

Package ‘hsem’

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Description We present this package for fitting structural equation models using the hierarchical likelihood method. This package allows extended structural equation model, including dynamic structural equation model. We illustrate the use of our packages with well-known data sets. Therefore, this package are able to handle two serious problems inadmissible solution and factor indeterminacy <[doi:10.3390/sym13040657](https://doi.org/10.3390/sym13040657)>.

Depends R (>= 3.6.0), methods, Matrix, numDeriv, boot, mvtnorm

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hsem-package

Hierarchical Structural Equation Models

Description

This package allows different models for multivariate response variables with a hierarchical structural equation models (HSEMs).

Details

```

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```

This is version 1.0 of the hsem package.

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hsemfit

Fitting Hierarchical Structural Equation Models using h-likelihood Approach

Description

The hsemfit is used to fit a hierarchical structural equation models (HSEMs) allowing different models for multivariate response variables. A variety of distributions and link functions for both response and the random effects are allowed. To call the fitting function hsemfit, models for the mean and dispersion must be specified by hsemmodeling object preferably created by calling the hsemmodeling function.

Usage

```

hsemfit(RespDist = "gaussian", BinomialDen = NULL,
DataMain, MeanModel, DispersionModel = NULL,
PhiFix = NULL, LamFix = NULL, structure = "correlated",
mord = 0, dord = 1, convergence = 1e-05,
Init_Corr = NULL, EstimateCorrelations = TRUE)

```

Arguments

RespDist	The distribution of the response is set by the option RespDist. The user can set it to: "gaussian" (default), "binomial", "poisson", or "gamma".
BinomialDen	When RespDist="binomial", one should use the option BinomialDen to specify the denominator for the binomial distribution. This should be "NULL" (default) or a numeric vector of length equal to the length of DataMain. When specified as BinomialDen=NULL and RespDist="binomial", the denominator is 1.
DataMain	The option DataMain determines the data frame to be used (non-optional).
MeanModel	For the mean model, this option requires DGHLMODELING object which should be specified by the option Model="mean".
DispersionModel	For the overdispersion model, this option requires DGHLMODELING object which should be specified by the option Model="dispersion".
PhiFix	The option for overdispersion parameters (phi) to be estimated or maintained constant. Specifying defaults such as PhiFix =NULL implies that phi is to be estimated. If not, phi is fixed at a value specified by PhiFix.
LamFix	The option for random-effect variance (lambda) to be estimated or maintained constant. Specifying defaults such as LamFix =NULL implies that lambda is to be estimated. If not, lambda is fixed at a value specified by LamFix.
structure	The option structure determines structure of random effects. When structure="correlated" (or "shared"), correlated (or shared) random-effects model is specified.
mord	The option mord specifies the order of Laplace approximation to the marginal likelihood for fitting the mean parameters. The choice is either 0 or 1 (default).
dord	The option dord specifies the order of adjusted profile likelihood for fitting the dispersion parameters. The choice is either 1 (default) or 2.
convergence	Setting this option determines the criterion for convergence, which is computed as the absolute difference between the values of all the estimated parameters in the previous and current iterations. The default criterion is 1e-06.
Init_Corr	Setting initial values of correlation (or shared parameters) between random effects
EstimateCorrelations	Correlation are estimated or fixed when EstimateCorrelations=TRUE (default) or EstimateCorrelations=FALSE.

Value

res	the output class resulted from jointfit_correlated.
-----	---

Examples

```
data(ml2)

MM1<-hsemmodeling(Model="mean",Link="identity",
  LinPred=urge~urge1+dep1+(1|id)+(urge1|id)+(dep1|id),
  RandDist=c("gaussian","gaussian","gaussian"))
```

```

DM1<-hsemmodeling(Model="dispersion",Link = "log",
  LinPred=phi~(1|id),RandDist=c("gaussian"))
MM2<-hsemmodeling(Model="mean",Link="identity",
  LinPred=dep~urge1+dep1+(1|id)+(urge1|id)+(dep1|id),
  RandDist=c("gaussian","gaussian","gaussian"))
DM2<-hsemmodeling(Model="dispersion",Link = "log",
  LinPred=phi~(1|id),RandDist=c("gaussian"))
res<-hsemfit(RespDist=c("gaussian","gaussian"),DataMain=list(ml2,ml2),
  structure="independent",MeanModel=list(MM1,MM2),
  DispersionModel=list(DM1,DM2))

```

hsemmodeling

Defining the Fixed and Random Models for the Mean and Dispersion parameters in HSEMs

Description

The hsemmodeling specifies a GLM, HGLM, DHGLM model for the mean parameters (μ), and a GLM, HGLM model for the overdispersion parameters (ϕ). GLM for μ , and GLM for ϕ are specified by adding only fixed terms to the linear predictors for the μ and ϕ , respectively.

Usage

```

hsemmodeling(Model="mean",Link=NULL,LinPred="constant",RandDist=NULL,
  Offset=NULL,LMatrix=NULL,LinkRandVariance=NULL,LinPredRandVariance=NULL,
  RandDistRandVariance="gaussian",
  LinkRandVariance2=NULL,LinPredRandVariance2=NULL)

```

Arguments

Model	This option specifies a GLM, HGLM or DHGLM model for μ when Model="mean" (default), and a GLM or HGLM for ϕ when Model="dispersion".
Link	The link function for the linear predictor is specified by the option Link. For Model="mean", Link can be "identity", "logit", "probit", "cloglog", "log", or "inverse". For Model="dispersion", the choice is either "log" or "inverse". The default, specified as NULL link, is "identity" for Model="mean" and "log" for Model="dispersion".
LinPred	The option LinPred specifies the fixed and random terms for the linear predictor for μ when specified as Model="mean" or for ϕ when Model="dispersion". For Model="mean", LinPred=y~x1+x2+(1 id1)+(1 id2) specifies y as the main response, x1 and x2 as fixed covariates and id1 and id2 as random terms. For Model="dispersion", the main response should be ϕ , e.g. $\phi \sim x1+x2+(1 id1)+(1 id2)$. This option can specify the model without random effects, e.g., LinPred= $\phi \sim x1+x2$. The default is "constant", which is set to intercept only the model for the corresponding linear predictors.

RandDist	The option RandDist specifies the distributions of the random terms represented in the option LinPred. It is set as a vector of distribution names from "gaussian" (default), "beta", "gamma", or "inverse-gamma" when Model="mean". For Model="dispersion", the choice is "gaussian" (default), "gamma", or "inverse-gamma". When more than one random terms are specified, e.g., $y \sim x_1 + x_2 + (1 id_1) + (1 id_2)$ in the option LinPred, the different distributions for each random term can be specified, e.g., <code>c("gaussian", "gamma")</code> , which assumes normal distribution for the random term "id1" and gamma distribution for the random term "id2", respectively.
Offset	The option Offset can be used to specify a known component to be included in the linear predictor specified by LinPred during fitting. This should be the default (NULL) or a numeric vector of length equal to that of the appropriate data.
LMatrix	The option LMatrix sets a matrix that is used as a post-multiplier for the model matrix of the corresponding random effects. This option allows correlation structures to be defined for random effects. For example, when specified as Model="mean" and Lmatrix=L1+L2, the linear predictor for mu takes $X \beta + Z_1 L_1 r_1 + Z_2 L_2 r_2$, where Z1 and Z2 are the model matrices for the random effects $v_1 = L_1 r_1$ and $v_2 = L_2 r_2$, specified in the option LinPred.
LinkRandVariance	The option LinkRandVariance specifies the link function for the linear predictor of the random-effect variances. The choice is either "log" (default) or "inverse". When more than two random terms are specified in the option LinPred, the user can set different link functions, e.g., <code>LinkRandVariance=c("log","inverse")</code> for each random term.
LinPredRandVariance	The option LinPredRandVariance specifies the fixed and random terms for the linear predictor of the random-effect variances for Model="mean". When $y \sim x_1 + x_2 + (1 id_1) + (1 id_2)$ is specified in the option LinPred, <code>LinPredRandVariance=c(lambda~xx1+(1 id11),lambda~xx2+(1 id12))</code> specifies xx1 and xx2 as fixed covariates and id11 and id12 as random terms in the linear predictors for the variances of the random terms id1 and id2, respectively. For Model="dispersion", the random term is not allowed in the linear predictor of the random-effect variance. The default (NULL) is set to intercept only model for the corresponding linear predictors.
RandDistRandVariance	The option RandDistRandVariance specifies the distributions for the random terms in the LinPredRandVariance. The choice is "gaussian" (default), "gamma", or "inverse-gamma".
LinkRandVariance2	This option specifies the link function for the linear predictor of the variance of random effects, which are specified in the option LinPredRandVariance. The choice is either "log" (default) or "inverse".
LinPredRandVariance2	This option specifies the fixed terms for the linear predictor of the variance of random effects, which is specified in the option LinPredRandVariance. For example, when <code>LinPredRandVariance=c(lambda~xx1+(1 id11),lambda~xx1+(1 id12))</code>

is specified, `LinPredRandVariance2=c(~xxx1,~xxx2)` specifies `xxx1` and `xxx2` as fixed covariates for the linear predictor of random-effect variances for `id11` and `id12`, respectively. The default (NULL) is set to constant variance for the random effects in `LinPredRandVariance`.

m12

simulated urge to smoke data

Description

By using an example for urge to smoke in the McNeish and Hamaker (2020), this data set is a simulated subset. It consists of 10 repetitions on regular time scales for 20 different individuals. For response variable, urge to Smoke is on a standardized scale average 0 and the standard deviation 1.

Usage

```
data("m12")
```

Format

A data frame with 200 observations on the following 6 variables.

`urge` standardized urge to smoke

`urge1` previous urge to smoke

`dep` standardized depression

`dep1` previous depression

`id` individual indicator

`time` time indicator

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