

Preface

Given that the opening chapter by Bruggeman et al. will provide an introduction to systems biology, it is not our intention in this preface to cover this; rather we will give an overview of the contents of this book and outline our reasoning for compiling it in the way that we have. This book is intended to give a comprehensive overview of the research field, which given its diversity, should have appeal to graduate students wanting to broaden their knowledge as well as to specialists of any of the genomic sub-disciplines. The overall structure of our book is inspired by the different consequences of gene expression, ranging from DNA, via RNA to proteins and metabolites, before the last chapters dealing with computational considerations concerning data standardization, storage, distribution and finally integration.

Given the origins of systems biology, the opening chapter deals with theoretical and mathematical approaches toward understanding the cellular hierarchy of biological systems with the chapters that follow dealing either with the acquisition of multi-factorial datasets or with their subsequent bioinformatical and biological interpretation. First among these, the chapter by Causse and Rothan, explains the collection or generation and identification of genetic variance suitable for systems biology. Herein both reverse (genotype to phenotype) and forward (phenotype to genotype) genetic strategies are discussed as methods of studying the effect of allelic variation as a method of perturbing biological systems with particular focus on quantitative genetics approaches and on the technological advances that will likely facilitate systems biology in plants. The third chapter by Foyer et al. utilizes the signaling functions of ascorbate to present a case study for experimental and interpretational analysis of global transcription profiling. This chapter thus provides three important functions firstly providing an important example of the use of environmental perturbation as a method to study plant systems, secondly presenting important considerations that need to be borne in mind both in experimental planning and equally importantly in data analysis of microarray experimentation and finally illustrating how biological information can be extracted from such studies. As an alternative experimental strategy, collection and evaluation of experimental data across a time course to allow an analysis of the kinetic response to a given perturbation. In a complementary chapter to Foyer et al., Hennig and Köhler explore this approach using case studies involving the analysis of the function of the transcription factors PHERES and LEAFY. The approach they introduce is the complementation of mutants by reintroduction of an unmutated copy of the gene in question

under the control of an inducible promoter. Hennig and Köhler lay a special emphasis on discussing experimental design strategies to accept, or reject a hypothesis generated from the high-throughput data. The final chapter concerned with transcriptional regulation that by Sundaresan, describes advances in the understanding of RNA interference presenting methods for their identification via computational analysis as well as discussing strategies to experimentally verify their function. RNA interference introduces an additional layer of regulation into a cellular system and may have an impact on how we understand RNA stability and posttranscriptional regulation in a complex biological "system".

Jumping to the next level of the cellular hierarchy, the subsequent two chapters deal with the analysis and characterization of proteins – those molecules that determine the metabolic and regulatory capacities of cells. Their high-throughput analysis has become possible by two parallel scientific achievements: the acquisition of genome information and the development of soft peptide ionization techniques for mass spectrometric applications. Brunner et al.'s chapter provides a thorough overview of different methods for the quantification of proteins, e.g. by comparing gel- and mass-spectral based proteomics methods for the differential display of proteins in two different samples and for their accurate quantification. Schuchardt and Sickmann's chapter provides a thorough overview of state-of-the art mass spectrometry (MS) equipment that is currently available for systematic protein analyses. Because mass spectrometric methods differ considerably each method has specific strength and weaknesses that determine its applicability to special experimental strategies. Therefore, this chapter has a special emphasis on the discussion of MS equipment for a certain experimental design. It furthermore covers the analysis of posttranslational modifications using phosphorylation as an example and lastly touches upon emerging issues of data analysis in proteomics.

The chapters by Steinhäuser/Kopka and Sumner et al. deal with experimental considerations for measuring primary and secondary metabolites, respectively. Steinhäuser and Kopka provide an overview of the requirements for establishing a GC-MS based metabolite profiling platform covering the entire experimental time frame from conceptual design through sample extraction and analysis to data analysis. The chapter additionally addresses the issue of quality by defining the widely used terminologies of fingerprinting, profiling and target application. Sumner et al. focus on the larger and more chemically diverse secondary metabolites. In this chapter Sumner and co-authors discuss the current state of the art in identifying and quantifying secondary metabolites of plant origin, and highlight the difficulties in doing so, as well as discussing potential solutions for the future. While the two preceding chapters are concerned with analysis of steady-state levels of metabolites, Dieuaide-Noubhani et al.'s chapter deals with the considerably more complex task of dynamic analysis of metabolism using techniques of metabolite flux analysis. The chapter covers both theoretical and experimental aspects of flux determination and also reviews recent key papers that attempt to integrate both experimental data and bioinformatic modeling in order to allow a more comprehensive understanding of plant metabolism.

Having covered protocols for data acquisition the final module of this book will focus on what to do with global data sets post-acquisition. The first chapter in this

section that of Nikiforova and Willmitzer describes the utility of correlation network visualisation and analysis utilizing the authors own studies on plant responses to nutrient deprivation to illustrate the power of this tool when applied to post-genomic datasets. The serious problem of non-standard ontology and the current status in adapting to a common language in the naming of both genes and proteins is discussed in Ahrens et al.'s chapter. As part of this issue, the authors highlight strategies to make data available to a wide scientific community in order to promote data distribution for the benefit of research progress.

The final chapters are both concerned with the integration of data from several different multi-factorial experiments and using them to model a biological system such that its reaction on a perturbation can be precisely predicted. Both of these chapters, by Steinfath et al. and by Schöner et al. highlight potentials and challenges of current modeling strategies and comment on their ability to retrieve biologically meaningful data. These final two chapters provide the full circle to the opening chapter, in wrapping up more theoretical considerations about biological systems that involve mathematical models and novel computer algorithms. We sincerely hope that our book presents an informative basic overview of the emergent discipline of systems biology from both experimental and theoretic perspectives and we both hope you enjoy reading it – we certainly did!

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