methods that cannot be easily pigeonholed.

While the definition of what plant systems biology really is may still be evolving, its key leading figures have clearly emerged and who they are is largely beyond dispute. Indeed, it is quite obvious who is driving the field forward and paving the way for others who follow in their wake and broaden the path. It is for that reason that the foreword to this volume is written by Philip Benfey, whose pioneering studies in the field of systems biology of gene expression have received wide recognition far beyond the plant community.

While the natural evolution of the field has been rapid and successful, it has become quite obvious that the time has come for setting up dedicated training programs in order to sustain this remarkable progress. This is already happening of course, in the form of IGERT and other training grants, iPlant initiative, etc., but additional modalities are needed. It is also the hope of the editor that this volume will make a contribution to achieving this goal as well.

In closing, I would like to acknowledge the contributions of the members of my own group over the years, and particularly that of Julia Chekanova, as well as the expert editorial assistance of Teresa Crew, without whom this volume would never have seen the light of day. Gene expression studies in my lab have been supported by grants from NSF, USDA, BARD, and NIH.

*Dmitry A. Belostotsky*

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