Parameter Estimation

About Parameter Estimation

Parameter estimation lets you estimate the values of unknown parameters in a model by fitting the model simulation results to experimental data. This technique is especially useful for parameters that you do not measure directly. This technique is appropriate when you have a fairly complete data set for one individual.

Estimating Parameters of a Model

You estimate one or more parameters in your model using the `sbioparamestim` function.

If you do not have Optimization Toolbox™ installed, then `sbioparamestim` uses the MATLAB function `fminsearch` as the default method for the parameter estimation.

If you have Optimization Toolbox and, optionally, Global Optimization Toolbox installed, then `sbioparamestim` uses the `lsqnonlin` function as the default method for the parameter estimation. However, you can specify other optimization functions from these toolboxes as the parameter estimation method.

Specifying Solver Type and Options for Parameter Estimation

If you specify a stochastic solver and options in the `Configset object` associated with your model, be aware that during parameter estimation SimBiology temporarily changes:

- `SolverType` property to the default solver of `ode15s`

- `SolverOptions` property to the options last configured for a deterministic solver

See Also

For more information on parameter estimation, see the `sbioparamestim` reference page.

For examples of estimating parameters, see:

- [Estimate Parameters](#)

- [Parameter Scanning, Parameter Estimation, and Sensitivity Analysis in the Yeast Heterotrimeric G Protein Cycle](#)

Individual and Population Fitting

SimBiology lets you perform individual and population fitting, which is parameter estimation for grouped sets of experimental data. This functionality requires Statistics Toolbox™ Version 7.3 or later. This type of parameter estimation is useful for pharmacokinetic/pharmacodynamic (PKPD) models, in which you typically want to fit your model to a population of data. This technique is appropriate when you have an incomplete data set for many

individuals.

You perform individual fitting using the `sbionlinfit` function.

You perform population fitting using the `sbionlmefit` or `sbionlmefitsa` function.

For more information, see the following:

- Creating Pharmacokinetic Models
- About Data Fitting in PKPD Models
- Performing Data Fitting with PKPD Models
- Modeling the Population Pharmacokinetics of Phenobarbital in Neonates

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