Package 'babelmixr2'

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Type Package

Title Use 'nlmixr2' to Interact with Open Source and Commercial Software

Version 0.1.8

Description Run other estimation and simulation software via the 'nlmixr2' (Fidler et al (2019) <doi:10.1002/psp4.12445>) interface including 'PKNCA', 'NONMEM' and 'Monolix'. While not required, you can get/install the 'lixoftConnectors' package in the 'Monolix' installation, as described at the following url <https://monolixsuite.slp-software.com/r-functions/2024R1/installation-and-initialization>. When 'lixoftConnectors' is available, 'Monolix' can be run directly instead of setting up command line usage.

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URL https://nlmixr2.github.io/babelmixr2/, https://github.com/nlmixr2/babelmixr2/

NeedsCompilation yes

Encoding UTF-8

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Contents

`.setupPopEDdatabase` *Setup the poped database*

Description

Setup the poped database

Usage

```
.setupPopEDdatabase(ui, data, control)
```

Arguments

`ui`	rxode2 ui function
`data`	babelmixr2 design data
`control`	PopED control

Value

PopED database

Author(s)

Matthew L. Fidler

`as.nlmixr2` *Convert an object to a nlmixr2 fit object*

Description

Convert an object to a nlmixr2 fit object

Usage

```
as.nlmixr2(
  x,
  ...,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  ci = 0.95
)

as.nlmixr(
  x,
  ...,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  ci = 0.95
)
```

Arguments

`x`	Object to convert
`...`	Other arguments
`table`	is the `nlmixr2est::tableControl()` options
`rxControl`	is the `rxode2::rxControl()` options, which is generally needed for how `addl` doses are handled in the translation
`ci`	is the confidence interval of the residual differences calculated (by default 0.95)

Value

nlmixr2 fit object

Author(s)

Matthew L. Fidler

Examples

```
# First read in the model (but without residuals)
mod <- nonmem2rx(system.file("mods/cpt/runODE032.ctl", package="nonmem2rx"),
                 determineError=FALSE, lst=".res", save=FALSE)

# define the model with residuals (and change the name of the
# parameters) In this step you need to be careful to not change the
# estimates and make sure the residual estimates are correct (could
# have to change var to sd).

 mod2 <-function() {
   ini({
     lcl <- 1.37034036528946
     lvc <- 4.19814911033061
     lq <- 1.38003493562413
     lvp <- 3.87657341967489
     RSV <- c(0, 0.196446108190896, 1)
     eta.cl ~ 0.101251418415006
     eta.v ~ 0.0993872449483344
     eta.q ~ 0.101302674763154
     eta.v2 ~ 0.0730497519364148
   })
   model({
     cmt(CENTRAL)
     cmt(PERI)
     cl <- exp(lcl + eta.cl)
     v <- exp(lvc + eta.v)
     q <- exp(lq + eta.q)
     v2 <- exp(lvp + eta.v2)
     v1 <- v
     scale1 <- v
     k21 <- q/v2
     k12 <- q/v
     d/dt(CENTRAL) <- k21 * PERI - k12 * CENTRAL - cl * CENTRAL/v1
     d/dt(PERI) <- -k21 * PERI + k12 * CENTRAL
     f <- CENTRAL/scale1
     f ~ prop(RSV)
   })
 }

# now we create another nonmem2rx object that validates the model above:

new <- as.nonmem2rx(mod2, mod)

# once that is done, you can translate to a full nlmixr2 fit (if you wish)
```

```
fit <- as.nlmixr2(new)

print(fit)
```

`babel.poped.database` *Expand a babelmixr2 PopED database*

Description

Expand a babelmixr2 PopED database

Usage

```
babel.poped.database(popedInput, ..., optTime = NA)
```

Arguments

`popedInput`	The babelmixr2 generated PopED database
`...`	other parameters sent to `PopED::create.poped.database()`
`optTime`	boolean to indicate if the global time indexer inside of babelmixr2 is reset if the times are different. By default this is `TRUE`. If `FALSE` you can get slightly better run times and possibly slightly different results. When `optTime` is `FALSE` the global indexer is reset every time the PopED rxode2 is setup for a problem or when a poped dataset is created. You can manually reset with `popedMultipleEndpointResetTimeIndex`

Value

babelmixr2 PopED database (with $babelmixr2 in database)

Author(s)

Matthew L. Fidler

`babelBpopIdx` *Get the bpop_idx by variable name for a poped database created by* `babelmixr2`

Description

This may work for other poped databases if the population parameters are named.

Usage

```
babelBpopIdx(popedInput, var)
```

Arguments

popedInput	The babelmixr2 created database
var	variable to query

Value

index of the variable

Author(s)

Matthew L. Fidler

Examples

```
if (requireNamespace("PopED", quietly=TRUE)) {

f <- function() {
  ini({
    tV <- 72.8
    tKa <- 0.25
    tCl <- 3.75
    tF <- fix(0.9)
    pedCL <- 0.8

    eta.v ~ 0.09
    eta.ka ~ 0.09
    eta.cl ~0.25^2

    prop.sd <- fix(sqrt(0.04))
    add.sd <- fix(sqrt(5e-6))

  })
  model({
    V<-tV*exp(eta.v)
    KA<-tKa*exp(eta.ka) * (pedCL**isPediatric) # add covariate for pediatrics
    CL<-tCl*exp(eta.cl)
    Favail <- tF

    N <-  floor(t/TAU)+1
    y <- (DOSE*Favail/V)*(KA/(KA - CL/V)) *
      (exp(-CL/V * (t - (N - 1) * TAU)) *
         (1 - exp(-N * CL/V * TAU))/(1 - exp(-CL/V * TAU)) -
         exp(-KA * (t - (N - 1) * TAU)) * (1 - exp(-N * KA * TAU))/(1 - exp(-KA * TAU)))

    y ~ prop(prop.sd) + add(add.sd)
  })
}

e <- et(c( 1,8,10,240,245))

babel.db <- nlmixr2(f, e, "poped",
```

```
                    popedControl(m = 2,
                                 groupsize=20,
                                 bUseGrouped_xt=TRUE,
                                 a=list(c(DOSE=20,TAU=24,isPediatric = 0),
                                        c(DOSE=40, TAU=24,isPediatric = 0))))

babelBpopIdx(babel.db, "pedCL")

}
```

---

bblDatToMonolix *Convert nlmixr2-compatible data to other formats (if possible)*

Description

Convert nlmixr2-compatible data to other formats (if possible)

Usage

```
bblDatToMonolix(
  model,
  data,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  env = NULL
)

bblDatToNonmem(
  model,
  data,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  env = NULL
)

bblDatToRxode(
  model,
  data,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  env = NULL
)

bblDatToMrgsolve(
  model,
  data,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
```

```
  env = NULL
)

bblDatToPknca(
  model,
  data,
  table = nlmixr2est::tableControl(),
  rxControl = rxode2::rxControl(),
  env = NULL
)
```

Arguments

model	rxode2 model for conversion
data	Input dataset.
table	is the table control; this is mostly to figure out if there are additional columns to keep.
rxControl	is the rxode2 control options; This is to figure out how to handle the addl dosing information.
env	When NULL (default) nothing is done. When an environment, the function nlmixr2est::.foceiPreProce env, model, rxControl) is called on the provided environment.

Value

With the function bblDatToMonolix() return a list with:

- Monolix compatible dataset ($monolix)
- Monolix ADM information ($adm)

With the function nlmixrDataToNonmem() return a dataset that is compatible with NONMEM.

With the function nlmixrDataToMrgsolve() return a dataset that is compatible with mrgsolve. Unlike NONMEM, it supports replacement events with evid=8 (note with rxode2 replacement evid is 5).

With the function nlmixrDataToRxode() this will normalize the dataset to use newer evid definitions that are closer to NONMEM instead of any classic definitions that are used at a lower level

Author(s)

Matthew L. Fidler

Examples

```
pk.turnover.emax3 <- function() {
  ini({
    tktr <- log(1)
    tka <- log(1)
    tcl <- log(0.1)
    tv <- log(10)
```

```
    ##
    eta.ktr ~ 1
    eta.ka ~ 1
    eta.cl ~ 2
    eta.v ~ 1
    prop.err <- 0.1
    pkadd.err <- 0.1
    ##
    temax <- logit(0.8)
    tec50 <- log(0.5)
    tkout <- log(0.05)
    te0 <- log(100)
    ##
    eta.emax ~ .5
    eta.ec50  ~ .5
    eta.kout ~ .5
    eta.e0 ~ .5
    ##
    pdadd.err <- 10
  })
  model({
    ktr <- exp(tktr + eta.ktr)
    ka <- exp(tka + eta.ka)
    cl <- exp(tcl + eta.cl)
    v <- exp(tv + eta.v)
    emax = expit(temax+eta.emax)
    ec50 =  exp(tec50 + eta.ec50)
    kout = exp(tkout + eta.kout)
    e0 = exp(te0 + eta.e0)
    ##
    DCP = center/v
    PD=1-emax*DCP/(ec50+DCP)
    ##
    effect(0) = e0
    kin = e0*kout
    ##
    d/dt(depot) = -ktr * depot
    d/dt(gut) =  ktr * depot -ka * gut
    d/dt(center) =  ka * gut - cl / v * center
    d/dt(effect) = kin*PD -kout*effect
    ##
    cp = center / v
    cp ~ prop(prop.err) + add(pkadd.err)
    effect ~ add(pdadd.err) | pca
  })
}

bblDatToMonolix(pk.turnover.emax3, nlmixr2data::warfarin)

bblDatToNonmem(pk.turnover.emax3, nlmixr2data::warfarin)

bblDatToMrgsolve(pk.turnover.emax3, nlmixr2data::warfarin)
```

```
bblDatToRxode(pk.turnover.emax3, nlmixr2data::warfarin)
```

`getStandardColNames` *Determine standardized rxode2 column names from data*

Description

Determine standardized rxode2 column names from data

Usage

```
getStandardColNames(data)
```

Arguments

`data`	A data.frame as the source for column names

Value

A named character vector where the names are the standardized names and the values are either the name of the column from the data or `NA` if the column is not present in the data.

Examples

```
getStandardColNames(data.frame(ID=1, DV=2, Time=3, CmT=4))
```

`modelUnitConversion` *Unit conversion for pharmacokinetic models*

Description

Unit conversion for pharmacokinetic models

Usage

```
modelUnitConversion(
  dvu = NA_character_,
  amtu = NA_character_,
  timeu = NA_character_,
  volumeu = NA_character_
)
```

Arguments

`dvu`, `amtu`, `timeu`	The units for the DV, AMT, and TIME columns in the data
`volumeu`	The units for the volume parameters in the model

Value

A list with names for the units associated with each parameter ("amtu", "clearanceu", "volumeu", "timeu", "dvu") and the numeric value to multiply the modeled estimate (for example, cp) so that the model is consistent with the data units.

See Also

Other Unit conversion: `simplifyUnit()`

Examples

```
modelUnitConversion(dvu = "ng/mL", amtu = "mg", timeu = "hr", volumeu = "L")
```

---

monolixControl *Monolix Controller for nlmixr2*

Description

Monolix Controller for nlmixr2

Usage

```
monolixControl(
  nbSSDoses = 7,
  useLinearization = FALSE,
  stiff = FALSE,
  addProp = c("combined2", "combined1"),
  exploratoryAutoStop = FALSE,
  smoothingAutoStop = FALSE,
  burnInIterations = 5,
  smoothingIterations = 200,
  exploratoryIterations = 250,
  simulatedAnnealingIterations = 250,
  exploratoryInterval = 200,
  exploratoryAlpha = 0,
  omegaTau = 0.95,
  errorModelTau = 0.95,
  variability = c("none", "firstStage", "decreasing"),
  runCommand = getOption("babelmixr2.monolix", ""),
  rxControl = NULL,
  sumProd = FALSE,
  optExpression = TRUE,
  calcTables = TRUE,
  compress = TRUE,
  ci = 0.95,
  sigdigTable = NULL,
  absolutePath = FALSE,
```

```
  modelName = NULL,
  muRefCovAlg = TRUE,
  run = TRUE,
  ...
)
```

Arguments

`nbSSDoses`	Number of steady state doses (default 7)
`useLinearization`	Use linearization for log likelihood and fim.
`stiff`	boolean for using the stiff ODE solver
`addProp`	specifies the type of additive plus proportional errors, the one where standard deviations add (combined1) or the type where the variances add (combined2). The combined1 error type can be described by the following equation: $$y = f + (a + b \times f^c) \times \varepsilon$$ The combined2 error model can be described by the following equation: $$y = f + \sqrt{a^2 + b^2 \times f^{2 \times c}} \times \varepsilon$$ Where: - y represents the observed value - f represents the predicted value - a is the additive standard deviation - b is the proportional/power standard deviation - c is the power exponent (in the proportional case c=1)
`exploratoryAutoStop`	logical to turn on or off exploratory phase auto-stop of SAEM (default 250)
`smoothingAutoStop`	Boolean indicating if the smoothing should automatically stop (default `FALSE`)
`burnInIterations`	Number of burn in iterations
`smoothingIterations`	Number of smoothing iterations
`exploratoryIterations`	Number of iterations for exploratory phase (default 250)
`simulatedAnnealingIterations`	Number of simulating annealing iterations
`exploratoryInterval`	Minimum number of iterations in the exploratory phase (default 200)
`exploratoryAlpha`	Convergence memory in the exploratory phase (only used when `exploratoryAutoStop` is `TRUE`)
`omegaTau`	Proportional rate on variance for simulated annealing

errorModelTau	Proportional rate on error model for simulated annealing
variability	This describes the methodology for parameters without variability. It could be: - Fixed throughout (none) - Variability in the first stage (firstStage) - Decreasing until it reaches the fixed value (decreasing)
runCommand	is a shell command or function to run monolix; You can specify the default by `options("babelmixr2.monolix"="runMonolix")`. If it is empty and 'lixoftConnectors' is available, use lixoftConnectors to run monolix. See details for function usage.
rxControl	'rxode2' ODE solving options during fitting, created with 'rxControl()'
sumProd	Is a boolean indicating if the model should change multiplication to high precision multiplication and sums to high precision sums using the PreciseSums package. By default this is FALSE.
optExpression	Optimize the rxode2 expression to speed up calculation. By default this is turned on.
calcTables	This boolean is to determine if the foceiFit will calculate tables. By default this is TRUE
compress	Should the object have compressed items
ci	Confidence level for some tables. By default this is 0.95 or 95% confidence.
sigdigTable	Significant digits in the final output table. If not specified, then it matches the significant digits in the 'sigdig' optimization algorithm. If 'sigdig' is NULL, use 3.
absolutePath	Boolean indicating if the absolute path should be used for the monolix runs
modelName	Model name used to generate the NONMEM output. If NULL try to infer from the model name (could be x if not clear). Otherwise use this character for outputs.
muRefCovAlg	This controls if algebraic expressions that can be mu-referenced are treated as mu-referenced covariates by: 1. Creating a internal data-variable 'nlmixrMuDerCov#' for each algebraic mu-referenced expression 2. Change the algebraic expression to 'nlmixrMuDerCov# * mu_cov_theta' 3. Use the internal mu-referenced covariate for saem 4. After optimization is completed, replace 'model()' with old 'model()' expression 5. Remove 'nlmixrMuDerCov#' from nlmix2 output In general, these covariates should be more accurate since it changes the system to a linear compartment model. Therefore, by default this is 'TRUE'.
run	Should monolix be run and the results be imported to nlmixr2? (Default is TRUE)
...	Ignored parameters

Details

If runCommand is given as a string, it will be called with the system() command like:

runCommand mlxtran.

For example, if `runCommand="'/path/to/monolix/mlxbsub2021' -p "` then the command line used would look like the following:

`'/path/to/monolix/mlxbsub2021' monolix.mlxtran`

If `runCommand` is given as a function, it will be called as `FUN(mlxtran, directory, ui)` to run Monolix. This allows you to run Monolix in any way that you may need, as long as you can write it in R. babelmixr2 will wait for the function to return before proceeding.

If `runCommand` is `NA`, `nlmixr()` will stop after writing the model files and without starting Monolix.

Note that you can get the translated monolix components from a parsed/compiled rxode2 ui object with `ui$monolixModel` and `ui$mlxtran`

Value

A monolix control object

Author(s)

Matthew Fidler

`nlmixr2Est.pknca` *Estimate starting parameters using PKNCA*

Description

Estimate starting parameters using PKNCA

Usage

```
## S3 method for class 'pknca'
nlmixr2Est(env, ...)
```

Arguments

`env`	Environment for the nlmixr2 estimation routines. This needs to have: - rxode2 ui object in '$ui' - data to fit in the estimation routine in '$data' - control for the estimation routine's control options in '$ui'
`...`	Other arguments provided to 'nlmixr2Est()' provided for flexibility but not currently used inside nlmixr

Details

Parameters are estimated as follows:

- ka 4 half-lives to Tmax but not higher than 3: `log(2)/(tmax/4)`
- vc Inverse of dose-normalized Cmax
- cl Estimated as the median clearance
- vp, vp2 2- and 4-fold the vc, respectively by default, controlled by the `vpMult` and `vp2Mult` arguments to `pkncaControl`
- q, q2 0.5- and 0.25-fold the cl, respectively by default, controlled by the `qMult` and `q2Mult` arguments to `pkncaControl`

The bounds for the parameter estimates are set to 10% of the first percentile and 10 times the 99th percentile. (For ka, the lower bound is set to the lower of 10% of the first percentile or 0.03 and the upper bound is not modified from 10 times the 99th percentile.)

Parameter estimation methods may be changed in a future version.

Value

A model with updated starting parameters. In the model a new element named "nca" will be available which includes the PKNCA results used for the calculation.

---

nonmemControl *NONMEM estimation control*

Description

NONMEM estimation control

Usage

```
nonmemControl(
  est = c("focei", "imp", "its", "posthoc"),
  advanOde = c("advan13", "advan8", "advan6"),
  cov = c("r,s", "r", "s", ""),
  maxeval = 1e+05,
  tol = 6,
  atol = 12,
  sstol = 6,
  ssatol = 12,
  sigl = 12,
  sigdig = 3,
  print = 1,
  extension = getOption("babelmixr2.nmModelExtension", ".nmctl"),
  outputExtension = getOption("babelmixr2.nmOutputExtension", ".lst"),
  runCommand = getOption("babelmixr2.nonmem", ""),
  iniSigDig = 5,
```

```
  protectZeros = FALSE,
  muRef = TRUE,
  addProp = c("combined2", "combined1"),
  rxControl = NULL,
  sumProd = FALSE,
  optExpression = TRUE,
  calcTables = TRUE,
  compress = TRUE,
  ci = 0.95,
  sigdigTable = NULL,
  readRounding = FALSE,
  readBadOpt = FALSE,
  niter = 100L,
  isample = 1000L,
  iaccept = 0.4,
  iscaleMin = 0.1,
  iscaleMax = 10,
  df = 4,
  seed = 14456,
  mapiter = 1,
  mapinter = 0,
  noabort = TRUE,
  modelName = NULL,
  muRefCovAlg = TRUE,
  run = TRUE,
  ...
)
```

Arguments

est	NONMEM estimation method
advanOde	The ODE solving method for NONMEM
cov	The NONMEM covariance method
maxeval	NONMEM's maxeval (for non posthoc methods)
tol	NONMEM tolerance for ODE solving advan
atol	NONMEM absolute tolerance for ODE solving
sstol	NONMEM tolerance for steady state ODE solving
ssatol	NONMEM absolute tolerance for steady state ODE solving
sigl	NONMEM sigl estimation option
sigdig	the significant digits for NONMEM
print	The print number for NONMEM
extension	NONMEM file extensions
outputExtension	Extension to use for the NONMEM output listing
runCommand	Command to run NONMEM (typically the path to "nmfe75") or a function. See the details for more information.

`iniSigDig` How many significant digits are printed in $THETA and $OMEGA when the estimate is zero. Also controls the zero protection numbers

`protectZeros` Add methods to protect divide by zero

`muRef` Automatically mu-reference the control stream

`addProp`, `sumProd`, `optExpression`, `calcTables`, `compress`, `ci`, `sigdigTable` Passed to `nlmixr2est::foceiControl`

`rxControl` Options to pass to `rxode2::rxControl` for simulations

`readRounding` Try to read NONMEM output when NONMEM terminated due to rounding errors

`readBadOpt` Try to read NONMEM output when NONMEM terminated due to an apparent failed optimization

`niter` number of iterations in NONMEM estimation methods

`isample` Isample argument for NONMEM ITS estimation method

`iaccept` Iaccept for NONMEM ITS estimation methods

`iscaleMin` parameter for IMP NONMEM method (ISCALE_MIN)

`iscaleMax` parameter for IMP NONMEM method (ISCALE_MAX)

`df` degrees of freedom for IMP method

`seed` is the seed for NONMEM methods

`mapiter` the number of map iterations for IMP method

`mapinter` is the MAPINTER parameter for the IMP method

`noabort` Add the `NOABORT` option for `$EST`

`modelName` Model name used to generate the NONMEM output. If `NULL` try to infer from the model name (could be `x` if not clear). Otherwise use this character for outputs.

`muRefCovAlg` This controls if algebraic expressions that can be mu-referenced are treated as mu-referenced covariates by:

1. Creating a internal data-variable 'nlmixrMuDerCov#' for each algebraic mu-referenced expression
2. Change the algebraic expression to 'nlmixrMuDerCov# * mu_cov_theta'
3. Use the internal mu-referenced covariate for saem
4. After optimization is completed, replace 'model()' with old 'model()' expression
5. Remove 'nlmixrMuDerCov#' from nlmix2 output

In general, these covariates should be more accurate since it changes the system to a linear compartment model. Therefore, by default this is 'TRUE'.

`run` Should NONMEM be run (and the files imported to nlmixr2); default is TRUE, but FALSE will simply create the NONMEM control stream and data file.

`...` optional `genRxControl` argument controlling automatic `rxControl` generation.

Details

If runCommand is given as a string, it will be called with the system() command like:

runCommand controlFile outputFile.

For example, if runCommand="'/path/to/nmfe75'" then the command line used would look like the following:

'/path/to/nmfe75' one.cmt.nmctl one.cmt.lst

If runCommand is given as a function, it will be called as FUN(ctl, directory, ui) to run NONMEM. This allows you to run NONMEM in any way that you may need, as long as you can write it in R. babelmixr2 will wait for the function to return before proceeding.

If runCommand is NA, nlmixr() will stop after writing the model files and without starting NONMEM.

Value

babelmixr2 control option for generating NONMEM control stream and reading it back into babelmixr2/nlmixr2

Author(s)

Matthew L. Fidler

Examples

```
nonmemControl()
```

---

pkncaControl *PKNCA estimation control*

Description

PKNCA estimation control

Usage

```
pkncaControl(
  concu = NA_character_,
  doseu = NA_character_,
  timeu = NA_character_,
  volumeu = NA_character_,
  vpMult = 2,
  qMult = 1/2,
  vp2Mult = 4,
  q2Mult = 1/4,
  dvParam = "cp",
  groups = character(),
  sparse = FALSE,
```

```
  ncaData = NULL,
  ncaResults = NULL,
  rxControl = rxode2::rxControl()
)
```

Arguments

concu, doseu, timeu	concentration, dose, and time units from the source data (passed to PKNCA::pknca_units_table()).
volumeu	compartment volume for the model (if NULL, simplified units from source data will be used)
vpMult, qMult, vp2Mult, q2Mult	Multipliers for vc and cl to provide initial estimates for vp, q, vp2, and q2
dvParam	The parameter name in the model that should be modified for concentration unit conversions. It must be assigned on a line by itself, separate from the residual error model line.
groups	Grouping columns for NCA summaries by group (required if sparse = TRUE)
sparse	Are the concentration-time data sparse PK (commonly used in small nonclinical species or with terminal or difficult sampling) or dense PK (commonly used in clinical studies or larger nonclinical species)?
ncaData	Data to use for calculating NCA parameters. Typical use is when a subset of the original data are informative for NCA.
ncaResults	Already computed NCA results (a PKNCAresults object) to bypass automatic calculations. At least the following parameters must be calculated in the NCA: tmax, cmax.dn, cl.last
rxControl	Control options sent to rxode2::rxControl()

Value

A list of parameters

---

popedControl *Control for a PopED design task*

Description

Control for a PopED design task

Usage

```
popedControl(
  stickyRecalcN = 4,
  maxOdeRecalc = 5,
  odeRecalcFactor = 10^(0.5),
  maxn = NULL,
```

```
 rxControl = NULL,
 sigdig = 4,
 important = NULL,
 unimportant = NULL,
iFIMCalculationType = c("reduced", "full", "weighted", "loc", "reducedPFIM", "fullABC",
   "largeMat", "reducedFIMABC"),
 iApproximationMethod = c("fo", "foce", "focei", "foi"),
 iFOCENumInd = 1000,
 prior_fim = matrix(0, 0, 1),
 d_switch = c("d", "ed"),
 ofv_calc_type = c("lnD", "d", "a", "Ds", "inverse"),
 strEDPenaltyFile = "",
 ofv_fun = NULL,
 iEDCalculationType = c("mc", "laplace", "bfgs-laplace"),
 ED_samp_size = 45,
 bLHS = c("hypercube", "random"),
 bUseRandomSearch = TRUE,
 bUseStochasticGradient = TRUE,
 bUseLineSearch = TRUE,
 bUseExchangeAlgorithm = FALSE,
 bUseBFGSMinimizer = FALSE,
 bUseGrouped_xt = FALSE,
 EACriteria = c("modified", "fedorov"),
 strRunFile = "",
 poped_version = NULL,
 modtit = "PopED babelmixr2 model",
 output_file = "PopED_output_summary",
 output_function_file = "PopED_output_",
 strIterationFileName = "PopED_current.R",
 user_data = NULL,
 ourzero = 1e-05,
 dSeed = NULL,
 line_opta = NULL,
 line_optx = NULL,
 bShowGraphs = FALSE,
 use_logfile = FALSE,
 m1_switch = c("central", "complex", "analytic", "ad"),
 m2_switch = c("central", "complex", "analytic", "ad"),
 hle_switch = c("central", "complex", "ad"),
 gradff_switch = c("central", "complex", "analytic", "ad"),
 gradfg_switch = c("central", "complex", "analytic", "ad"),
 grad_all_switch = c("central", "complex"),
 rsit_output = 5,
 sgit_output = 1,
 hm1 = 1e-05,
 hlf = 1e-05,
 hlg = 1e-05,
 hm2 = 1e-05,
```

```
    hgd = 1e-05,
    hle = 1e-05,
    AbsTol = 1e-06,
    RelTol = 1e-06,
    iDiffSolverMethod = NULL,
    bUseMemorySolver = FALSE,
    rsit = 300,
    sgit = 150,
    intrsit = 250,
    intsgit = 50,
    maxrsnullit = 50,
    convergence_eps = 1e-08,
    rslxt = 10,
    rsla = 10,
    cfaxt = 0.001,
    cfaa = 0.001,
    bGreedyGroupOpt = FALSE,
    EAStepSize = 0.01,
    EANumPoints = FALSE,
    EAConvergenceCriteria = 1e-20,
    bEANoReplicates = FALSE,
    BFGSProjectedGradientTol = 1e-04,
    BFGSTolerancef = 0.001,
    BFGSToleranceg = 0.9,
    BFGSTolerancex = 0.1,
    ED_diff_it = 30,
    ED_diff_percent = 10,
    line_search_it = 50,
    Doptim_iter = 1,
    iCompileOption = c("none", "full", "mcc", "mpi"),
    compileOnly = FALSE,
    iUseParallelMethod = c("mpi", "matlab"),
    MCC_Dep = NULL,
    strExecuteName = "calc_fim.exe",
    iNumProcesses = 2,
    iNumChunkDesignEvals = -2,
    Mat_Out_Pre = "parallel_output",
    strExtraRunOptions = "",
    dPollResultTime = 0.1,
    strFunctionInputName = "function_input",
    bParallelRS = FALSE,
    bParallelSG = FALSE,
    bParallelMFEA = FALSE,
    bParallelLS = FALSE,
    groupsize = NULL,
    time = "time",
    timeLow = "low",
    timeHi = "high",
```

```
  id = "id",
  m = NULL,
  x = NULL,
  ni = NULL,
  maxni = NULL,
  minni = NULL,
  maxtotni = NULL,
  mintotni = NULL,
  maxgroupsize = NULL,
  mingroupsize = NULL,
  maxtotgroupsize = NULL,
  mintotgroupsize = NULL,
  xt_space = NULL,
  a = NULL,
  maxa = NULL,
  mina = NULL,
  a_space = NULL,
  x_space = NULL,
  use_grouped_xt = FALSE,
  grouped_xt = NULL,
  use_grouped_a = FALSE,
  grouped_a = NULL,
  use_grouped_x = FALSE,
  grouped_x = NULL,
  our_zero = NULL,
  auto_pointer = "",
  user_distribution_pointer = "",
  minxt = NULL,
  maxxt = NULL,
  discrete_xt = NULL,
  discrete_a = NULL,
  fixRes = FALSE,
  script = NULL,
  overwrite = TRUE,
  literalFix = TRUE,
  opt_xt = FALSE,
  opt_a = FALSE,
  opt_x = FALSE,
  opt_samps = FALSE,
  optTime = TRUE,
  literalFixRes = FALSE,
  ...
)
```

Arguments

stickyRecalcN	The number of bad ODE solves before reducing the atol/rtol for the rest of the problem.

`maxOdeRecalc` Maximum number of times to reduce the ODE tolerances and try to resolve the system if there was a bad ODE solve.

`odeRecalcFactor`
The ODE recalculation factor when ODE solving goes bad, this is the factor the rtol/atol is reduced

`maxn` Maximum number of design points for optimization; By default this is declared by the maximum number of design points in the babelmixr2 dataset (when `NULL`)

`rxControl` 'rxode2' ODE solving options during fitting, created with 'rxControl()'

`sigdig` Optimization significant digits. This controls:

- The tolerance of the inner and outer optimization is `10^-sigdig`
- The tolerance of the ODE solvers is `0.5*10^(-sigdig-2)`; For the sensitivity equations and steady-state solutions the default is `0.5*10^(-sigdig-1.5)` (sensitivity changes only applicable for liblsoda)
- The tolerance of the boundary check is `5 * 10 ^ (-sigdig + 1)`

`important` character vector of important parameters or NULL for default. This is used with Ds-optimality

`unimportant` character vector of unimportant parameters or NULL for default. This is used with Ds-optimality

`iFIMCalculationType`
can be either an integer or a named value of the Fisher Information Matrix type:

- 0/"full" = Full FIM
- 1/"reduced" = Reduced FIM
- 2/"weighted" = weighted models
- 3/"loc" = Loc models
- 4/"reducedPFIM" = reduced FIM with derivative of SD of sigma as in PFIM
- 5/"fullABC" = FULL FIM parameterized with A,B,C matrices & derivative of variance
- 6/"largeMat" = Calculate one model switch at a time, good for large matrices
- 7/"reducedFIMABC" = =Reduced FIM parameterized with A,B,C matrices & derivative of variance

`iApproximationMethod`
Approximation method for model, 0=FO, 1=FOCE, 2=FOCEI, 3=FOI

`iFOCENumInd` integer; number of individuals in focei solve

`prior_fim` matrix; prior FIM

`d_switch` integer or character option:

- 0/"ed" = ED design
- 1/"d" = D design

`ofv_calc_type` objective calculation type:

- 1/"d" = D-optimality". Determinant of the FIM: det(FIM)
- 2/"a" = "A-optimality". Inverse of the sum of the expected parameter variances: 1/trace_matrix(inv(FIM))

- 4/"lnD" = "lnD-optimality". Natural logarithm of the determinant of the FIM: log(det(FIM))
- 6/"Ds" = "Ds-optimality". Ratio of the Determinant of the FIM and the Determinant of the uninteresting rows and columns of the FIM: det(FIM)/det(FIM_u)
- 7/"inverse" = Inverse of the sum of the expected parameter RSE: 1/sum(get_rse(FIM,poped.db,use_pe

`strEDPenaltyFile`
: Penalty function name or path and filename, empty string means no penalty. User defined criterion can be defined this way.

`ofv_fun`
: User defined function used to compute the objective function. The function must have a poped database object as its first argument and have "..." in its argument list. Can be referenced as a function or as a file name where the function defined in the file has the same name as the file. e.g. "cost.txt" has a function named "cost" in it.

`iEDCalculationType`
: ED Integral Calculation type:

- 0/"mc" = Monte-Carlo-Integration
- 1/"laplace" = Laplace Approximation
- 2/"bfgs-laplace" = BFGS Laplace Approximation

`ED_samp_size`
: Sample size for E-family sampling

`bLHS`
: How to sample from distributions in E-family calculations. 0=Random Sampling, 1=LatinHyperCube –

`bUseRandomSearch`

- ********START OF Optimization algorithm SPECIFICATION OPTIONS************

: Use random search (1=TRUE, 0=FALSE)

`bUseStochasticGradient`
: Use Stochastic Gradient search (1=TRUE, 0=FALSE)

`bUseLineSearch`
: Use Line search (1=TRUE, 0=FALSE)

`bUseExchangeAlgorithm`
: Use Exchange algorithm (1=TRUE, 0=FALSE)

`bUseBFGSMinimizer`
: Use BFGS Minimizer (1=TRUE, 0=FALSE)

`bUseGrouped_xt`
: Use grouped time points (1=TRUE, 0=FALSE).

`EACriteria`
: Exchange Algorithm Criteria:

- 1/"modified" = Modified
- 2/"fedorov" = Fedorov

`strRunFile`
: Filename and path, or function name, for a run file that is used instead of the regular PopED call.

`poped_version`

- ********START OF Labeling and file names SPECIFICATION OPTIONS************

: The current PopED version

`modtit`
: The model title

`output_file`
: Filename and path of the output file during search

`output_function_file`
: Filename suffix of the result function file

`strIterationFileName`
: Filename and path for storage of current optimal design

`user_data`
- ******START OF Miscellaneous SPECIFICATION OPTIONS**********

: User defined data structure that, for example could be used to send in data to the model

`ourzero`
: Value to interpret as zero in design

`dSeed`
: The seed number used for optimization and sampling – integer or -1 which creates a random seed `as.integer(Sys.time())` or NULL.

`line_opta`
: Vector for line search on continuous design variables (1=TRUE,0=FALSE)

`line_optx`
: Vector for line search on discrete design variables (1=TRUE,0=FALSE)

`bShowGraphs`
: Use graph output during search

`use_logfile`
: If a log file should be used (0=FALSE, 1=TRUE)

`m1_switch`
: Method used to calculate M1:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference
  - 20/"analytic" = Analytic derivative
  - 30/"ad" = Automatic differentiation

`m2_switch`
: Method used to calculate M2:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference
  - 20/"analytic" = Analytic derivative
  - 30/"ad" = Automatic differentiation

`hle_switch`
: Method used to calculate linearization of residual error:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference
  - 30/"ad" = Automatic differentiation

`gradff_switch`
: Method used to calculate the gradient of the model:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference
  - 20/"analytic" = Analytic derivative
  - 30/"ad" = Automatic differentiation

`gradfg_switch`
: Method used to calculate the gradient of the parameter vector g:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference
  - 20/"analytic" = Analytic derivative
  - 30/"ad" = Automatic differentiation

`grad_all_switch`
: Method used to calculate all the gradients:
  - 1/"central" = Central difference
  - 0/"complex" = Complex difference

rsit_output	Number of iterations in random search between screen output
sgit_output	Number of iterations in stochastic gradient search between screen output
hm1	Step length of derivative of linearized model w.r.t. typical values
hlf	Step length of derivative of model w.r.t. g
hlg	Step length of derivative of g w.r.t. b
hm2	Step length of derivative of variance w.r.t. typical values
hgd	Step length of derivative of OFV w.r.t. time
hle	Step length of derivative of model w.r.t. sigma
AbsTol	The absolute tolerance for the diff equation solver
RelTol	The relative tolerance for the diff equation solver
iDiffSolverMethod	The diff equation solver method, NULL as default.
bUseMemorySolver	If the differential equation results should be stored in memory (1) or not (0)
rsit	Number of Random search iterations
sgit	Number of stochastic gradient iterations
intrsit	Number of Random search iterations with discrete optimization.
intsgit	Number of Stochastic Gradient search iterations with discrete optimization
maxrsnullit	Iterations until adaptive narrowing in random search
convergence_eps	Stochastic Gradient convergence value, (difference in OFV for D-optimal, difference in gradient for ED-optimal)
rslxt	Random search locality factor for sample times
rsla	Random search locality factor for covariates
cfaxt	Stochastic Gradient search first step factor for sample times
cfaa	Stochastic Gradient search first step factor for covariates
bGreedyGroupOpt	Use greedy algorithm for group assignment optimization
EAStepSize	Exchange Algorithm StepSize
EANumPoints	Exchange Algorithm NumPoints
EAConvergenceCriteria	Exchange Algorithm Convergence Limit/Criteria
bEANoReplicates	Avoid replicate samples when using Exchange Algorithm
BFGSProjectedGradientTol	BFGS Minimizer Convergence Criteria Normalized Projected Gradient Tolerance
BFGSTolerancef	BFGS Minimizer Line Search Tolerance f
BFGSToleranceg	BFGS Minimizer Line Search Tolerance g
BFGSTolerancex	BFGS Minimizer Line Search Tolerance x

`ED_diff_it` Number of iterations in ED-optimal design to calculate convergence criteria

`ED_diff_percent`
ED-optimal design convergence criteria in percent

`line_search_it` Number of grid points in the line search

`Doptim_iter` Number of iterations of full Random search and full Stochastic Gradient if line search is not used

`iCompileOption` Compile options for PopED

- "none"/-1 = No compilation
- "full/0 or 3 = Full compilation
- "mcc"/1 or 4 = Only using MCC (shared lib)
- "mpi"/2 or 5 = Only MPI,

When using numbers, option 0,1,2 runs PopED and option 3,4,5 stops after compilation.

When using characters, the option `compileOnly` determines if the model is only compiled (and PopED is not run).

`compileOnly` logical; only compile the model, do not run PopED (in conjunction with `iCompileOption`)

`iUseParallelMethod`
Parallel method to use

- 0/"matlab"= Matlab PCT
- 1/"mpi" = MPI

`MCC_Dep` Additional dependencies used in MCC compilation (mat-files), if several space separated

`strExecuteName` Compilation output executable name

`iNumProcesses` Number of processes to use when running in parallel (e.g. 3 = 2 workers, 1 job manager)

`iNumChunkDesignEvals`
Number of design evaluations that should be evaluated in each process before getting new work from job manager

`Mat_Out_Pre` The prefix of the output mat file to communicate with the executable

`strExtraRunOptions`
Extra options send to e$g. the MPI executable or a batch script, see execute_parallel$m for more information and options

`dPollResultTime`
Polling time to check if the parallel execution is finished

`strFunctionInputName`
The file containing the popedInput structure that should be used to evaluate the designs

`bParallelRS` If the random search is going to be executed in parallel

`bParallelSG` If the stochastic gradient search is going to be executed in parallel

`bParallelMFEA` If the modified exchange algorithm is going to be executed in parallel

`bParallelLS` If the line search is going to be executed in parallel

`groupsize` Vector defining the size of the different groups (num individuals in each group). If only one number then the number will be the same in every group.

`time` string that represents the time in the dataset (ie xt)

`timeLow` string that represents the lower design time (ie minxt)

`timeHi` string that represents the upper design time (ie maxmt)

`id` The id variable

`m` Number of groups in the study. Each individual in a group will have the same design.

`x` A matrix defining the initial discrete values for the model Each row is a group/individual.

`ni` Vector defining the number of samples for each group.

`maxni`

- ********START OF DESIGN SPACE OPTIONS************

Max number of samples per group/individual

`minni` Min number of samples per group/individual

`maxtotni` Number defining the maximum number of samples allowed in the experiment.

`mintotni` Number defining the minimum number of samples allowed in the experiment.

`maxgroupsize` Vector defining the max size of the different groups (max number of individuals in each group)

`mingroupsize` Vector defining the min size of the different groups (min num individuals in each group) –

`maxtotgroupsize`

The total maximal groupsize over all groups

`mintotgroupsize`

The total minimal groupsize over all groups

`xt_space` Cell array `cell` defining the discrete variables allowed for each xt value. Can also be a vector of values `c(1:10)` (same values allowed for all xt), or a list of lists `list(1:10, 2:23, 4:6)` (one for each value in xt in row major order or just for one row in xt, and all other rows will be duplicated).

`a` Matrix defining the initial continuous covariate values. n_rows=number of groups, n_cols=number of covariates. If the number of rows is one and the number of groups > 1 then all groups are assigned the same values.

`maxa` Vector defining the max value for each covariate. If a single value is supplied then all a values are given the same max value

`mina` Vector defining the min value for each covariate. If a single value is supplied then all a values are given the same max value

`a_space` Cell array `cell` defining the discrete variables allowed for each a value. Can also be a list of values `list(1:10)` (same values allowed for all a), or a list of lists `list(1:10, 2:23, 4:6)` (one for each value in a).

`x_space` Cell array `cell` defining the discrete variables for each x value.

`use_grouped_xt` Group sampling times between groups so that each group has the same values (`TRUE` or `FALSE`).

`grouped_xt` Matrix defining the grouping of sample points. Matching integers mean that the points are matched. Allows for finer control than `use_grouped_xt`

use_grouped_a
: Group continuous design variables between groups so that each group has the same values (TRUE or FALSE).

grouped_a
: Matrix defining the grouping of continuous design variables. Matching integers mean that the values are matched. Allows for finer control than use_grouped_a.

use_grouped_x
: Group discrete design variables between groups so that each group has the same values (TRUE or FALSE).

grouped_x
: Matrix defining the grouping of discrete design variables. Matching integers mean that the values are matched. Allows for finer control than use_grouped_x.

our_zero
: Value to interpret as zero in design.

auto_pointer
: Filename and path, or function name, for the Autocorrelation function, empty string means no autocorrelation

user_distribution_pointer
: Filename and path, or function name, for user defined distributions for E-family designs

minxt
: Matrix or single value defining the minimum value for each xt sample. If a single value is supplied then all xt values are given the same minimum value

maxxt
: Matrix or single value defining the maximum value for each xt sample. If a single value is supplied then all xt values are given the same maximum value.

discrete_xt
: Cell array cell defining the discrete variables allowed for each xt value. Can also be a list of values list(1:10) (same values allowed for all xt), or a list of lists list(1:10, 2:23, 4:6) (one for each value in xt). See examples in create_design_space.

discrete_a
: Cell array cell defining the discrete variables allowed for each a value. Can also be a list of values list(1:10) (same values allowed for all a), or a list of lists list(1:10, 2:23, 4:6) (one for each value in a). See examples in create_design_space.

fixRes
: boolean; Fix the residuals to what is specified by the model

script
: write a PopED/rxode2 script that can be modified for more fine control. The default is NULL.

  When script is TRUE, the script is returned as a lines that would be written to a file and with the class babelmixr2popedScript. This allows it to be printed as the script on screen.

  When script is a file name (with an R extension), the script is written to that file.

overwrite
: [logical(1)]
  If TRUE, an existing file in place is allowed if it it is both readable and writable. Default is FALSE.

literalFix
: boolean, substitute fixed population values as literals and re-adjust ui and parameter estimates after optimization; Default is 'TRUE'.

opt_xt
: boolean to indicate if this is meant for optimizing times

opt_a
: boolean to indicate if this is meant for optimizing covariates

opt_x
: boolean to indicate if the discrete design variables be optimized

opt_samps	boolean to indicate if the sample optimizer is used (not implemented yet in PopED)
optTime	boolean to indicate if the global time indexer inside of babelmixr2 is reset if the times are different. By default this is TRUE. If FALSE you can get slightly better run times and possibly slightly different results. When optTime is FALSE the global indexer is reset every time the PopED rxode2 is setup for a problem or when a poped dataset is created. You can manually reset with popedMultipleEndpointResetTimeIndex
literalFixRes	boolean, substitute fixed population values as literals and re-adjust ui and parameter estimates after optimization; Default is 'TRUE'.
...	other parameters for PopED control

Value

popedControl object

Author(s)

Matthew L. Fidler

---

popedGetMultipleEndpointModelingTimes

Get Multiple Endpoint Modeling Times

Description

This function takes a vector of times and a corresponding vector of IDs, groups the times by their IDs, initializes an internal C++ global TimeIndexer, that is used to efficiently lookup the final output from the rxode2 solve and then returns the sorted unique times.

The popedMultipleEndpointIndexDataFrame() function can be used to visualize the internal data structure inside R, but it does not show all the indexes in the case of time ties for a given ID. Rather it shows one of the indexs and the total number of indexes in the data.frame

Usage

```
popedGetMultipleEndpointModelingTimes(times, modelSwitch, sorted = FALSE)

popedMultipleEndpointIndexDataFrame(print = FALSE)
```

Arguments

times	A numeric vector of times.
modelSwitch	An integer vector of model switch indicator corresponding to the times
sorted	A boolean indicating if the returned times should be sorted
print	boolean for popedMultipleEndpointIndexDataFrame() when TRUE show each id/index per time even though it may not reflect in the returned data.frame

Value

A numeric vector of unique times.

Examples

```
times <- c(1.1, 1.2, 1.3, 2.1, 2.2, 3.1)
modelSwitch <- c(1, 1, 1, 2, 2, 3)
sortedTimes <- popedGetMultipleEndpointModelingTimes(times, modelSwitch, TRUE)
print(sortedTimes)

# now show the output of the data frame representing the model
# switch to endpoint index

popedMultipleEndpointIndexDataFrame()

# now show a more complex example with overlaps etc.

times <- c(1.1, 1.2, 1.3, 0.5, 2.2, 1.1, 0.75,0.75)
modelSwitch <- c(1, 1, 1, 2, 2, 2, 3, 3)
sortedTimes <- popedGetMultipleEndpointModelingTimes(times, modelSwitch, TRUE)
print(sortedTimes)

popedMultipleEndpointIndexDataFrame(TRUE) # Print to show individual matching
```

---

popedMultipleEndpointResetTimeIndex

Reset the Global Time Indexer for Multiple Endpoint Modeling

Description

This clears the memory and resets the global time indexer used for multiple endpoint modeling.

Usage

```
popedMultipleEndpointResetTimeIndex()
```

Value

NULL, called for side effects

Examples

```
popedMultipleEndpointResetTimeIndex()
```

`rxToMonolix` *Convert RxODE syntax to monolix syntax*

Description

Convert RxODE syntax to monolix syntax

Usage

```
rxToMonolix(x, ui)
```

Arguments

`x`	Expression
`ui`	rxode2 ui

Value

Monolix syntax

Author(s)

Matthew Fidler

`rxToNonmem` *Convert RxODE syntax to NONMEM syntax*

Description

Convert RxODE syntax to NONMEM syntax

Usage

```
rxToNonmem(x, ui)
```

Arguments

`x`	Expression
`ui`	rxode2 ui

Value

NONMEM syntax

Author(s)

Matthew Fidler

`simplifyUnit` *Simplify units by removing repeated units from the numerator and denominator*

Description

Simplify units by removing repeated units from the numerator and denominator

Usage

```
simplifyUnit(numerator = "", denominator = "")
```

Arguments

`numerator`	The numerator of the units (or the whole unit specification)
`denominator`	The denominator of the units (or NULL if `numerator` is the whole unit specification)

Details

`NA` or `""` for `numerator` and `denominator` are considered unitless.

Value

The units specified with units that are in both the numerator and denominator cancelled.

See Also

Other Unit conversion: `modelUnitConversion()`

Examples

```
simplifyUnit("kg", "kg/mL")
# units that don't match exactly are not cancelled
simplifyUnit("kg", "g/mL")
```

Index