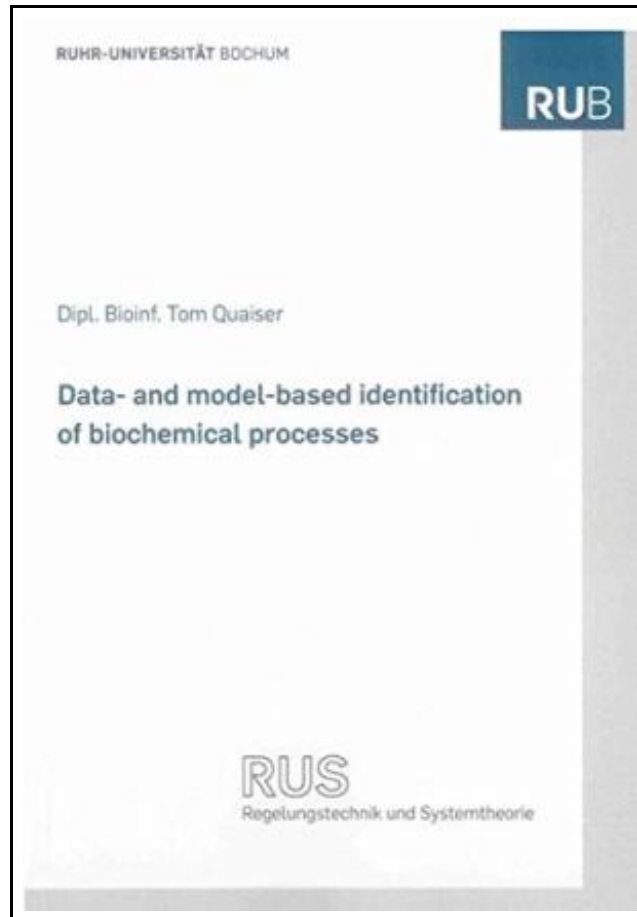


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Shaker Verlag Aug 2012, 2012. Taschenbuch. Book Condition: Neu. 21x14.8x cm. Neuware - In the last decade a paradigm shift has taken place in biochemical research: while traditionally biochemical processes have often been studied on a qualitative level, more and more research now focuses on quantitative time-resolved aspects of biochemical processes. However, on a quantitative dynamic level the complexity of these processes increases significantly and the need of mathematical models arises. Once a model is fitted to experimental data it can be used to simulate and study the dynamic behavior of a given process. Furthermore, a fitted model allows it to test new experiments and hypothesis *in silico* before time and cost intensive real experiments need to be conducted. The interplay between biochemical experimentation and mathematical modeling - known as systems biology - is an integral part of this thesis. Identifying a predictive model starts with the formulation of an initial model, which combines a priori knowledge with new to be tested hypotheses. The initial model is refined in an iterative process of performing quantitative experiments, estimating unknown model parameters, model validation and hypothesis testing. When constructing a model, it is tempting to incorporate all known interactions between biochemical species, which results in models with a large number of unknown parameters, which subsequently have to be estimated from experimental data. However, parameter estimation can only provide valid results, if the complexity of the model and the amount and quality of data are in balance with one another. If this is the case the model is said to be identifiable for the given data. In Chapter 2 of this thesis we describe a new automatic approach to test the identifiability of model parameters. We compare our new method - the eigenvalue method - to three well established methods for identifiability testing....



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