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Autore	Kramer Andrei
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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.
