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Nota di contenuto	Methods in Bioengineering: Systems Analysis of Biological Networks; Contents; Chapter 1 Quantitative Immunofluorescence for Measuring Spatial Compartmentation of Covalently Modified Signaling Proteins; 1.1 Introduction; 1.2 Experimental Design; 1.3 Materials; 1.3.1 Cell culture; 1.3.2 Buffers/reagents; 1.3.3 Immunofluorescence reagents; 1.4 Methods; 1.4.1 Cell culture and stimulation for phospho-ERK measurements; 1.4.2 Antibody labeling of phosphorylated ERK (ppERK); 1.4.3 Fluorescence microscopy imaging of ppERK and automated imageanalysis 1.5 Data Acquisition, Anticipated Results, and Interpretation1.6 Statistical Guidelines; 1.7 Discussion and Commentary; 1.8 Application Notes; 1.9 Summary Points; Acknowledgments; References; Chapter 2 Development of Green Fluorescent Protein-Based Reporter Cell Lines for Dynamic Profiling of Transcription Factor and Kinase Activation; 2.1 Introduction; 2.2 Materials; 2.2.1 Cell and bacterial culture; 2.2.2 Buffers and reagents; 2.2.3 Cloning; 2.2.4 Microscopy; 2.3 Methods; 2.3.1 3T3-L1 cell culture; 2.3.2 Transcription factor reporter

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2.4 Application Notes2.4.1 Electroporation of TF reporter plasmids into 3T3-L1 preadipocytes; 2.4.2 Monitoring activation of ERK in HepG2 cells; 2.5 Data Acquisition, Anticipated Results, and Interpretation; 2.6 Discussion and Commentary; 2.7 Summary Points; Acknowledgments; References; Chapter 3 Comparison of Algorithms for Analyzing Fluorescent Microscopy Images and Computation of Transcription Factor Profiles; 3.1 Introduction; 3.2 Preliminaries; 3.2.1 Principles of GFP reporter systems; 3.2.2 Wavelets; 3.2.3 K-means clustering; 3.2.4 Principal component analysis
3.2.5 Mathematical description of digital images and image analysis3.3 Methods; 3.3.1 Image analysis based on wavelets and a bidirectional search; 3.3.2 Image analysis based on K-means clustering and PCA; 3.3.3 Determining fluorescence intensity of an image; 3.3.4 Comparison of the two image analysis procedures; 3.4 Data Acquisition, Anticipated Results, and Interpretation; 3.4.1 Developing a model describing the relationship between the transcription factor concentration and the observed fluorescence intensity
3.4.2 Solution of an inverse problem for determining transcription factor concentrations3.5 Application Notes; 3.6 Summary and Conclusions; Acknowledgments; References; Chapter 4 Data-Driven, Mechanistic Modeling of Biochemical Reaction Networks; 4.1 Introduction; 4.2 Principles of Data-Driven Modeling; 4.2.1 Types of experimental data; 4.2.2 Data processing and normalization; 4.2.3 Suitability of models used in conjunction with quantitative data; 4.2.4 Issues related to parameter specification and estimation; 4.3 Examples of Data-Driven Modeling
4.3.1 Example 1: Systematic analysis of crosstalk in the PDGF receptor signaling network

Sommario/riassunto

This practical book is part of the new Artech House Methods in Bioengineering series - volumes designed to offer detailed guidance on authoritative methods for addressing specific bioengineering challenges. Written and edited by recognized experts in the field, each book provides research engineers, scientists, and students with step-by-step procedures, clear examples, and effective ways to overcome problems that may be encountered. This volume focuses on the design of state-of-the art methods for investigating complex biological systems and the development of complex models to analyze the data. Professionals find how-to guidance on experimental approaches for investigating cellular behavior in health and disease.