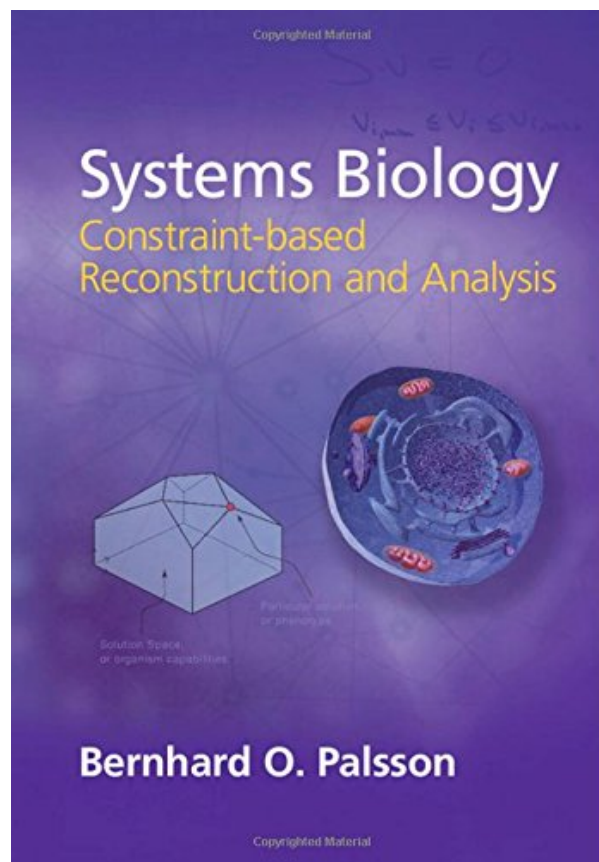


# SYSTEMS BIOLOGY: CONSTRAINT-BASED RECONSTRUCTION AND ANALYSIS BY BERNHARD Ø. PALSSON



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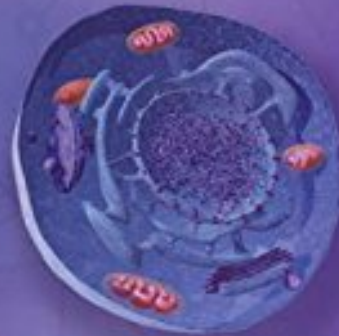
# Systems Biology

## Constraint-based Reconstruction and Analysis



Solution Space  
or organism capabilities

Particular solution  
or phenotype



# Bernhard O. Palsson

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## **Review**

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"... a very important and novel contribution to the systems biology literature. The field of systems biology is still in the phase of being defined as an independent field with a clear curriculum, but Palsson gives his very clear contributions to this. His definition of the paradigm of systems biology as components, networks, computer models and physiology is clearly explained and linked to educational modules, educational values and specific prerequisites. Thus, not only is he providing a fantastic novel textbook that enables teaching about network reconstruction and analysis, but he is also clearly defining this as the core of systems biology."

I am therefore confident that the very well thought through structure of this textbook, where the reader is introduced to the different layers of network reconstruction and analysis, will be widely used for teaching systems biology worldwide."

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#### About the Author

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Recent technological advances have enabled comprehensive determination of the molecular composition of living cells. The chemical interactions between many of these molecules are known, giving rise to genome-scale reconstructed biochemical reaction networks underlying cellular functions. Mathematical descriptions of the totality of these chemical interactions lead to genome-scale models that allow the computation of physiological functions. Reflecting these recent developments, this textbook explains how such quantitative and computable genotype-phenotype relationships are built using a genome-wide basis of information about the gene portfolio of a target organism. It describes how biological knowledge is assembled to reconstruct biochemical reaction networks, the formulation of computational models of biological functions, and how these models can be used to address key biological questions and enable predictive biology. Developed through extensive classroom use, the book is designed to provide students with a solid conceptual framework and an invaluable set of modeling tools and computational approaches.

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