Package 'pamm'

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Description Simulation functions to assess or explore the power of a dataset to estimates significant random effects (intercept or slope) in a mixed model. The functions are based on the `lme4` and `lmerTest` packages.

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Description

Simulation functions to assess or explore the power of a dataset to estimate significant random effects (intercept or slope) in a mixed model. The functions are based on the "lme4" and "lmerTest" packages.

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See Also

Useful links:

- [https://github.com/JulienGAMartin/pamm_R](https://github.com/JulienGAMartin/pamm_R)
- Report bugs at [https://github.com/JulienGAMartin/pamm_R/issues](https://github.com/JulienGAMartin/pamm_R/issues)

Usage

```r
EAMM(
  numsim,
  group,
  repl,
  fixed = c(0, 1, 0),
  VI = seq(0.05, 0.95, 0.05),
  VS = seq(0.05, 0.5, 0.05),
  CoIS = 0,
  relIS = "cor",
  n.X = NA,
  autocorr.X = 0,
  X.dist = "gaussian",
  intercept = 0,
)```
heteroscedasticity = c("null"),
mer.sim = TRUE,
mer.model = NULL
)

Arguments

numsim  number of simulation for each step

group  number of group

repl  number of replicates per group

fixed  vector of length 3 with mean, variance and estimate of fixed effect to simulate. Default: c(0, 1, 0)

VI  variance component of intercept. Could be specified as a vector. Default: seq(0.05, 0.95, 0.05)

VS  Variance component of the slope or IxE. Could be specified as a vector. Default: seq(0.05, 0.5, 0.05)

CoIS  value of correlation or covariance between random intercept and random slope. Default: 0

relIS  "cor" or "cov" set the type of relation give in CoIS. By default the relation is set to correlation

n.X  number of different values to simulate for the fixed effect (covariate). If NA, all values of X are independent between groups. If the value specified is equivalent to the number of replicates per group, repl, then all groups are observed for the same values of the covariate. Default: NA

autocorr.X  correlation between two successive covariate value for a group. Default: 0

X.dist  specify the distribution of the fixed effect. Only "gaussian" (normal distribution) and "unif" (uniform distribution) are accepted actually. Default: "gaussian"

intercept  a numeric value giving the expected intercept value. Default: 0

heteroscedasticity  a vector specifying heterogeneity in residual variance across X. If c("null") residual variance is homogeneous across X. If c("power",t1,t2) models heterogeneity with a constant plus power variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v) \) denote the variance function evaluated at \( v \), the constant plus power variance function is defined as \( \sigma^2(v) = (\theta_1 + |v|^{\theta_2})^2 \), where \( \theta_1, \theta_2 \) are the variance function coefficients. If c("exp",t) models heterogeneity with an exponential variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v) \) denote the variance function evaluated at \( v \), the exponential variance function is defined as \( \sigma^2(v) = e^{2*\theta*v} \), where \( \theta \) is the variance function coefficient. Default:"Null"

mer.sim  Use the simulate.merMod function to simulate the data. Potentially faster for large dataset but more restricted in terms of options

mer.model  Simulate the data based on a existing data and model structure from a lmer object. Should be specified as a list of 3 components: a mer object fitted via lmer, an environmental covariate for which to test the random slope, a random effect (e.g. list(fm1,"Days","Subject"))
Details

P-values for random effects are estimated using a log-likelihood ratio test between two models with and without the effect. Power represent the percentage of simulations providing a significant p-value for a given random structure. Residual variance, e, is calculated as 1-VI.

Value

data frame reporting estimated P-values and power with CI for random intercept and random slope

See Also

[PAMM()], [SSF()] for other simulations [plot.EAMM()] for plotting output

Examples

```r
## Not run:
ours <- EAMM(
  numsim = 10, group = 10, repl = 4, fixed = c(0, 1, 1),
  VI = seq(0.1, 0.3, 0.05), VS = seq(0.05, 0.2, 0.05)
) plot(ours, "both")

(fm1 <- lmer(Reaction ~ Days + (Days | Subject), sleepstudy))
ours2 <- EAMM(
  numsim = 10,
  mer.model = list(model = fm1, env = "Days", random = "Subject"),
  VI = seq(0.3, 0.5, 0.1), VS = seq(0.05, 0.2, 0.05)
) plot(ours2, "both")
## End(Not run)
```

PAMM

Simulation function to assess power of mixed models

Description

Given a specific variance-covariance structure for random effect, the function simulate different group size and assess p-values and power of random intercept and random slope

Usage

PAMM(
  numsim, group, repl, randompart,
fixed = c(0, 1, 0),
n.X = NA,
autocorr.X = 0,
X.dist = "gaussian",
intercept = 0,
heteroscedasticity = c("null"),
ftype = "lmer",
mer.sim = FALSE
)

Arguments

numsim number of simulation for each step

group number of group. Could be specified as a vector

repl number of replicates per group. Could be specified as a vector

randompart vector of length 4 or 5, with 1: variance component of intercept, VI; 2: variance component of slope, VS; 3: residual variance, VR; 4: relation between random intercept and random slope; 5: "cor" or "cov" determine if the relation 4 between I ans S is a correlation or a covariance. Default: "cor"

fixed vector with mean, variance and estimate of fixed effect to simulate. Default: c(0, 1, 0)

n.X number of different values to simulate for the fixed effect (covariate). If NA, all values of X are independent between groups. If the value specified is equivalent to the number of replicates per group, repl, then all groups are observed for the same values of the covariate. Default: NA

autocorr.X correlation between two successive covariate value for a group. Default: 0

X.dist specify the distribution of the fixed effect. Only "gaussian" (normal distribution) and "unif" (uniform distribution) are accepted actually. Default: "gaussian"

intercept a numeric value giving the expected intercept value. Default: 0

heteroscedasticity a vector specifying heterogeneity in residual variance across X. If c("null") residual variance is homogeneous across X. If c("power", t1, t2) models heterogeneity with a constant plus power variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v) \) denote the variance function evaluated at \( v \), the constant plus power variance function is defined as \( \sigma^2(v) = (\theta_1 + |v|^\theta_2)^2 \), where \( \theta_1, \theta_2 \) are the variance function coefficients. If c("exp", t), models heterogeneity with an exponential variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v) \) denote the variance function evaluated at \( v \), the exponential variance function is defined as \( \sigma^2(v) = e^{2\theta v} \), where \( \theta \) is the variance function coefficient.

ftype character value "lmer", "lme" or "MCMCglmm" specifying the function to use to fit the model. Actually "lmer" only is accepted

mer.sim simulate the data using simulate.merMod from lme4. Faster for large sample size but not as flexible.
Details

P-values for random effects are estimated using a log-likelihood ratio test between two models with and without the effect. Power represent the percentage of simulations providing a significant p-value for a given random structure.

Value

data frame reporting estimated P-values and power with CI for random intercept and random slope.

@seealso [EAMM()], [SSF()], [plot.PAMM()]

Examples

## Not run:
oirs <- PAMM(numsim = 10, group = c(seq(10, 50, 10), 100), repl = c(3, 4, 6), randompart = c(0.4, 0.1, 0.5, 0.1), fixed = c(0, 1, 0.7))
plot(ours, "both")

## End(Not run)
Examples

```r
## Not run:
ours <- EAMM(numsim=10, group=10, repl=4,
              VI=seq(0.1,0.95,0.05), VS=c(0.05,0.1) )
plot(ours, "both")
plot(ours, "VI", vs=0.1)
plot(ours, "VS", vi=0.2)

## End(Not run)
```

### plot.PAMM

**Graphic output of the PAMM function**

#### Description

Provide graphic interpretation of the simulation results

#### Usage

```r
## S3 method for class 'PAMM'
plot(x, graphtype = "both", nbgroup, nbrepl, fun3D = "wireframe", ...)
```

#### Arguments

- `x`: a PAMM object
- `graphtype`: "group", "repl" or "both". "group" give graphs with varying number of ID and with a fixed number of replicates specified in `nbrepl`. "repl" give graphs with varying number of replicates and with a fixed number of ID specified in `nbgroup`. "both" 3-D plot. see also `fun3D` argument. Note: useful only with multiple group size and multiple number of replicates.
- `nbgroup`: number of group for which plots the output. Necessary for "repl" type of graph
- `nbrepl`: number of replicates for which plots the output. Necessary for "group" type of graph
- `fun3D`: plot function used to plot the 3D graph. "wireframe" uses lattice, "persp" uses graphics and "open3d" uses rgl
- `...`: potentially further arguments to pass to methods

#### Details

Parameters `phi`, `theta`, `ticktype` ("simple" or "detailed"), `nticks`, `nbcol` from `persp()` function could also be specified for 3D plots. In addition, color schemes ("grey", "cm.colors" and "rainbow") and `coltype` ("restricted" or "0-1") parameters could also be specified for 3D plots.
Examples

```r
## Not run:
ours <- PAMM(numsim=10, group=c(seq(10, 50, 10), 100), repl=c(3, 4, 6),
               randompart=c(0.4, 0.1, 0.5, 0.1), fixed=c(0, 1, 0.7))
plot(ours, "both")
plot(ours, "group", nbrepl=4)
plot(ours, "repl", nbgp=20)

## End(Not run)
```

---

**plot.SSF**

*Graphic output of the PAMM function*

**Description**

Provide graphic interpretation of the simulation results

**Usage**

```r
## S3 method for class 'SSF'
plot(x, ...)
```

**Arguments**

- `x` an SSF object
- `...` potentially further arguments to pass to methods

**Examples**

```r
## Not run:
oursSSF <- SSF(50, 100, 10, c(0.4, 0.1, 0.6, 0))
plot(oursSSF)

## End(Not run)
```
Description

Given a specific total number of observations and variance-covariance structure for random effect, the function simulates different association of number of group and replicates, giving the specified sample size, and assess p-values and power of random intercept and random slope.

Usage

```
SSF(
  numsim, tss, nbstep = 10, randompart, fixed = c(0, 1, 0), n.X = NA,
  autocorr.X = 0, X.dist = "gaussian", intercept = 0, exgr = NA,
  exrepl = NA, heteroscedasticity = c("null")
)
```

Arguments

- `numsim`: number of simulation for each step
- `tss`: total sample size, nb group * nb replicates
- `nbstep`: number of group*replicates associations to simulate
- `randompart`: vector of lenght 4 or 5 with 1: variance component of intercept, VI; 2: variance component of slope, VS; 3: residual variance, VR; 4: relation between random intercept and random slope; 5: "cor" or "cov" determine id the relation between I ans S is correlation or covariance, set to "cor" by default
- `fixed`: vector of lenght 3 with mean, variance and estimate of fixed effect to simulate
- `n.X`: number of different values to simulate for the fixed effect (covariate). If NA, all values of X are independent between groups. If the value specified is equivalent to the number of replicates per group, repl, then all groups are observed for the same values of the covariate. Default: NA
- `autocorr.X`: correlation between two successive covariate value for a group. Default: 0
- `X.dist`: specify the distribution of the fixed effect. Only "gaussian" (normal distribution) and "unif" (uniform distribution) are accepted actually. Default: "gaussian"
- `intercept`: a numeric value giving the expected intercept value. Default: 0
exgr  a vector specifying minimum and maximum value for number of group. Default: `c(2, tss/2)`

exrepl  a vector specifying minimum and maximum value for number of replicates. Default: `c(2, tss/2)`

heteroscedasticity  a vector specifying heterogeneity in residual variance across X. If `c("null")` residual variance is homogeneous across X. If `c("power", t1, t2)` models heterogeneity with a constant plus power variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v)s^2(v) \) denote the variance function evaluated at \( v \), the constant plus power variance function is defined as \( \sigma^2(v) = (\theta_1 + |v|^{t_2})^2s^2(v) = (t_1 + |v|^2)^2 \), where \( \theta_1, \theta_2, t_1, t_2 \) are the variance function coefficients. If `c("exp", t)` models heterogeneity with an exponential variance function. Letting \( v \) denote the variance covariate and \( \sigma^2(v)s^2(v) \) denote the variance function evaluated at \( v \), the exponential variance function is defined as \( \sigma^2(v) = e^{2*\theta*v}s^2(v) = exp(2*t*v) \), where \( \theta \) is the variance function coefficient.

Details

P-values for random effects are estimated using a log-likelihood ratio test between two models with and without the effect. Power represent the percentage of simulations providing a significant p-value for a given random structure.

Value

data frame reporting estimated P-values and power with CI for random intercept and random slope

See Also

PAMM(), EAMM() for other simulation functions plot.SSF() for plotting

Examples

```r
## Not run:
oursSSF <- SSF(10, 100, 10, c(0.4, 0.1, 0.6, 0))
plot(oursSSF)

## End(Not run)
```
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