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## Torsten

Torsten: A Pharmacokinetic/Pharmacodynamic Model Library for  
Stan

User's Guide  
(Torsten Version 0.88rc, Stan version 2.25.0)

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## Individuals

We thank the Stan Development Team for giving us guidance on how to create new Stan functions and adding features to Stan’s core language that facilitate building ODE-based models.

We also thank Kyle Baron and Hunter Ford for helpful advice on coding in C++ and using GitHub, Curtis Johnston for reviewing the User Manual, and Yaming Su for using Torsten and giving us feedback.

## Introduction

Stan is an open source probabilistic programming language designed primarily to do Bayesian data analysis [3]. Several of its features make it a powerful tool to specify and fit complex models. First, its language is very expressive and flexible. Secondly, it implements a variant of No U-Turn Sampler(NUTS), an adaptive Hamiltonian Monte Carlo algorithm that was proven more efficient than commonly used Monte Carlo Markov Chains (MCMC) samplers for complex high dimensional problems [7, 2]. Our goal is to harness these innovations and make Stan a better software for pharmacometrics modeling. Our efforts are twofold:

- (1) We contribute to the development of features, such as functions that support differential equations based models, and implement them directly into Stan’s core language.
- (2) We develop Torsten, an extension with specialized pharmacometrics functions.

Throughout the process, we work very closely with the Stan Development Team. We have benefited immensely from their mentorship, advice, and feedback. Just like Stan, Torsten is an open source project that fosters collaborative work. Interested in contributing? Comment at Torsten repository

<https://github.com/metrumresearchgroup/Torsten>

or email us ([billg@metrumrg.com](mailto:billg@metrumrg.com), [yiz@metrumrg.com](mailto:yiz@metrumrg.com)) and we will help you help us!

Torsten is licensed under the BSD 3-clause license.

**WARNING:** The current version of Torsten is a *prototype*. It is being released for review and comment, and to support limited research applications. It has not been rigorously tested and should not be used for critical applications without further testing or cross-checking by comparison with other methods.

We encourage interested users to try Torsten out and are happy to assist. Please report issues, bugs, and feature requests on [our GitHub page](#).

### 1.1. Overview

Torsten is a collection of Stan functions to facilitate analysis of pharmacometric data using Stan. The current version includes:

- Specific linear compartment models:
  - One compartment model with first order absorption.
  - Two compartment model with elimination from and first order absorption into central compartment
- General linear compartment model described by a system of first-order linear Ordinary Differential Equations (ODEs).
- General compartment model described by a system of first order ODEs.
- Mix compartment model with PK forcing function described by a linear one or two compartment model.

The models and data format are based on NONMEM<sup>1</sup>/NMTRAN/PREDPP conventions including:

- Recursive calculation of model predictions
  - This permits piecewise constant covariate values
- Bolus or constant rate inputs into any compartment
- Single dose and multiple dose events
- Handles steady state dosing events
- Implemented NMTRAN data items include: TIME, EVID, CMT, AMT, RATE, ADDL, II, SS

---

<sup>1</sup>NONMEM® is licensed and distributed by ICON Development Solutions.

In general, all real variables may be passed as model parameters. A few exceptions apply /to functions which use a numerical integrator(i.e. the general and the mix compartment models). The below listed cases present technical difficulties, which we expect to overcome in Torsten's next release:

- In the case of a multiple truncated infusion rate dosing regimen:
  - The bioavailability (F) and the amount (AMT) must be fixed.

This library provides Stan language functions that calculate amounts in each compartment, given an event schedule and an ODE system.

### 1.2. Implementation summary

- Current Torsten v0.88 is based on Stan v2.25.0.
- All functions are programmed in C++ and are compatible with the Stan math automatic differentiation library [4]
- One and two compartment models are based on analytical solutions of governing ODEs.
- General linear compartment models are based on semi-analytical solutions using the built-in matrix exponential function
- General compartment models are solved numerically using built-in ODE integrators in Stan. The tuning parameters of the solver are adjustable. The steady state solution is calculated using a numerical algebraic solver.
- A mix compartment model's PK forcing function is solved analytically, and its forced ODE system is solved numerically.

### 1.3. Development plans

Our current plans for future development of Torsten include the following:

- Build a system to easily share packages of Stan functions (written in C++ or in the Stan language)
- Optimize Matrix exponential functions
  - Function for the action of Matrix Exponential on a vector
  - Hand-coded gradients
  - Special algorithm for matrices with special properties
- Develop new method for large-scale hierarchical models with costly ODE solving.
- Fix issue that arises when computing the adjoint of the lag time parameter (in a dosing compartment) evaluated at  $t_{\text{lag}} = 0$ .
- Extend formal tests
  - More unit tests and better CD/CI support.
  - Comparison with simulations from the R package `mrgsolve` and the software NONMEM®
  - Recruit non-developer users to conduct beta testing

## Changelog

### Version 0.88 <2020-12-18 Fri>.

- Added
  - Bioavailability, lag time, ODE real & integer data are optional in PMX function signatures.
  - Support all EVID options from NM-TRAN and `mrgsolve`.
  - Support steady-state infusion through multiple interdose intervals.
- Changed
  - More efficient memory management of COVDES implementation.
  - Update of MPI framework to adapt multilevel parallelism.
  - Update to Stan version 2.25.0.
  - Use `cmdstanr` as R interface.
  - Stop supporting `rstan` as R interface.

### Version 0.87 <2019-07-26 Fri>.

- Added
  - MPI dynamic load balance for Torsten's population ODE integrators
    - \* `pmx_integrate_ode_group_adams`

- \* pmx\_integrate\_ode\_group\_bdf
- \* pmx\_integrate\_ode\_group\_rk45

To invoke dynamic load balance instead of default static balance for MPI, issue `TORSTEN_MPI=2` in `make/local`.

- Support `RATE` as parameter in `pmx_solve_rk45/bdf/adams` functions.
- Changed
  - Some fixes on steady-state solvers
  - Update to `rstan` version 2.19.2.

#### Version 0.86 <2019-05-15 Wed>.

- Added
  - Torsten's ODE integrator functions
    - \* pmx\_integrate\_ode\_adams
    - \* pmx\_integrate\_ode\_bdf
    - \* pmx\_integrate\_ode\_rk45
 and their counterparts to solve a population/group of subjects governed by an ODE
    - \* pmx\_integrate\_ode\_group\_adams
    - \* pmx\_integrate\_ode\_group\_bdf
    - \* pmx\_integrate\_ode\_group\_rk45
  - Torsten's population PMX solver functions for general ODE models
    - \* pmx\_solve\_group\_adams
    - \* pmx\_solve\_group\_bdf
    - \* pmx\_solve\_group\_rk45
  - Support time step `ts` as parameter in `pmx_integrate_ode_XXX` solvers.
- Changed
  - Renaming Torsten functions in previous releases, the old-new name mapping is
    - \* PKModelOneCpt → pmx\_solve\_onecpt
    - \* PKModelTwoCpt → pmx\_solve\_onecpt
    - \* linOdeModel → pmx\_solve\_linode
    - \* generalOdeModel\_adams → pmx\_solve\_adams
    - \* generalOdeModel\_bdf → pmx\_solve\_bdf
    - \* generalOdeModel\_rk45 → pmx\_solve\_rk45
    - \* mixOde1CptModel\_bdf → pmx\_solve\_onecpt\_bdf
    - \* mixOde1CptModel\_rk45 → pmx\_solve\_onecpt\_rk45
    - \* mixOde2CptModel\_bdf → pmx\_solve\_twocpt\_bdf
    - \* mixOde2CptModel\_rk45 → pmx\_solve\_twocpt\_rk45
 Note that the new version of the above functions return the *transpose* of the matrix returned by the old versions, in order to improve memory efficiency. The old version are retained but will be deprecated in the future.
  - Update to Stan version 2.19.1.

#### Version 0.85 <2018-12-04 Tue>.

- Added
  - Dosing rate as parameter
- Changed
  - Update to Stan version 2.18.0.

#### Version 0.84 <2018-02-24 Sat>.

- Added
  - Piecewise linear interpolation function.
  - Univariate integral functions.
- Changed
  - Update to Stan version 2.17.1.
  - Minor revisions to User Manual.
  - Bugfixes.



**Version 0.83 <2017-08-02 Wed>.**

- Added
  - Work with TorstenHeaders
  - Each chain has a different initial estimate
- Changed
  - User manual
  - Fix misspecification in ODE system for TwoCpt example.
  - Other bugfixes

**Version 0.82 <2017-01-29 Sun>.**

- Added
  - Allow parameter arguments to be passed as 1D or 2D arrays
  - More unit tests
  - Unit tests check automatic differentiation against finite differentiation.
- Changed
  - Split the parameter argument into three arguments: pMatrix (parameters for the ODEs – note: for `linOdeModel`, pMatrix is replaced by the constant rate matrix K), biovar (parameters for the biovariability), and tlag (parameters for the lag time).
  - bugfixes

**Version 0.81 <2016-09-27 Tue>.**

- Added `linCptModel` (linear compartmental model) function

**Version 0.80a <2016-09-21 Wed>.**

- Added `check_finite` statements in `pred_1` and `pred_2` to reject metropolis proposal if initial conditions are not finite

## Installation

Currently Torsten is based on a forked version of Stan and hosted on GitHub

- <https://github.com/metrumresearchgroup/Torsten>

The latest v0.88 is compatible with Stan v2.25.0. Torsten can be accessed from command line for cmdstan interface and cmdstanr (<https://mc-stan.org/cmdstanr/>) for R interface. It requires a modern C++11 compiler as well as a Make utility. See [9] for details of installation and required toolchain. In particular, we recommend the following versions of C++ compilers:

- Linux: g++ >=7.5 or clang >=8.0,
- macOS: the XCode version of clang,
- Windows: g++ 8.1 (available with RTools 4.0).

On windows, the Make utility mingw32-make can be installed as part of RTools.

### 2.1. Command line interface

The command line interface cmdstan is available along with Torsten and can be found at Torsten/cmdstan.

After installation, one can use the following command to build a Torsten model `model_name` in `model_path`

```
cd Torsten/cmdstan
make model_path/model_name # replace "make" with "mingw32-make" on Windows platform
```

### 2.2. R interface

After installing cmdstanr from <https://mc-stan.org/cmdstanr/>, use the following command to set path

```
cmdstanr::set_cmdstan_path("Torsten/cmdstan")
```

Then one can follow <https://mc-stan.org/cmdstanr/articles/cmdstanr.html> to compile and run Torsten models.

### 2.3. MPI support

Torsten's MPI support is of a different flavour than `reduce_sum` found in Stan. To be able to utilize MPI parallelisation, one first needs to ensure an MPI library such as

- <https://www.mpich.org/downloads/>
- <https://www.open-mpi.org/software/ompi/>

is available. Torsten's implementation is tested on both MPICH and OpenMPI.

To use MPI-supported population/group solvers, add/edit `make/local`

```
TORSTEN_MPI=1

# path to MPI headers
CXXFLAGS += -isystem /usr/local/include
# if you are using Metrum's metworx platform, add MPICH3's
```

```
# headers with  
# CXXFLAGS += -isystem /usr/local/mpich3/include
```

Note that currently TORSTEN\_MPI and STAN\_MPI flags conflict on processes management and cannot be used in a same Stan model, and MPI support is only available through cmdstan interface.

## 2.4. Testing

Models in example-models directory are for tutorial and demonstration. The following shows how to build and run the two-compartment model using cmdstanr, and use bayesplot to examine posterior density of CL.

```
library("cmdstanr")  
set_cmdstan_path("Torsten/cmdstan")  
file.dir <- file.path("Torsten", "example-models", "pk2cpt")  
file <- file.path(file.dir, "pk2cpt.stan")  
model <- cmdstan_model(file)  
fit <- model$sample(data = file.path(file.dir, "pk2cpt.data.R"),  
                   init = file.path(file.dir, "pk2cpt.init.R"),  
                   seed = 123,  
                   chains = 4,  
                   parallel_chains = 2,  
                   refresh = 500)  
bayesplot::mcmc_dens_overlay(fit$draws("CL"))
```

## Using Torsten

The reader should have a basic understanding of how Stan works before reading this chapter. There are excellent resources online to get started with Stan (<http://mc-stan.org/documentation>). In this section we go through the different functions Torsten adds to Stan. The code for the examples can be found at the `example-models` folder.

Torsten's functions are prefixed with `pmx_`. For some of their arguments we adopt NM-TRAN format for events specification (Table 3.1). All the `real[]` arguments above are allowed to be `parameters` in a Stan

TABLE 3.1. NM-TRAN compatible event specification arguments. All arrays should have the same length corresponding to the number of events.

Argument Name	Definition	Stan data type
<code>time</code>	time	<code>real[]</code>
<code>amt</code>	amount	<code>real[]</code>
<code>rate</code>	infusion rate	<code>real[]</code>
<code>ii</code>	interdose interval	<code>real[]</code>
<code>evid</code>	event ID	<code>int[]</code>
<code>cmt</code>	event compartment	<code>int[]</code>
<code>addl</code>	additional identical doses	<code>int[]</code>
<code>ss</code>	steady-state dosing flag	<code>int[]</code>

model. In addition, Torsten functions support optional arguments and overloaded signatures. Optional arguments are indicated by surrounding square bracket `[]`. Table below shows three commonly used PMX model arguments that support overloading. In the rest of this document we assume this convention unless indicated otherwise.

TABLE 3.2. PMX model parameter overloadings. One can use 1d array `real[]` to indicate constants of all events, or 2d array `real[, ]` so that the  $i$ th row of the array describes the model arguments for time interval  $(t_{i-1}, t_i)$ , and the number of the rows equals to the size of `time`.

Argument Name	Definition	Stan data type	Optional
<code>theta</code>	model parameters	<code>real[]</code> or <code>real[, ]</code>	N
<code>biovar</code>	bioavailability fraction	<code>real[]</code> or <code>real[, ]</code>	Y (default to 1.0)
<code>tlag</code>	lag time	<code>real[]</code> or <code>real[, ]</code>	Y (default to 0.0)

### 3.1. One Compartment Model

**3.1.1. Description.** Function `pmx_solve_onecpt` solves a one-compartment PK model (Figure 3.1). The model obtains plasma concentrations of parent drug  $c = y_2/V_2$  by solving for the mass of drug in the central compartment  $y_2$  from ordinary differential equations (ODEs)

$$y_1' = -k_a y_1, \quad (3.1a)$$

$$y_2' = k_a y_1 - \left( \frac{CL}{V_2} + \frac{Q}{V_2} \right) y_2. \quad (3.1b)$$

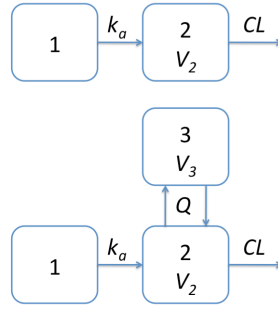


FIGURE 3.1. One and two compartment models with first order absorption implemented in Torsten.

### 3.1.2. Usage.

```
matrix = pmx_solve_onecpt(time, amt, rate, ii, evid, cmt, addl, ss, theta [, biovar, tlag ] )
```

### 3.1.3. Arguments.

See Table 3.1 and Table 3.2.

**3.1.4. Return value.** An ncmt-by-nt matrix, where nt is the number of time steps and ncmt=2 is the number of compartments.

### 3.1.5. Note.

- ODE Parameters **theta** should consist of  $CL$ ,  $V_2$ ,  $k_a$ , in that order.
- **biovar** and **tlag** are optional, so that the following are allowed:

```
pmx_solve_onecpt(..., theta);
pmx_solve_onecpt(..., theta, biovar);
pmx_solve_onecpt(..., theta, biovar, tlag);
```

- Setting  $k_a = 0$  eliminates the first-order absorption.

## 3.2. Two Compartment Model

**3.2.1. Description.** Function **pmx\_solve\_twocpt** solves a two-compartment PK model (Figure 3.1). The model obtains plasma concentrations of parent drug  $c = y_2/V_2$  by solving for the mass of drug in the central compartment  $y_2$  from ordinary differential equations(ODEs)

$$y_1' = -k_a y_1 \quad (3.2a)$$

$$y_2' = k_a y_1 - \left( \frac{CL}{V_2} + \frac{Q}{V_2} \right) y_2 + \frac{Q}{V_3} y_3 \quad (3.2b)$$

$$y_3' = \frac{Q}{V_2} y_2 - \frac{Q}{V_3} y_3 \quad (3.2c)$$

### 3.2.2. Usage.

```
matrix = pmx_solve_twocpt(time, amt, rate, ii, evid, cmt, addl, ss, theta [, biovar, tlag ] )
```

### 3.2.3. Arguments.

See Table 3.1 and Table 3.2.

**3.2.4. Return value.** An ncmt-by-nt matrix, where nt is the number of time steps and ncmt=3 is the number of compartments.

**3.2.5. Note.**

- ODE Parameters **theta** consists of  $CL$ ,  $Q$ ,  $V_2$ ,  $V_3$ ,  $k_a$ .
- **biovar** and **tlag** are optional, so that the following are allowed:

```
pmx_solve_twocpt(..., theta);
pmx_solve_twocpt(..., theta, biovar);
pmx_solve_twocpt(..., theta, biovar, tlag);
```

- Setting  $k_a = 0$  eliminates the first-order absorption.

**3.3. General Linear ODE Model Function**

**3.3.1. Description.** Function **pmx\_solve\_linode** solves a (piecewise) linear ODEs model with coefficients in form of matrix  $K$

$$y'(t) = Ky(t) \quad (3.3)$$

For example, in a two-compartment model with first order absorption,  $K$  is

$$K = \begin{bmatrix} -k_a & 0 & 0 \\ k_a & -(k_{10} + k_{12}) & k_{21} \\ 0 & k_{12} & -k_{21} \end{bmatrix} \quad (3.4)$$

where  $k_{10} = CL/V_2$ ,  $k_{12} = Q/V_2$ , and  $k_{21} = Q/V_3$ .

**3.3.2. Usage.**

```
matrix = pmx_solve_linode(time, amt, rate, ii, evid, cmt, addl, ss, K, biovar, tlag )
```

**3.3.3. Arguments.**

- **K** System parameters. **K** can be either
  - a **matrix** for constant parameters in all events, or
  - an array of matrices **matrix**  $K[nt]$  so that the  $i$ th entry of the array describes the model parameters for time interval  $(t_{i-1}, t_i)$ , and the number of the rows equals to the number of event time **nt**.
- See Table 3.1 and Table 3.2 for the rest of arguments.

**3.3.4. Return value.** An  $n$ -by- $nt$  matrix, where  $nt$  is the number of time steps and  $n$  is the number of rows(columns) of square matrix **K**.

**3.4. General ODE Model Function**

**3.4.1. Description.** Function **pmx\_solve\_adams**, **pmx\_solve\_bdf**, and **pmx\_solve\_rk45** solve a first-order ODE system specified by user-specified right-hand-side function **ODE\_rhs**  $f$

$$y'(t) = f(t, y(t))$$

In the case where the **rate** vector  $r$  is non-zero, this equation becomes:

$$y'(t) = f(t, y(t)) + r$$

**3.4.2. Usage.**

```
matrix pmx_solve_[adams || rk45 || bdf](ODE_rhs, int nCmt, time, amt, rate, ii, evid, cmt,
  ↳ addl, ss, theta, [ biovar, tlag, real[:,] x_r, int[:,] x_i, real rel_tol, real abs_tol,
  ↳ int max_step, real as_rel_tol, real as_abs_tol, int as_max_step ] );
```

Here [adams || rk45 || bdf] indicates the function name can use any of the three suffixes. See below.

### 3.4.3. Arguments.

- **ODE\_rhs** ODE right-hand-side  $f$ . It should be defined in `functions` block and has the following format

```
real[] = f(real t, real[] y, real[] param, real[] dat_r, int[] dat_i) {...}
```

Here **t** is time, **y** the unknowns of ODE, **param** the parameters, **dat\_r** the real data, **dat\_i** the integer data. **param**, **dat\_r**, and **dat\_i** are from the entry of **theta**, **x\_r**, and **x\_i** corresponding to **t**, respectively.  $f$  should not include dosing rates in its definition, as Torsten automatically update  $f$  when the corresponding event indicates infusion dosage.

- **nCmt** The number of compartments, equivalently, the dimension of the ODE system.
- **x\_r** 2d array real data to be passed to ODE RHS. If specified, its 1st dimension should have the same size as **time**.
- **x\_i** 2d array integer data to be passed to ODE RHS. If specified, its 1st dimension should have the same size as **time**.
- **rel\_tol** The relative tolerance for numerical integration, default to 1.0E-6.
- **abs\_tol** The absolute tolerance for numerical integration, default to 1.0E-6.
- **max\_step** The maximum number of steps in numerical integration, default to  $10^6$ .
- **as\_rel\_tol** The relative tolerance for algebra solver for steady state solution, default to 1.0E-6.
- **as\_abs\_tol** The absolute tolerance for algebra solver for steady state solution, default to 1.0E-6.
- **as\_max\_step** The maximum number of iterations in algebra solver for steady state solution, default to  $10^2$ .
- See Table 3.1 and Table 3.2 for the rest of arguments.

**3.4.4. Return value.** An **nCmt**-by-**nt** matrix, where **nt** is the size of **time**.

### 3.4.5. Note.

- See section 3.7.5 for different types of integrator and general guidance.
- See section 3.7.5 for comments on accuracy and tolerance.
- The default values of **atol**, **rtol**, and **max\_step** are based on a limited amount of PKPD test problems and should not be considered as universally applicable. We strongly recommend user to set these values according to physical intuition and numerical tests. See also Section 3.7.5.
- With optional arguments indicated by square bracket, the following calls are allowed:

```
pmx_solve_[adams || rk45 || bdf](..., theta);
pmx_solve_[adams || rk45 || bdf](..., theta, rel_tol, abs_tol, max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, rel_tol, abs_tol, max_step, as_rel_tol,
  ↳ as_abs_tol, as_max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, rel_tol, abs_tol, max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, rel_tol, abs_tol, max_step, as_rel_tol,
  ↳ as_abs_tol, as_max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, rel_tol, abs_tol, max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, rel_tol, abs_tol, max_step,
  ↳ as_rel_tol, as_abs_tol, as_max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, rel_tol, abs_tol, max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, rel_tol, abs_tol, max_step,
  ↳ as_rel_tol, as_abs_tol, as_max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i, rel_tol, abs_tol,
  ↳ max_step);
pmx_solve_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i, rel_tol, abs_tol,
  ↳ max_step, as_rel_tol, as_abs_tol, as_max_step);
```

### 3.5. Coupled ODE Model Function

**3.5.1. Description.** When the ODE system consists of two subsystems in form of

$$\begin{aligned} y_1' &= f_1(t, y_1), \\ y_2' &= f_2(t, y_1, y_2), \end{aligned}$$

with  $y_1$ ,  $y_2$ ,  $f_1$ , and  $f_2$  being vector-valued functions, and  $y_1'$  independent of  $y_2$ , the solution can be accelerated if  $y_1$  admits an analytical solution which can be introduced into the ODE for  $y_2$  for numerical integration. This structure arises in PK/PD models, where  $y_1$  describes a forcing PK function and  $y_2$  the PD effects. In the example of a Friberg-Karlsson semi-mechanistic model(see below), we observe an average speedup of  $\sim 47 \pm 18\%$  when using the mix solver in lieu of the numerical integrator. In the context, currently the couple solver supports one- & two-compartment for PK model, and **rk45** & **bdf** integrator for nonlinear PD model.

**3.5.2. Usage.**

```
matrix pmx_solve_onecpt_[ rk45 || bdf ](reduced_ODE_system, int nOde, time, amt, rate, ii,
  ↳ evid, cmt, addl, ss, theta, biovar, tlag [, real rel_tol, real abs_tol, int max_step,
  ↳ real as_rel_tol, real as_abs_tol, int as_max_step ] );
matrix pmx_solve_twocpt_[ rk45 || bdf ](reduced_ODE_system, int nOde, time, amt, rate, ii,
  ↳ evid, cmt, addl, ss, theta, biovar, tlag [, real rel_tol, real abs_tol, int max_step,
  ↳ real as_rel_tol, real as_abs_tol, int as_max_step ] );
```

**3.5.3. Arguments.**

- **reduced\_ODE\_rhs** The system numerically solve ( $y_2$  in the above discussion, also called the *reduced system* and **nOde** the number of equations in the *reduced* system. The function that defines a reduced system has an almost identical signature to that used for a full system, but takes one additional argument:  $y_1$ , the PK states, i.e. solution to the PK ODEs.

```
real[] reduced_ODE_rhs(real t, real[] y2, real[] y1, real[] theta, real[] x_r,
  ↳ int[] x_i)
```

- **nCmt** The number of compartments. Equivalently, the dimension of the ODE system.
- **rel\_tol** The relative tolerance for numerical integration, default to 1.0E-6.
- **abs\_tol** The absolute tolerance for numerical integration, default to 1.0E-6.
- **max\_step** The maximum number of steps in numerical integration, default to  $10^6$ .
- See Table 3.1 and Table 3.2 for the rest of arguments.

**3.5.4. Return value.** An  $nPk + nOde$ -by- $nt$  matrix, where  $nt$  is the size of **time**, and  $nPk$  equals to 2 in **pmx\_solve\_onecpt\_** functions and 3 in **pmx\_solve\_twocpt\_** functions.

### 3.6. General ODE-based Population Model Function

**3.6.1. Description.** All the previous functions solves for a single subject. Torsten also provides population modeling counterparts for ODE solutions. The functions solve for a population that share an ODE model but with subject-level parameters and event specifications and have similar signatures to single-subject functions, except that now events arguments **time**, **amt**, **rate**, **ii**, **evid**, **cmt**, **addl**, **ss** specifies the entire population, one subject after another.

**3.6.2. Usage.**

```
matrix pmx_solve_group_[adams || rk45 || bdf](ODE_rhs, int nCmt, int[] len, time, amt, rate,
  ↳ ii, evid, cmt, addl, ss, theta, [ biovar, tlag, real[,] x_r, int [,] x_i, real rel_tol,
  ↳ real abs_tol, int max_step, real as_rel_tol, real as_abs_tol, int as_max_step ] );
```

Here **[adams || rk45 || bdf]** indicates the function name can be of any of the three suffixes. See section 3.7.5.



### 3.6.3. Arguments.

- **time**, **amt**, **rate**, **ii**, **evid**, **cmt**, **addl**, **ss** 2d-array arguments that describe data record for the entire population (see also Table 3.1 and Table 3.2). They must have same size in the first dimension. Take **evid** for example. Let  $N$  be the population size, then **evid**[1 to **evid**[**n1** specifies events ID for subject 1, **evid**[**n1** + 1 to **evid**[**n1** + **n2** for subject 2, etc. With  $n_i$  being the number of events for subject  $i$ ,  $i = 1, 2, \dots, N$ , the size of **evid**'s first dimension is  $\sum_i n_i$ .
- **len** The length of data for each subject within the above events arrays. The size of **len** equals to population size  $N$ .
- **ODE\_rhs** ODE right-hand-side  $f$ . It should be defined in **functions** block and has the following format

```
real[] = f(real t, real[] y, real[] param, real[] dat_r, int[] dat_i) {...}
```

Here **t** is time, **y** the unknowns of ODE, **param** the parameters, **dat\_r** the real data, **dat\_i** the integer data. **param**, **dat\_r**, and **dat\_i** are from the entry of **theta**, **x\_r**, and **x\_i** corresponding to **t**, respectively.  $f$  should not include dosing rates in its definition, as Torsten automatically update  $f$  when the corresponding event indicates infusion dosage.

- **nCmt** The number of compartments. Equivalently, the dimension of the ODE system.
- **x\_r** 2d array real data to be passed to ODE RHS. If specified, its 1st dimension should have the same size as **time**.
- **x\_i** 2d array integer data to be passed to ODE RHS. If specified, its 1st dimension should have the same size as **time**.
- **rel\_tol** The relative tolerance for numerical integration, default to 1.0E-6.
- **abs\_tol** The absolute tolerance for numerical integration, default to 1.0E-6.
- **max\_step** The maximum number of steps in numerical integration, default to  $10^6$ .
- **as\_rel\_tol** The relative tolerance for algebra solver for steady state solution, default to 1.0E-6.
- **as\_abs\_tol** The absolute tolerance for algebra solver for steady state solution, default to 1.0E-6.
- **as\_max\_step** The maximum number of iterations in algebra solver for steady state solution, default to  $10^2$ .

**3.6.4. Return value.** An **nCmt**-by-**nt** matrix, where **nt** is the total size of events  $\sum_i n_i$ .

### 3.6.5. Note.

- Similar to single-subject solvers, three numerical integrator are provided:
  - **pmx\_solve\_group\_adams**: Adams-Moulton method,
  - **pmx\_solve\_group\_bdf**: Backward-differentiation formula,
  - **pmx\_solve\_group\_rk45**: Runge-Kutta 4/5 method.
- With optional arguments indicated by square bracket, the following calls are allowed:

```
pmx_solve_group_[adams || rk45 || bdf](..., theta);
pmx_solve_group_[adams || rk45 || bdf](..., theta, rel_tol, abs_tol, max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, rel_tol, abs_tol, max_step, as_rel_tol,
  ↳ as_abs_tol, as_max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, rel_tol, abs_tol, max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, rel_tol, abs_tol, max_step,
  ↳ as_rel_tol, as_abs_tol, as_max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, tlag);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, tlag, rel_tol, abs_tol, max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, tlag, rel_tol, abs_tol, max_step,
  ↳ as_rel_tol, as_abs_tol, as_max_step);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r);
pmx_solve_group_[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, rel_tol, abs_tol,
  ↳ max_step);
```

```
pmx_solve_group[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, rel_tol, abs_tol,
  ↪ max_step, as_rel_tol, as_abs_tol, as_max_step);
pmx_solve_group[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i);
pmx_solve_group[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i, rel_tol, abs_tol,
  ↪ max_step);
pmx_solve_group[adams || rk45 || bdf](..., theta, biovar, tlag, x_r, x_i, rel_tol, abs_tol,
  ↪ max_step, as_rel_tol, as_abs_tol, as_max_step);
```

- The group solvers support parallelisation through Message Passing Interface(MPI). One can access this feature through cmdstan or cmdstanr interface.

```
# cmdstan interface user need to add "TORSTEN_MPI=1" and
# "TBB_CXX_TYPE=gcc" in "cmdstan/make/local" file. In linux & macos
# this can be done as
echo "TORSTEN_MPI=1" > cmdstan/make/local
echo "TBB_CXX_TYPE=gcc" > cmdstan/make/local # "gcc" should be replaced by user's C compiler
make path-to-model/model_name
mpiexec -n number_of_processes model_name sample... # additional cmdstan options
```

```
library("cmdstanr")
cmdstan_make_local(cpp_options = list("TORSTEN_MPI" = "1", "TBB_CXX_TYPE"="gcc")) # "gcc"
  ↪ should be replaced by user's C compiler
rebuild_cmdstan()
mod <- cmdstan_model(path-to-model-file, quiet=FALSE, force_recompile=TRUE)
f <- mod$sample_mpi(data = ..., chains = 1, mpi_args = list("n" = number_of_processes),
  ↪ refresh = 200)
```

Here  $n$  denotes number of MPI processes, so that  $N$  ODE systems (each specified by a same RHS function and subject-dependent events) are distributed to and solved by  $n$  processes evenly. Note that to access this feature user must have MPI installed, and some MPI installation may require set additional compiler arguments, such as CXXLFLAGS and LDFLAGS.

### 3.7. ODE integrator Function

**3.7.1. Description.** Torsten provides its own implementation of ODE solvers that solves

$$y'(t) = f(t, y(t)), \quad y(t_0) = y_0$$

for  $y$ . These solvers are customized for Torsten applications and different from those found in Stan. The general ODE PMX solvers in previous sections are internally powered by these functions.

**3.7.2. Usage.**

```
real[ , ] pmx_integrate_ode[ adams || bdf || rk45 ](ODE_rhs, real[] y0, real t0, real[] ts,
  ↪ real[] theta, real[] x_r, int[] x_i [ , real rtol, real atol, int max_step ]);
```

**3.7.3. Arguments.**

- **ODE\_rhs** Function that specifies the right-hand-side  $f$ . It should be defined in functions block and has the following format

```
real[] = f(real t, real[] y, real[] param, real[] dat_r, int[] dat_i) {...}
```

Here  $t$  is time,  $y$  the unknowns of ODE,  $param$  the parameters,  $dat_r$  the real data,  $dat_i$  the integer data.

- $y_0$  Initial condition  $y_0$ .
- $t_0$  Initial time  $t_0$ .

- **ts** Output time when solution is seeked.
- **theta** Parameters to be passed to **ODE\_rhs** function.
- **x\_r** Real data to be passed to **ODE\_rhs** function.
- **x\_i** Integer data to be passed to **ODE\_rhs** function.
- **rtol** Relative tolerance, default to 1.e-6(**rk45**) and 1.e-8(**adams** and **bdf**).
- **atol** Absolute tolerance, default to 1.e-6(**rk45**) and 1.e-8(**adams** and **bdf**).
- **max\_step** Maximum number of steps allowed between neighboring time in **ts**, default to 100000.

**3.7.4. Return value.** An n-by-nd 2d-array, where n is the size of **ts** and nd the dimension of the system.

#### 3.7.5. Note.

- Three numerical integrator are provided:
  - **pmx\_integrate\_ode\_adams**: Adams-Moulton method,
  - **pmx\_integrate\_ode\_bdf**: Backward-differentiation formula,
  - **pmx\_integrate\_ode\_rk45**: Runge-Kutta 4/5 method.

When not equipped with further understanding of the ODE system, as a rule of thumb we suggest user try **rk45** integrator first, **bdf** integrator when the system is suspected to be stiff, and **adams** when a non-stiff system needs to be solved with higher accuracy/smaller tolerance.

- All three integrators support adaptive stepping. To achieve that, at step  $i$  estimated error  $e_i$  is calculated and compared with given tolerance so that

$$e_i < \|rtol \times \tilde{y} + atol\| \quad (3.5)$$

Here  $\tilde{y}$  is the numerical solution of  $y$  at current step and  $\|\cdot\|$  indicates certain norm. When the above check fails, the solver attempts to reduce step size and retry. The default values of **atol**, **rtol**, and **max\_step** are based on Stan's ODE functions and should not be considered as optimal. User should make problem-dependent decision on **rtol** and **atol**, according to estimated scale of the unknowns, so that the error would not affect inference on statistical variance of quantities that enter the Stan model. In particular, when an unknown can be neglected below certain threshold without affecting the rest of the dynamic system, setting **atol** greater than that threshold will avoid spurious and error-prone computation. See [6] and 1.4 of [8] for details.

- With optional arguments indicated by square bracket, the following calls are allowed:

```
pmx_integrate_ode_[adams || rk45 || bdf](..., x_i);
pmx_integrate_ode_[adams || rk45 || bdf](..., x_i, rel_tol, abs_tol, max_step);
```

## 3.8. ODE group integrator Function

**3.8.1. Description.** All the previous functions solves for a single ODE system. Torsten also provides group modeling counterparts for ODE integrators. The functions solve for a group of ODE systems that share an ODE RHS but with different parameters. They have similar signatures to single-ODE integration functions.

#### 3.8.2. Usage.

```
matrix pmx_integrate_ode_group_[adams || rk45 || bdf](ODE_system, real[ , ] y0, real t0,
  ↳ int[] len, real[] ts, real[ , ] theta, real[ , ] x_r, int[ , ] x_i, [ real rtol, real
  ↳ atol, int max_step ] );
```

Here [adams || rk45 || bdf] indicates the function name can be of any of the three suffixes. See section 3.7.5.

- **ODE\_rhs** Function that specifies the right-hand-side  $f$ . See Section 3.7.3.
- **y0** Initial condition  $y_0$  for each subsystem in the group. The first dimension equals to the size of the group.
- **t0** Initial time  $t_0$ .

- **len** A vector that contains the number of output time points for each subsystem. The length of the vector equals to the size of the group.
- **ts** Output time when solution is sought, consisting of **ts** of each subsystem concatenated.
- **theta** 2d-array parameters to be passed to **ODE\_rhs** function. Each row corresponds to one subsystem.
- **x\_r** 2d-array real data to be passed to **ODE\_rhs** function. Each row corresponds to one subsystem.
- **x\_i** 2d-array integer data to be passed to **ODE\_rhs** function. Each row corresponds to one subsystem.
- **rtol** Relative tolerance.
- **atol** Absolute tolerance.
- **max\_step** Maximum number of steps allowed between neighboring time in **ts**.

**3.8.3. Return value.** An  $n$ -by- $nd$  matrix, where  $n$  is the size of **ts** and  $nd$  the dimension of the system.

#### 3.8.4. Note.

- With optional arguments indicated by square bracket, the following calls are allowed:

```
pmx_integrate_group_[adams || rk45 || bdf](..., x_i);
pmx_integrate_group_[adams || rk45 || bdf](..., x_i, rel_tol, abs_tol, max_step);
```

- The group integrators support parallelisation through Message Passing Interface(MPI). One can access this feature through `cmdstan` or `cmdstanr` interface.

```
# cmdstan interface user need to add "TORSTEN_MPI=1" and
# "TBB_CXX_TYPE=gcc" in "cmdstan/make/local" file. In linux & macos
# this can be done as
echo "TORSTEN_MPI=1" > cmdstan/make/local
echo "TBB_CXX_TYPE=gcc" > cmdstan/make/local # "gcc" should be replaced by user's C compiler
make path-to-model/model_name
mpiexec -n number_of_processes model_name sample... # additional cmdstan options
```

```
library("cmdstanr")
cmdstan_make_local(cpp_options = list("TORSTEN_MPI" = "1", "TBB_CXX_TYPE"="gcc")) # "gcc"
  ↳ should be replaced by user's C compiler
rebuild_cmdstan()
mod <- cmdstan_model(path-to-model-file, quiet=FALSE, force_recompile=TRUE)
f <- mod$sample_mpi(data = ..., chains = 1, mpi_args = list("n" = number_of_processes),
  ↳ refresh = 200)
```

Here  $n$  denotes number of MPI processes, so that  $N$  ODE systems are distributed to and solved by  $n$  processes evenly. Note that to access this feature user must have MPI installed, and some MPI installation may require set additional compiler arguments, such as `CXXFLAGS` and `LDFLAGS`.

### 3.9. Univariate integral

```
real univariate_integral_rk45(f, t0, t1, theta, x_r, x_i)
```

```
real univariate_integral_bdf(f, t0, t1, theta, x_r, x_i)
```

Based on the ODE solver capability in Stan, Torsten provides functions calculating the integral of a univariate function. The integrand function  $f$  must follow the signature

```

real f(real t, real[] theta, real[] x_r, int[] x_i) {
    /* ... */
}

```

### 3.10. Piecewise linear interpolation

```

real linear_interpolation(real xout, real[] x, real[] y)

```

```

real[] linear_interpolation(real[] xout, real[] x, real[] y)

```

Torsten also provides function `linear_interpolation` for piecewise linear interpolation over a set of  $x$ ,  $y$  pairs. It returns the values of a piecewise linear function at specified values `xout` of the first function argument. The function is specified in terms of a set of  $x$ ,  $y$  pairs. Specifically, `linear_interpolation` implements the following function

$$y_{\text{out}} = \begin{cases} y_1, & x_{\text{out}} < x_1 \\ y_i + \frac{y_{i+1} - y_i}{x_{i+1} - x_i} (x_{\text{out}} - x_i), & x_{\text{out}} \in [x_i, x_{i+1}) \\ y_n, & x_{\text{out}} \geq x_n \end{cases}$$

- The  $x$  values must be in increasing order, i.e.  $x_i < x_{i+1}$ .
- All three arguments may be data or parameters.

## Examples

All the PMX models in this chapter can be found in `Torsten/example-models` directory:

- `Torsten/example-models/pk2cpt` (Section 4.1).
- `Torsten/example-models/pk2cpt_linode` (Section 4.2).
- `Torsten/example-models/pk2cpt_ode` (Section 4.3).
- `Torsten/example-models/FK_coupled` (Section 4.4).
- `Torsten/example-models/twocpt_population` (Section 4.5).
- `Torsten/example-models/lotka_volterra_ode_group_model` (Section 4.6).
- `Torsten/example-models/effCpt` (Section 4.9).
- `Torsten/example-models/FribergKarlsson` (Section 4.10).

### 4.1. Two-compartment model for single patient

We model drug absorption in a single patient and simulate plasma drug concentrations:

- Multiple Doses: 1250 mg, every 12 hours, for a total of 15 doses
- PK measured at 0.083, 0.167, 0.25, 0.5, 0.75, 1, 1.5, 2, 4, 6, 8, 10 and 12 hours after 1st, 2nd, and 15th dose. In addition, the PK is measured every 12 hours throughout the trial.

With the plasma concentration  $\hat{c}$  solved from two-compartment ODEs in 3.2, we simulate  $c$  according to:

$$\begin{aligned}\log(c) &\sim N(\log(\hat{c}), \sigma^2) \\ (CL, Q, V_2, V_3, ka) &= (5 \text{ L/h}, 8 \text{ L/h}, 20 \text{ L}, 70 \text{ L}, 1.2 \text{ h}^{-1}) \\ \sigma^2 &= 0.01\end{aligned}$$

The data are generated using the R package `mrgsolve` [1].

Code below shows how `Torsten` function `pmx_solve_twocpt` can be used to fit the above model.

```
data{
  int<lower = 1> nt; // number of events
  int<lower = 1> nObs; // number of observation
  int<lower = 1> iObs[nObs]; // index of observation

  // NONMEM data
  int<lower = 1> cmt[nt];
  int evid[nt];
  int addl[nt];
  int ss[nt];
  real amt[nt];
  real time[nt];
  real rate[nt];
  real ii[nt];

  vector<lower = 0>[nObs] cObs; // observed concentration (Dependent Variable)
}

transformed data{
  vector[nObs] logCObs = log(cObs);
  int nTheta = 5; // number of ODE parameters in Two Compartment Model
  int nCmt = 3; // number of compartments in model
```

```

}

parameters{
  real<lower = 0> CL;
  real<lower = 0> Q;
  real<lower = 0> V1;
  real<lower = 0> V2;
  real<lower = 0> ka;
  real<lower = 0> sigma;
}

transformed parameters{
  real theta[nTheta]; // ODE parameters
  row_vector<lower = 0>[nt] cHat;
  vector<lower = 0>[nObs] cHatObs;
  matrix<lower = 0>[nCmt, nt] x;

  theta[1] = CL;
  theta[2] = Q;
  theta[3] = V1;
  theta[4] = V2;
  theta[5] = ka;

  x = pmx_solve_twocpt(time, amt, rate, ii, evid, cmt, addl, ss, theta);

  cHat = x[2, :] ./ V1; // we're interested in the amount in the second compartment

  cHatObs = cHat[iObs]; // predictions for observed data recors
}

model{
  // informative prior
  CL ~ lognormal(log(10), 0.25);
  Q ~ lognormal(log(15), 0.5);
  V1 ~ lognormal(log(35), 0.25);
  V2 ~ lognormal(log(105), 0.5);
  ka ~ lognormal(log(2.5), 1);
  sigma ~ cauchy(0, 1);

  logCObs ~ normal(log(cHatObs), sigma);
}

```

Four MCMC chains of 2000 iterations (1000 warmup iterations and 1000 sampling iterations) are simulated. 1000 samples per chain were used for the subsequent analyses. The MCMC history plots (Figure 4.1) suggest that the 4 chains have converged to common distributions for all of the key model parameters. The fit to the plasma concentration data (Figure 4.3) are in close agreement with the data, which is not surprising since the fitted model is identical to the one used to simulate the data. Similarly the parameter posterior density can be examined in Figure 4.2 and shows consistency with the values used for simulation. Another way to summarize the posterior is through `cmdstanr`'s `summary` method.

```

## fit is a CmdStanMCMC object returned by sampling. See cmdstanr reference.
> pars = c("CL", "Q", "V1", "V2", "ka", "sigma")
> fit$summary(pars)
# A tibble: 6 x 10
  variable mean median sd mad q5 q95 rhat ess_bulk ess_tail
  <chr>    <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
1 CL      4.82  4.83  0.0910 0.0870 4.68  4.97  1.00  1439.  1067.
2 Q       7.56  7.55  0.588  0.586  6.61  8.56  1.00  1256.  1235.
3 V1     21.1  21.1  2.50  2.45  17.1  25.3  1.00  1057.  1177.
4 V2     76.1  76.1  5.33  4.93  67.5  84.9  1.01  1585.  1372.
5 ka      1.23  1.23  0.175  0.174  0.958  1.52  1.00  1070.  1122.
6 sigma   0.109 0.108 0.0117 0.0111 0.0911 0.130 1.01  1414.  905.

```

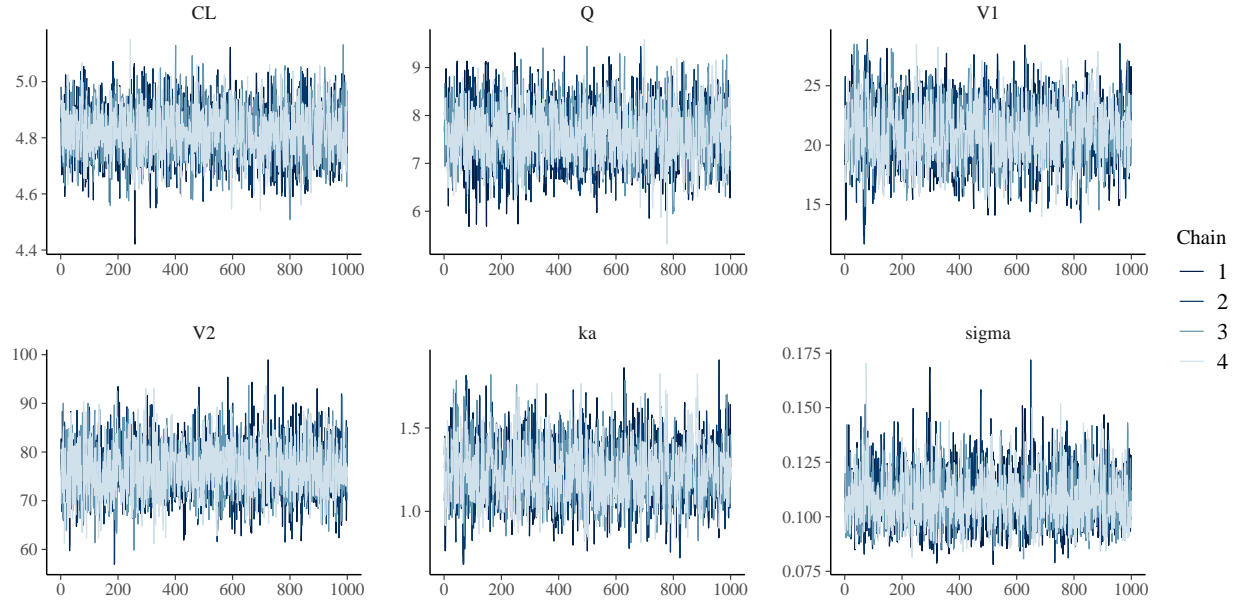


FIGURE 4.1. MCMC history plots for the parameters of a two compartment model with first order absorption (each color corresponds to a different chain)

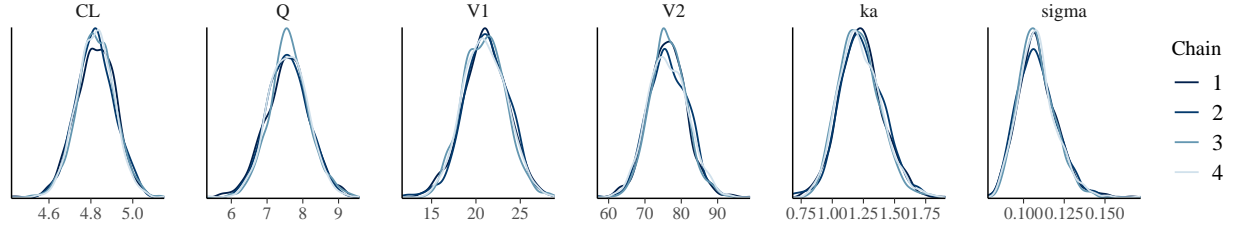


FIGURE 4.2. Posterior marginal densities of the Model Parameters of a two compartment model with first order absorption (each color corresponds to a different chain)

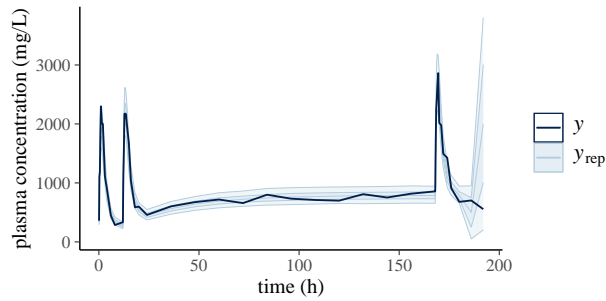


FIGURE 4.3. Predicted ( $y_{\text{rep}}$ ) and observed ( $y$ ) plasma drug concentrations of a two compartment model with first order absorption.  $y_{\text{rep}}$  is shown with posterior median, 50%, 90% credible intervals.



## 4.2. Two-compartment model as a linear ODE model for single patient

Using `pmx_solve_linode`, the following example fits a two-compartment model with first order absorption. We omit data and `model` block as they are identical to Section 4.1.

```
transformed data{
  row_vector[nObs] logCObs = log(cObs);
  int nCmt = 3;
  real biovar[nCmt];
  real tlag[nCmt];

  for (i in 1:nCmt) {
    biovar[i] = 1;
    tlag[i] = 0;
  }
}

parameters{
  real<lower = 0> CL;
  real<lower = 0> Q;
  real<lower = 0> V1;
  real<lower = 0> V2;
  real<lower = 0> ka;
  real<lower = 0> sigma;
}

transformed parameters{
  matrix[3, 3] K;
  real k10 = CL / V1;
  real k12 = Q / V1;
  real k21 = Q / V2;
  row_vector<lower = 0>[nt] cHat;
  row_vector<lower = 0>[nObs] cHatObs;
  matrix<lower = 0>[3, nt] x;

  K = rep_matrix(0, 3, 3);

  K[1, 1] = -ka;
  K[2, 1] = ka;
  K[2, 2] = -(k10 + k12);
  K[2, 3] = k21;
  K[3, 2] = k12;
  K[3, 3] = -k21;

  x = pmx_solve_linode(time, amt, rate, ii, evid, cmt, addl, ss, K, biovar, tlag);

  cHat = row(x, 2) ./ V1;

  for(i in 1:nObs){
    cHatObs[i] = cHat[iObs[i]]; // predictions for observed data records
  }
}
```

## 4.3. Two-compartment model solved by numerical integrator for single patient

Using `pmx_solve_rk45`, the following example fits a two-compartment model with first order absorption. User-defined function `ode_rhs` describes the RHS of the ODEs.

```
functions{
  real[] ode_rhs(real t, real[] x, real[] parms, real[] x_r, int[] x_i){
    real CL = parms[1];
```

```

    real Q = parms[2];
    real V1 = parms[3];
    real V2 = parms[4];
    real ka = parms[5];

    real k10 = CL / V1;
    real k12 = Q / V1;
    real k21 = Q / V2;

    real y[3];

    y[1] = -ka*x[1];
    y[2] = ka*x[1] - (k10 + k12)*x[2] + k21*x[3];
    y[3] = k12*x[2] - k21*x[3];

    return y;
}

```

We omit data and model block as they are identical to Section 4.1.

```

transformed data {
    row_vector[nObs] logCObs = log(cObs);
    int nTheta = 5;    // number of parameters
    int nCmt = 3;    // number of compartments
}

parameters {
    real<lower = 0> CL;
    real<lower = 0> Q;
    real<lower = 0> V1;
    real<lower = 0> V2;
    real<lower = 0> ka;
    real<lower = 0> sigma;
}

transformed parameters {
    real theta[nTheta];
    row_vector<lower = 0>[nt] cHat;
    row_vector<lower = 0>[nObs] cHatObs;
    matrix<lower = 0>[3, nt] x;

    theta[1] = CL;
    theta[2] = Q;
    theta[3] = V1;
    theta[4] = V2;
    theta[5] = ka;

    x = pmx_solve_rk45(ode_rhs, 3, time, amt, rate, ii, evid, cmt, addl, ss, theta, 1e-5,
        ↪ 1e-8, 1e5);

    cHat = x[2, ] ./ V1;

    for(i in 1:nObs){
        cHatObs[i] = cHat[iObs[i]]; // predictions for observed data records
    }
}

model{

```

#### 4.4. Joint PK-PD model

A Friberg-Karlsson Semi-Mechanistic model [5] couples a PK model with a PD effect. In the current example, we use the two compartment model in section 3.2 for PK model.

Neutropenia is observed in patients receiving an ME-2 drug. Our goal is to model the relation between neutrophil counts and drug exposure. Using a feedback mechanism, the body maintains the number of neutrophils at a baseline value (Figure 4.4). While in the patient's blood, the drug impedes the production of neutrophils. As a result, the neutrophil count goes down. After the drug clears out, the feedback mechanism kicks in and brings the neutrophil count back to baseline.

$$\log(ANC_i) \sim N(\log(Circ), \sigma_{ANC}^2) \quad (4.1)$$

$$Circ = f_{FK}(MTT, Circ_0, \alpha, \gamma, c) \quad (4.2)$$

$$(MTT, Circ_0, \alpha, \gamma, ktr) = (125, 5.0, 3 \times 10^{-4}, 0.17) \quad (4.3)$$

$$\sigma_{ANC}^2 = 0.001 \quad (4.4)$$

where  $c$  is the drug concentration in the blood we get from the Two Compartment model, and  $Circ$  is obtained by solving the following system of nonlinear ODEs:

$$y'_{prol} = k_{prol}y_{prol}(1 - E_{drug}) \left( \frac{Circ_0}{y_{circ}} \right)^\gamma - k_{tr}y_{prol} \quad (4.5a)$$

$$y'_{trans1} = k_{tr}y_{prol} - k_{tr}y_{trans1} \quad (4.5b)$$

$$y'_{trans2} = k_{tr}y_{trans1} - k_{tr}y_{trans2} \quad (4.5c)$$

$$y'_{trans3} = k_{tr}y_{trans2} - k_{tr}y_{trans3} \quad (4.5d)$$

$$y'_{circ} = k_{tr}y_{trans3} - k_{tr}y_{circ} \quad (4.5e)$$

where  $E_{drug} = \alpha c$ .

The ODEs specifying the Two Compartment Model (Equation (3.2a)) do not depend on the PD ODEs (Equation (4.5)) and can be solved analytically using Torsten's `pmx_solve_twocpt` function. We therefore specify our model using a coupled solver function. We do not expect our system to be stiff and use the Runge-Kutta 4th/5th order integrator.

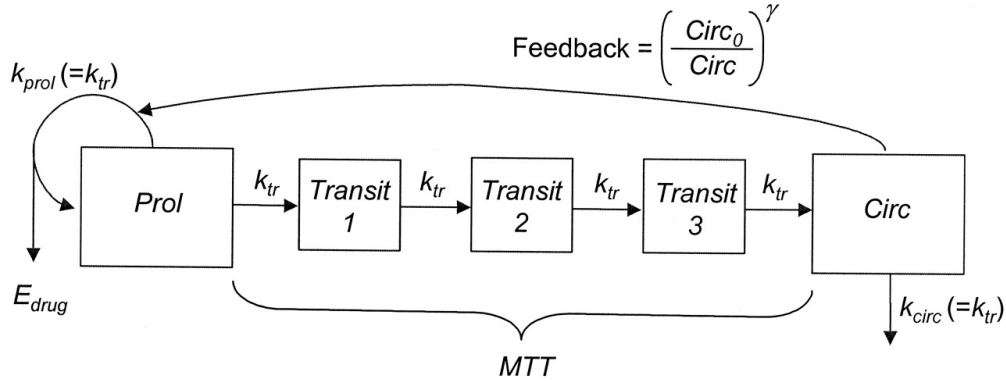


FIGURE 4.4. Friberg-Karlsson semi-mechanistic Model.

```
functions{
  real[] FK_ODE(real t, real[] y, real[] y_pk, real[] theta, real[] rdummy, int[] idummy){
    /* PK variables */
    real VC = theta[3];

    /* PD variable */
    real mtt = theta[6];
```

```

    real circ0      = theta[7];
    real alpha      = theta[8];
    real gamma      = theta[9];
    real ktr        = 4.0 / mtt;
    real prol       = y[1] + circ0;
    real transit1    = y[2] + circ0;
    real transit2    = y[3] + circ0;
    real transit3    = y[4] + circ0;
    real circ       = fmax(machine_precision(), y[5] + circ0);
    real conc       = y_pk[2] / VC;
    real EDrug      = alpha * conc;

    real dydt[5];

    dydt[1] = ktr * prol * ((1 - EDrug) * ((circ0 / circ)^gamma) - 1);
    dydt[2] = ktr * (prol - transit1);
    dydt[3] = ktr * (transit1 - transit2);
    dydt[4] = ktr * (transit2 - transit3);
    dydt[5] = ktr * (transit3 - circ);

    return dydt;
}
}

data{
    int<lower = 1> nt;
    int<lower = 1> nObsPK;
    int<lower = 1> nObsPD;
    int<lower = 1> iObsPK[nObsPK];
    int<lower = 1> iObsPD[nObsPD];
    real<lower = 0> amt[nt];
    int<lower = 1> cmt[nt];
    int<lower = 0> evid[nt];
    real<lower = 0> time[nt];
    real<lower = 0> ii[nt];
    int<lower = 0> addl[nt];
    int<lower = 0> ss[nt];
    real rate[nt];
    vector<lower = 0>[nObsPK] cObs;
    vector<lower = 0>[nObsPD] neutObs;

    real<lower = 0> circ0Prior;
    real<lower = 0> circ0PriorCV;
    real<lower = 0> mttPrior;
    real<lower = 0> mttPriorCV;
    real<lower = 0> gammaPrior;
    real<lower = 0> gammaPriorCV;
    real<lower = 0> alphaPrior;
    real<lower = 0> alphaPriorCV;
}

transformed data{
    int nOde = 5;
    vector[nObsPK] logCObs;
    vector[nObsPD] logNeutObs;

    int nTheta = 9; // number of parameters
    int nIIV = 7; // parameters with IIV

    int n = 8; // ODE dimension */
    real rtol = 1e-8;
    real atol = 1e-8;;
    int max_step = 100000;

```

```

    logCObs = log(cObs);
    logNeutObs = log(neutObs);
}

parameters{

    real<lower = 0> CL;
    real<lower = 0> Q;
    real<lower = 0> VC;
    real<lower = 0> VP;
    real<lower = 0> ka;
    real<lower = 0> mtt;
    real<lower = 0> circ0;
    real<lower = 0> alpha;
    real<lower = 0> gamma;
    real<lower = 0> sigma;
    real<lower = 0> sigmaNeut;

    // IIV parameters
    cholesky_factor_corr[nIIV] L;
    vector<lower = 0>[nIIV] omega;
}

transformed parameters{
    row_vector[nt] cHat;
    vector<lower = 0>[nObsPK] cHatObs;
    row_vector[nt] neutHat;
    vector<lower = 0>[nObsPD] neutHatObs;
    real<lower = 0> theta[nTheta];
    matrix[nOde + 3, nt] x;
    real biovar[nTheta] = rep_array(1.0, nTheta);
    real tlag[nTheta] = rep_array(0.0, nTheta);

    theta[1] = CL;
    theta[2] = Q;
    theta[3] = VC;
    theta[4] = VP;
    theta[5] = ka;
    theta[6] = mtt;
    theta[7] = circ0;
    theta[8] = alpha;
    theta[9] = gamma;

    x = pmx_solve_twocpt_rk45(FK_ODE, nOde, time, amt, rate, ii, evid, cmt, addl, ss, theta,
        ↪ biovar, tlag, rtol, atol, max_step);

    cHat = x[2, ] / VC;
    neutHat = x[8, ] + circ0;

    for(i in 1:nObsPK) cHatObs[i] = cHat[iObsPK[i]];
    for(i in 1:nObsPD) neutHatObs[i] = neutHat[iObsPD[i]];
}

model {
    // Priors
    CL ~ normal(0, 20);
    Q ~ normal(0, 20);
    VC ~ normal(0, 100);
    VP ~ normal(0, 1000);
    ka ~ normal(0, 5);
    sigma ~ cauchy(0, 1);

```

```

mtt      ~ lognormal(log(mttPrior), mttPriorCV);
circ0    ~ lognormal(log(circ0Prior), circ0PriorCV);
alpha    ~ lognormal(log(alphaPrior), alphaPriorCV);
gamma    ~ lognormal(log(gammaPrior), gammaPriorCV);
sigmaNeut ~ cauchy(0, 1);

// Parameters for Matt's trick
L ~ lkj_corr_cholesky(1);
omega ~ cauchy(0, 1);

// observed data likelihood
logCObs ~ normal(log(cObs), sigma);
logNeutObs ~ normal(log(neutObs), sigmaNeut);
}

```

#### 4.5. Two-compartment population model

Using `pmx_solve_group_bdf`, the following example fits a two-compartment population model.

```

functions{
  // define ODE system for two compartment model
  real[] twoCptModelODE(real t,
                        real[] x,
                        real[] parms,
                        real[] rate, // in this example, rate is treated as data
                        int[] dummy){

    // Parameters
    real CL = parms[1];
    real Q = parms[2];
    real V1 = parms[3];
    real V2 = parms[4];
    real ka = parms[5];

    // Re-parametrization
    real k10 = CL / V1;
    real k12 = Q / V1;
    real k21 = Q / V2;

    // Return object (derivative)
    real y[3]; // 1 element per compartment of
               // the model

    // PK component of the ODE system
    y[1] = -ka*x[1];
    y[2] = ka*x[1] - (k10 + k12)*x[2] + k21*x[3];
    y[3] = k12*x[2] - k21*x[3];

    return y;
  }
}

data{
  int<lower = 1> np; // population size */
  int<lower = 1> nt; // number of events
  int<lower = 1> nObs; // number of observations
  int<lower = 1> iObs[nObs]; // index of observation

  // NONMEM data
  int<lower = 1> cmt[np * nt];
  int evid[np * nt];
  int addl[np * nt];
  int ss[np * nt];
}

```

```

real amt[np * nt];
real time[np * nt];
real rate[np * nt];
real ii[np * nt];

real<lower = 0> cObs[np*nObs]; // observed concentration (dependent variable)
}

transformed data {
  real logCObs[np*nObs];
  int<lower = 1> len[np];
  int<lower = 1> len_theta[np];
  int<lower = 1> len_biovar[np];
  int<lower = 1> len_tlag[np];

  int nTheta = 5; // number of parameters
  int nCmt = 3; // number of compartments
  real biovar[np * nt, nCmt];
  real tlag[np * nt, nCmt];

  logCObs = log(cObs);

  for (id in 1:np) {
    for (j in 1:nt) {
      for (i in 1:nCmt) {
        biovar[(id - 1) * nt + j, i] = 1;
        tlag[(id - 1) * nt + j, i] = 0;
      }
    }
    len[id] = nt;
    len_theta[id] = nt;
    len_biovar[id] = nt;
    len_tlag[id] = nt;
  }
}

parameters{
  real<lower = 0> CL[np];
  real<lower = 0> Q[np];
  real<lower = 0> V1[np];
  real<lower = 0> V2[np];
  real<lower = 0> ka[np];
  real<lower = 0> sigma[np];
}

transformed parameters{
  real theta[np * nt, nTheta];
  vector<lower = 0>[nt] cHat[np];
  real<lower = 0> cHatObs[np*nObs];
  matrix[3, nt * np] x;

  for (id in 1:np) {
    for (it in 1:nt) {
      theta[(id - 1) * nt + it, 1] = CL[id];
      theta[(id - 1) * nt + it, 2] = Q[id];
      theta[(id - 1) * nt + it, 3] = V1[id];
      theta[(id - 1) * nt + it, 4] = V2[id];
      theta[(id - 1) * nt + it, 5] = ka[id];
    }
  }
}

x = pmx_solve_group_bdf(twoCptModelODE, 3, len,
                        time, amt, rate, ii, evid, cmt, addl, ss,

```

```

                                theta, biovar, tlag);

  for (id in 1:np) {
    for (j in 1:nt) {
      cHat[id][j] = x[2, (id - 1) * nt + j] ./ V1[id];
    }
  }

  for (id in 1:np) {
    for (i in 1:nObs) {
      cHatObs[(id - 1)*nObs + i] = cHat[id][iObs[i]]; // predictions for observed data
      ↪ records
    }
  }
}

model{
  // informative prior
  for(id in 1:np){
    CL[id] ~ lognormal(log(10), 0.25);
    Q[id] ~ lognormal(log(15), 0.5);
    V1[id] ~ lognormal(log(35), 0.25);
    V2[id] ~ lognormal(log(105), 0.5);
    ka[id] ~ lognormal(log(2.5), 1);
    sigma[id] ~ cauchy(0, 1);

    for(i in 1:nObs){
      logCObs[(id - 1)*nObs + i] ~ normal(log(cHatObs[(id - 1)*nObs + i]), sigma[id]);
    }
  }
}

```

When the above model is compiled with MPI support(see Section 2.3), one can run it with within-chain parallelization:

```

mpiexec -n nproc ./twocpt_population sample data file=twocpt_population.data.R
↪ init=twocpt_population.init.R

```

Here `nproc` indicates the number of parallel processes participating ODE solution. For example, with `np=8` for a population of 8, `nproc=4` indicates solving 8 subjects' ODEs in parallel, with each process solving 2 subjects.

#### 4.6. Lotka-Volterra group model

Using `pmx_integrate_ode_group_rk45`, the following example fits a Lotka-Volterra group model, based on Stan's case study.

```

functions {
  real[] dz_dt(real t,          // time
               real[] z,        // system state {prey, predator}
               real[] theta,    // parameters
               real[] x_r,      // unused data
               int[] x_i) {
    real u = z[1];
    real v = z[2];

    real alpha = theta[1];
    real beta = theta[2];
    real gamma = theta[3];
    real delta = theta[4];
  }
}

```



```

    real du_dt = (alpha - beta * v) * u;
    real dv_dt = (-gamma + delta * u) * v;
    return { du_dt, dv_dt };
}
}
data {
  int<lower = 0> N_subj;          // number of subjects
  int<lower = 0> N;               // number of measurement times
  real ts_0[N];                 // measurement times > 0
  real y0_0[2];                 // initial measured populations
  real<lower = 0> y_0[N, 2];     // measured populations
}
transformed data {
  int len[N_subj] = rep_array(N, N_subj);
  real y0[N_subj, 2] = rep_array(y0_0, N_subj);
  real y[N_subj, N, 2] = rep_array(y_0, N_subj);
  real ts[N_subj * N];
  for (i in 1:N_subj) {
    ts[((i-1)*N + 1) : (i*N)] = ts_0;
  }
}
parameters {
  real<lower = 0> theta[N_subj, 4]; // { alpha, beta, gamma, delta }
  real<lower = 0> z_init[N_subj, 2]; // initial population
  real<lower = 0> sigma[N_subj, 2]; // measurement errors
}
transformed parameters {
  matrix[2, N_subj * N] z;
  z = pmx_integrate_ode_group_rk45(dz_dt, z_init, 0, len, ts, theta,
    ↪ rep_array(rep_array(0.0, 0), N_subj), rep_array(rep_array(0, 0), N_subj));
}
model {
  for (isub in 1:N_subj) {
    theta[isub, {1, 3}] ~ normal(1, 0.5);
    theta[isub, {2, 4}] ~ normal(0.05, 0.05);
    sigma[isub] ~ lognormal(-1, 1);
    z_init[isub] ~ lognormal(10, 1);
    for (k in 1:2) {
      y0[isub, k] ~ lognormal(log(z_init[isub, k]), sigma[isub, k]);
      y[isub, , k] ~ lognormal(log(z[k, ((isub-1)*N + 1):(isub*N)]), sigma[isub, k]);
    }
  }
}

```

#### 4.7. Univariate integral of a quadratic function

integral of a quadratic function. This example shows how to use `univariate_integral_rk45` to calculate the integral of a quadratic function.

```

functions {
  real fun_ord2(real t, real[] theta, real[] x_r, int[] x_i) {
    real a = 2.3;
    real b = 2.0;
    real c = 1.5;
    real res;
    res = a + b * t + c * t * t;
    return res;
  }
}
data {
  real t0;
}

```

```

    real t1;
    real dtheta[2];
    real x_r[0];
    int x_i[0];
}
transformed data {
    real univar_integral;
    univar_integral = univariate_integral_rk45(func, t0, t1, dtheta,
                                              x_r, x_i);
}
/* ... */

```

#### 4.8. Linear interpolation

This example illustrates how to use `linear_interpolationi` to fit a piecewise linear function to a data set consisting of  $(x, y)$  pairs.

```

data{
    int nObs;
    real xObs[nObs];
    real yObs[nObs];
    int nx;
    int nPred;
    real xPred[nPred];
}

transformed data{
    real xmin = min(xObs);
    real xmax = max(xObs);
}

parameters{
    real y[nx];
    real<lower = 0> sigma;
    simplex[nx - 1] xSimplex;
}

transformed parameters{
    real yHat[nObs];
    real x[nx];

    x[1] = xmin;
    x[nx] = xmax;
    for(i in 2:(nx-1))
        x[i] = x[i-1] + xSimplex[i-1] * (xmax - xmin);

    yHat = linear_interpolation(xObs, x, y);
}

model{
    xSimplex ~ dirichlet(rep_vector(1, nx - 1));
    y ~ normal(0, 25);
    yObs ~ normal(yHat, sigma);
}

generated quantities{
    real yHatPred[nPred];
    real yPred[nPred];

    yHatPred = linear_interpolation(xPred, x, y);
    for(i in 1:nPred)
        yPred[i] = normal_rng(yHatPred[i], sigma);
}

```

### 4.9. Effect Compartment Population Model

Here we expand the example in 3.2 to a population model fitted to the combined data from phase I and phase IIa studies. The parameters exhibit inter-individual variations (IIV), due to both random effects and to the patients' body weight, treated as a covariate and denoted  $bw$ .

#### 4.9.1. Population Model for Plasma Drug Concentration $c$ .

$$\begin{aligned}
 \log(c_{ij}) &\sim N(\log(\hat{c}_{ij}), \sigma^2), \\
 \hat{c}_{ij} &= f_{2cpt}(t_{ij}, D_j, \tau_j, CL_j, Q_j, V_{1j}, V_{2j}, k_{aj}), \\
 \log(CL_j, Q_j, V_{ssj}, k_{aj}) &\sim N\left(\log\left(\widehat{CL}\left(\frac{bw_j}{70}\right)^{0.75}, \widehat{Q}\left(\frac{bw_j}{70}\right)^{0.75}, \widehat{V}_{ss}\left(\frac{bw_j}{70}\right), \widehat{k}_a\right), \Omega\right), \\
 V_{1j} &= f_{V_1} V_{ssj}, \\
 V_{2j} &= (1 - f_{V_1}) V_{ssj}, \\
 (\widehat{CL}, \widehat{Q}, \widehat{V}_{ss}, \widehat{k}_a, f_{V_1}) &= (10 \text{ L/h}, 15 \text{ L/h}, 140 \text{ L}, 2 \text{ h}^{-1}, 0.25), \\
 \Omega &= \begin{pmatrix} 0.25^2 & 0 & 0 & 0 \\ 0 & 0.25^2 & 0 & 0 \\ 0 & 0 & 0.25^2 & 0 \\ 0 & 0 & 0 & 0.25^2 \end{pmatrix}, \\
 \sigma &= 0.1
 \end{aligned}$$

Furthermore we add a fourth compartment in which we measure a PD effect(Figure 4.5).

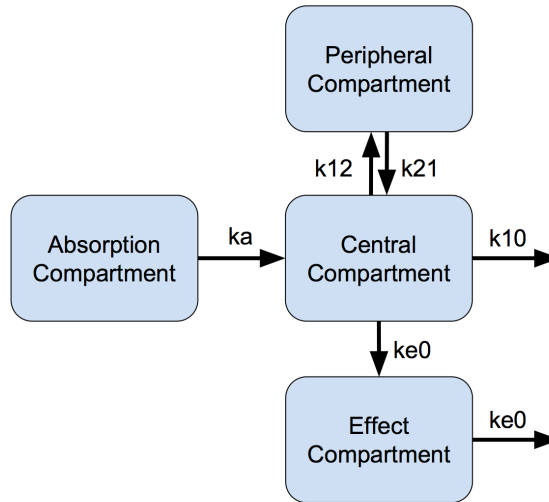


FIGURE 4.5. Effect Compartment Model

#### 4.9.2. Effect Compartment Model for PD response $R$ .

$$\begin{aligned}
 R_{ij} &\sim N\left(\widehat{R}_{ij}, \sigma_R^2\right), \\
 \widehat{R}_{ij} &= \frac{E_{max} c_{eij}}{EC_{50j} + c_{eij}}, \\
 c'_{e \cdot j} &= k_{e0j} (c_{\cdot j} - c_{e \cdot j}), \\
 \log(EC_{50j}, k_{e0j}) &\sim N\left(\log\left(\widehat{EC}_{50}, \widehat{k}_{e0}\right), \Omega_R\right), \\
 (E_{max}, \widehat{EC}_{50}, \widehat{k}_{e0}) &= (100, 100.7, 1), \\
 \Omega_R &= \begin{pmatrix} 0.2^2 & 0 \\ 0 & 0.25^2 \end{pmatrix}, \quad \sigma_R = 10.
 \end{aligned}$$

The PK and the PD data are simulated using the following treatment.

- Phase I study
  - Single dose and multiple doses
  - Parallel dose escalation design
  - 25 subjects per dose
  - Single doses: 5, 10, 20, and 40 mg
  - PK: plasma concentration of parent drug ( $c$ )
  - PD response: Emax function of effect compartment concentration ( $R$ )
  - PK and PD measured at 0.125, 0.25, 0.5, 0.75, 1, 2, 3, 4, 6, 8, 12, 18, and 24 hours
- Phase IIa trial in patients
  - 100 subjects
  - Multiple doses: 20 mg
  - sparse PK and PD data (3-6 samples per patient)

The model is simultaneously fitted to the PK and the PD data. For this effect compartment model, we construct a constant rate matrix and use `pmx_solve_linode`. Correct use of Torsten requires the user pass the entire event history (observation and dosing events) for an individual to the function. Thus the Stan model shows the call to `pmx_solve_linode` within a loop over the individual subjects rather than over the individual observations. Note that the correlation matrix  $\rho$  does not explicitly appear in the model, but it is used to construct  $\Omega$ , which parametrizes the PK IIV.

```

data{
  int<lower = 1> nSubjects;
  int<lower = 1> nt;
  int<lower = 1> nObs;
  int<lower = 1> iObs[nObs];
  real<lower = 0> amt[nt];
  int<lower = 1> cmt[nt];
  int<lower = 0> evid[nt];
  int<lower = 1> start[nSubjects];
  int<lower = 1> end[nSubjects];
  real<lower = 0> time[nt];
  vector<lower = 0>[nObs] cObs;
  vector[nObs] respObs;
  real<lower = 0> weight[nSubjects];
  real<lower = 0> rate[nt];
  real<lower = 0> ii[nt];
  int<lower = 0> addl[nt];
  int<lower = 0> ss[nt];
}

transformed data{
  vector[nObs] logCObs = log(cObs);
  int<lower = 1> nRandom = 5;
  int nCmt = 4;
}

```

```

    real biovar[nCmt] = rep_array(1.0, nCmt);
    real tlag[nCmt] = rep_array(0.0, nCmt);
}

parameters{
    real<lower = 0> CLHat;
    real<lower = 0> QHat;
    real<lower = 0> V1Hat;
    real<lower = 0> V2Hat;
    // real<lower = 0> kaHat;
    real<lower = (CLHat / V1Hat + QHat / V1Hat + QHat / V2Hat +
        sqrt((CLHat / V1Hat + QHat / V1Hat + QHat / V2Hat)^2 -
            4 * CLHat / V1Hat * QHat / V2Hat)) / 2> kaHat; // ka > lambda_1
    real<lower = 0> ke0Hat;
    real<lower = 0> EC50Hat;
    vector<lower = 0>[nRandom] omega;
    corr_matrix[nRandom] rho;
    real<lower = 0> omegaKe0;
    real<lower = 0> omegaEC50;
    real<lower = 0> sigma;
    real<lower = 0> sigmaResp;

    // reparameterization
    vector[nRandom] logtheta_raw[nSubjects];
    real logKe0_raw[nSubjects];
    real logEC50_raw[nSubjects];
}

transformed parameters{
    vector<lower = 0>[nRandom] thetaHat;
    cov_matrix[nRandom] Omega;
    real<lower = 0> CL[nSubjects];
    real<lower = 0> Q[nSubjects];
    real<lower = 0> V1[nSubjects];
    real<lower = 0> V2[nSubjects];
    real<lower = 0> ka[nSubjects];
    real<lower = 0> ke0[nSubjects];
    real<lower = 0> EC50[nSubjects];
    matrix[nCmt, nCmt] K;
    real k10;
    real k12;
    real k21;
    row_vector<lower = 0>[nt] cHat;
    row_vector<lower = 0>[nObs] cHatObs;
    row_vector<lower = 0>[nt] respHat;
    row_vector<lower = 0>[nObs] respHatObs;
    row_vector<lower = 0>[nt] ceHat;
    matrix[nCmt, nt] x;

    matrix[nRandom, nRandom] L;
    vector[nRandom] logtheta[nSubjects];
    real logKe0[nSubjects];
    real logEC50[nSubjects];

    thetaHat[1] = CLHat;
    thetaHat[2] = QHat;
    thetaHat[3] = V1Hat;
    thetaHat[4] = V2Hat;
    thetaHat[5] = kaHat;

    Omega = quad_form_diag(rho, omega); // diag_matrix(omega) * rho * diag_matrix(omega)
    L = cholesky_decompose(Omega);

```

```

for(j in 1:nSubjects){
  logtheta[j] = log(thetaHat) + L * logtheta_raw[j];
  logKe0[j] = log(ke0Hat) + logKe0_raw[j] * omegaKe0;
  logEC50[j] = log(EC50Hat) + logEC50_raw[j] * omegaEC50;

  CL[j] = exp(logtheta[j, 1]) * (weight[j] / 70)^0.75;
  Q[j] = exp(logtheta[j, 2]) * (weight[j] / 70)^0.75;
  V1[j] = exp(logtheta[j, 3]) * weight[j] / 70;
  V2[j] = exp(logtheta[j, 4]) * weight[j] / 70;
  ka[j] = exp(logtheta[j, 5]);
  ke0[j] = exp(logKe0[j]);
  EC50[j] = exp(logEC50[j]);

  k10 = CL[j] / V1[j];
  k12 = Q[j] / V1[j];
  k21 = Q[j] / V2[j];

  K = rep_matrix(0, nCmt, nCmt);

  K[1, 1] = -ka[j];
  K[2, 1] = ka[j];
  K[2, 2] = -(k10 + k12);
  K[2, 3] = k21;
  K[3, 2] = k12;
  K[3, 3] = -k21;
  K[4, 2] = ke0[j];
  K[4, 4] = -ke0[j];

  x[, start[j]:end[j]] = pmx_solve_linode(time[start[j]:end[j]], amt[start[j]:end[j]],
                                           rate[start[j]:end[j]], ii[start[j]:end[j]],
                                           evid[start[j]:end[j]], cmt[start[j]:end[j]],
                                           addl[start[j]:end[j]], ss[start[j]:end[j]], K,
                                           ↪ biovar, tlag);

  cHat[start[j]:end[j]] = 1000 * x[2, start[j]:end[j]] ./ V1[j];
  ceHat[start[j]:end[j]] = 1000 * x[4, start[j]:end[j]] ./ V1[j];
  respHat[start[j]:end[j]] = 100 * ceHat[start[j]:end[j]] ./
    (EC50[j] + ceHat[start[j]:end[j]]);
}

cHatObs = cHat[iObs];
respHatObs = respHat[iObs];
}

model{
  // Prior
  CLHat ~ lognormal(log(10), 0.2);
  QHat ~ lognormal(log(15), 0.2);
  V1Hat ~ lognormal(log(30), 0.2);
  V2Hat ~ lognormal(log(100), 0.2);
  kaHat ~ lognormal(log(5), 0.25);
  ke0Hat ~ lognormal(log(10), 0.25);
  EC50Hat ~ lognormal(log(1.0), 0.2);
  omega ~ normal(0, 0.2);
}

```

**4.9.3. Results.** We use the same diagnosis tools as for the previous examples. Table 4.1 summarises the statistics and diagnostics of the parameters. In particular, `rhat` for all parameters being close to 1.0 indicates convergence of the 4 chains. Figure 4.6 shows the posterior density of the parameters.

Posterior prediction check (PPC) in Figure 4.7-4.11 show that the fits to the plasma concentration are in close agreement with the data, notably for the sparse data case (phase IIa study). The fits to the PD data (Figure 4.12-4.16) look reasonable considering data being more noisy so the model produces larger credible intervals. Both the summary table and PPC plots show that the estimated values of the parameters are consistent with the values used to simulate the data.

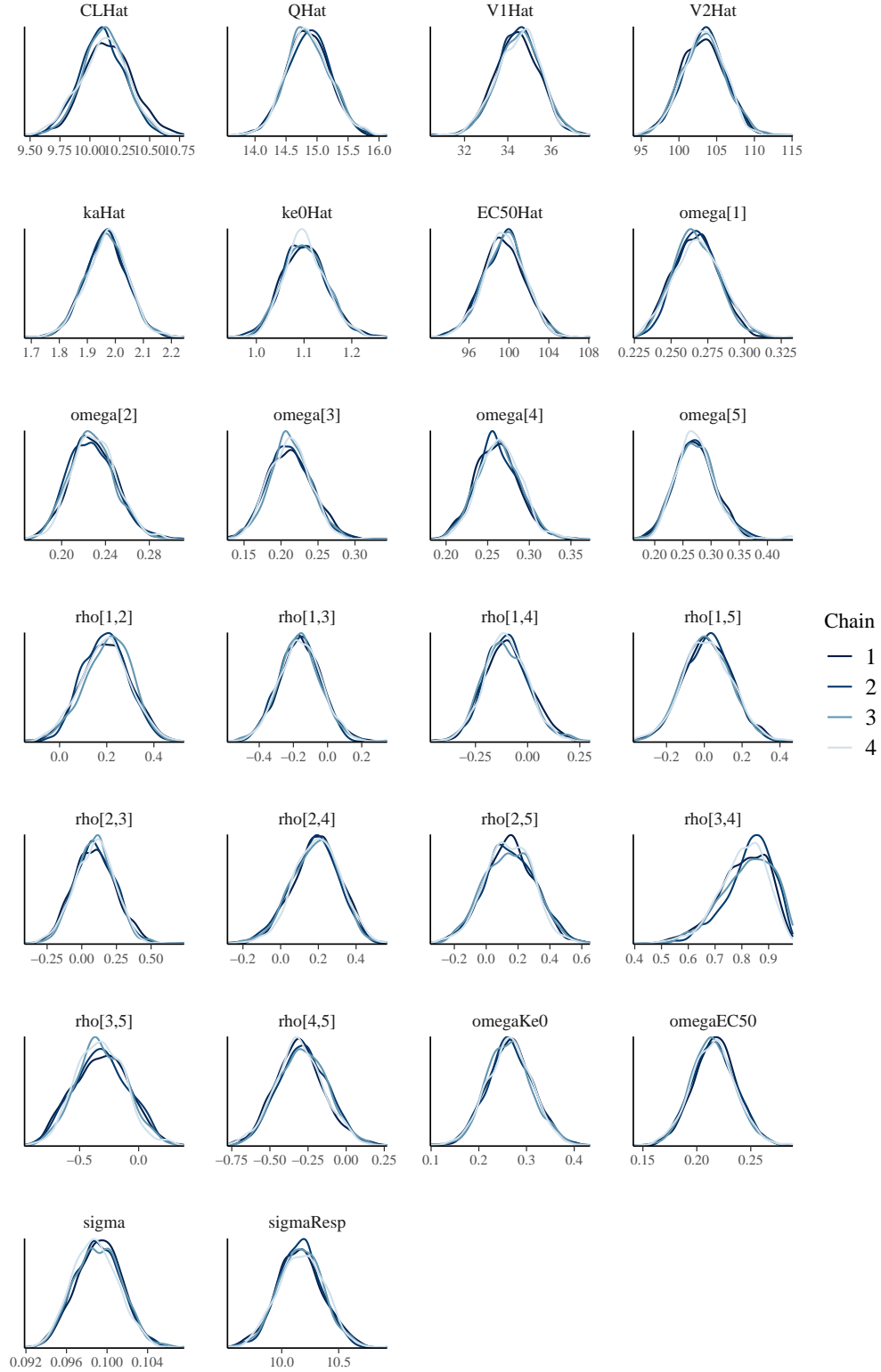


FIGURE 4.6. Posterior marginal densities of the model parameters of the effect compartment model.

TABLE 4.1. Summary of the MCMC simulations of the marginal posterior distributions of the model parameters for the effect compartment model example.

variable	mean	median	sd	mad	q5	q95	rhat	ess <sub>bulk</sub>	ess <sub>tail</sub>
CLHat	10.121	10.120	0.195	0.192	9.797	10.445	1.007	319.942	630.619
QHat	14.858	14.853	0.347	0.344	14.301	15.432	1.000	1106.126	1712.821
V1Hat	34.493	34.516	1.004	0.995	32.814	36.086	1.004	671.777	1563.396
V2Hat	103.269	103.291	2.876	2.878	98.568	108.019	1.002	1689.165	2580.382
kaHat	1.968	1.969	0.076	0.074	1.843	2.087	1.001	1204.531	1747.427
ke0Hat	1.102	1.100	0.046	0.045	1.030	1.180	1.001	4008.337	3167.030
EC50Hat	99.512	99.542	2.124	2.098	95.981	102.987	1.000	2557.436	2773.519
omega[1]	0.268	0.267	0.016	0.016	0.242	0.295	1.008	594.842	978.297
omega[2]	0.229	0.228	0.021	0.021	0.195	0.264	1.002	1245.453	1966.911
omega[3]	0.212	0.211	0.029	0.029	0.165	0.261	1.005	623.820	1692.248
omega[4]	0.263	0.262	0.026	0.026	0.221	0.306	1.002	1396.611	2260.425
omega[5]	0.272	0.271	0.036	0.035	0.217	0.335	1.008	293.132	728.867
rho[1,2]	0.197	0.200	0.100	0.101	0.029	0.360	1.003	1322.261	1955.862
rho[1,3]	-0.161	-0.161	0.122	0.121	-0.361	0.042	1.001	1609.160	2270.515
rho[1,4]	-0.101	-0.105	0.107	0.107	-0.270	0.083	1.001	1685.591	2353.498
rho[1,5]	0.016	0.015	0.128	0.128	-0.192	0.226	1.000	2039.767	2939.988
rho[2,3]	0.091	0.092	0.144	0.148	-0.143	0.328	1.008	718.187	1550.836
rho[2,4]	0.186	0.190	0.125	0.125	-0.025	0.384	1.005	948.704	1819.199
rho[2,5]	0.146	0.145	0.157	0.161	-0.111	0.402	1.003	626.620	1546.157
rho[3,4]	0.815	0.827	0.093	0.094	0.646	0.947	1.010	309.098	736.635
rho[3,5]	-0.318	-0.323	0.219	0.228	-0.678	0.055	1.016	200.806	607.958
rho[4,5]	-0.295	-0.299	0.161	0.162	-0.551	-0.019	1.008	546.998	1151.092
omegaKe0	0.265	0.265	0.047	0.047	0.188	0.346	1.001	1731.276	2049.892
omegaEC50	0.216	0.216	0.020	0.020	0.182	0.249	1.001	1599.567	1844.056
sigma	0.099	0.099	0.002	0.002	0.095	0.103	1.002	1726.283	2836.027
sigmaResp	10.165	10.166	0.198	0.198	9.844	10.495	1.002	4788.527	2923.203



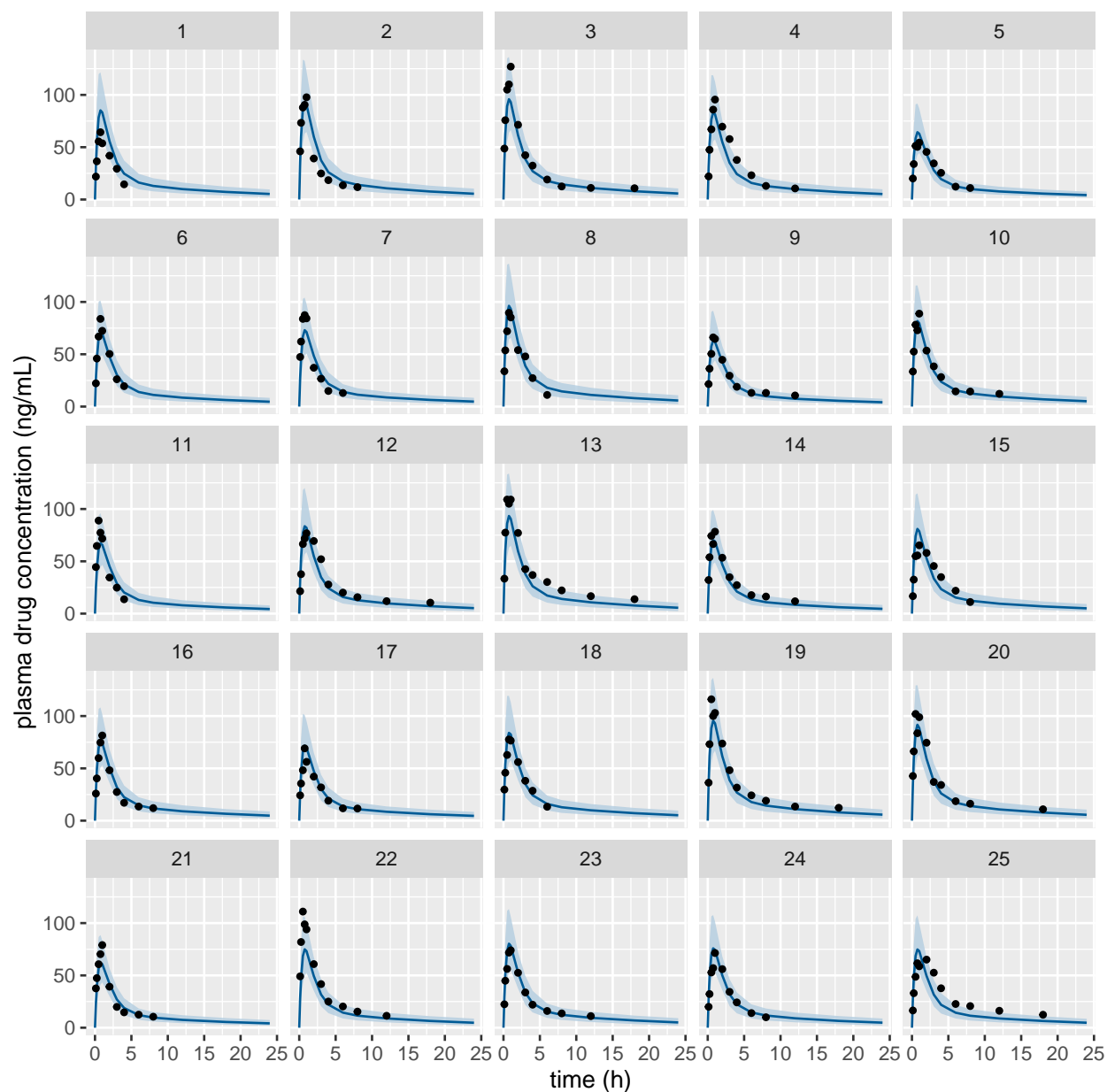


FIGURE 4.7. Predicted (90% credible interval and median) and observed individual plasma drug concentrations in study 1 (5mg dose).

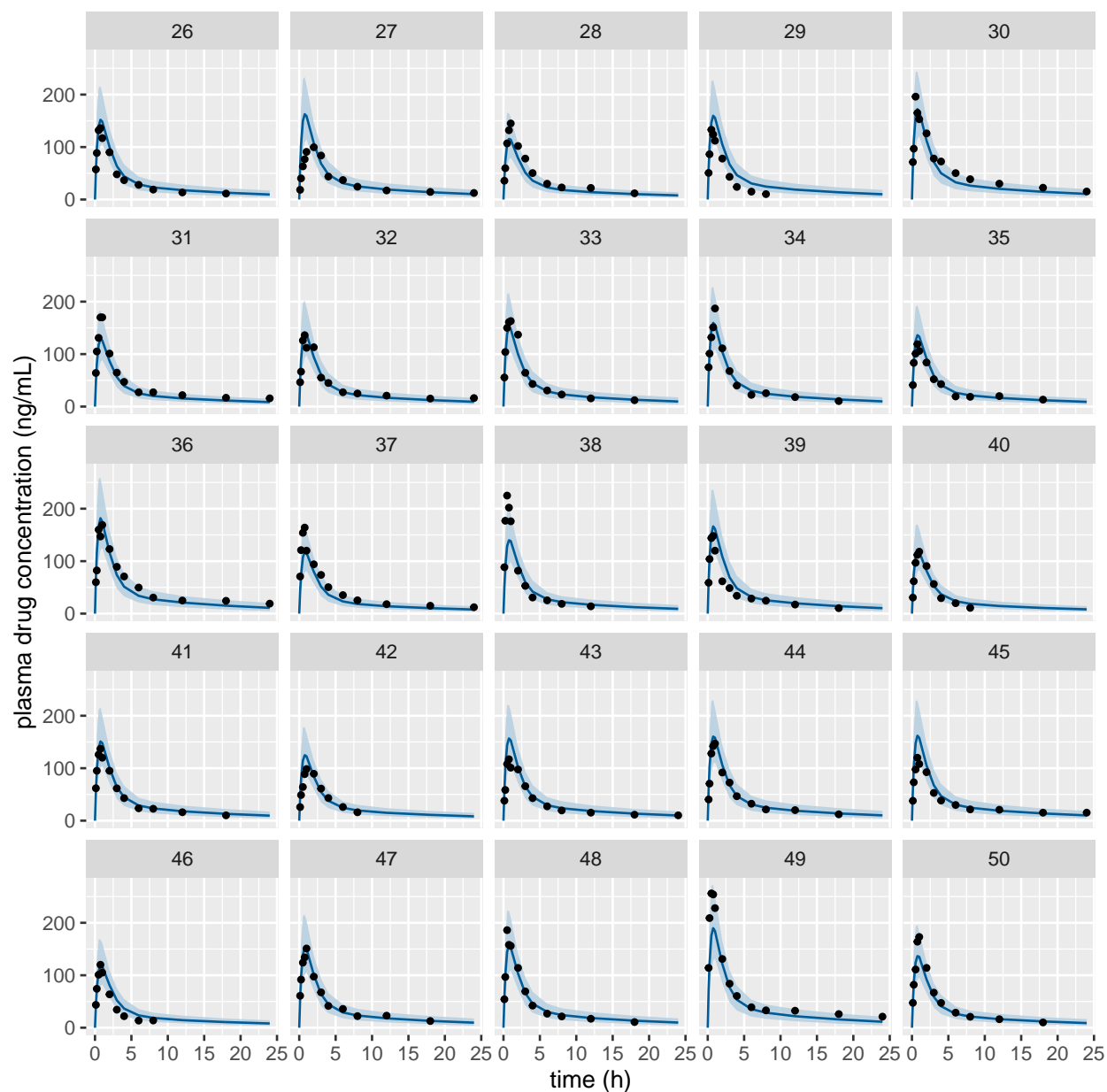


FIGURE 4.8. Predicted (90% credible interval and median) and observed individual plasma drug concentrations in study 1 (10mg dose).

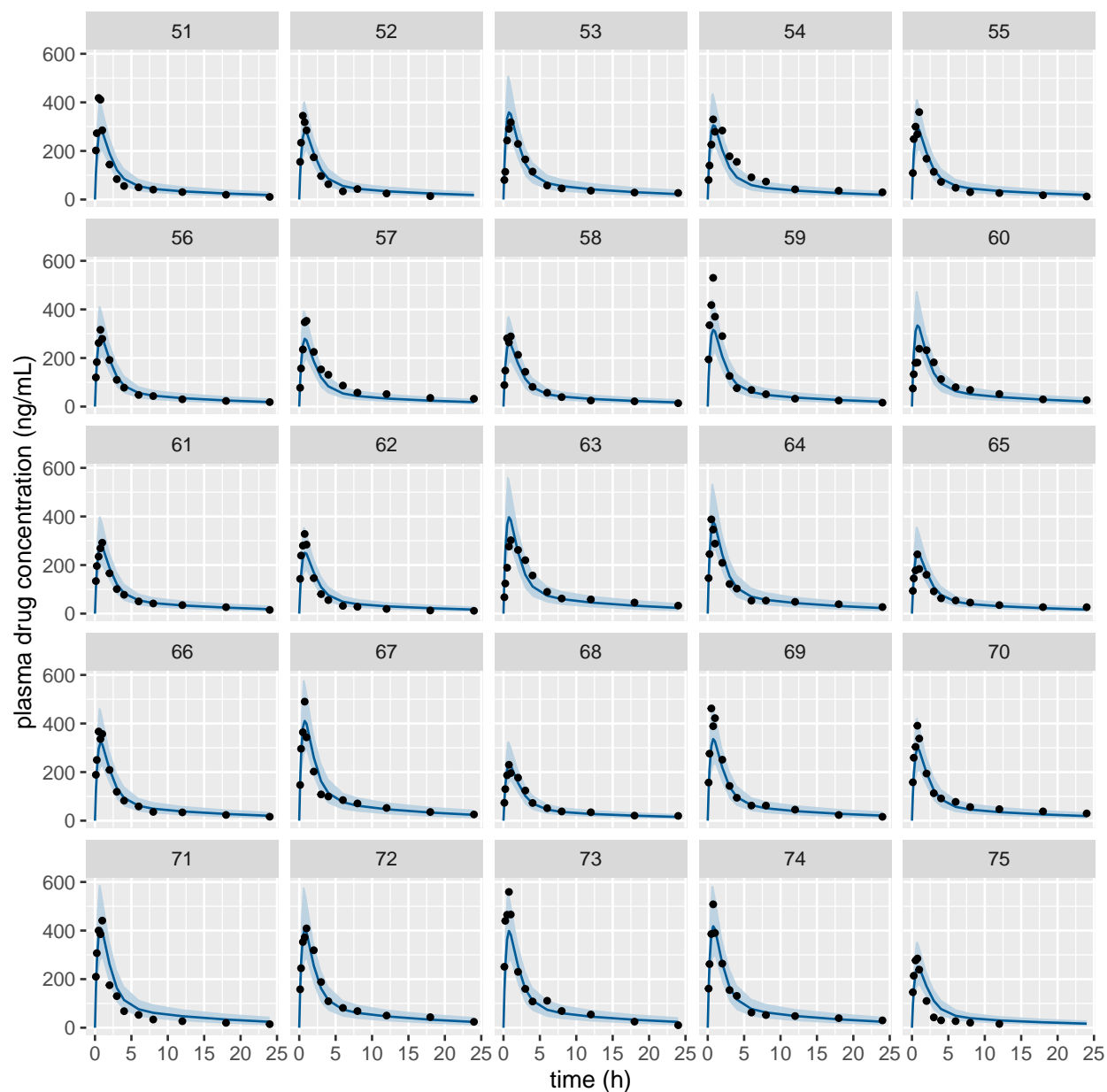


FIGURE 4.9. Predicted (90% credible interval and median) and observed individual plasma drug concentrations in study 1 (20mg dose).

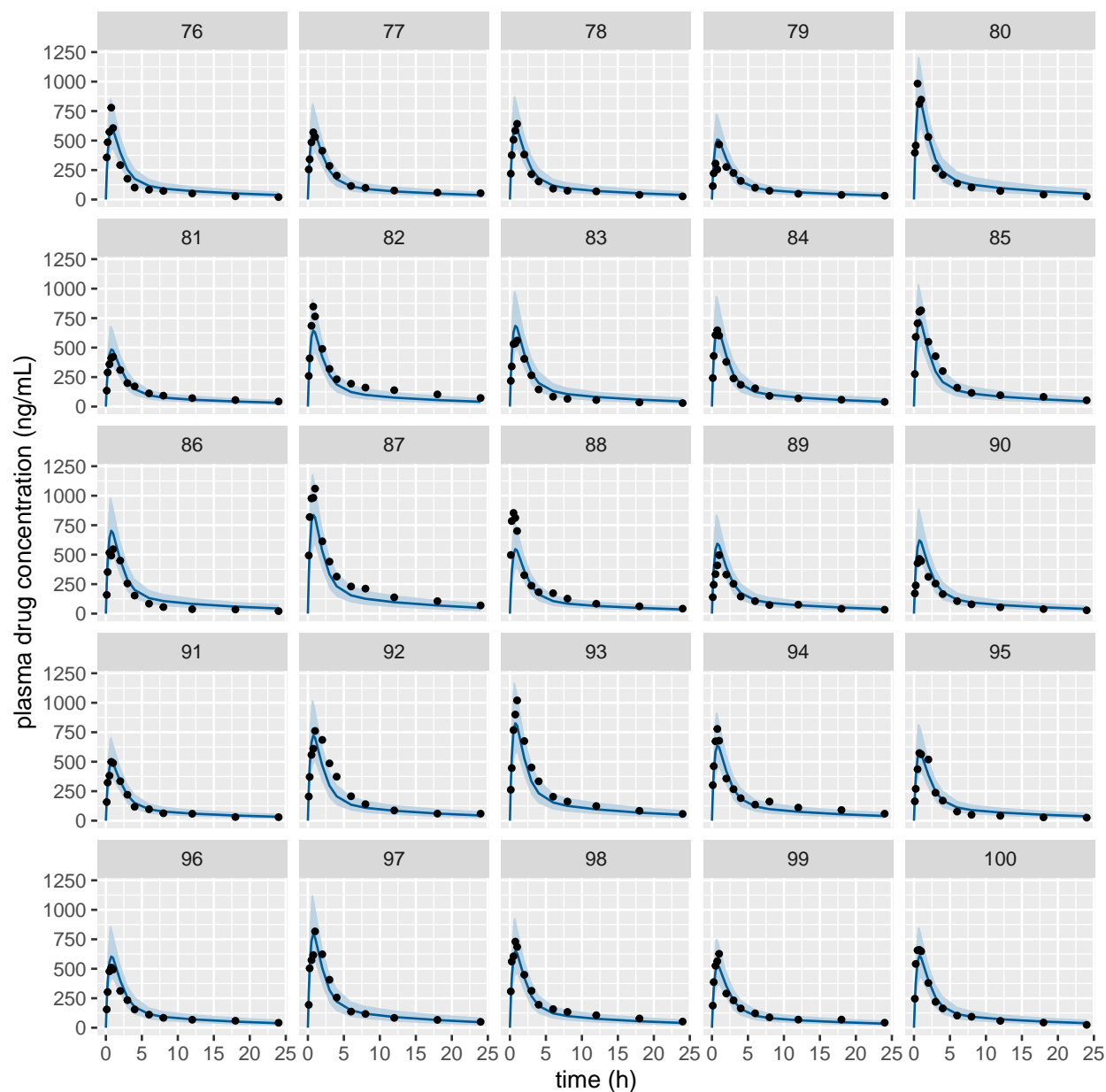


FIGURE 4.10. Predicted (90% credible interval and median) and observed individual plasma drug concentrations in study 1 (40mg dose).

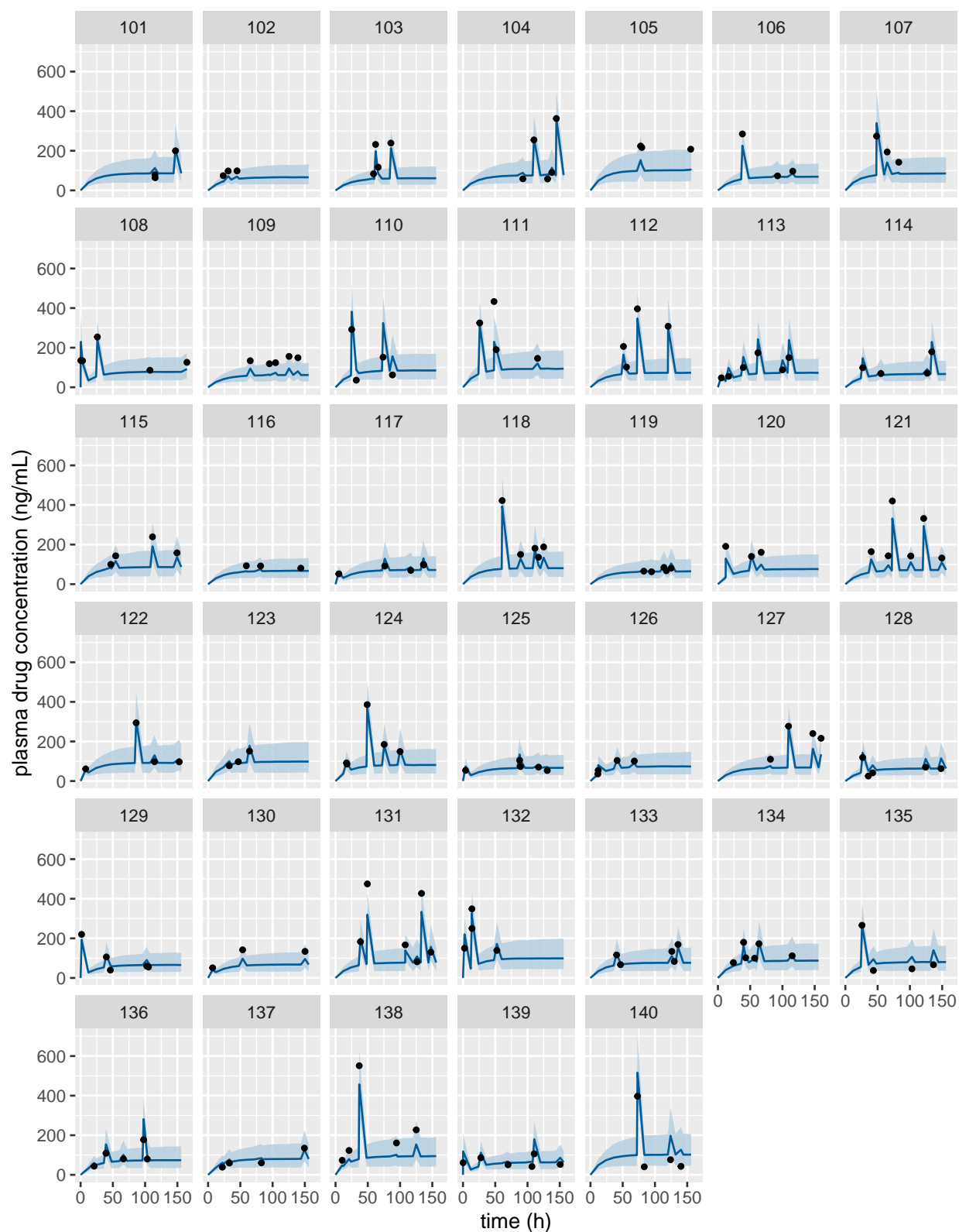


FIGURE 4.11. Predicted (90% credible interval and median) and observed individual plasma drug concentrations in study 2 (first 40 subjects).

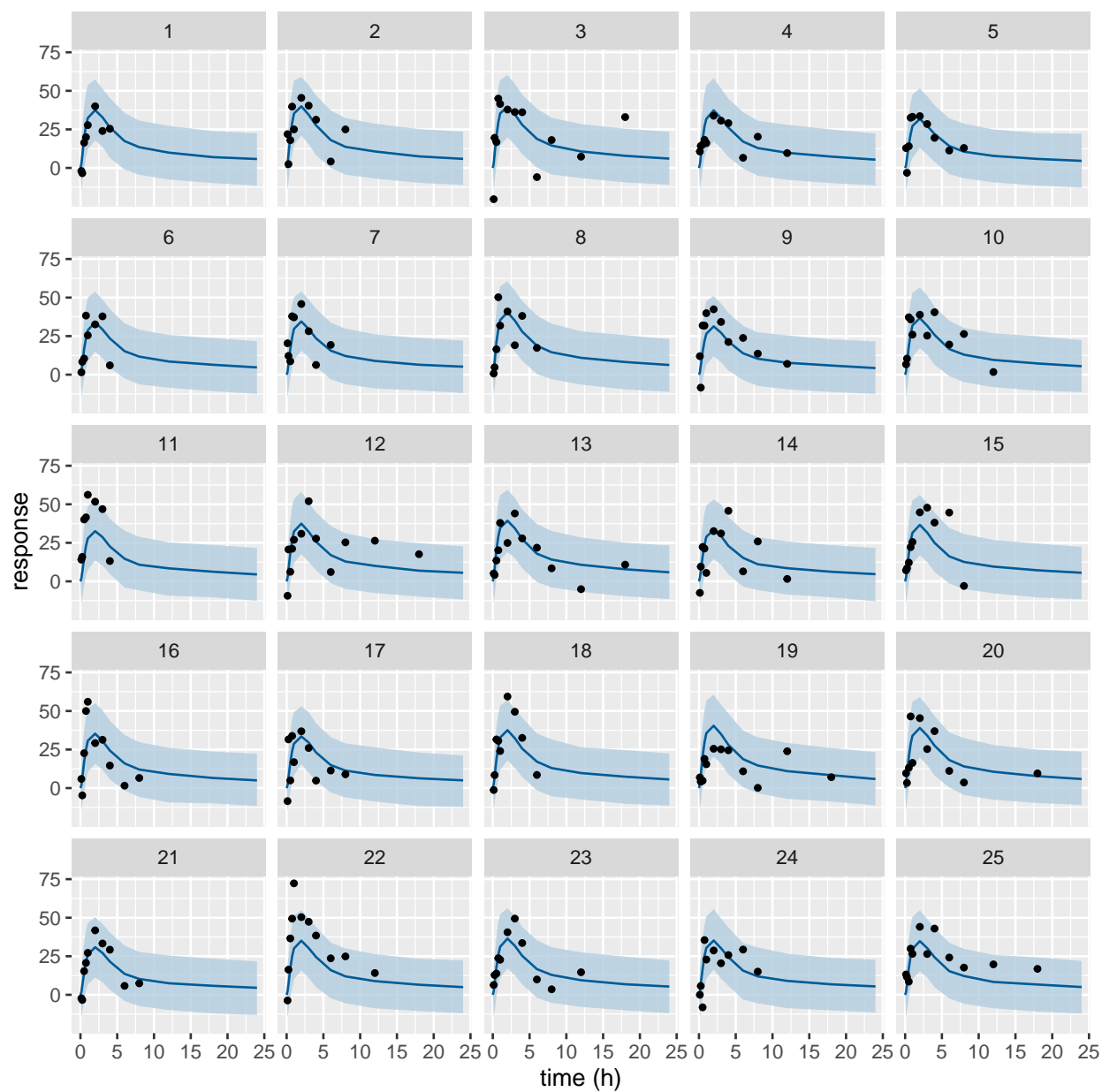


FIGURE 4.12. Predicted (90% credible interval and median) and observed individual PD response in study 1 (5mg dose).

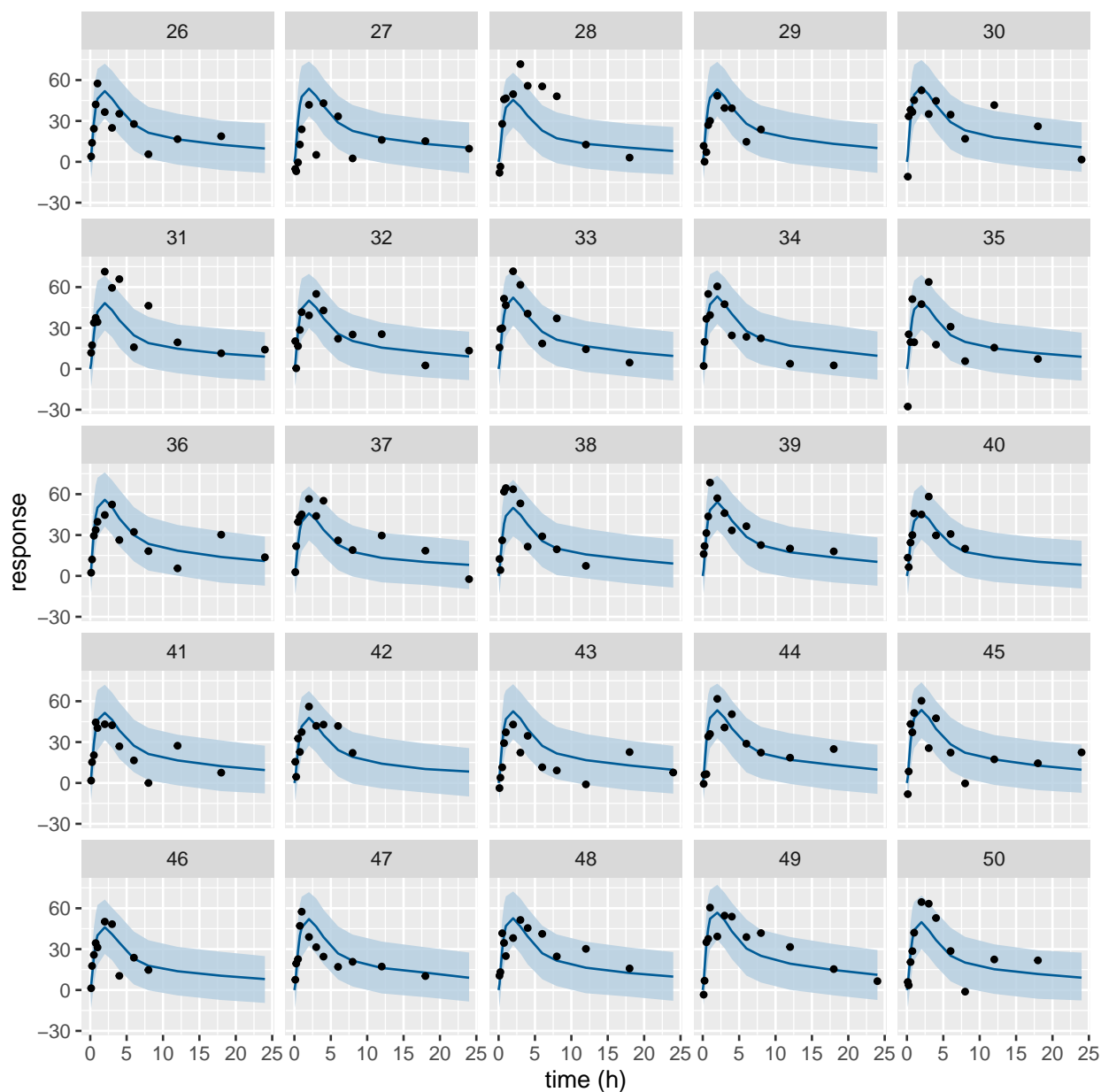


FIGURE 4.13. Predicted (90% credible interval and median) and observed individual PD response in study 1 (10mg dose).

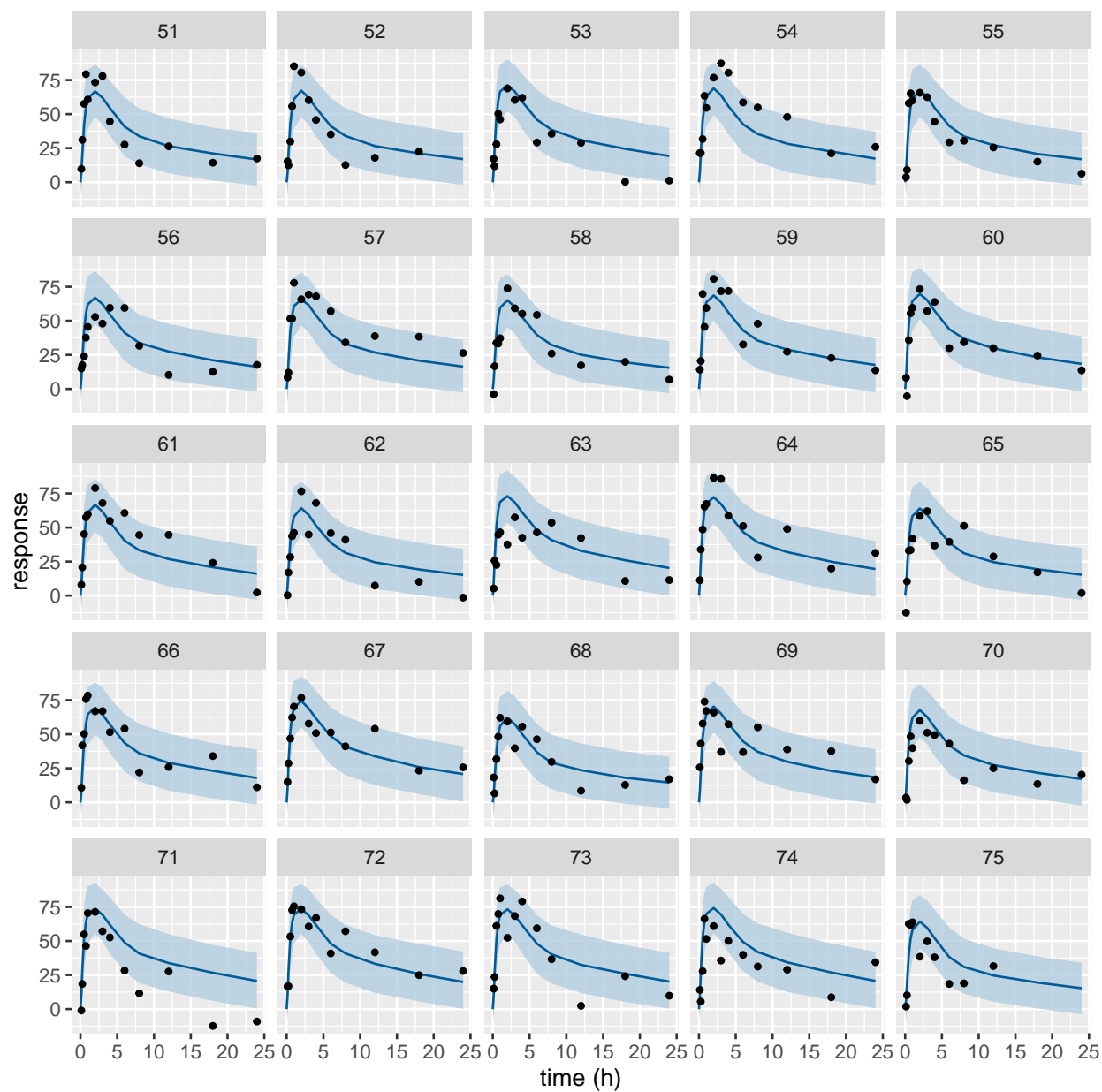


FIGURE 4.14. Predicted (90% credible interval and median) and observed individual PD response in study 1 (20mg dose).



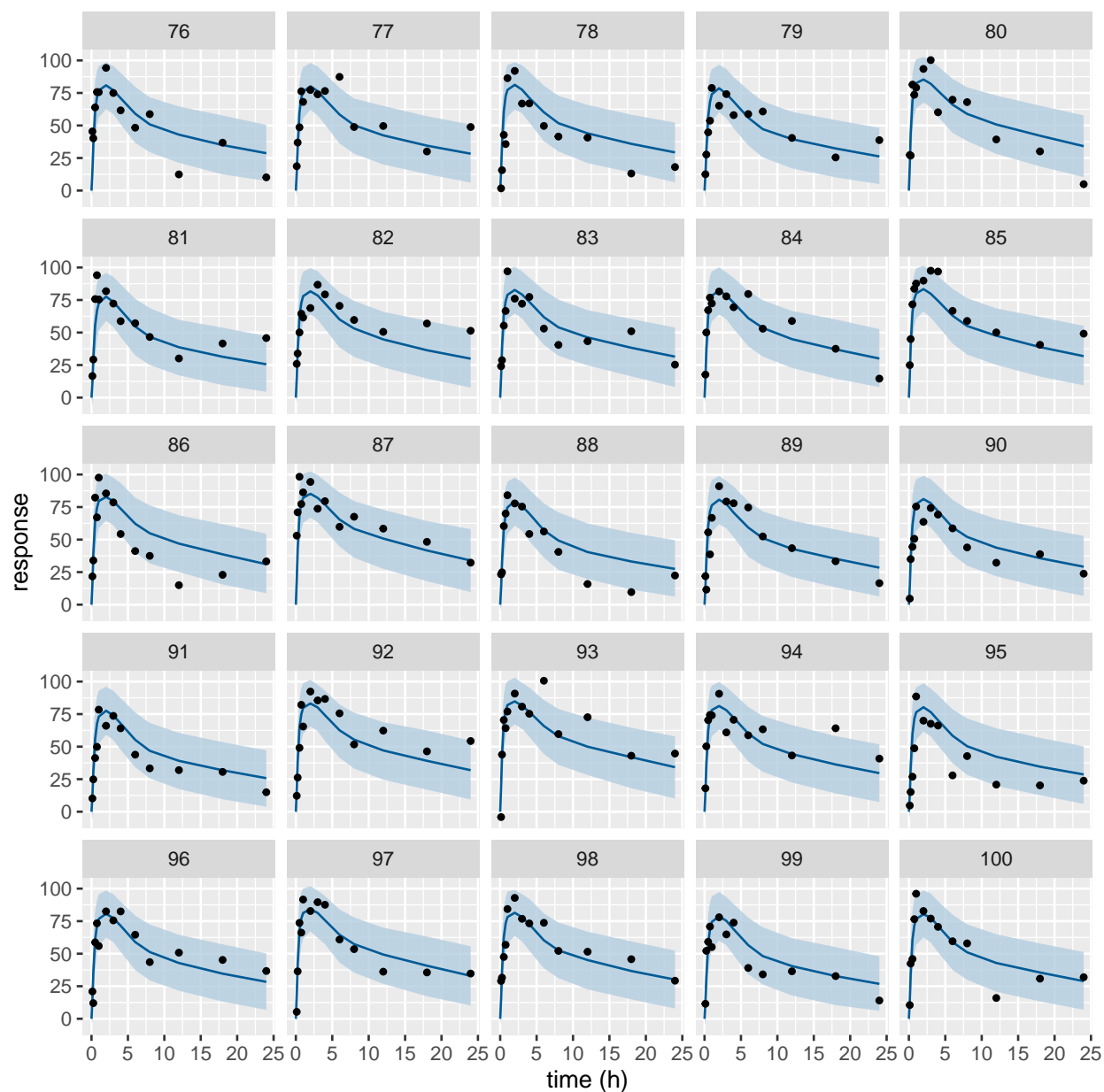


FIGURE 4.15. Predicted (90% credible interval and median) and observed individual PD response in study 1 (40mg dose).

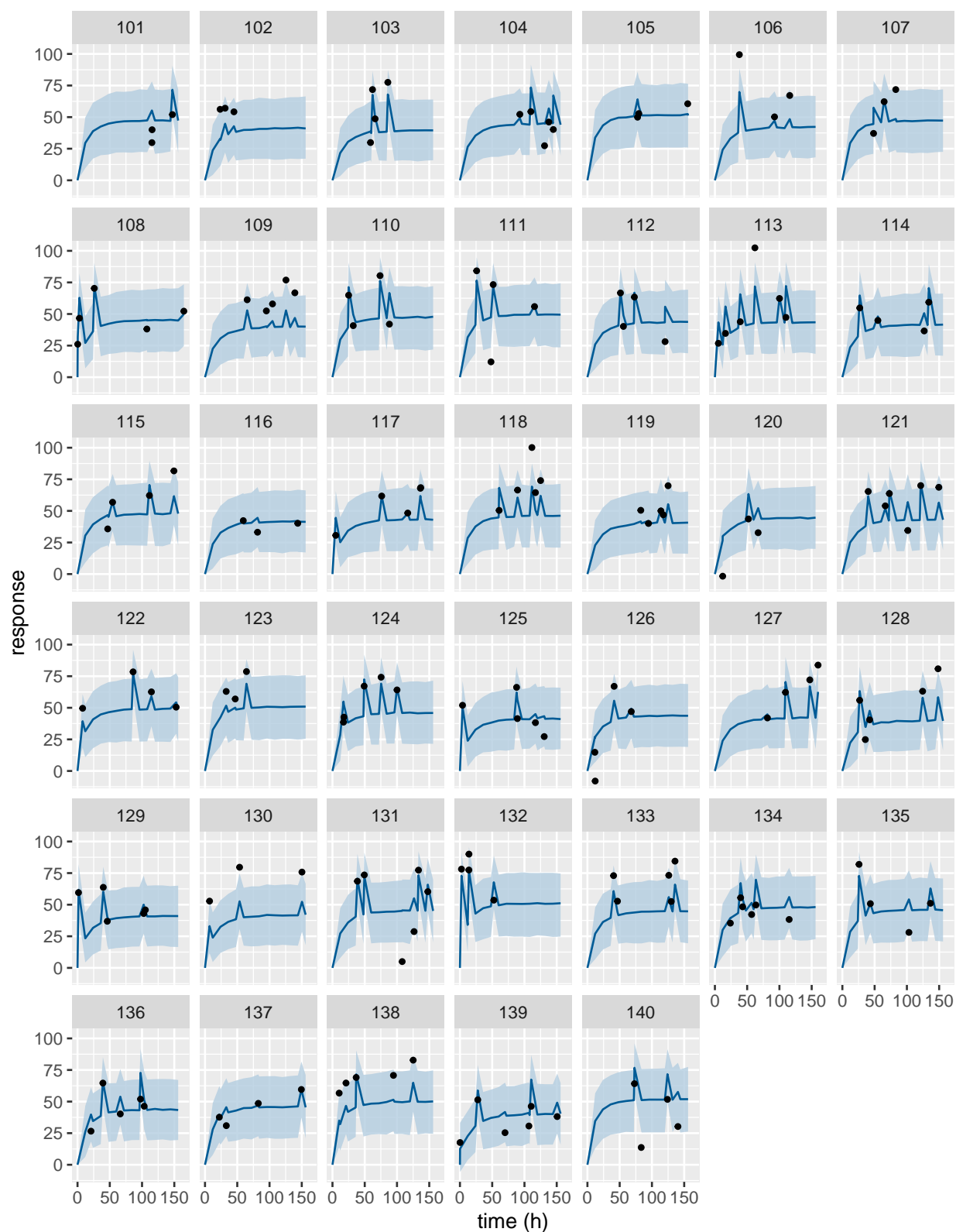


FIGURE 4.16. Predicted (90% credible interval and median) and observed individual PD response in study 2 (first 40 subjects).

#### 4.10. Friberg-Karlsson Semi-Mechanistic Population Model

We now return to the example in Section 4.4 and extend it to a population model. While we recommend using the coupled solver, and this time we solve it using group solver. We leave it as an exercise to the reader to rewrite the model with coupled solver.

##### 4.10.1. Friberg-Karlsson Population Model for drug-induced myelosuppression (*ANC*).

$$\begin{aligned} \log(ANC_{ij}) &\sim N(Circ_{ij}, \sigma_{ANC}^2), \\ \log(MTT_j, Circ_{0j}, \alpha_j) &\sim N\left(\log(\widehat{MTT}, \widehat{Circ_0}, \widehat{\alpha}), \Omega_{ANC}\right), \\ (\widehat{MTT}, \widehat{Circ_0}, \widehat{\alpha}, \gamma) &= (125, 5, 2, 0.17), \\ \Omega_{ANC} &= \begin{pmatrix} 0.2^2 & 0 & 0 \\ 0 & 0.35^2 & 0 \\ 0 & 0 & 0.2^2 \end{pmatrix}, \\ \sigma_{ANC} &= 0.1, \\ \Omega_{PK} &= \begin{pmatrix} 0.25^2 & 0 & a0 & 0 & 0 \\ 0 & 0.4^2 & 0 & 0 & 0 \\ 0 & 0 & 0.25^2 & 0 & 0 \\ 0 & 0 & 0 & 0.4^2 & 0 \\ 0 & 0 & 0 & 0 & 0.25^2 \end{pmatrix} \end{aligned}$$

The PK and the PD data are simulated using the following treatment.

- Phase IIa trial in patients
  - Multiple doses: 80,000 mg
  - Parallel dose escalation design
  - 15 subjects
  - PK: plasma concentration of parent drug (*c*)
  - PD response: Neutrophil count (*ANC*)
  - PK measured at 0.083, 0.167, 0.25, 0.5, 0.75, 1, 2, 3, 4, 6, 8, 12, 18, and 24 hours
  - PD measured once every two days for 28 days.

Once again, we simultaneously fit the model to the PK and the PD data. It pays off to construct informative priors. For instance, we could fit the PK data first, as was done in example 1, and get informative priors on the PK parameters. The PD parameters are drug independent, so we can use information from the neutropenia literature. In this example, we choose to use strongly informative priors on both PK and PD parameters.

The ODE is defined as

```
functions{
  real[] twoCptNeutModelODE(real t, real[] x, real[] parms, real[] rdummy, int[] idummy){
    real k10;
    real k12;
    real k21;
    real CL;
    real Q;
    real V1;
    real V2;
    real ka;
    real mtt;
    real circ0;
    real gamma;
    real alpha;
    real ktr;
    real dxdt[8];
    real conc;
    real EDrug;
```

```

real transit1;
real transit2;
real transit3;
real circ;
real prol;

CL = parms[1];
Q = parms[2];
V1 = parms[3];
V2 = parms[4];
ka = parms[5];
mtt = parms[6];
circ0 = parms[7];
gamma = parms[8];
alpha = parms[9];

k10 = CL / V1;
k12 = Q / V1;
k21 = Q / V2;

ktr = 4 / mtt;

dxdt[1] = -ka * x[1];
dxdt[2] = ka * x[1] - (k10 + k12) * x[2] + k21 * x[3];
dxdt[3] = k12 * x[2] - k21 * x[3];
conc = x[2]/V1;
EDrug = alpha * conc;
// x[4], x[5], x[6], x[7] and x[8] are differences from circ0.
prol = x[4] + circ0;
transit1 = x[5] + circ0;
transit2 = x[6] + circ0;
transit3 = x[7] + circ0;
circ = fmax(machine_precision(), x[8] + circ0); // Device for implementing a modeled
// initial condition

dxdt[4] = ktr * prol * ((1 - EDrug) * ((circ0 / circ)^gamma) - 1);
dxdt[5] = ktr * (prol - transit1);
dxdt[6] = ktr * (transit1 - transit2);
dxdt[7] = ktr * (transit2 - transit3);
dxdt[8] = ktr * (transit3 - circ);

return dxdt;
}
}

```

We use the `pmx_solve_group_rk45` function to solve the entire population's events.

```

transformed parameters{
  row_vector[nt] cHat;
  vector[nObsPK] cHatObs;
  row_vector[nt] neutHat;
  vector[nObsPD] neutHatObs;
  matrix[8, nt] x;
  real<lower = 0> parms[nSubjects, nTheta]; // The [1] indicates the parameters are constant

  // variables for Matt's trick
  vector<lower = 0>[nIIV] thetaHat;
  matrix<lower = 0>[nSubjects, nIIV] thetaM;

  // Matt's trick to use unit scale
  thetaHat[1] = CLHat;
  thetaHat[2] = QHat;
  thetaHat[3] = V1Hat;

```

```

thetaHat[4] = V2Hat;
thetaHat[5] = mttHat;
thetaHat[6] = circ0Hat;
thetaHat[7] = alphaHat;
thetaM = (rep_matrix(thetaHat, nSubjects) .*
          exp(diag_pre_multiply(omega, L * etaStd)))';

for(i in 1:nSubjects) {
  parms[i, 1] = thetaM[i, 1] * (weight[i] / 70)^0.75; // CL
  parms[i, 2] = thetaM[i, 2] * (weight[i] / 70)^0.75; // Q
  parms[i, 3] = thetaM[i, 3] * (weight[i] / 70); // V1
  parms[i, 4] = thetaM[i, 4] * (weight[i] / 70); // V2
  parms[i, 5] = kaHat; // ka
  parms[i, 6] = thetaM[i, 5]; // mtt
  parms[i, 7] = thetaM[i, 6]; // circ0
  parms[i, 8] = gamma;
  parms[i, 9] = thetaM[i, 7]; // alpha
}

/* group solver */
x = pmx_solve_group_rk45(twoCptNeutModelODE, 8, len,
                        time, amt, rate, ii, evid, cmt, addl, ss,
                        parms,
                        1e-6, 1e-6, 500);

for(i in 1:nSubjects) {
  cHat[start[i]:end[i]] = x[2, start[i]:end[i]] / parms[i, 3]; // divide by V1
  neutHat[start[i]:end[i]] = x[8, start[i]:end[i]] + parms[i, 7]; // Add baseline
}

for(i in 1:nObsPK) cHatObs[i] = cHat[iObsPK[i]];
for(i in 1:nObsPD) neutHatObs[i] = neutHat[iObsPD[i]];
}

```

This allows us to use within-chain parallelisation to reduce simulation time. When run from cmdstan, each MPI run generates one chain, and we use 4 MPI runs to generate 4 chains.

```

# chain 1
mpiexec -n nproc ./FribergKarlsson sample adapt delta=0.95 data file=fribergkarlsson.data.R
↳ init=fribergkarlsson.init.R random seed=8765 id=1 output file=output.1.csv
# chain 2
mpiexec -n nproc ./FribergKarlsson sample adapt delta=0.95 data file=fribergkarlsson.data.R
↳ init=fribergkarlsson.init.R random seed=8765 id=2 output file=output.2.csv
# chain 3
mpiexec -n nproc ./FribergKarlsson sample adapt delta=0.95 data file=fribergkarlsson.data.R
↳ init=fribergkarlsson.init.R random seed=8765 id=3 output file=output.3.csv
# chain 4
mpiexec -n nproc ./FribergKarlsson sample adapt delta=0.95 data file=fribergkarlsson.data.R
↳ init=fribergkarlsson.init.R random seed=8765 id=4 output file=output.4.csv

```

**4.10.2. Results.** Table 4.2 summarizes the sampling and some diagnostics output. estimation reflects the real value of the parameters (Table 4.2 and Figure 4.17. Similar to the previous example, PPCs shown in Figure 4.18 and 4.19 indicate the model is a good fit.

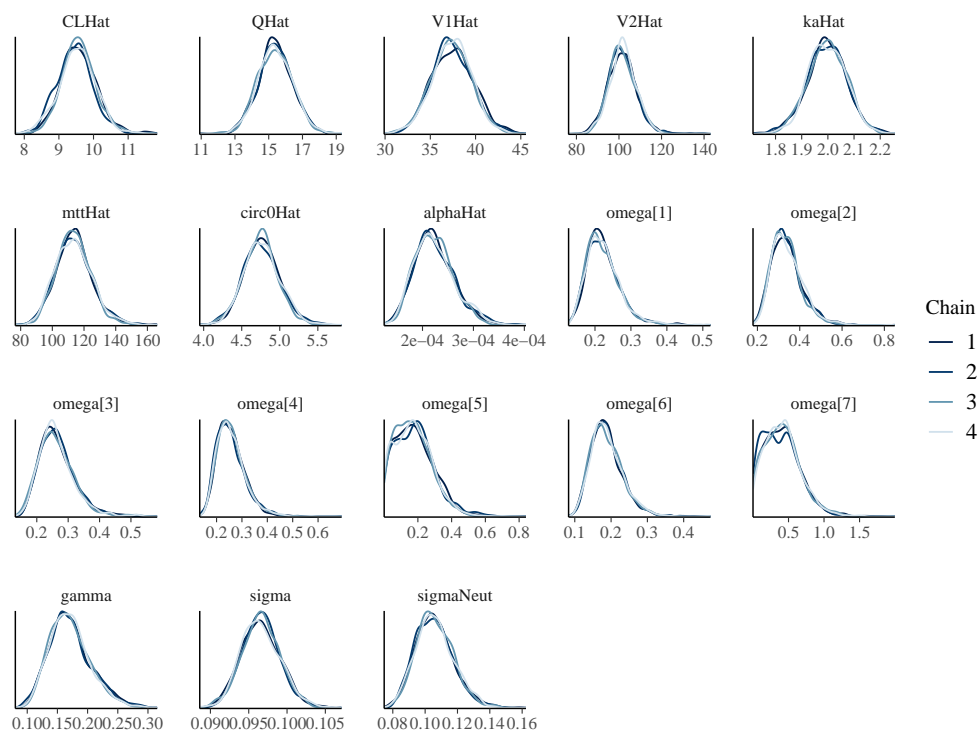


FIGURE 4.17. Posterior marginal densities of the model parameters of the Friberg-Karlsson population model.

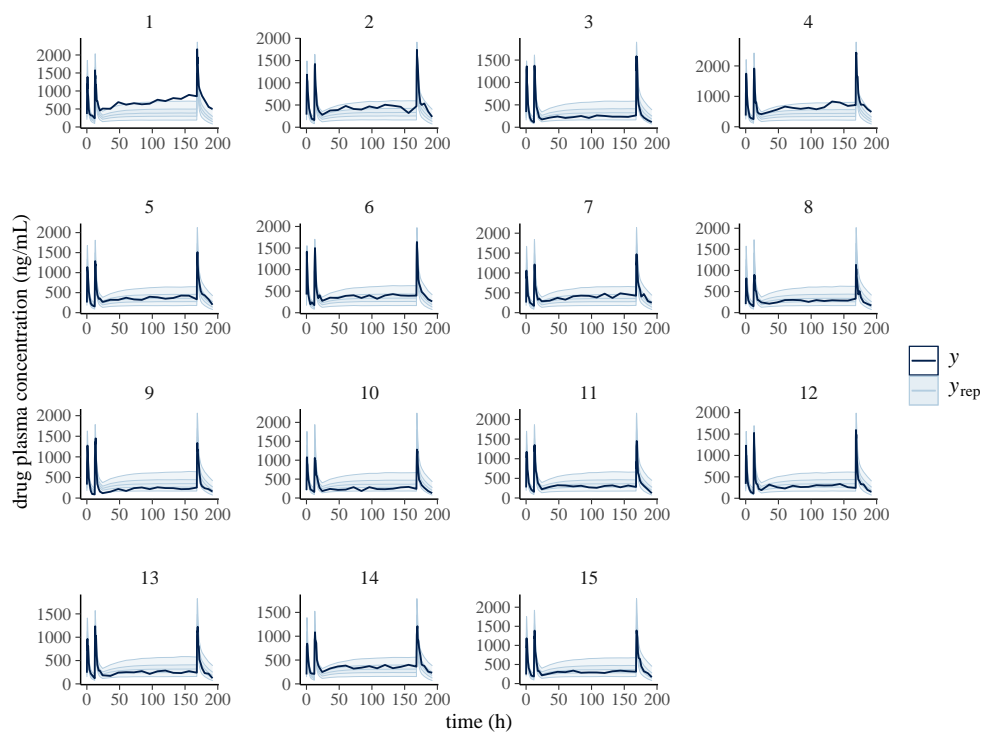


FIGURE 4.18. Predicted (50%, 90% credible interval and median) and observed individual drug plasma concentration.

TABLE 4.2. Summary of the MCMC simulations of the marginal posterior distributions of the model parameters for the Friberg-Karlsson population model example.

variable	mean	median	sd	mad	q5	q95	rhat	essbulk	esstail
CLHat	9.539	9.535	0.522	0.487	8.692	10.401	1.006	971.369	1655.449
QHat	15.401	15.386	1.018	1.000	13.742	17.090	1.000	2263.843	2447.006
V1Hat	37.396	37.360	2.244	2.228	33.762	41.058	1.001	1936.476	2372.815
V2Hat	101.698	101.394	6.503	6.119	91.529	112.538	1.001	2580.227	2592.925
kaHat	1.997	1.997	0.074	0.074	1.873	2.115	1.001	7056.877	2993.406
mttHat	113.681	113.204	11.506	10.910	95.807	133.514	1.001	4255.900	3269.646
circ0Hat	4.760	4.752	0.241	0.229	4.375	5.163	1.002	3774.920	2783.663
omega[1]	0.223	0.217	0.047	0.042	0.160	0.307	1.000	1751.864	2235.607
omega[2]	0.339	0.329	0.073	0.067	0.239	0.473	1.001	2363.843	2607.056
omega[3]	0.264	0.256	0.057	0.051	0.186	0.367	1.002	2128.660	2018.425
omega[4]	0.257	0.249	0.056	0.051	0.182	0.361	1.003	2293.877	2937.673
omega[5]	0.177	0.169	0.112	0.118	0.019	0.376	1.000	1550.483	2045.025
omega[6]	0.188	0.183	0.044	0.041	0.127	0.269	1.000	2377.698	2965.713
omega[7]	0.409	0.394	0.256	0.259	0.045	0.865	1.003	1386.987	2015.873
gamma	0.171	0.168	0.035	0.033	0.121	0.235	1.000	8809.668	3189.676
sigma	0.097	0.096	0.003	0.003	0.093	0.101	1.002	5436.508	2899.706
sigmaNeut	0.106	0.105	0.012	0.011	0.088	0.127	1.000	2809.059	3031.605
alphaHat	2.24e-4	2.19e-4	3.97e-05	3.80e-05	1.66e-4	2.96e-4	1.000	5138.105	2807.328

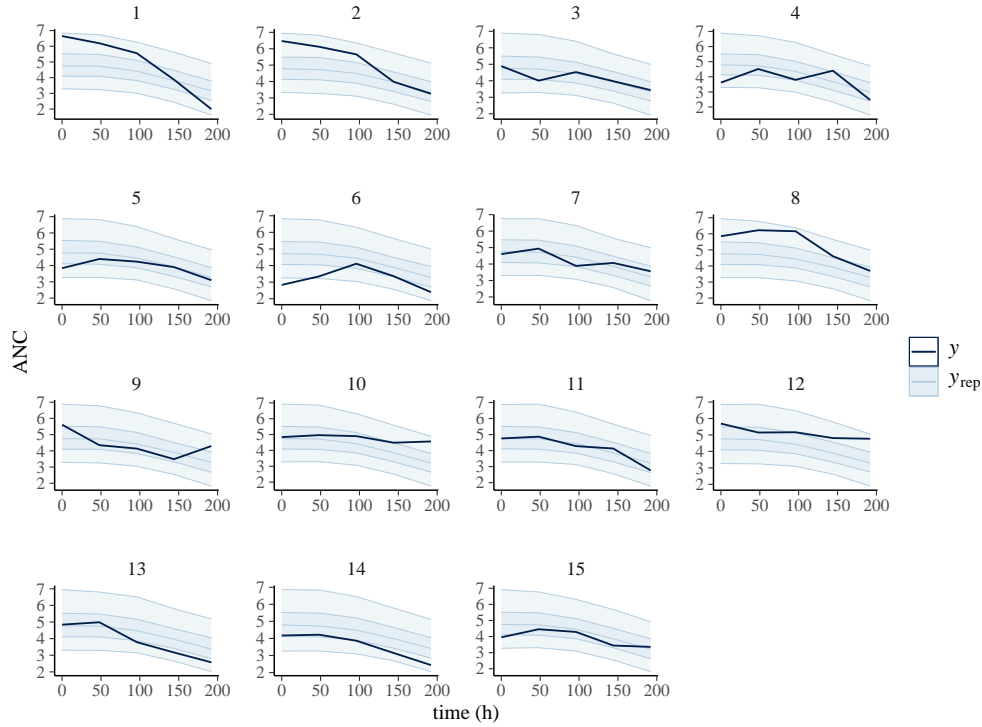


FIGURE 4.19. Predicted (50%, 90% credible interval and median) and observed individual Neutrophil counts.

## Compiling constants

Torsten uses compiling flags to control some solver behavior. These flags can be used in `cmdstan/make/local` file, or in `cmdstanr::set_make_local` function.

- **TORSTEN\_MPI=1** turns on within-chain parallelisation of MPI-enable functions. To use this option one must also point **TBB\_CXX\_TYPE** to proper C compiler. See also section 3.6.5 and 3.8.4.
- **TORSTEN\_CVS\_JAC\_DQ=1** makes BDF and Adams integrator use CVODES' default method to calculate Jacobian matrix in nonlinear solver [6].



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