1.

Record Nr.	UNINA990008403320403321
Autore	Paret, Peter
Titolo	Art as history : episodes in the culture and politics of nineteenth-century germany / Peter Paret
Pubbl/distr/stampa	Princeton, : Princeton University Press, 1988
ISBN	0-691-05541-6
Descrizione fisica	227 p. : ill. ; 26 cm
Disciplina	700.43
Locazione	FLFBC
Collocazione	701.03 PARP 01
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia

2.

Record Nr.	UNINA9910819512503321
Autore	Kramer Andrei
Titolo	Stochastic methods for parameter estimation and design of experiments in systems biology / / vorgelegt von Andrei Kramer
Pubbl/distr/stampa	Berlin, Germany : , : Logos Verlag, , [2016] ©2016
ISBN	3-8325-8795-0
Descrizione fisica	1 online resource (xii,137 pages) : illustrations
Disciplina	570.113
Soggetti	Stochastic analysis - Mathematical models Systems biology - Statistical mehods Biological systems - Data processing
Lingua di pubblicazione	Inglese
Formato	Materiale a stampa
Livello bibliografico	Monografia
Note generali	"Von der Fakultat Konstruktions-, Produktions- und Fahrzeugtechnik der Universitat Stuttgart zur Erlangung der Wurde eines Doktor-Ingenieurs (Dr.-Ing.) genehmigte Abhandlung."

Nota di bibliografia	Includes bibliographical references (pages 127-137).
Sommario/riassunto	Long description: Markov Chain Monte Carlo (MCMC) methods are sampling based techniques, which use random numbers to approximate deterministic but unknown values. They can be used to obtain expected values, estimate parameters or to simply inspect the properties of a non-standard, high dimensional probability distribution. Bayesian analysis of model parameters provides the mathematical foundation for parameter estimation using such probabilistic sampling. The strengths of these stochastic methods are their robustness and relative simplicity even for nonlinear problems with dozens of parameters as well as a built-in uncertainty analysis. Because Bayesian model analysis necessarily involves the notion of prior knowledge, the estimation of unidentifiable parameters can be regularised (by priors) in a straight forward way. This work draws the focus on typical cases in systems biology: relative data, nonlinear ordinary differential equation models and few data points. It also investigates the consequences of parameter estimation from steady state data; consequences such as performance benefits. In biology the data is almost exclusively relative, the raw measurements (e.g. western blot intensities) are normalised by control experiments or a reference value within a series and require the model to do the same when comparing its output to the data. Several sampling algorithms are compared in terms of effective sampling speed and necessary adaptations to relative and steady state data are explained.