How to use `nma` S3 methods

Introduction

This document describes how to use the main functions of `NMA` to run a network meta-analysis.

Example

```
library(NMA)
library(dplyr)
library(purrr)
```

Settings

Define the BUGS parameters for MCMC.

```
bugs_params <-
  list(
    PROG = "openBugs",
    N.BURNIN = 10,#00,
    N.SIMS = 150,#0,
    N.CHAINS = 2,
    N.THIN = 1,
    PAUSE = TRUE)
```

Define the scenario we will use for the analysis. We will load in a dataframe of values.

```
analyses_params <-
  read.csv(
    here::here("raw_data", "AnalysisList.csv"),
    as.is = TRUE,
    na.strings = c("NR", "NA")) %>%
  filter(Endpoint_type == "Surv") %>%
  dplyr::rename(name = Analysis_name,
                type = Analysis_Type)
```

For demonstration purposes we will select the first scenario to run.

```
analysis <- analyses_params[1, ]

# fixed effects RANDOM=FALSE, random effects RANDOM=TRUE
RANDOM <- analysis$Model_effects == "RE"

REFTX <- analysis$REFTX

# indicator for availability of binary endpoint data
is_bin <- analysis$BinData == "YES"

# indicator for availability of median endpoint data
is_med <- analysis$MedData == "YES"
```

Read in datasets

The trials data consist of upto 3 separate dataframes. A main table, `subData`, and optional tables for median event time and binary data, `subDataMed` and `subDataBin` respectively.

```
file_name <- paste0(here::here("raw_data"), "/survdata_", analysis$Endpoint, "_")

subData <-
  read.csv(paste0(file_name, analysis$type, ".csv"),
           header = TRUE,
           as.is = TRUE)

subDataBin <-
  if (is_bin) {
    read.csv(paste0(file_name, "bin.csv"),
             header = TRUE,
             as.is = TRUE)
  } else {NA}

subDataMed <-
  if (is_med) {
    read.csv(paste0(file_name, "med.csv"),
             header = TRUE,
             as.is = TRUE) %>%
      mutate(medR = floor(medR))
  } else {NA}
```

Build model

Now we can create the NMA object to use in the modelling.

```
nma_model <-
  new_NMA(subData = subData,
          subDataMed = subDataMed,
          subDataBin = subDataBin,
          bugs_params = bugs_params,
          is_random = RANDOM,
          refTx = REFTX ,
          effectParam = "beta",
          modelParams = "totresdev",
          label = analysis$name,
          endpoint = analysis$Endpoint)

nma_model
#> $dat
#> $dat$inits
#> function() {
#>       list(
#>         beta = c(NA, rnorm(nTx - 1, 0, 2)),
#>         sd = 0.1,
#>         alpha = rnorm(nStudies)) %>%
#>         .[param_names]
#>     }
#> <bytecode: 0x00000174580ede80>
#> <environment: 0x000001745825eed8>
#>
```

```
#> $dat$subData
#>     X                              study                  base            tx       Lmean       Ls
#> 1   6                ARCHER 1050 (Wu, 2017)               ERL/GEF           DAC -0.47803580 0.113440
#> 2   9                 CONVINCE (Shi 2017)                CIS+PEM           ICO -0.43078292 0.154626
#> 3  26       CTRI/2015/08/006113 (Patil 2017)            CARBO+PEM       ERL/GEF -0.41551544 0.129116
#> 4  15   CTRI/2016/08/007149 (Noronha 2019b)               ERL/GEF GEF+CARBO+PEM -0.67330000 0.134210
#> 5  22                    ENSURE (Wu 2015)               GEM+CIS       ERL/GEF -1.07880966 0.214485
#> 6   5                 FLAURA (Soria 2018)               ERL/GEF           OSI -0.77652879 0.110238
#> 7   4                 GOAL (Campelo 2018)               ERL/GEF       GEF+OLA -0.28768207 0.186450
#> 8   3                  INCREASE (Li 2018)                   ICO ICO high-dose -0.30110509 0.175849
#> 9  17 JO25567 (JapicCTI-111390) (Seto 2014)               ERL/GEF       ERL+BEV -0.61618614 0.200492
#> 10  2            LUX-Lung 3 (Sequist 2013)               CIS+PEM           AFA -0.71334989 0.143742
#> 11 24              LUX-Lung 6 (Wu 2014a)\n               GEM+CIS           AFA -1.34707365 0.163030
#> 12 25              LUX-Lung 7 (Park 2016)               ERL/GEF           AFA -0.24846136 0.123532
#> 13 20             NCT01017874 (Yang, 2014)              ERL/GEF CIS+PEM+GEF_m -0.18632958 0.344369
#> 14  7             NCT01221077 (Leighl 2017              ERL/GEF       LIN+ERL  0.31188676 0.297077
#> 15 18             NCT01469000 (Yang, 2020)              ERL/GEF       GEF+PEM -0.40047757 0.149945
#> 16 16       NCT01532089 (Stinchcombe 2019)              ERL/GEF       ERL+BEV -0.21072103 0.245707
#> 17 21                NCT01769066 (Yu 2014)              CIS+PEM CIS+PEM+GEF_m -1.60943791 0.690829
#> 18 28                NCT01864681 (Li 2019)              ERL/GEF       GEF+MET  0.03922071 0.168174
#> 19  8       NCT01897480 (Scagliotti, 2020)              ERL/GEF       EMI+ERL -0.11653382 0.165827
#> 20 12              NCT02148380 (Han, 2017)              ERL/GEF     CARBO+PEM  1.04982212 0.470613
#> 21 10              NCT02148380 (Han, 2017)              ERL/GEF       ERL/GEF  0.00000000 0.215255
#> 22 11              NCT02148380 (Han, 2017)              ERL/GEF GEF+CARBO+PEM -0.73396918 0.453945
#> 23 13      NEJ005/TCOG0902 (Sugawara, 2015) GEF+CARBO+PEM (Alter) GEF+CARBO+PEM -0.34249031 0.267811
#> 24 27  NEJ009 (UMIN000006340) (Hosomi 2019)              ERL/GEF GEF+CARBO+PEM -0.71334989 0.118258
#> 25 19                 NEJ026 (Saito 2019)               ERL/GEF       ERL+BEV -0.50252682 0.189648
#> 26  1               RELAY (Nakagawa, 2019)              ERL/GEF       RAM+ERL -0.52593926 0.127530
#> 27 14            SWOG S1403 (Goldberg 2018)                 AFA       AFA+CET  0.15700375 0.196751
#> 28 23                TORCH (Gridelli 2012)              GEM+CIS       ERL/GEF -0.51082562 0.353646
#>
#> $dat$subDataBin
#>                       study    base      tx BinR BinN Btx Bbase Bstudy
#> 1 NCT01039948 (Mok, 2016) ERL/GEF ERL/GEF   34   38   1     1     33
#> 2 NCT01039948 (Mok, 2016) ERL/GEF GEF+FIC   27   33  14     1     33
#>
#> $dat$subDataMed
#>                                     study          base            tx median medN medR mediantx medi
#> 1                                 An 2016       ERL/GEF       ERL/GEF   14.0   45   22        1
#> 2                                 An 2016       ERL/GEF       GEF+PEM   18.0   45   22       17
#> 3  CALGB 30406 (NCT00126581) (Janne 2012)       ERL/GEF       ERL/GEF   14.1   33   16        1
#> 4  CALGB 30406 (NCT00126581) (Janne 2012)       ERL/GEF ERL+PAC+CARBO   17.2   33   16       10
#> 5      GENOA / NCT02319577 (Genova, 2019)       ERL/GEF       ERL/GEF    9.5   21   10        1
#> 6      GENOA / NCT02319577 (Genova, 2019)       ERL/GEF       VIN+GEF    6.2   23   11       24
#> 7        IFCT-1503 ACE-Lung (Cortot 2019)           AFA           AFA   11.1   59   29        2
#> 8        IFCT-1503 ACE-Lung (Cortot 2019)           AFA       AFA+CET   12.8   59   29        3
#> 9                  NCT01502202 (Lee 2016) CIS+PEM+GEF_m       CIS+PEM    7.8   37   18        5
#> 10                 NCT01502202 (Lee 2016) CIS+PEM+GEF_m CIS+PEM+GEF_m   13.3   39   19        6
#> 11        UMIN000013586 (Kitagawa, 2019)       ERL/GEF       ERL/GEF   15.1   10    5        1
#> 12        UMIN000013586 (Kitagawa, 2019)       ERL/GEF       GEF+BEV    5.4    6    3       11
#>
#> $dat$bugsData
#> $dat$bugsData$Lstudy
```

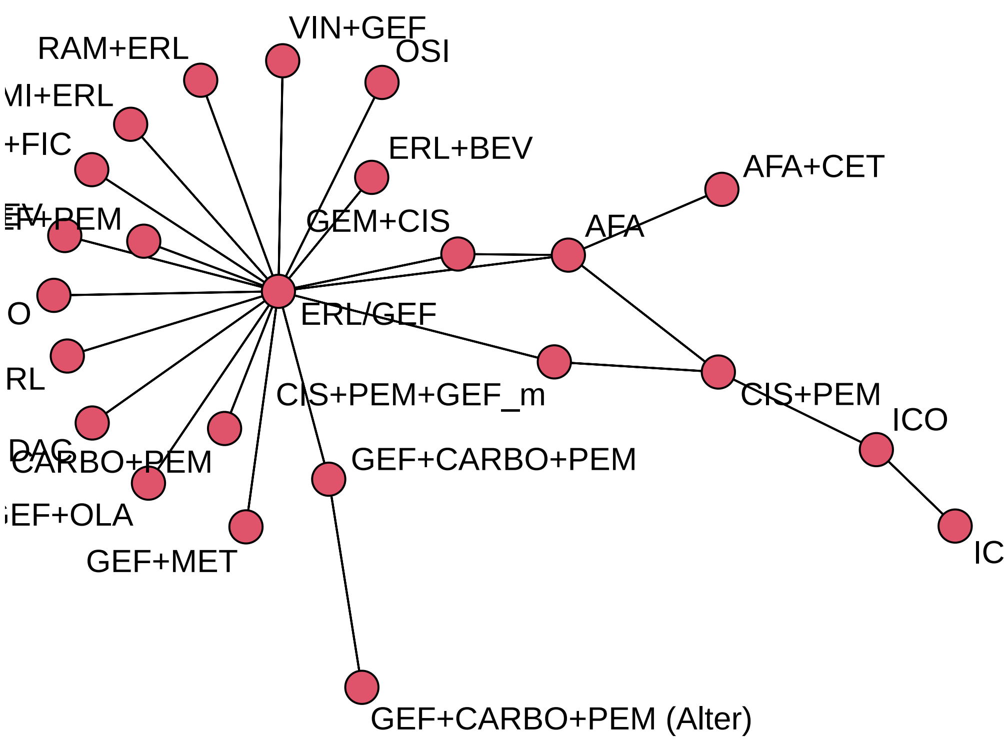
```
#>  [1]  6  9 24 13 20  5  4  3 15  2 22 23 18  7 16 14 19 26  8 10 10 10 11 25 17  1 12 21
#>
#> $dat$bugsData$Ltx
#>  [1]  7 19  1 12  1 22 16 20  9  2  2  2  6 21 17  9  6 15  8  4  1 12 12 12  9 23  3  1
#>
#> $dat$bugsData$Lbase
#>  [1]  1  5  4  1 18  1  1 19  1  5 18  1  1  1  1  1  5  1  1  1  1  1 13  1  1  1  2 18
#>
#> $dat$bugsData$Lmean
#>  [1] -0.47803580 -0.43078292 -0.41551544 -0.67330000 -1.07880966 -0.77652879 -0.28768207 -0.30110509
#> [17] -1.60943791  0.03922071 -0.11653382  1.04982212  0.00000000 -0.73396918 -0.34249031 -0.71334989
#>
#> $dat$bugsData$Lse
#>  [1] 0.1134403 0.1546265 0.1291164 0.1342100 0.2144855 0.1102381 0.1864509 0.1758496 0.2004921 0.143
#> [21] 0.2152550 0.4539455 0.2678118 0.1182584 0.1896482 0.1275307 0.1967513 0.3536465
#>
#> $dat$bugsData$multi
#>  [1] 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 1 1 1 0 0 0 0 0 0
#>
#> $dat$bugsData$LnObs
#> [1] 28
#>
#> $dat$bugsData$nTx
#> [1] 24
#>
#> $dat$bugsData$nStudies
#> [1] 33
#>
#> $dat$bugsData$medianStudy
#>  [1] 27 27 30 30 32 32 29 29 31 31 28 28
#>
#> $dat$bugsData$medianTx
#>  [1]  1 17  1 10  1 24  2  3  5  6  1 11
#>
#> $dat$bugsData$medianBase
#>  [1] 1 1 1 1 1 1 2 2 6 6 1 1
#>
#> $dat$bugsData$Bstudy
#> [1] 33 33
#>
#> $dat$bugsData$Btx
#> [1]  1 14
#>
#> $dat$bugsData$Bbase
#> [1] 1 1
#>
#> $dat$bugsData$medianN
#>  [1] 45 45 33 33 21 23 59 59 37 39 10  6
#>
#> $dat$bugsData$medianR
#>  [1] 22 22 16 16 10 11 29 29 18 19  5  3
#>
#> $dat$bugsData$median
```

```
#>  [1] 14.0 18.0 14.1 17.2  9.5  6.2 11.1 12.8  7.8 13.3 15.1  5.4
#>
#> $dat$bugsData$medianNObs
#> [1] 12
#>
#> $dat$bugsData$Bn
#> [1] 38 33
#>
#> $dat$bugsData$Br
#> [1] 34 27
#>
#> $dat$bugsData$BnObs
#> [1] 2
#>
#>
#> $dat$txList
#>  [1] "ERL/GEF"               "AFA"                   "AFA+CET"               "CARBO+PEM"
#>  [9] "ERL+BEV"               "ERL+PAC+CARBO"         "GEF+BEV"               "GEF+CARBO+PEM"
#> [17] "GEF+PEM"               "GEM+CIS"               "ICO"                   "ICO high-dose"
#>
#>
#> $is_med
#> [1] TRUE
#>
#> $is_bin
#> [1] TRUE
#>
#> $bugs_params
#> $bugs_params$PROG
#> [1] "openBugs"
#>
#> $bugs_params$N.BURNIN
#> [1] 10
#>
#> $bugs_params$N.SIMS
#> [1] 150
#>
#> $bugs_params$N.CHAINS
#> [1] 2
#>
#> $bugs_params$N.THIN
#> [1] 1
#>
#> $bugs_params$PAUSE
#> [1] TRUE
#>
#> $bugs_params$run_bugs
#> [1] TRUE
#>
#>
#> $bugs_fn
#> function(...)
#>         bugs(program = "openbugs", ...)
```

```
#> <bytecode: 0x000001745392bbc8>
#> <environment: 0x000001745e367750>
#>
#> $is_random
#> [1] FALSE
#>
#> $refTx
#> [1] "ERL/GEF"
#>
#> $effectParam
#> [1] "beta"
#>
#> $modelParams
#> [1] "totresdev"
#>
#> $label
#> [1] "BC_PFS_mFE"
#>
#> $endpoint
#> [1] "PFS"
#>
#> attr(,"class")
#> [1] "nma"
#> attr(,"CALL")
#> attr(,"CALL")$subData
#> subData
#>
#> attr(,"CALL")$subDataMed
#> subDataMed
#>
#> attr(,"CALL")$subDataBin
#> subDataBin
#>
#> attr(,"CALL")$bugs_params
#> bugs_params
#>
#> attr(,"CALL")$is_random
#> RANDOM
#>
#> attr(,"CALL")$refTx
#> REFTX
#>
#> attr(,"CALL")$effectParam
#> [1] "beta"
#>
#> attr(,"CALL")$modelParams
#> [1] "totresdev"
#>
#> attr(,"CALL")$label
#> analysis$name
#>
#> attr(,"CALL")$endpoint
#> analysis$Endpoint
```

We can view the network graph.

```
library(sna)
plotNetwork(nma_model)
```



Run MCMC

```
nma_res <- NMA_run(nma_model)
#> Loading required namespace: BRugs
#> Welcome to BRugs connected to OpenBUGS version 3.2.3
#> model is syntactically correct
#> data loaded
#> model compiled
#> Initializing chain 1:
#> initial values loaded and chain initialized but another chain contain uninitialized variables
#> Initializing chain 2:
#> model is initialized
```

```
#> model is already initialized
#> Sampling has been started ...
#> 10 updates took 0 s
#> deviance set
#> monitor set for variable 'beta'
#> monitor set for variable 'totresdev'
#> monitor set for variable 'deviance'
#> 150 updates took 0 s
#> Warning in dir.create(path = here(folder)): 'C:\Users\Nathan\Documents\ICON\NMA\output' already exis

nma_res
#> Inference for Bugs model at "C:/Users/Nathan/Documents/ICON/NMA/inst/FE_med_bin.txt", fit using Open
#>  2 chains, each with 160 iterations (first 10 discarded)
#>  n.sims = 300 iterations saved
#>            mean    sd  2.5%   25%   50%   75%  97.5% Rhat n.eff
#> beta[2]     0.2   0.7  -0.7  -0.5   0.1   0.7    1.3  2.2     4
#> beta[3]    -0.9   0.9  -2.2  -2.0  -0.5  -0.1    0.0  7.0     2
#> beta[4]     0.5   0.1   0.2   0.4   0.4   0.5    0.7  1.0   210
#> beta[5]     1.4   0.6   0.1   1.2   1.4   1.8    2.3  2.0     4
#> beta[6]     0.8   0.7  -0.2   0.4   0.9   1.1    2.8  1.5     6
#> beta[7]    -0.5   0.1  -0.7  -0.5  -0.5  -0.4   -0.2  1.0   300
#> beta[8]    -0.1   0.2  -0.4  -0.2  -0.1   0.0    0.2  1.0   190
#> beta[9]    -0.5   0.1  -0.7  -0.6  -0.5  -0.4   -0.3  1.0   210
#> beta[10]   -0.2   0.7  -1.3  -0.5  -0.2   0.1    0.7  1.2   230
#> beta[11]    0.9   0.8  -0.6   0.4   1.0   1.4    2.2  1.1    26
#> beta[12]   -0.7   0.1  -0.9  -0.8  -0.7  -0.6   -0.5  1.0   300
#> beta[13]   -0.4   0.3  -0.9  -0.6  -0.4  -0.2    0.3  1.0   150
#> beta[14]   -0.3   0.2  -0.7  -0.4  -0.3  -0.2    0.2  1.1    21
#> beta[15]    0.0   0.2  -0.3  -0.1   0.0   0.1    0.3  1.0   110
#> beta[16]   -0.3   0.2  -0.6  -0.4  -0.3  -0.2    0.1  1.0   300
#> beta[17]   -0.9   0.6  -2.1  -1.5  -0.6  -0.4   -0.2  1.0    91
#> beta[18]    1.3   0.4   0.7   0.9   1.3   1.6    1.9  2.1     4
#> beta[19]    0.9   0.6  -0.4   0.6   0.9   1.4    1.9  2.8     3
#> beta[20]    0.6   0.6  -0.7   0.3   0.7   1.1    1.7  2.6     3
#> beta[21]    0.3   0.3  -0.3   0.1   0.3   0.5    0.8  1.0   300
#> beta[22]   -0.8   0.1  -1.0  -0.8  -0.8  -0.7   -0.6  1.0   300
#> beta[23]   -0.5   0.1  -0.8  -0.6  -0.5  -0.4   -0.3  1.0   200
#> beta[24]    0.4   0.6  -0.7   0.0   0.3   0.8    1.4  1.2    11
#> totresdev 655.5 578.3 110.6 293.6 385.8 919.6 1813.1  1.1    41
#> deviance  670.8 578.7 126.9 309.2 400.9 933.8 1833.6  1.1    45
#>
#> 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 = 349.8 and DIC = 1021.0
#> DIC is an estimate of expected predictive error (lower deviance is better).

# diagnostics(nma_res)
# nma_outputs(nma_res)
```

Reconfigure model

It is simple to modify an existing analysis without repeating the previous steps. For example, we can run the NMA for a random effects model version of the same model.

```
nma_model2 <-
  NMA_update(nma_model,
             is_random = TRUE)

nma_res2 <- NMA_run(nma_model2,
                    output_dir = "RE output")
#> model is syntactically correct
#> data loaded
#> model compiled
#> Initializing chain 1:
#> initial values loaded but chain contain uninitialized variables
#> Initializing chain 2:
#> initial values loaded but chain contain uninitialized variables
#> initial values generated, model initialized
#> Sampling has been started ...
#> 10 updates took 0 s
#> deviance set
#> monitor set for variable 'beta'
#> monitor set for variable 'totresdev'
#> monitor set for variable 'deviance'
#> 150 updates took 0 s
#> Warning in dir.create(path = here(folder)): 'C:\Users\Nathan\Documents\ICON\NMA\RE output' already e

nma_res2
#> Inference for Bugs model at "C:/Users/Nathan/Documents/ICON/NMA/inst/RE_med_bin.txt", fit using Open
#>  2 chains, each with 160 iterations (first 10 discarded)
#>  n.sims = 300 iterations saved
#>           mean  sd  2.5%  25%  50%  75% 97.5% Rhat n.eff
#> beta[2]   -0.6 5.4  -7.0 -6.3  0.1  4.6   5.9 12.1     2
#> beta[3]   -5.5 3.2 -10.1 -9.2 -3.4 -2.6  -1.8  5.3     2
#> beta[4]    0.4 1.7  -2.1 -1.5  0.9  1.9   2.8  6.3     2
#> beta[5]    1.1 1.1  -0.9  0.4  0.7  2.3   3.1  1.7     6
#> beta[6]    0.8 3.9  -5.4 -3.9  2.6  4.3   5.1  5.2     2
#> beta[7]   -1.1 1.2  -3.5 -2.2 -0.9 -0.1   0.7  1.9     4
#> beta[8]   -2.2 0.9  -3.7 -2.9 -2.3 -1.7  -0.1  1.0   300
#> beta[9]   -0.9 1.0  -2.8 -1.3 -0.7 -0.2   0.7  1.2    26
#> beta[10]  -1.8 1.3  -3.6 -2.6 -2.2 -0.9   0.9  3.5     3
#> beta[11]   2.0 1.3  -1.0  1.3  2.2  2.9   4.3  1.1    15
#> beta[12]  -1.2 0.5  -2.0 -1.5 -1.3 -1.0  -0.3  2.0     4
#> beta[13]  -2.6 2.2  -6.5 -3.8 -2.5 -0.8   0.8  3.6     3
#> beta[14]  -0.7 1.1  -2.1 -1.5 -1.0  0.2   1.6  1.9     4
#> beta[15]   0.1 1.2  -2.0 -0.8 -0.1  1.1   2.2  3.4     3
#> beta[16]   1.7 0.8   0.0  1.1  1.8  2.4   2.9  1.0   260
#> beta[17]   3.2 3.0  -0.3  0.6  0.8  6.2   7.8  4.0     2
#> beta[18]   0.8 2.1  -2.4 -1.1  0.7  2.6   4.4  6.2     2
#> beta[19]   1.7 2.4  -1.2 -0.5  0.8  4.4   5.3  6.0     2
#> beta[20]   1.4 1.3  -0.7  0.3  1.5  2.6   3.7  4.3     2
#> beta[21]   2.0 1.5  -1.7  1.2  2.2  3.2   4.3  1.2    24
#> beta[22]   1.3 1.5  -0.5  0.2  0.7  2.8   4.3  2.7     3
#> beta[23]  -2.3 1.0  -3.8 -2.9 -2.5 -1.9   0.0  1.7     5
```

```
#> beta[24]     0.5   1.2  -1.7  -0.5   0.7   1.7    2.3  3.8     2
#> totresdev 423.5 398.4  69.8 104.6 394.6 580.1 1670.6  5.3     2
#> deviance  440.8 401.0  84.7 121.1 412.8 594.5 1699.7  5.3     2
#>
#> 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 = 216.0 and DIC = 656.8
#> DIC is an estimate of expected predictive error (lower deviance is better).

# diagnostics(nma_res2, save = TRUE)
# nma_outputs(nma_res2, save = TRUE)
```