

Running an NMA with a Reference file

Borrowing from the approach in the **heemod** package, as well as defining the analysis in an **R** script it is also possible to specify the analysis with only file inputs. This vignette will show how to do this with a simple example.

Introduction

The idea is to create folder with all of the information needed to run the NMA analysis contained in files within. The meta information about the contents of the folder is contained in a *reference file*. The reference file is called **REFERENCE.csv**.

Reference file

This file contains two columns called **type** and **file**. Rows in the **type** column must contain one of the following keywords:

- **bugs**: File containing the BUGS input parameters for MCMC
- **analysis**: File containing the scenario information
- **subData**: Mandatory NMA data. Required column headings of **tx**, **base**, **study**, **Lmean**, **Lse**, **multi_arm**
- **subDataBin**: Optional binary data. Required column headings of **tx**, **base**, **study**, **BinN**, **BinR**
- **subDataMed**: Optional median time data. Required column headings of **tx**, **base**, **study**, **medN**, **medR**, **median**

type	file
bugs	bugs.csv
analysis	analysis.csv
subData	subData.csv

Parameter files

bugs.csv includes: OpenBUGS or WinBUGS option **PROG**, **N.BURNIN**, **N.SIMS**, **N.CHAINS**, **N.THIN**, **PAUSE**. For example,

```
PROG, openBugs
N.BURNIN, 1000
N.SIMS, 1500
N.CHAINS, 2
N.THIN, 1
PAUSE, TRUE
```

and **analysis.csv** includes: whether a random effects model, **RANDOM**; the reference treatment, **REFTX**; **effectParam**, **modelParams**, **label** and **endpoint**. For example,

```
is_random, FALSE
refTx, ERL/GEF
effectParam, beta
modelParams, totresdev
label, BC_PFS_mFE
endpoint, PFS
```

Running an NMA

A single call sets-up the NMA represented by the contents of the folder.

```
nma_model <- new_NMA_dir(data_dir = here::here("inst/analysis_folder"))
```

Run MCMC

The NMA MCMC function calls the appropriate BUGS model in the usual way.

```
nma_res <- NMA_run(nma_model)
#> ===== RUNNING BUGS MODEL
#> Warning in dir.create(path = here(folder)): 'C:\Users\Nathan\Documents\R\NMA\output' already exists

nma_res
#> Inference for Bugs model at "C:/Users/Nathan/Documents/R/NMA/inst/FE.txt",
#> 2 chains, each with 2500 iterations (first 1000 discarded)
#> n.sims = 3000 iterations saved
#>      mean sd 2.5% 25% 50% 75% 97.5% Rhat n.eff
#> beta[2] -0.3 0.1 -0.5 -0.3 -0.3 -0.2 -0.1 1 370
#> beta[3] -0.1 0.2 -0.6 -0.3 -0.1 0.0 0.3 1 480
#> beta[4] 0.5 0.1 0.2 0.4 0.5 0.5 0.7 1 3000
#> beta[5] 0.5 0.2 0.1 0.4 0.5 0.6 0.8 1 420
#> beta[6] -0.4 0.3 -1.0 -0.6 -0.4 -0.2 0.2 1 540
#> beta[7] -0.5 0.1 -0.7 -0.6 -0.5 -0.4 -0.3 1 1900
#> beta[8] -0.1 0.2 -0.4 -0.2 -0.1 0.0 0.2 1 850
#> beta[9] -0.5 0.1 -0.7 -0.6 -0.5 -0.4 -0.2 1 3000
#> beta[10] -0.7 0.1 -0.9 -0.8 -0.7 -0.6 -0.5 1 3000
#> beta[11] -0.4 0.3 -0.9 -0.5 -0.4 -0.2 0.2 1 3000
#> beta[12] 0.0 0.2 -0.3 -0.1 0.0 0.2 0.4 1 3000
#> beta[13] -0.3 0.2 -0.7 -0.4 -0.3 -0.2 0.1 1 3000
#> beta[14] -0.4 0.1 -0.7 -0.5 -0.4 -0.3 -0.1 1 1700
#> beta[15] 1.0 0.1 0.7 0.9 1.0 1.1 1.3 1 2700
#> beta[16] 0.1 0.2 -0.4 -0.1 0.0 0.2 0.5 1 530
#> beta[17] -0.2 0.3 -0.8 -0.4 -0.2 -0.1 0.3 1 1400
#> beta[18] 0.3 0.3 -0.3 0.1 0.3 0.5 0.9 1 3000
#> beta[19] -0.8 0.1 -1.0 -0.8 -0.8 -0.7 -0.6 1 3000
#> beta[20] -0.5 0.1 -0.8 -0.6 -0.5 -0.4 -0.3 1 3000
#> totresdev 27.0 6.4 16.6 22.3 26.3 31.0 40.8 1 3000
#> deviance -11.9 6.4 -22.3 -16.6 -12.5 -7.9 2.0 1 3000
#>
#> For each parameter, n.eff is a crude measure of effective sample size,
#> and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
#>
#> DIC info (using the rule, pD = Dbar-Dhat)
#> pD = 19.9 and DIC = 8.0
#> DIC is an estimate of expected predictive error (lower deviance is better).
```