

nlmixr: an R package for population PKPD modeling

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Welcome to population modeling with R

The fact that you are here suggest you have an interest to do population modeling in R ! Maybe you found this through our nlmixr website. Maybe via Twitter, LinkedIn, GitHub. Either way: **welcome and join us in our journey to do population modeling with R !**

This book is intended to get you started with nlmixr, an R package for Nonlinear Mixed Effects Models in Population Pharmacokinetics and Pharmacodynamics. You'll get information on the package itself, its installation, interesting use cases and more.

nlmixr is licensed under GPL-2 | GPL-3 [expanded from: GPL (≥ 2)].



Preface

In pharmacometrics there are several population pharmacokinetic and pharmacodynamic modeling software packages. The **nlmixr** R package was developed for fitting general dynamic models, pharmacokinetic (PK) models and pharmacokinetic-pharmacodynamic (PKPD) models in particular, with either individual data or population data. The interesting part about **nlmixr** is that it is open-source and the whole workflow of modeling can be done solely in R !

About this book

This book provides guidance to using **nlmixr** and serves as a first reference manual, without the intent to cover every aspect of modeling or **nlmixr**.

We assume readers have a background in pharmacometric modeling and know how to use R. Basic knowledge is required and assumed on installing other software packages, such as Python. The installation of **nlmixr** and related software and packages is described in Chapter 2.

Acknowledgements

We are thankful for the time people are willing to spend on this project. There have been various interactions and contributions on GitHub. We would like to thank

Chapter 1

Introduction

1.1 Prerequisites

There are several packages and pieces of software that together create an environment that enables you to use `nlmixr`.

These packages and software are:

- R (and related GUIs, such as RGui and `Rstudio`)
- Python - i.e., `SymPy`
- `RxODE`
- `nlmixr`

Related custom packages used by `nlmixr` are:

- `PreciseSums`
- `SnakeCharmer`

Packages to support the use of `nlmixr` are:

- `ShinyMixR`
- `xpose.nlmixr`

More on the installation of packages and software in Chapter 2.

1.2 Workflow

The ability to perform population modeling in R provides an opportunity to work via a single unified workflow for data management, data exploration, data analysis and report writing.

`nlmixr` can be used directly from the R command line and there is another option: `ShinyMixR`. This package provides a means to build a project-centric workflow around `nlmixr` from the R command line and from a streamlined `Shiny` application. This project tool was developed to enhance the usability and attractiveness of `nlmixr`, facilitating dynamic and interactive use in real-time for rapid model development. More on the use of `ShinyMixR` in Chapter 3.1.

Chapter 2

Installation

Needs rewrite because of the CRAN and GitHub versions of `RxODE` and `nlmixr`

`nlmixr` can be used on several platforms. The installation can be easy to challenging depending on the platform. We are in the process of making sure the installation works every time. Any help or suggestions are appreciated !

2.1 `nlmixr`

2.1.1 Windows installer

For those not interested in customized installation on Windows, we **recommend** you download a Windows installer for your platform from the following link

2.1.2 Installation on Windows

To replicate the environment that was used in Windows for `nlmixr` development, you will need administrator rights, and you should perform the following steps:

1. Install R 3.4.1 (or later) from the R website.
 - For best results, we suggest you use `C:\R\R-3.4.1`, but you can also use the default location (`C:\Program Files\R\R-3.4.1`) as well, if really needed.
 - For 64-bit Windows, it is best practice to include *only* the 64-bit version. If you include 32-bit files, some packages may not run correctly. Additionally, both the 32- and 64-bit binaries have to be compiled for every package. Similarly, if on 32-bit Windows, install only the 32-bit version of R (and Python, and Rtools).
2. Install the appropriate version of Rtools for Windows, currently version 3.4, from here.
 - This is an absolute requirement, since it includes C++ and related compilers not usually available under Windows.
 - For best results, use the default location of `c:\Rtools`
 - `RxODE`, a required component of `nlmixr`, checks and sets up the path based on the following:
 - a. `Rtools` is in the path (fastest and recommended option)

- b. `Rtools` was installed with information saved to the Windows registry, and `RxODE` can find the installation.
 - c. `Rtools` is on a hard drive installed in either `Rtools` or `RBuildTools`
 - If you are on 64-bit windows, please *do not install* the R 3.3.x 32-bit toolchain. These files can interfere with some packages that compile binaries, with unpredictable consequences. Similarly, only install 32-bit `Rtools` on 32-bit versions of Windows.
 - Make sure the compilers have been added to the Windows `PATH` environment variable, or `RxODE` and `nlmixr` will not work (this should be done automatically during installation).
3. Install a version of Python for Windows.
- This is used for its symbolic algebra package `SymPy`.
 - A very robust Python distribution that includes `SymPy` and many packages that may be useful to the data scientist and/or pharmacometrician is `Anaconda`. Although very straightforward and easy to install, it is quite a large download and contains much more than you will need to run `nlmixr`. When installing, use the Python 3.6 version. During the installation, `Anaconda` provides the option of adding itself to the `PATH` environment variable, but advises against it; please do this anyway (despite the red warning).
 - Another option is to use official Python, although you will need to install `SymPy` separately if you go this route, which is sometimes not straightforward under Windows 10 owing to folder permissions (see here for a few workarounds). Nonetheless, see here for instructions for installation from source or using `pip`. Note that if you approach us for support, we are going to recommend that you use `Anaconda`.
 - Regardless of the option you choose, please use like with like (64-bit Python for 64-bit Windows, for example).
 - Once again, make sure Python has been added to the Windows `PATH` environment variable, or `RxODE` and `nlmixr` will not work, no matter what `Anaconda` might say.
3. Install `devtools`.
- This package is required to install packages from Github, amongst other things.
 - This can be done from a clean R session by `install.packages("devtools")`.
4. Load `devtools` using `library(devtools)`.
5. Install `RxODE`.
- Currently the new version of `RxODE` is in the process of being uploaded to CRAN. `nlmixr` needs this newer version of `RxODE` to function correctly. To install this version, use the command: `install_github("nlmixrdevelopment/RxODE")`.
 - Once installed, type `RxODE::rxWinPythonSetup()` to install the required package `SnakeCharmR` and make sure Python and `SymPy` are working properly.
 - Restart your R session.
 - As a quick test, you can make sure that R and Python can communicate by typing the command `library(SnakeCharmR)`.
 - To validate or test the installation of `RxODE` completely, you can type the following `library(RxODE); rxTest()`; and it will run all of the unit tests in `RxODE` to make sure it is running correctly on your system. (Note that the `testthat` package is required for this, and it will take a long time.)
6. Install `nlmixr`.
- Load `devtools` again using `library(devtools)`
 - Install `nlmixr` by running `install_github("nlmixrdevelopment/nlmixr")`

2.1.3 Installation on Linux

Instructions for Ubuntu-like distributions are given here (specifically, Ubuntu 16.04 Xenial Xerus), but all current Linux distributions are supported, in principle.

1. Install R 3.4.1 (or later) from an appropriate repository (Ubuntu Xenial shown below, based on instructions provided here).
 - You will need administrator privileges (i.e. access to `sudo`). Provide your admin password when asked.
 - Add the official CRAN repository for Ubuntu: `sudo apt-key adv --keyserver keyserver.ubuntu.com --recv-keys E298A3A825C0D65DFD57CBB651716619E084DAB9`
 - Add the official CRAN repository for Ubuntu: `sudo add-apt-repository 'deb [arch=amd64,i386] https://cran.rstudio.com/bin/linux/ubuntu xenial/'`. If you aren't using Ubuntu Xenial, change `xenial` to match your distribution's codename.
 - Now refresh the package list using `sudo apt-get update`.
 - We can now install base R and required development libraries, and their dependencies: `sudo apt-get install r-base r-base-dev libssl-dev`
2. Install Python dependencies.
 - Enter this: `sudo apt-get install python-sympy python-pip python-setuptools python3-pip python-dev python3-dev`.
3. Install devtools and dependencies.
 - This package is required to install packages from Github, amongst other things.
 - Some Linux distributions don't include build tools out of the box. To be safe, check this: `sudo apt-get install build-essential`
 - Install devtools from a clean R session by entering `install.packages("devtools")`.
4. In R, load devtools using `library(devtools)`.
5. Install RxODE.
 - Currently the new version of RxODE is in the process of being uploaded to CRAN. `nlmixr` needs this newer version of RxODE to function correctly. To install this version, use the command: `install_github("nlmixrdevelopment/RxODE")`.
 - Install SnakeCharmR using `install_github("nlmixrdevelopment/SnakeCharmR")`.
 - Restart your R session.
 - As a quick test, you can make sure that R and Python can communicate by typing the command `library(SnakeCharmR)`.
 - To validate or test the installation of RxODE completely, you can type the following `library(RxODE); rxTest()`; and it will run all of the unit tests in RxODE to make sure it is running correctly on your system. (Note that the `testthat` package is required for this, and it will take a long time.)
6. Install `nlmixr`.
 - This can be done by `install_github("nlmixrdevelopment/nlmixr")`

2.1.4 Installation on macOS

Instructions for macOS 10.12 Sierra are provided here. They should be broadly extensible to all recent releases of macOS.

The general logic is to first install any external software and then install the R packages.

1. Check the Python version in the terminal: `python --version`. On macOS the standard version is 2.7, which is used by `nlmixr`. If there are other versions of Python available, set the `$PATH` to the 2.7 version and/or remove other versions of Python, if possible (this step can be a challenge).
2. Install R 3.4.1 (or later) from the R website.
 - Download and install `R-3.4.1.pkg` (or later) from CRAN.
3. Install Python dependencies.
 - Install `pip` from the macOS or RStudio terminal prompt: `sudo easy_install pip`.
 - Install `sympy` using `pip`: `sudo -H pip install sympy`.
4. Install build tools.
 - Install Xcode from the App Store.
 - Read the license by entering the following at the macOS terminal: `sudo xcodebuild -license`
 - Scroll through it all, reading it carefully, and type `agree` at the end. (If you don't, you can't use `nlmixr` or anything else that requires compilation on macOS. Don't yell at us, yell at Apple.)
 - Install `gfortran`: download the appropriate macOS installer from here and run it. Another option is to run the installation for the appropriate macOS version from the terminal by typing: `brew cask install gfortran` to automatically install the version of `gfortran` on macOS needed by R from the Terminal (Mac or RStudio).

Now install the R packages:

5. Install `devtools` and dependencies.
 - This package is required to install packages from Github, amongst other things.
 - Install `devtools` from a clean R session by entering `install.packages("devtools")`.
6. In R, load `devtools` using `library(devtools)`.
7. Install `RxODE`.
 - Currently the new version of `RxODE` is in the process of being uploaded to CRAN. `nlmixr` needs this newer version of `RxODE` to function correctly. To install this version, use the command: `install_github("nlmixrdevelopment/RxODE")` or use `install.packages('RxODE')`.
 - Install `SnakeCharmR` using `install_github("nlmixrdevelopment/SnakeCharmR")`.
 - Restart your R session.
 - As a quick test, you can make sure that R and Python can communicate by typing the command `library(SnakeCharmR)`.
 - `SnakeCharmR` wants to install the Python package `sympy` and the latest macOS version does not allow this (installation of packages cannot be done system wide and has to be done on user level). To do this, open the terminal (in macOS or Rstudio) and type: `pip install sympy --user` (the user flag is important !).

- To validate or test the installation of RxODE completely, you can type the following `library(RxODE); rxTest();` and it will run all of the unit tests in RxODE to make sure it is running correctly on your system. (Note that the `testthat` package is required for this, and it will take a long time.)

8. Install `nlmixr`.

- This can be done by `install_github("nlmixrdevelopment/nlmixr")` or `install.packages('nlmixr')`.

2.2 ShinyMixR: project management tool for nlmixr

A user-friendly tool was developed for `nlmixr` based on Shiny and `shinydashboards`, which facilitates a workflow around an `nlmixr` project.

This `ShinyMixR` package provides a means to build a project-centric workflow around `nlmixr` from the R command line and from a streamlined Shiny application. This project tool was developed to enhance the usability and attractiveness of `nlmixr`, facilitating dynamic and interactive use in real-time for rapid model development. More on the use of `ShinyMixR` in Chapter 3.1.

To install the package, use:

```
devtools::install_github("richardhooijmaijers/shinyMixR")
```


Chapter 3

nlmixr vignettes

Some *significant* applications are demonstrated in this chapter; the vignettes will be discussing the application in more depth.

3.1 ShinyMixR - project-centric interface

3.1.1 Introduction

The `nlmixr` package can be accessed through command line in `R` and `RStudio`, and through an graphical user interface `ShinyMixR` supported by the `nlmixr` team. Both command line and interface support the integration with `xpose.nlmixr`.

`ShinyMixR` aims to provide a user-friendly tool for `nlmixr` based on `Shiny`, which facilitates a workflow around an `nlmixr` project. It is build as a project-centric, instead of interface-centric, workflow around `nlmixr` from the `R` command line and from a streamlined `Shiny` application. The `shinydashboard` package was used to set up a structure for controlling and tracking runs with an `nlmixr` project, and was the basis for setting up the modular interface.

This project tool enhances the usability and attractiveness of `nlmixr`, facilitating dynamic and interactive use in real-time for rapid model development. In this project-oriented structure, the command line and dashboard can be used independently and/or interdependently. This means that many of the functions within the package can also be used outside the interface within an interactive `R` session.

Using the `ShinyMixR`, the user specifies and controls an `nlmixr` project workflow entirely in `R`. Within a project folder, a structure can be created to include separate folders for models, data and runs. Functionality is available to edit and run model code, summarize and compare model outputs in a tabular fashion, and view model development using a tree paradigm. Inputs, outputs and metadata are stored in relation to the model code within the project structure (a discrete `R` object) to ensure traceability.

Results are visualized by using modifications of existing packages (such as `xpose.nlmixr`, user-written functions and packages, or pre-existing plotting functionality included in the `ShinyMixR` package. Results are reported using the `R3port` package in pdf and html format.

How the package can be used and what the most important functions are, is described in this section. When working with this package, there are two important assumptions:

1. A specific folder structure is in place. The package uses this structure to read and write certain files (the folder structure can be generated automatically using the `create_proj` function).
2. Within a folder structure, multiple models can be present and is considered a “project”. The package creates and manages a project object which is available in the global environment.

An introduction on how to use the **ShinyMixR** interface can be found here. To get started, first install the package and use the library.

3.1.2 Getting started

To get started, first install the package using:

```
devtools::install_github("richardhooijmaijers/shinyMixR")
```

Be aware that the **nlmixr**, **nlmixr.xpose** and **R3port** package should be installed before installing **shinyMixR**, e.g.:

```
devtools::install_github("richardhooijmaijers/R3port")
devtools::install_github("nlmixrdevelopment/nlmixr")
devtools::install_github("nlmixrdevelopment/xpose.nlmixr")
```

The easiest way to get to know the package is to create the folder structure (which include some example models):

```
library(shinyMixR,quietly = TRUE)
create_proj()
```

By default, a folder structure is created within the current directory. The following folders are created:

- **analysis**: in this folder all plots and tables are saved in a structured way to make them accesible to the interface
- **data**: data files used by the models in R data format (.rds)
- **models**: models, available as separate R scripts according the unified user interface in **nlmixr**
- **scripts**: generic analysis scipts made available in the interface
- **shinyMixR**: folder used by the interface to store temporarily files and results files

The interface monitors what happens in these folders. This is important to know because new models and/or data can be copied into these folders or files can be removed. This will then be recognized within the app (after refreshing the overview). This way it is possible to work on data and models separately and plug it in to **shinyMixR** at a later stage.

Once there is a folder structure present the interface can be started:

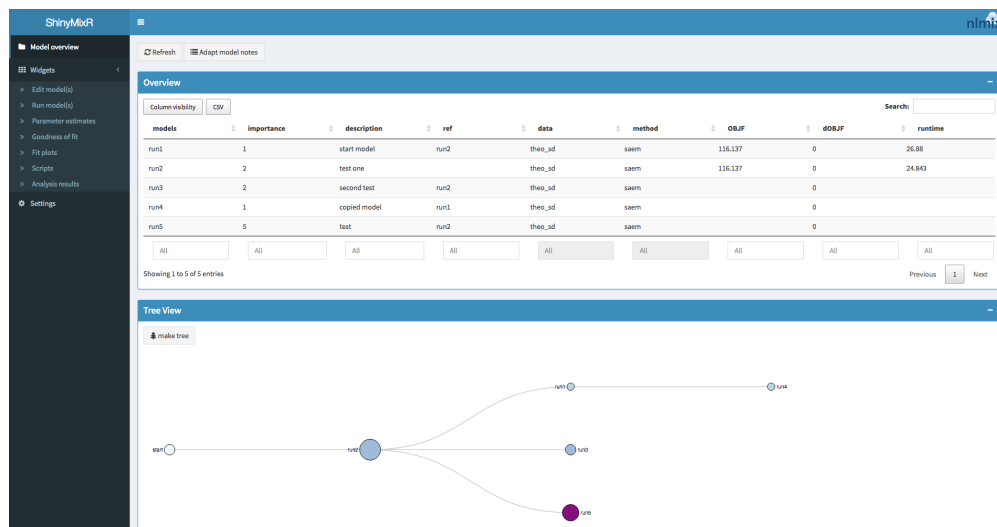
```
run_shinymixr(launch.browser = TRUE)
```

The interface will be started and a project object will be created in the global environment in which all information is kept/managed. If correct, the interface will open in the default browser and the following will be seen:

On the left side, there is sidebar with various menu items. The content of the main body will open with the model overview but will change based on the selected menu item in the sidebar. The sidebar can be collapsed by clicking the three lines in the top bar, providing more room for the main body.

3.1.3 Overview

The overview page can be used to see which models are present in a project, the relationship between models and to adapt model meta data. The overview can be exported to a CSV file and a selection of columns can be made that should be displayed (all using the **DT** package).



3.1.4 Edit models

The edit tab can be used to edit existing models within an editor including syntax coloring (using `shinyAce`). It is also possible to create new models using various templates or to duplicate existing models.

3.1.5 Run models

The run tab can be used to run models within a project. It is possible to run one or multiple models at once. Also it is possible to assess the intermediate output or progress for an nlmixr run.

3.1.6 Parameter estimates

The parameter estimates tab can be used to generate a table with parameter estimates. In case multiple models are selected the table will show the results of each run in a separate column. This page is reactive which means that in case a different model is selected, the table is directly updated. There is also the possibility to save the table to a latex/pdf or html file.

3.1.7 Goodness of fit

The goodness of fit tab can be used to generate a combination of 4 goodness of fit plots combined. By default nlmixr.xpose is used but direct ggplot can also be used by specifying this in the settings. Also here the plots can be saved to a latex/pdf or html file.

3.1.8 Fit plots

The fit plots tab can be used to generate a individual fit plots. The same options are present here as for the goodness of fit plots.

3.1.9 Scripts

It is possible to write your own scripts that can be used to analyse model results. This script can be used to process the result for one or multiple models at once (the interface will include the name of the selected models in the script). An example of how such a script will look like is included in the package.

Model(s)

run1 ▼

```

1 run1 <- function() {
2   data = "theo_sd"
3   desc = "start model"
4   ref = "run2"
5   imp = 1
6   est = "saem"
7   control<-list()
8   ini({
9     tka <- .5
10    tcl <- -3.2
11    tv <- -1

```

Model(s)

run1 run2

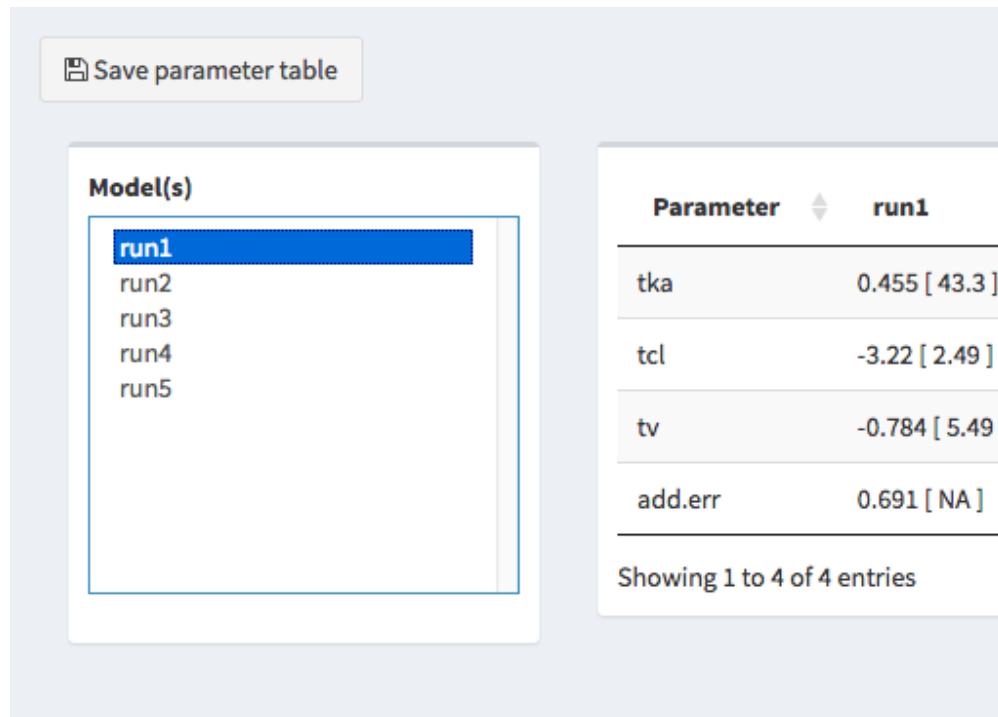
▶ Run Model(s) ⚙ Show progress

```

*****./shinyMixR/temp/run1.prog.txt*
Loading required package: nlme
Loading required package: RxODE
Compiling RxODE differential equations...done.
clang++ -I/Library/Frameworks/R.framework/Reso

*****./shinyMixR/temp/run2.prog.txt*
Loading required package: nlme
Loading required package: RxODE

```



The screenshot shows the ShinyMIXR interface. At the top left is a button labeled 'Save parameter table'. Below it is a panel titled 'Model(s)' containing a list of models: 'run1', 'run2', 'run3', 'run4', and 'run5'. 'run1' is selected and highlighted in blue. To the right of the model list is a table showing parameters for the selected model, 'run1'.

Parameter	run1
tka	0.455 [43.3]
tcl	-3.22 [2.49]
tv	-0.784 [5.49]
add.err	0.691 [NA]

Below the table, it says 'Showing 1 to 4 of 4 entries'.

3.1.10 Results

It is possible to view and combine the results from the models within a project within the last tab.

3.1.11 Interactive session

When working in an interactive R session, many functions used by the interface are also available from an interactive R session. When working outside the interface it is important to know how to interact with the project object. This object should be created as one of the first steps because other function rely on the availability of this object:

```
proj_obj <- get_proj()
```

This function will look in the folder structure to create or update the available information. The result is a list that is build-up as follows:

```
object
|--- run 1
|   |--- model location
|   |--- model meta data
|   |--- model high level results
|
|--- ...
|
|--- meta data (time of last refresh)
```

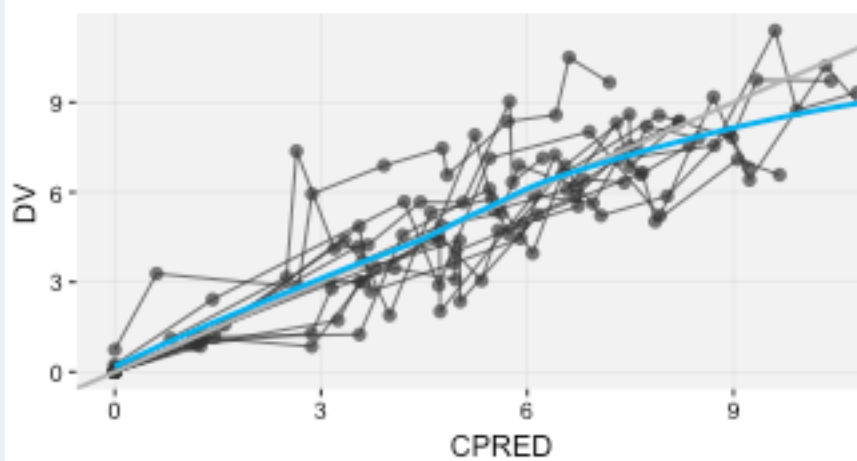
In case this object is not present it will be created by looking at the files present in the current folder structure. In case the object is already present it will check if newer files are present in the current folder

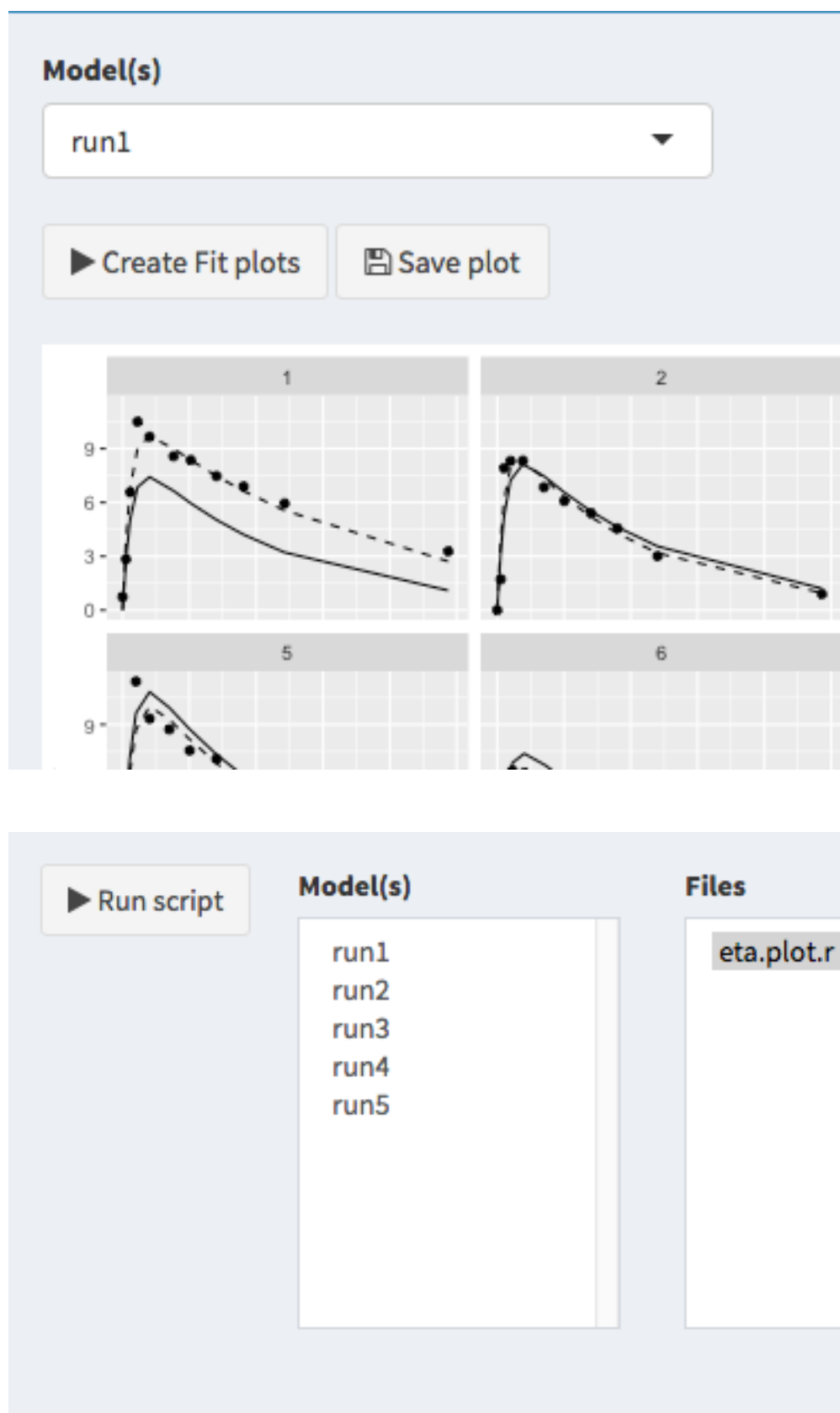
Model(s)

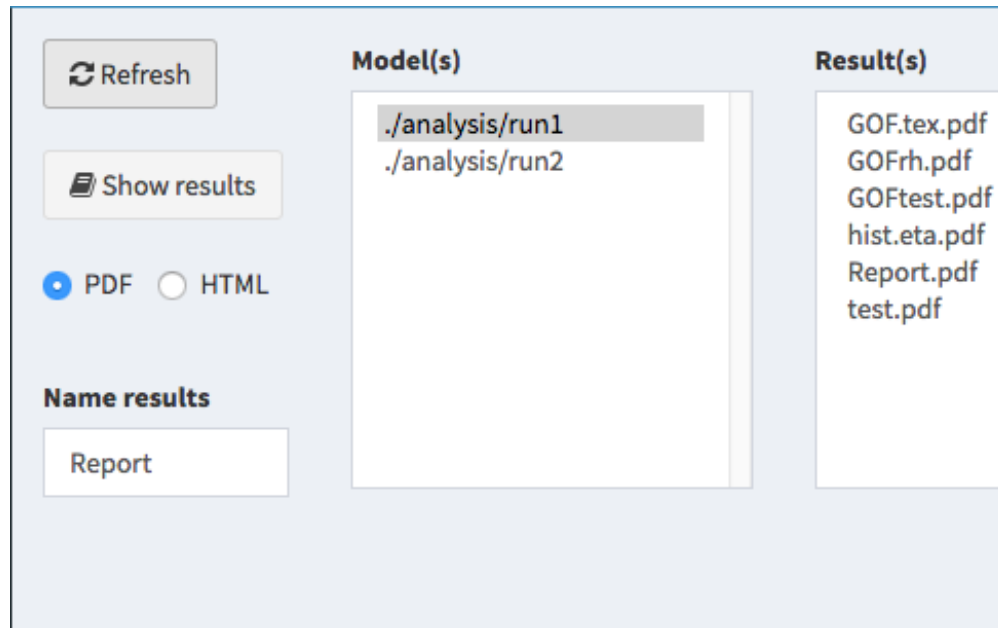
run1

▶ Create GOF

📄 Save plot

A**C**





and will update the object with this information. Therefore one have to be aware that this function should be submitted manually in case new information is present in the one of the folders.

Once a folder structure is in place and the project object is created, an overview can be created for the available models and, if models are submitted, high level results. It is also possible to display a collapsible d3 tree view of the models. This is mainly useful in case reference to models is provided to show the hierarchy of the models within a project:

```
overview()
tree_overview()
```

Although the `nlmixr` package obviously has the possibility to run `nlmixr` models, the `shinyMixR` package also have a function available named `run_nmx`. the main reason this function was written is the option to run the model in an external R session. This is necessary within the interface to overcome the application from freezing when a model is submitted. Also within an interactive R session it is convenient because you do not have to wait for a run to finish. An example how this can be used is given below:

```
#proj_obj <- get_proj()
#run_nmx("run1",proj=proj_obj)
```

```
run_nmx("run1",proj=proj_obj)
# progress of a run is written to external text file
# this can be read-in for intermediate assessment
readLines("shinyMixR/temp/run1.prog.txt")
```

The current version of the package has three functions for assessing the model results. The first function is to create a simple parameter table `par_table`. By default this function returns a data.frame. In case multiple models are selected, each column will have the results of the selected model. The results can also be written to a PDF (using latex) or html file using the `R3port` package:


```
par_table(proj_obj,c("run1","run2"))
# par_table(proj_obj, models="run1", outnm="par.tex")
```

For assessing the goodness of fit, the `gof_plot` function can be used. This function will by default use the `nlmixr.xpose` package to create 4 different types of plots. It is also possible to directly create `ggplot2` types of plots. By default the plots will be created within the R session but can also be written to pdf/html using the `R3port` package:

```
res <- readRDS("./shinyMixR/run1.res.rds")
gof_plot(res)
# gof_plot(res, mdlnm="run1", outnm="gof.tex")
```

The last plot is an individual fit plot `fit_plot`. This function will also by default use the `nlmixr.xpose` package to create a plot per individual including the observed data, individual and population predictions. Also here it is possible to create `ggplot2` types of plots and plots can be outputted to pdf/html:

```
fit_plot(res, type="user")
# fit_plot(res, mdlnm="run1", outnm="fit.html")
```

3.2 nlmixr modeling mini-language:

```
library(nlmixr)
?nlmixr
```

Under the hood `nlmixr` has five main modules:

1. `dynmodel()` and its mcmc cousin `dynmodel.mcmc()` for nonlinear dynamic models of individual data;
2. `nlme_lin_cmpt()` for one to three linear compartment models of population data with first order absorption, or i.v. bolus, or i.v. infusion using the `nlme` algorithm;
3. `nlme_ode()` for general dynamic models defined by ordinary differential equations (ODEs) of population data using the `nlme` algorithm;
4. `saem_fit` for general dynamic models defined by ordinary differential equations (ODEs) of population data by the Stochastic Approximation Expectation-Maximization (SAEM) algorithm;
5. `gnlmm` for generalized non-linear mixed-models (possibly defined by ordinary differential equations) of population data by the adaptive Gaussian quadrature algorithm.

3.2.1 Rationale

`nlmixr` estimation routines each have their own way of specifying models. Often the models are specified in ways that are most intuitive for one estimation routine, but do not make sense for another estimation routine. Sometimes, legacy estimation routines like `[nlme]` have their own syntax that is outside of the control of the `nlmixr` package.

The unique syntax of each routine makes the routines themselves easier to maintain and expand, and allows interfacing with existing packages that are outside of `nlmixr` (like `[nlme]`). However, a model definition language that is common between estimation methods, and an output object that is uniform, will make it easier to switch between estimation routines and will facilitate interfacing output with external packages like `xpose` and other user-written packages.

The `nlmixr` mini-modeling language attempts to address this issue by incorporating a common language. This language is inspired by both R and NONMEM, since these languages are familiar to many pharmacometricians.

Initial Estimates and boundaries for population parameters

`nlmixr` models are contained in a R function with two blocks: `ini` and `model`. This R function can be named anything, but is not meant to be called directly from R. In fact if you try you will likely get an error such as `Error: could not find function "ini"`.

The `ini` model block

The `ini` model block is meant to hold the initial estimates for the model, and the boundaries of the parameters for estimation routines that support boundaries (note `nlmixr`'s `saem` and `[nlme]` do not currently support parameter boundaries).

To explain how these initial estimates are specified we will start with an annotated example:

```
f <- function(){ ## Note the arguments to the function are currently
                  ## ignored by `nlmixr`

  ini({
    ## Initial conditions for population parameters (sometimes
    ## called theta parameters) are defined by either `<-` or `=`
    lCl <- 1.6      #log CL (L/hr)
    ## Note that simple expressions that evaluate to a number are
    ## OK for defining initial conditions (like in R)
    lVc = log(90)  #log V (L)
    ## Also a comment on a parameter is captured as a parameter label
    lKa <- 1 #log Ka (1/hr)
    ## Bounds may be specified by c(lower, est, upper), like NONMEM:
    ## Residuals errors are assumed to be population parameters
    prop.err <- c(0, 0.2, 1)
  })
  ## The model block will be discussed later
  model({})
}
```

As shown in the above examples:

- Simple parameter values are specified as a R-compatible assignment
- Boundaries may be specified by `c(lower, est, upper)`.
- Like NONMEM, `c(lower,est)` is equivalent to `c(lower,est,Inf)`
- Also like NONMEM, `c(est)` does not specify a lower bound, and is equivalent to specifying the parameter without R's `c` function.
- The initial estimates are specified on the variance scale, and in analogy with NONMEM, the square roots of the diagonal elements correspond to coefficients of variation when used in the exponential IIV implementation

These parameters can be named almost any R compatible name. Please note that:

- Residual error estimates should be coded as population estimates (i.e. using an `'='` or `'<='` statement, not a `'~'`).
- Naming variables that start with `"_"` are not supported. Note that R does not allow variable starting with `"_"` to be assigned without quoting them.
- Naming variables that start with `"rx_"` or `"nlmixr_"` is not supported since `RxODE` and `nlmixr` use these prefixes internally for certain estimation routines and calculating residuals.

- Variable names are case sensitive, just like they are in R. “CL” is not the same as “Cl”.

Initial Estimates for between subject error distribution (NONMEM’s \$OMEGA)

In mixture models, multivariate normal individual deviations from the population parameters are estimated (in NONMEM these are called ETA parameters). Additionally the variance/covariance matrix of these deviations is also estimated (in NONMEM this is the OMEGA matrix). These also have initial estimates. In `nlmixr` these are specified by the `~` operator that is typically used in R for “modeled by”, and was chosen to distinguish these estimates from the population and residual error parameters.

Continuing the prior example, we can annotate the estimates for the between subject error distribution

```
f <- function(){
  ini({
    lCl <- 1.6      #log Cl (L/hr)
    lVc = log(90)   #log V (L)
    lKa <- 1        #log Ka (1/hr)
    prop.err <- c(0, 0.2, 1)
    ## Initial estimate for ka IIV variance
    ## Labels work for single parameters
    eta.ka ~ 0.1    #BSV Ka

    ## For correlated parameters, you specify the names of each
    ## correlated parameter separated by a addition operator `+`
    ## and the left handed side specifies the lower triangular
    ## matrix initial of the covariance matrix.
    eta.cl + eta.vc ~ c(0.1,
                        0.005, 0.1)

    ## Note that labels do not currently work for correlated
    ## parameters. Also do not put comments inside the lower
    ## triangular matrix as this will currently break the model.
  })
  ## The model block will be discussed later
  model({})
}
```

As shown in the above examples:

- Simple variances are specified by the variable name and the estimate separated by `~`.
- Correlated parameters are specified by the sum of the variable labels and then the lower triangular matrix of the covariance is specified on the left handed side of the equation. This is also separated by `~`. }

Currently the model syntax does not allow comments inside the lower triangular matrix.

Model Syntax for ODE based models (NONMEM’s \$PK, \$PRED, \$DES and \$ERROR)

The ini model block Once the initialization block has been defined, you can define a `model` block in terms of the defined variables in the `ini` block. You can also mix in `RxODE` blocks into the model.

The current method of defining an `nlmixr` model is to specify the parameters, and then possibly the `RxODE` lines:

Continuing describing the syntax with an annotated example:

```
f <- function(){
  ini({
    lCl <- 1.6      #log Cl (L/hr)
    lVc <- log(90)  #log Vc (L)
    lKA <- 0.1      #log Ka (1/hr)
    prop.err <- c(0, 0.2, 1)
    eta.Cl ~ 0.1 ## BSV Cl
    eta.Vc ~ 0.1 ## BSV Vc
    eta.KA ~ 0.1 ## BSV Ka
  })
  model({
    ## First parameters are defined in terms of the initial estimates
    ## parameter names.
    Cl <- exp(lCl + eta.Cl)
    Vc <- exp(lVc + eta.Vc)
    KA <- exp(lKA + eta.KA)
    ## After the differential equations are defined
    kel <- Cl / Vc;
    d/dt(depot) = -KA*depot;
    d/dt(centr) = KA*depot - kel*centr;
    ## And the concentration is then calculated
    cp = centr / Vc;
    ## Last, nlmixr is told that the plasma concentration follows
    ## a proportional error (estimated by the parameter prop.err)
    cp ~ prop(prop.err)
  })
}
```

A few points to note:

- Parameters are defined before the differential equations. Currently directly defining the differential equations in terms of the population parameters is not supported.
- The differential equations, parameters and error terms are in a single block, instead of multiple sections.
- State names, calculated variables cannot start with either “rx_” or “nlmixr_” since these are used internally in some estimation routines.
- Errors are specified using the ~. Currently you can use either `add(parameter)` for additive error, `prop(parameter)` for proportional error or `add(parameter1) + prop(parameter2)` for additive plus proportional error. You can also specify `norm(parameter)` for the additive error, since it follows a normal distribution.
- Some routines, like `saem` require parameters in terms of `Pop.Parameter + Individual.Deviation.Parameter + Covariate*Covariate.Parameter`. The order of these parameters do not matter. This is similar to NONMEM’s mu-referencing, though not quite so restrictive.
- The type of parameter in the model is determined by the initial block; Covariates used in the model are missing in the `ini` block. These variables need to be present in the modeling dataset for the model to run.

Model Syntax for solved PK systems

Solved PK systems are also currently supported by `nlmixr` with the `linCmt()` pseudo-function. An annotated example of a solved system is below:

```
f <- function(){
  ini({
```

```

lCl <- 1.6      #log Cl (L/hr)
lVc <- log(90)  #log Vc (L)
lKA <- 0.1      #log Ka (1/hr)
prop.err <- c(0, 0.2, 1)
eta.Cl ~ 0.1 ## BSV Cl
eta.Vc ~ 0.1 ## BSV Vc
eta.KA ~ 0.1 ## BSV Ka
})
model({
  Cl <- exp(lCl + eta.Cl)
  Vc <- exp(lVc + eta.Vc)
  KA <- exp(lKA + eta.KA)
  ## Instead of specifying the ODEs, you can use
  ## the linCmt() function to use the solved system.
  ##
  ## This function determines the type of PK solved system
  ## to use by the parameters that are defined. In this case
  ## it knows that this is a one-compartment model with first-order
  ## absorption.
  linCmt() ~ prop(prop.err)
})
}

```

A few things to keep in mind:

- Currently the solved systems support either oral dosing, IV dosing or IV infusion dosing and does not allow mixing the dosing types.
- While RxODE allows mixing of solved systems and ODEs, this has not been implemented in `nlmixr` yet.
- The solved systems implemented are the one, two and three compartment models with or without first-order absorption. Each of the models support a lag time with a `tlag` parameter.
- In general the linear compartment model figures out the model by the parameter names. `nlmixr` currently knows about numbered volumes, V_c/V_p , Clearances in terms of both Cl and Q/CLD . Additionally `nlmixr` knows about elimination micro-constants (ie K_{12}). Mixing of these parameters for these models is currently not supported.

Checking model syntax

After specifying the model syntax you can check that `nlmixr` is interpreting it correctly by using the `nlmixr` function on it.

Using the above function we can get:

```

> `nlmixr`(f)
## 1-compartment model with first-order absorption in terms of Cl
## Initialization:
#####
Fixed Effects ($theta):
      lCl      lVc      lKA
1.60000 4.49981 0.10000

Omega ($omega):
      [,1] [,2] [,3]
[1,]  0.1  0.0  0.0

```

```

[2,] 0.0 0.1 0.0
[3,] 0.0 0.0 0.1

## Model:
#####
Cl <- exp(lCl + eta.Cl)
Vc <- exp(lVc + eta.Vc)
KA <- exp(lKA + eta.KA)
## Instead of specifying the ODEs, you can use
## the linCmt() function to use the solved system.
##
## This function determines the type of PK solved system
## to use by the parameters that are defined. In this case
## it knows that this is a one-compartment model with first-order
## absorption.
linCmt() ~ prop(prop.err)

```

In general this gives you information about the model (what type of solved system/RxODE), initial estimates as well as the code for the model block.

Using the model syntax for estimating a model

Once the model function has been created, you can use it and a dataset to estimate the parameters for a model given a dataset.

This dataset has to have RxODE compatible events IDs. Both Monolix and NONMEM use a different dataset description. You may convert these datasets to RxODE-compatible datasets with the `nmDataConvert` function. Note that steady state doses are not supported by RxODE, and therefore not supported by the conversion function.

As an example, you can use a simulated rich 1-compartment dataset.

```

d <- Oral_1CPT
d <- d[,names(d) != "SS"];
d <- nmDataConvert(d);

```

Once the data has been converted to the appropriate format, you can use the `nlmixr` function to run the appropriate code.

The method to estimate the model is:

```

fit <- nlmixr(model.function, rxode.dataset, est="est", control=estControl(options))

```

Currently `nlme` and `saem` are implemented. For example, to run the above model with `saem`, we could have the following:

```

> f <- function(){
  ini({
    lCl <- 1.6      #log Cl (L/hr)
    lVc <- log(90)  #log Vc (L)
    lKA <- 0.1      #log Ka (1/hr)
    prop.err <- c(0, 0.2, 1)
    eta.Cl ~ 0.1 ## BSV Cl
    eta.Vc ~ 0.1 ## BSV Vc
    eta.KA ~ 0.1 ## BSV Ka
  })
}

```

```

})
model({
  ## First parameters are defined in terms of the initial estimates
  ## parameter names.
  Cl <- exp(lCl + eta.Cl)
  Vc <- exp(lVc + eta.Vc)
  KA <- exp(lKA + eta.KA)
  ## After the differential equations are defined
  kel <- Cl / Vc;
  d/dt(depot) = -KA*depot;
  d/dt(centr) = KA*depot-kel*centr;
  ## And the concentration is then calculated
  cp = centr / Vc;
  ## Last, nlmixr is told that the plasma concentration follows
  ## a proportional error (estimated by the parameter prop.err)
  cp ~ prop(prop.err)
})
}
> fit.s <- nlmixr(f,d,est="saem",control=saemControl(n.burn=50,n.em=100,print=50));
Compiling RxODE differential equations...done.
c:/Rtools/mingw_64/bin/g++ -I"c:/R/R-34~1.1/include" -DNDEBUG -I"d:/Compiler/gcc-4.9.3/local330/in
In file included from c:/R/R-34~1.1/library/RCPAR~1/include/armadillo:52:0,
from c:/R/R-34~1.1/library/RCPAR~1/include/RcppArmadilloForward.h:46,
from c:/R/R-34~1.1/library/RCPAR~1/include/RcppArmadillo.h:31,
from saem3090757b4bd1x64.cpp:1:
c:/R/R-34~1.1/library/RCPAR~1/include/armadillo_bits/compiler_setup.hpp:474:96: note: #pragma message
#pragma message ("WARNING: use of OpenMP disabled; this compiler doesn't support OpenMP 3.0+")
~
c:/Rtools/mingw_64/bin/g++ -shared -s -static-libgcc -o saem3090757b4bd1x64.dll tmp.def saem3090757b4b
done.
1: 1.8174 4.6328 0.0553 0.0950 0.0950 0.0950 0.6357
50: 1.3900 4.2039 0.0001 0.0679 0.0784 0.1082 0.1992
100: 1.3894 4.2054 0.0107 0.0686 0.0777 0.1111 0.1981
150: 1.3885 4.2041 0.0089 0.0683 0.0778 0.1117 0.1980
Using sympy via SnakeCharmR
## Calculate ETA-based prediction and error derivatives:
Calculate Jacobian.....done.
Calculate sensitivities.....
done.
## Calculate d(f)/d(eta)
## ...
## done
## ...
## done
The model-based sensitivities have been calculated.
It will be cached for future runs.
Calculating Table Variables...
done

```

The options for `saem` are controlled by `saemControl`. You may wish to make sure the minimization is complete in the case of `saem`. You can do that with `traceplot` which shows the iteration history with the divided by burn-in and EM phases. In this case, the burn seems reasonable; you may wish to increase the number of iterations in the EM phase of the estimation. Overall it is probably a semi-reasonable solution.

nlmixr output objects

In addition to unifying the modeling language sent to each of the estimation routines, the outputs currently have a unified structure.

You can see the fit object by typing the object name:

```
> fit.s
nlmixr SAEM fit (ODE)

      OBJF      AIC      BIC Log-likelihood
62335.96 62349.96 62397.88      -31167.98

Time (sec; $time):
      saem setup FOCEi Evaulate covariance table
elapsed 379.32  2.9      1.71      0 19.11

Parameters ($par.fixed):
      Parameter Estimate      SE      CV Untransformed      (95%CI)
1Cl      log Cl (L/hr)      1.39 0.0240      1.7%      4.01 (3.82, 4.20)
1Vc      log Vc (L)      4.20 0.0256      0.6%      67.0 (63.7, 70.4)
1KA      log Ka (1/hr) 0.00890 0.0307 344.9%      1.01 (0.950, 1.07)
prop.err      0.198      19.8%

Omega ($omega):
      eta.Cl      eta.Vc      eta.KA
eta.Cl 0.06833621 0.00000000 0.000000
eta.Vc 0.00000000 0.07783316 0.000000
eta.KA 0.00000000 0.00000000 0.111673

Fit Data (object is a modified data.frame):
      ID      TIME      DV      IPRED      PRED      IRES      RES      IWRES
1: 1 0.25 204.8 194.859810 198.21076 9.94018953 6.589244 0.25766777
2: 1 0.50 310.6 338.006073 349.28827 -27.40607290 -38.688274 -0.40955290
3: 1 0.75 389.2 442.467750 463.78410 -53.26775045 -74.584098 -0.60809361
---
6945: 120 264.00 11.3 13.840800 70.58248 -2.54080024 -59.282475 -0.92725039
6946: 120 276.00 3.9 4.444197 34.41018 -0.54419655 -30.510177 -0.61851500
6947: 120 288.00 1.4 1.427006 16.77557 -0.02700637 -15.375569 -0.09559342
      WRES      CWRES      CPRED      CRES      eta.Cl      eta.Vc
1: 0.07395107 0.07349997 198.41341 6.38659 0.09153143 0.1366395
2: -0.26081216 -0.27717947 349.82730 -39.22730 0.09153143 0.1366395
3: -0.39860485 -0.42988445 464.55651 -75.35651 0.09153143 0.1366395
---
6945: -0.77916115 -1.34050999 41.10189 -29.80189 0.32007359 -0.1381479
6946: -0.65906613 -1.28359979 15.51100 -11.61100 0.32007359 -0.1381479
6947: -0.56746681 -1.22839732 5.72332 -4.32332 0.32007359 -0.1381479
      eta.KA
1: 0.1369685
2: 0.1369685
3: 0.1369685
---
6945: -0.2381078
6946: -0.2381078
6947: -0.2381078
```


This example shows what is typical printout of an `nlmixr` fit object. The elements of the fit are:

- The type of fit (`nlme`, `saem`, etc)
- Metrics of goodness of fit (AIC, BIC, and `logLik`).
 - To align the comparison between methods, the FOCEi likelihood objective is calculated regardless of the method used and used for goodness of fit metrics.
 - This FOCEi likelihood has been compared to NONMEM’s objective function and gives the same values (based on the data in **Wang 2007 (INCLUDE REF)**)
 - Also note that `saem` does not calculate an objective function, and the FOCEi is used as the only objective function for the fit.
 - Even though the objective functions are calculated in the same manner, caution should be used when comparing fits from various estimation routines.

The next item is the timing of each of the steps of the fit.

- These can be also accessed by (`fit.s$time`).
- As a mnemonic, the access for this item is shown in the printout. This is true for almost all of the other items in the printout.

After the timing of the fit, the parameter estimates are displayed (can be accessed by `fit.s$par.fixed`

- While the items are rounded for R printing, each estimate without rounding is still accessible by the `$` syntax. For example, the `$Untransformed` gives the untransformed parameter values.
- The Untransformed parameter takes log-space parameters and back-transforms them to normal parameters. Not the CIs are listed on the back-transformed parameter space.
- Proportional Errors are converted to %CV on the untransformed space
- Omega block (accessed by `fit.s$omega`)

The table of fit data. Please note:

- An `nlmixr` fit object is actually a data frame. Saving it as a Rdata object and then loading it without `nlmixr` will just show the data by itself. Don’t worry; the fit information has not vanished, you can bring it back by simply loading `nlmixr`, and then accessing the data.
- Special access to fit information (like the `$omega`) needs `nlmixr` to extract the information.

If you use the `$` to access information, the order of precedence is:

- Fit data from the overall data.frame
- Information about the parsed `nlmixr` model (via `$uif`)
- Parameter history if available (via `$par.hist` and `$par.hist.stacked`)
- Fixed effects table (via `$par.fixed`)
- Individual differences from the typical population parameters (via `$eta`)
- Fit information from the list of information generated during the post-hoc residual calculation.
- Fit information from the environment where the post-hoc residual were calculated
- Fit information about how the data and options interacted with the specified model (such as estimation options or if the solved system is for an infusion or an IV bolus).

While the printout may displays the data as a `data.table` object or `tbl` object, the data is NOT any of these objects, but rather a derived data frame. - Since the object `**is*` a `data.frame`, you can treat it like one.

In addition to the above properties of the fit object, there are a few additional that may be helpful for the modeler:

- `$theta` gives the fixed effects parameter estimates (in NONMEM the `thetas`). This can also be accessed in `nlme` function. Note that the residual variability is treated as a fixed effect parameter and is included in this list.
- `$eta` gives the random effects parameter estimates, or in NONMEM the `etas`. This can also be accessed in using the `random.effects` function.

Chapter 4

Applications of `nlmixr`

4.1 Demo Examples from GitHub

How can you run the examples from GitHub and what can you learn from these.

4.2 Posters and Presentations

Various posters were presented at different conferences where `nlmixr` was compared to `NONMEM`. These findings provide evidence that `nlmixr` may provide a viable open-source parameter estimation alternative for fitting nonlinear mixed effects pharmacometric models within the R environment.

PosterACoP2016

PosterWCoP2016

PosterACoP2017

PosterPAGE2017

On 8 December 2016, Rik Schoemaker presented a seminar on `nlmixr` at Uppsala University with the title: `nlmixr`: an open-source package for pharmacometric modelling in R (PresentationUppsala161208).

`nlmixr` was presented at the 12th Pharmacometrics Network Benelux Meeting (29 March 2018) with the title: Simulation (R_xODE) and parameter estimation in `nlmixr` (PresentationPNB180326).

4.3 Sparse data analysis with `nlmixr`

4.3.1 Examination of `nlmixr` estimation algorithm properties for sparse sample data

The nlme and SAEM parameter estimation algorithms were compared with `NONMEM` FOCE-I in a sparse-sampling data setting. To this end, 10,000 patients were simulated after 7 doses with 24 hour intervals with doses split between 10, 30, 60 and 120 mg. Four time points were randomly sampled in the 24 hours after the last dose. A first order absorption, one compartment distribution, and linear elimination model was used with population values of Clearance=4.0 L/hr, V_c=70 L, and K_A=1 /hr, 30% IIV for all three parameters (diagonal omega matrix), and 20% residual variability. Of these 10,000 patients, 600 patients were randomly sampled (stratified by dose, 150 subjects per dose), 500 times using PsN and analysed using `NONMEM`.

The code for the full analysis is provided here along with some output graphs to demonstrate the results. While these are interesting in their own right, the code also demonstrates how to perform parallel analysis of the estimations; with 500 datasets per analysis, it makes perfect sense to be able to run these analyses side-by-side providing you have access to a computer with multiple cores. As these approaches are completely OS-dependent, the code below for running in parallel is only applicable to Windows.

Installing the latest version of nlmixr can be performed with the following code:

```
library(devtools)
install_github("nlmixrdevelopment/PreciseSums")
install_github("nlmixrdevelopment/RxODE")
install_github("nlmixrdevelopment/nlmixr")
```

Load the packages and define the model using ODEs:

```
library(nlmixr)
library(data.table)

#Define the RxODE model
ode4 <- "
  d/dt(abs)      = -KA*abs;
  d/dt(centr)    =  KA*abs-(CL/V)*centr;
  C2=centr/V;
"

#Create the RxODE simulation object
mod4 <- RxODE(model = ode4, modName = 'mod4')
```

Generate the 10,000 sampled parameters:

```
#Population parameter values on log-scale
params1 <- c(CL = log(4),
             V = log(70),
             KA = log(1))

#make 10,000 subjects to sample from:
nsubg <- 2500 # subjects per dose
doses <- c(10, 30, 60, 120)
nsub <- nsubg * length(doses)

#IIV of 30% for each parameter
omega <- diag(c(0.09, 0.09, 0.09)) # IIV covariance matrix
sigma <- 0.2

#Sample from the multivariate normal
set.seed(98176247)
library(MASS)
mv <-
  mvrnorm(nsub, rep(0, dim(omega)[1]), omega) # Sample from covariance matrix

#Combine population parameters with IIV
params.all <-
  data.table(
    "ID" = seq(1:nsub),
    "CL" = exp(params1['CL'] + mv[, 1]),
    "V" = exp(params1['V'] + mv[, 2]),
    "KA" = exp(params1['KA'] + mv[, 3])
  )
```

```
#set the doses (looping through the 4 doses)
params.all[, AMT := 1000 * doses]
```

The do the simulation of all these profiles. The cool thing is to use lapply which is super efficient (the initial code with a for loop as suggested in the RxODE paper is about 20 times slower):

```
Startlapply <- Sys.time()

#Run the simulations using lapply for speed
s = lapply(1:nsub, function(i) {
#selects the parameters associated with the subject to be simulated
  params <- params.all[i]
#creates an eventTable with 7 doses every 24 hours
  ev <- eventTable()
  ev$add.dosing(
    dose = params$AMT,
    nbr.doses = 7,
    dosing.to = 1,
    dosing.interval = 24,
    rate = NULL,
    start.time = 0
  )
#generates 4 random samples in a 24 hour period for the last dose
  ev$add.sampling(6 * 24 + c(0, sort(round(sample(runif(600, 0, 1440), 4) / 60, 2))))
#runs the RxODE simulation
  x <- as.data.table(mod4$run(params, ev))
#merges the parameters and ID number to the simulation output
  x[, names(params) := params]
})

#runs the entire sequence of 10000 subjects and binds the results to the object res
res = as.data.table(do.call("rbind", s))

Stoplapply <- Sys.time()

Stoplapply - Startlapply
#10,000 subjects simulated in:
#Time difference of 29.36007 secs
```

Clean up the results and prepare for analysis using NONMEM:

```
setnames(res, "time", "TIME")
#administered dose:
Dose <- expand.grid(TIME = seq(0, 6 * 24, 24), ID = params.all$ID)
Dose <- data.table(merge(Dose, params.all, by = "ID"))
Dose[, C2 := 0]
Dose[, EVID := 101]
Dose[, DOSE := AMT / 1000]
res[, EVID := 0]
res[, centr := NULL]
res[, abs := NULL]
res[, DOSE := AMT / 1000]
res[, AMT := 0]
```

```

#take out the 'trough' (sampling)timepoint used for dosing in this case
res <- res[TIME != 144]
res <- rbind(res, Dose)
setkey(res, ID, TIME)
#Add residual error
res[, DV := C2 * exp(rnorm(length(C2), 0, sigma))]
res[, C2 := NULL]
res[, DV := round(DV)]
#NONMEM EVID is just 1 instead of the RxODE EVID of 101
res[, EVIDNM := as.numeric(EVID == 101)]
res <- res[, .(ID, DOSE, V, CL, KA, TIME, EVID, AMT, DV, EVIDNM)]
write.table(res, file="FullSIM160817.csv", sep=",", col.names=TRUE, quote=FALSE, row.names=FALSE)

```

Then PsN is used to sample 600 subjects stratified by dose from the 10,000 subjects and analyse these with NONMEM. This is repeated 500 times using PsN bootstrap functionality, creating both 500 sets of output and 500 data files to be analysed using nlmixr with the following PsN syntax:

```
bootstrap runN024.mod -samples=500 -sample_size=600 -stratify_on=DOSE -no-run_base_model -seed=12345 -t
```

and the following NONMEM syntax file:

```

$PROB    ORAL1_1CPT_KAVCL MULTIPLE DOSE FOCEI runN024
$INPUT    ID DOSE VI CLI KAI TIME EVIDNLMX AMT DV EVID
$DATA     FullSIM160817.csv IGNORE=@
$SUBR     ADVAN2,TRANS2
$PK
CL=EXP(THETA(1)+ETA(1))
V=EXP(THETA(2)+ETA(2))
KA=EXP(THETA(3)+ETA(3))
S2=V
$ERROR
IPRED = F
RESCV = THETA(4)
W      = IPRED*RESCV
IRES   = DV-IPRED
IWRES  = IRES/W
Y      = IPRED+W*EPS(1)
$THETA   1.6          ;CL
$THETA   4.5          ;V
$THETA   0.2          ;Ka
$THETA   (0,0.3,1) ;RSV
$OMEGA   0.15 0.15 0.15
$SIGMA   1 FIX
$EST      NSIG=3 PRINT=5 MAX=9999 NOABORT POSTHOC METHOD=COND INTER NOOBT
$COV

```

The NONMEM results will be provided separately, along with the PsN-generated data files that will be analysed in nlmixr. A function `do_nlmixr` is created that reads in the data file, defines the model, runs the parameter estimation, and then saves the output file, to be analysed at a later date. The code to analyse these data sets using SAEM with the solved equations implementation is:

```

#SAEM with solved equations:

do_nlmixr <- function(i) {
  datr <-
    read.csv(
      paste("D:\\nmrun\\nmrun1\\m1\\bs_pr1_", i, ".dta", sep = ""),
      header = TRUE,
      stringsAsFactors = F
    )

  #If using Microsoft R Open, you need to specify:
  #setMKLthreads(1)
  #Otherwise it accesses too much resources without any gain in speed

  one.compartment.oral.model.solved <- function() {
    ini({
      # Where initial conditions/variables are specified
      # '<-' or '=' defines population parameters
      # Simple numeric expressions are supported
      lCl <- 1      #log Cl (L/hr)
      lVc <- 4      #log V (L)
      lKA <- 0.1    #log V (L)
      # Bounds may be specified by c(lower, est, upper), like NONMEM:
      # Residuals errors are assumed to be population parameters
      prop.err <- c(0, 0.2, 1)
      # Between subject variability estimates are specified by '~'
      # Semicolons are optional
      eta.Cl ~ 0.1
      eta.Vc ~ 0.1
      eta.KA ~ 0.1
    })
    model({
      # Where the model is specified
      # The model uses the ini-defined variable names
      Cl <- exp(lCl + eta.Cl)
      Vc <- exp(lVc + eta.Vc)
      KA <- exp(lKA + eta.KA)
      # Solved equations:
      linCmt() ~ prop(prop.err)
    })
  }

  fit <-
    nlmixr(
      one.compartment.oral.model.solved,
      datr,
      est = "saem",
      control = saemControl(print = 50)
    )

  save(fit, file = paste("fit_SAEM_Solved_UUI_", i, ".Rdata", sep = ""))
}

```

Note that if you use Microsoft R-Open, this comes with the Intel MKL for parallel mathematical computing

software that interferes with nlmixr code. You need to actively tell R to only use a single thread using the command `setMKLthreads(1)`. Otherwise it appears to use a parallelised implementation but that only eats up hardware resources without any gain in speed (quite the opposite actually). The code for SAEM with an ODE implementation is:

```
#SAEM with ODE:

do_nlmixrODE <- function(i) {
  datr <-
    read.csv(
      paste("D:\\nmrun\\nmrun1\\m1\\bs_pr1_", i, ".dta", sep = ""),
      header = TRUE,
      stringsAsFactors = F
    )

  #If using Microsoft R Open, you need to specify:
  #setMKLthreads(1)
  #Otherwise it accesses too much resources without any gain in speed

  one.compartment.oral.model <- function() {
    ini({
      # Where initial conditions/variables are specified
      # '<-' or '=' defines population parameters
      # Simple numeric expressions are supported
      lCl <- 1      #log Cl (L/hr)
      lVc <- 4      #log V (L)
      lKA <- 0.1    #log V (L)
      # Bounds may be specified by c(lower, est, upper), like NONMEM:
      # Residuals errors are assumed to be population parameters
      prop.err <- c(0, 0.2, 1)
      # Between subject variability estimates are specified by '~'
      # Semicolons are optional
      eta.Cl ~ 0.1
      eta.Vc ~ 0.1
      eta.KA ~ 0.1
    })
    model({
      # Where the model is specified
      # The model uses the ini-defined variable names
      Cl <- exp(lCl + eta.Cl)
      Vc <- exp(lVc + eta.Vc)
      KA <- exp(lKA + eta.KA)
      # RxODE-style differential equations are supported
      d / dt(depot) = -KA * depot

      d / dt(centr) = KA * depot - (Cl / Vc) * centr

      ## Concentration is calculated
      cp = centr / Vc

      # And is assumed to follow proportional error estimated by prop.err
      cp ~ prop(prop.err)
    })
  }
}
```



```

}

fit <-
  nlmixr(
    one.compartment.oral.model,
    datr,
    est = "saem",
    control = saemControl(print = 50)
  )

save(fit, file = paste("fit_SAEM_ODE_UUI_", i, ".Rdata", sep = ""))
}

```

nlme with solved equations:

```

#nlme with solved equations:

do_nlmixr_nlme <- function(i) {
  datr <-
    read.csv(
      paste("D:\\nmrun\\nmrun1\\m1\\bs_pri_", i, ".dta", sep = ""),
      header = TRUE,
      stringsAsFactors = F
    )

  one.compartment.oral.model.solved <- function() {
    ini({
      # Where initial conditions/variables are specified
      # '<-' or '=' defines population parameters
      # Simple numeric expressions are supported
      lCl <- 1          #log Cl (L/hr)
      lVc <- 4          #log V (L)
      lKA <- 0.1        #log V (L)
      # Bounds may be specified by c(lower, est, upper), like NONMEM:
      # Residuals errors are assumed to be population parameters
      prop.err <- c(0, 0.2, 1)
      # Between subject variability estimates are specified by '~'
      # Semicolons are optional
      eta.Cl ~ 0.1
      eta.Vc ~ 0.1
      eta.KA ~ 0.1
    })
    model({
      # Where the model is specified
      # The model uses the ini-defined variable names
      Cl <- exp(lCl + eta.Cl)
      Vc <- exp(lVc + eta.Vc)
      KA <- exp(lKA + eta.KA)
      # Solved equations:
      linCmt() ~ prop(prop.err)
    })
  }
}

```

```

fit <-
  nlmixr(
    one.compartment.oral.model.solved,
    datr,
    est = "nlme",
    control = nlmeControl(pnlstol = .1)
  )

save(fit, file = paste("fit_NLME_Solved_UUI_", i, ".Rdata", sep = ""))
}

```

and finally nlme with ODE:

```

#nlme with ODE:

do_nlmixrODE_nlme <- function(i) {
  datr <-
    read.csv(
      paste("D:\\nmrun\\nmrun1\\m1\\bs_pr1_", i, ".dta", sep = ""),
      header = TRUE,
      stringsAsFactors = F
    )

  one.compartment.oral.model <- function() {
    ini({
      # Where initial conditions/variables are specified
      # '<-' or '=' defines population parameters
      # Simple numeric expressions are supported
      lCl <- 1          #log Cl (L/hr)
      lVc <- 4          #log V (L)
      lKA <- 0.1        #log V (L)
      # Bounds may be specified by c(lower, est, upper), like NONMEM:
      # Residuals errors are assumed to be population parameters
      prop.err <- c(0, 0.2, 1)
      # Between subject variability estimates are specified by '~'
      # Semicolons are optional
      eta.Cl ~ 0.1
      eta.Vc ~ 0.1
      eta.KA ~ 0.1
    })
    model({
      # Where the model is specified
      # The model uses the ini-defined variable names
      Cl <- exp(lCl + eta.Cl)
      Vc <- exp(lVc + eta.Vc)
      KA <- exp(lKA + eta.KA)
      # RxODE-style differential equations are supported
      d / dt(depot) = -KA * depot

      d / dt(centr) = KA * depot - (Cl / Vc) * centr

      ## Concentration is calculated
    })
  }
}

```

```

    cp = centr / Vc

    # And is assumed to follow proportional error estimated by prop.err
    cp ~ prop(prop.err)

  })
}

fit <-
  nlmixr(
    one.compartment.oral.model,
    datr,
    est = "nlme",
    control = nlmeControl(pnlsTol = .1)
  )

save(fit, file = paste("fit_NLME_ODE_UUI_", i, ".Rdata", sep = ""))
}

```

To run these analyses in parallel, you need to set up a local virtual cluster using the `doParallel` package, in this case with 15 cores, but adjust to your own hardware:

```

#install.packages("doParallel")
library(doParallel)
cl <- makeCluster(15)
registerDoParallel(cl)

```

And then run the 500 analyses using `foreach` syntax. SAEM with ODEs takes forever for 600 subjects and 4 samples per subject, and so this chunk only runs 15 analyses:

```

timeS_Sparse <- Sys.time()
nlmixr_out <-
  foreach(i = 1:15, .packages = c('nlmixr')) %dopar% do_nlmixrODE(i)
timeE_Sparse <- Sys.time()
timeE_Sparse - timeS_Sparse
#Time difference of 1.216711 hours for only 15 runs in parallel on a 15 core cluster

```

But SAEM with solved equations is much faster!:

```

timeS_Sparse <- Sys.time()
nlmixr_out <-
  foreach(i = 1:500, .packages = c('nlmixr')) %dopar% do_nlmixr(i)
timeE_Sparse <- Sys.time()
timeE_Sparse - timeS_Sparse
#Time difference of 3.656132 hours

```

nlme with solved systems is even faster:

```

timeS_Sparse <- Sys.time()
nlmixr_out <-
  foreach(i = 1:500, .packages = c('nlmixr')) %dopar% do_nlmixr_nlme(i)

```

```
timeE_Sparse <- Sys.time()
timeE_Sparse - timeS_Sparse
#Time difference of 43.58214 mins
```

and nlme with ODEs is still very doable:

```
timeS_Sparse <- Sys.time()
nlmixr_out <-
  foreach(i = 1:500, .packages = c('nlmixr')) %dopar% do_nlmixrODE_nlme(i)
timeE_Sparse <- Sys.time()
timeE_Sparse - timeS_Sparse
#Time difference of 2.432612 hours
```

You can then read in the output from the 500 nlmixr analyses. With the new Unified User Interface, uniform storage is obtained for all estimation routines, and so a single read routine suffices!

```
Read_nlmixr <- function(Identifier) {
  for (i in 1:500) {
    filename <- paste(Identifier, "_", i, ".Rdata", sep = "")

    if (file.exists(filename)) {
      load(filename)
      TMSE <- fit$par.fixed$SE
      TM <- fit$theta
      names(TMSE) <- paste(names(TM), "_SE", sep = "")
      Time <- c("Time" = fit$table.time["elapsed"])
      IIV <- sqrt(diag(fit$omega))
      run <- c("Run" = i)
      MISSING_CWRES <- c("MISSING_CWRES" = sum(is.na(fit$CWRES)))
      TM <- c(run, TM, TMSE, Time, IIV, MISSING_CWRES)
      TM <- as.data.frame(t(TM))
      fit <- NULL
      print(i)
      if (i == 1) {
        nlmixrpars <- TM
      } else {
        nlmixrpars <- rbind(nlmixrpars, TM)
      }
    }
  }

  save(nlmixrpars, file = paste(Identifier, ".Rdata", sep = ""))
}
```

```
Read_nlmixr(Identifier = "fit_NLME_Solved_UUI")
#Read_nlmixr(Identifier = "fit_NLME_ODE_UUI")
#Read_nlmixr(Identifier = "fit_SAEM_Solved_UUI")
```

These results can then be compared with the NONMEM output and plotted to see the results. Let's start with a comparison of nlme results and NONMEM estimates. The results generated for nlme using solved equations are provided in Figure 4.1.

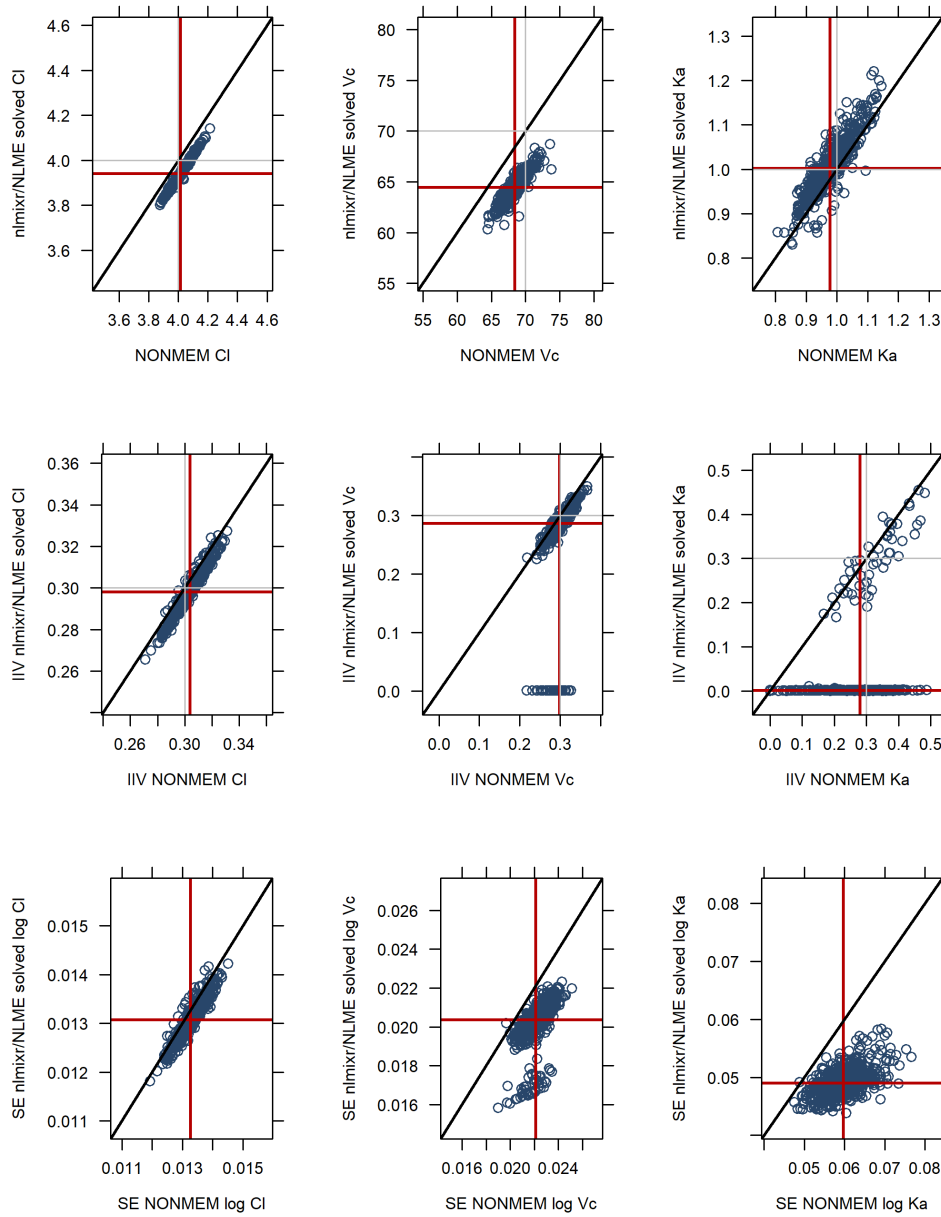


Figure 4.1: Sparse data analysis results: NONMEM FOCE-I solved vs. nlmixr/NLME solved. CI (left column), Vc (middle column), and Ka (right column), for the population parameter (top row), IIV (middle row), and SE of the log population estimate (bottom row)

Estimates for population parameters (Cl, Vc, Ka) match pretty well between NONMEM and nlme, and IIV for Cl works fine as well. However, when IIVs become a bit more difficult to estimate, like for Vc, and for Ka especially, nlme tends to return IIV values of zero quite frequently.

Next step is to compare the results for nlme with models implemented using solved equations vs. the ODE implementation (Figure 4.2).

As is clear from the graph, there is some discrepancy between the outcomes of the two model-definition methods, but this is to be expected with any numerical approach.

Next, SAEM results are compared with NONMEM FOCE-I. At this stage, estimating ODE models with a large number of subjects is prohibitively time-consuming using SAEM, and so only SAEM with solved solution results are presented (Figure 4.3).

These results show a near perfect match between NONMEM and nlmixr/SAEM population estimates, and a very good match for IIV estimates as well, where it is noted that for Ka, NONMEM estimates a number of IIVs at zero, while SAEM never does this. The standard errors for NONMEM are larger than for SAEM in all cases, but it is difficult to say which one is correct: for population parameters and IIVs, the values simulated from are known, but for standard errors this is not the case.

Finally, for a comparison between methods in terms of speed of calculations see Figure 4.4. It is clear that NONMEM is faster in virtually all cases (and SAEM with ODEs is not even reported) and these comparisons are with single-thread NONMEM. However, speeds are not so prohibitively high that use in daily practice is crippled.

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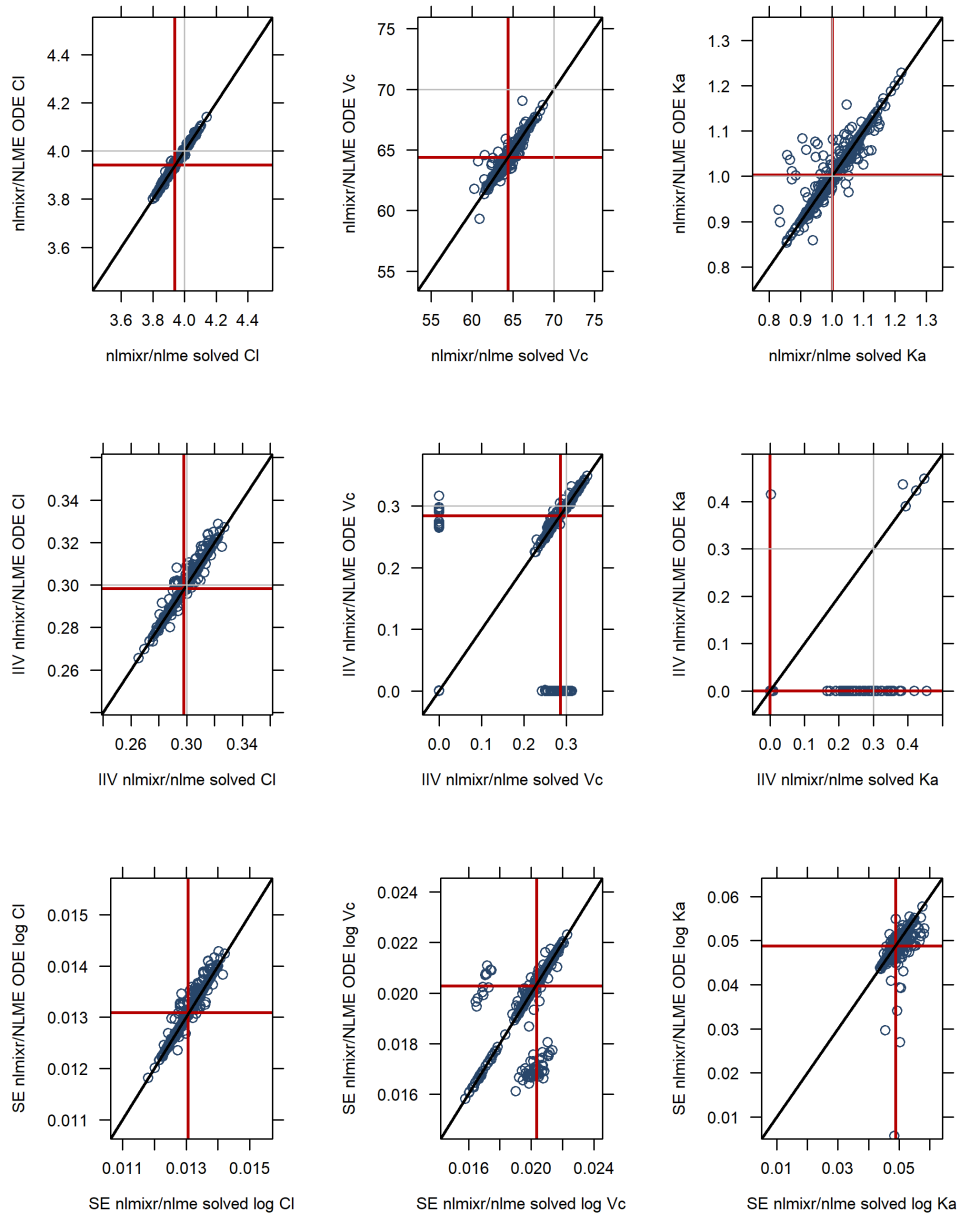


Figure 4.2: Sparse data analysis results: nlmixr/NLME solved vs. nlmixr/NLME ODE. CI (left column), Vc (middle column), and Ka (right column), for the population parameter (top row), IIV (middle row), and SE of the log population estimate (bottom row)

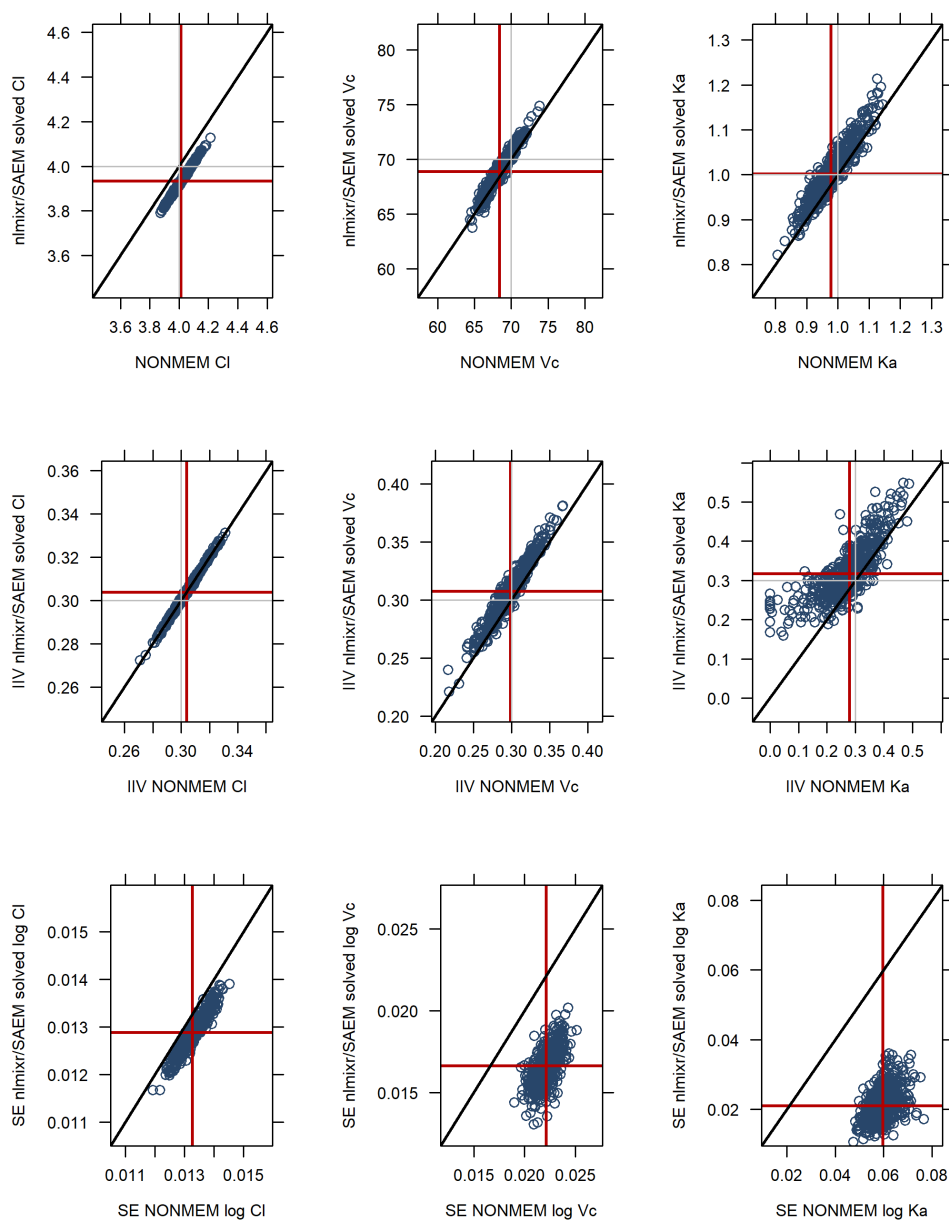


Figure 4.3: Sparse data analysis results: NONMEM FOCE I solved vs. nlmixr/SAEM solved. CI (left column), Vc (middle column), and Ka (right column), for the population parameter (top row), IIV (middle row), and SE of the log population estimate (bottom row)

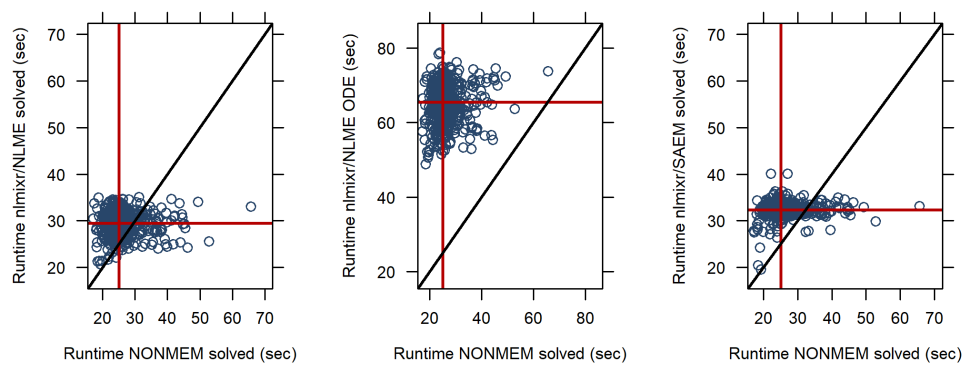


Figure 4.4: Comparison of runtimes vs NONMEM FOCE I: nlmixr/NLME solved (left), nlmixr/NLME ODE (middle), SAEM solved (right)