

# Package ‘gmusim’

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**Title** Growth Modelling using a Shape Invariant Model with Random Effects

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**Description** Functions for fitting growth curves using SIM (Shape Invariant Model) with random effects (Beath, 2007) involved in time independent covariates and computing some public health statistics, such as age at peak velocity (apv), peak velocity (pv) and height (or weight) at peak velocity (ypv). This package is based on R package sitar and SIM model, and the basis of this model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve.

**License** GPL (>= 2)

**LazyData** true

**Depends** R (>= 3.0.0), nlme, splines

**Imports** sitar(>= 1.0.8)

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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exdataz

*Do interpolation for original time measurements and covariates.***Description**

This function evenly partitions time measurements and produces additional ones for an individual in his/her age range. It then uses `predict.gmusim` to obtain additional fitted values to calculate age at peak velocity (apv), peak velocity (pv) and height (or weight) at peak velocity (ypv).

**Usage**

```
exdataz(x, z, p, id, idmat, n = round(365 * diff(range(x))))
```

**Arguments**

x	vector of ages (assume x is centered).
z	data.frame of time independent covariates (assume z is centered).
p	number of columns in data.frame z.
id	factor of subject identifiers.
idmat	matrix of unique id, note that this matrix has been setted to 1 column.
n	time (age) measures after extension for computing aphv (default is round(365*diff(range(x)))).

**Details**

For some individuals, the number of measurements is small. In order to calculate accurate apv (age at peak velocity), pv (peak velocity) and ypv (height at peak velocity or weight at peak velocity), it is necessary to perform interpolation for original time measurements and obtain additional predictions for each individual. This function extends time (age) measurements between min(time) and max(time), as well as covariates z, note that output of z has been centralized.

**Value**

a data frame including expanded x(age), centralization covariates z and corresponding id.

**Author(s)**

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**Examples**

```
require(sitar)
data(heights)
x <- heights$age
h <- heights$height
id <- heights$id
men <- heights$men
men <- abs(men)-mean(abs(men))
z <- data.frame(z1=men)
p <- 1
idmat <- matrix(unique(id), ncol = 1)
newdata <- exdataz(x, z, p, id, idmat)
```

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gmusim	<i>Fit a growth curve model using the Shape Invariant Model with random effects</i>
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## Description

The basis of the Shape Invariant Model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve. After fitting a growth model using the Shape Invariant Model, this function can compute apv, pv and ypv of each individual by the numerical method.

## Usage

```
gmusim(x, y, id, df, knots, len, cal = FALSE, fixed = random,
       random = "a+b+c", bounds = 0.04, start, bstart, verbose = FALSE,
       correlation = NULL, weights = NULL, subset = NULL, method = "ML",
       na.action = na.fail, control = nlmeControl(returnObject = TRUE))
```

## Arguments

x	vector of ages.
y	vector of measurements.
id	factor of subject identifiers.
df	degrees of freedom for cubic regression spline.
knots	vector of values for knots (default df quantiles of x distribution).
len	time (age) measures after extension for computing aphv, if it is missing, then it equals round(365*diff(range(x))); if cal=FALSE, it is useless.
cal	control for whether to calculate pv, apv and height at pv or not (default FALSE).
fixed	character string specifying a, b, c fixed effects (default random).
random	character string specifying a, b, c random effects (default "a+b+c").
bounds	span of x for regression spline, or fractional extension of range (default 0.04).
start	optional numeric vector of initial estimates for the fixed effects, or list of initial estimates for the fixed and random effects (see <a href="#">nlme</a> ).
bstart	optional starting value for fixed effect b, if it is missing, then it equals to mean(x) when calculating.
verbose	optional logical value to print information on the evolution of the iterative algorithm (see <a href="#">nlme</a> ).
correlation	optional corStruct object describing the within-group correlation structure (see <a href="#">nlme</a> ).
weights	optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure (see <a href="#">nlme</a> ).
subset	optional expression indicating the subset of the rows of data that should be used in the fit (see <a href="#">nlme</a> ).
method	character string, either "REML" or "ML" (default) (see <a href="#">nlme</a> ).
na.action	function for when the data contain NAs (see <a href="#">nlme</a> ).
control	list of control values for the estimation algorithm (see <a href="#">nlme</a> ).

## Details

**Start** is an initial estimation vector for fixed effect parameters, it is suggested that the initial values for a, b, c are 0, mean(x) and 0, respectively. Note that a, b, c are corresponding to  $\alpha_0$ ,  $\beta_0$  and  $-\beta_1$  in model (7) of Beath (2007). One method for improving the initial guess for coefficients of fixed effects is to fit the model without random effects to the pooled data using a standard nonlinear least squares package. **bstart** allows the origin of b to be varied. Changing the origin of b affects its random effect variance.

## Value

An object inheriting from class `gmusim` representing the nonlinear mixed-effects model fit, includes all the components returned by `nlme` (see [nlmeObject](#) for a full description) plus the following components:

**bstart**: the value of arg `bstart`.

**call.gmusim**: the internal `gmusim` call that produced the object.

**fitnlme**: the function returning the predicted value of y.

**ns**: the `lm` object providing starting values for the B-spline curve.

**calindex**: APV(age at pv), PV(peak velocity) and HPV(height at pv).

**fitted.values**: a data frame, including expanded x (age), fitted values (y) for corresponding expanded x and id.

Generic functions such as `print`, `plot`, `anova` and `summary` can be used to show the results of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, `random.effects`, `predict`, `getData`, `getGroups`, `getCovariate` and `getVarCov` can be used to extract some of `gmusim`'s components.

## Author(s)

Zhiqiang Cao <zcaoae@connect.ust.hk>, Man-Yu Wong <mamywong@ust.hk>

## References

Beath KJ. Infant growth modelling using a shape invariant model with random effects. *Statistics in Medicine* 2007;26:2547-2564.

Cole TJ, Donaldson MD, Ben-Shlomo Y. SITAR—a useful instrument for growth curve analysis. *Int J Epidemiol* 2010;39:1558-66.

## See Also

[sitar](#), [gmusim\\_both](#), [gmusim\\_com](#), [gmusim\\_gr](#), [gmusim\\_size](#).

## Examples

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
id <- heights$id
df <- 5
## Do not calculate phv, aphv and hphv
resu1 <- gmusim(x,y,id,df)
summary(resu1)
## Calculate phv, aphv and height at phv (hphv)
```

```

resu2 <- gmusim(x,y,id,df,cal=TRUE)
summary(resu2)
aphv <- resu2$calindex
fitted.values <- resu2$fitted.values

```

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gmusim_both	<i>Fit a growth curve model using the Shape Invariant Model with random effects involved in time independent covariates affecting both individual's size and growth rate.</i>
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## Description

The basis of the Shape Invariant Model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve. This function can deal with time independent covariates affecting both subject's size and growth rate, note that every covariate in data.frame z must have both size and growth rate effects.

## Usage

```

gmusim_both(x, y, z, p, n, id, df, knots, len, cal = FALSE, fixed = random,
  random = "a+b+c", bounds = 0.04, start, bstart, verbose = FALSE,
  correlation = NULL, weights = NULL, subset = NULL, method = "ML",
  na.action = na.fail, control = nlmeControl(returnObject = TRUE))

```

## Arguments

x	vector of ages.
y	vector of measurements.
z	data.frame of time independent covariates.
p	number of columns in data.frame z.
n	length of x.
id	factor of subject identifiers.
df	degrees of freedom for cubic regression spline.
knots	vector of values for knots (default df quantiles of x distribution).
len	time (age) measures after extension for computing aphv, if it is missing, then it equals round(365*diff(range(x))); if cal=FALSE, it is useless.
cal	control for whether to calculate pv, apv and height at pv or not (default FALSE).
fixed	character string specifying a, b, c fixed effects (default random).
random	character string specifying a, b, c random effects (default "a+b+c").
bounds	span of x for regression spline, or fractional extension of range (default 0.04).
start	optional numeric vector of initial estimates for the fixed effects, or list of initial estimates for the fixed and random effects (see <a href="#">nlme</a> ).
bstart	optional starting value for fixed effect b, if it is missing, then it equals to mean(x) when calculating.
verbose	optional logical value to print information on the evolution of the iterative algorithm (see <a href="#">nlme</a> ).

correlation	optional corStruct object describing the within-group correlation structure (see <a href="#">nlme</a> ).
weights	optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure (see <a href="#">nlme</a> ).
subset	optional expression indicating the subset of the rows of data that should be used in the fit (see <a href="#">nlme</a> ).
method	character string, either "REML" or "ML" (default) (see <a href="#">nlme</a> ).
na.action	function for when the data contain NAs (see <a href="#">nlme</a> ).
control	list of control values for the estimation algorithm (see <a href="#">nlme</a> ).

## Details

**Start** is an initial estimation vector for fixed effect parameters, it is suggested that the initial values for a, b, c are 0, mean(x) and 0, respectively. Note that a, b, c are corresponding to  $\alpha_0$ ,  $\beta_0$  and  $-\beta_1$  in model (7) of Beath (2007). One method for improving the initial guess for coefficients of fixed effects is to fit the model without random effects to the pooled data using a standard nonlinear least squares package. **bstart** allows the origin of b to be varied. Changing the original of b affects its random effect variance.

## Value

An object inheriting from class gmusim representing the nonlinear mixed-effects model fit, includes all the components returned by nlme (see [nlmeObject](#) for a full description) plus the following components:

**bstart**: the value of arg bstart.

**call.gmusim**: the internal gmusim\_both call that produced the object.

**fitnlme**: the function returning the predicted value of y.

**ns**: the lm object providing starting values for the B-spline curve.

**calindex**: APHV(age at phv), PHV(peak height velocity) and HPHV(height at phv).

**fitted.values**: a data frame, including expanded x, fitted values (y) for corresponding expanded x and id.

Generic functions such as print, plot, anova and summary can be used to show the results of the fit. The functions resid, coef, fitted, fixed.effects, random.effects, predict, getData, getGroups, getCovariate and getVarCov can be used to extract some of gmusim\_both's components.

## Author(s)

Zhiqiang Cao <zcaoae@connect.ust.hk>, Man-Yu Wong <mamywong@ust.hk>

## References

- Beath KJ. Infant growth modelling using a shape invariant model with random effects. *Statistics in Medicine* 2007;26:2547-2564.
- Cole TJ, Donaldson MD, Ben-Shlomo Y. SITAR—a useful instrument for growth curve analysis. *Int J Epidemiol* 2010;39:1558-66.

## See Also

[sitar](#), [gmusim](#), [gmusim\\_com](#), [gmusim\\_gr](#), [gmusim\\_size](#).

## Examples

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
men <- heights$men
id <- heights$id
df <- 5
#since negative value are censored, here use absolute value
z <- data.frame(z1=abs(men))
p <- 1
n <- length(x)
## Do not calculate phv, aphv and hphv
resu1 <- gmusim_both(x,y,z,p,n,id,df)
summary(resu1)
## Calculate phv, aphv and height at phv (hphv)
resu2 <- gmusim_both(x,y,z,p,n,id,df,cal=TRUE)
summary(resu2)
aphv <- resu2$calindex
fitted.values <- resu2$fitted.values
```

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gmusim\_com

*Fit a growth curve model using the Shape Invariant Model with random effects involved in time independent covariates having combined effects.*

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## Description

The basis of the Shape Invariant Model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve. This function can deal with time independent covariates having combined effects, that is, some covariates only have size effects, some only have growth rate effects and some others have both size and growth rate effects.

## Usage

```
gmusim_com(x, y, z, w, p1, p2, n, id, df, knots, len, cal = FALSE,
  fixed = random, random = "a+b+c", bounds = 0.04, start, bstart,
  verbose = FALSE, correlation = NULL, weights = NULL, subset = NULL,
  method = "ML", na.action = na.fail, control = nlmeControl(returnObject =
  TRUE))
```

## Arguments

x	vector of ages.
y	vector of measurements.
z	data.frame of covariates only affect subject's size.
w	data.frame of covariates only affect subject's growth rate.
p1	number of columns in data.frame z.
p2	number of columns in data.frame w.

<code>n</code>	length of <code>x</code> .
<code>id</code>	factor of subject identifiers.
<code>df</code>	degrees of freedom for cubic regression spline.
<code>knots</code>	vector of values for knots (default <code>df</code> quantiles of <code>x</code> distribution).
<code>len</code>	time (age) measures after extension for computing <code>aphv</code> , if it is missing, then it equals <code>round(365*diff(range(x)))</code> ; when <code>cal=FALSE</code> , it is useless.
<code>cal</code>	control for whether to calculate <code>pv</code> , <code>apv</code> and height at <code>pv</code> or not (default <code>FALSE</code> ).
<code>fixed</code>	character string specifying <code>a</code> , <code>b</code> , <code>c</code> fixed effects (default <code>random</code> ).
<code>random</code>	character string specifying <code>a</code> , <code>b</code> , <code>c</code> random effects (default <code>"a+b+c"</code> ).
<code>bounds</code>	span of <code>x</code> for regression spline, or fractional extension of range (default <code>0.04</code> ).
<code>start</code>	optional numeric vector of initial estimates for the fixed effects, or list of initial estimates for the fixed and random effects (see <a href="#">nlme</a> ).
<code>bstart</code>	optional starting value for fixed effect <code>b</code> , if it is missing, then it equals to <code>mean(x)</code> when calculating.
<code>verbose</code>	optional logical value to print information on the evolution of the iterative algorithm (see <a href="#">nlme</a> ).
<code>correlation</code>	optional <code>corStruct</code> object describing the within-group correlation structure (see <a href="#">nlme</a> ).
<code>weights</code>	optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure (see <a href="#">nlme</a> ).
<code>subset</code>	optional expression indicating the subset of the rows of data that should be used in the fit (see <a href="#">nlme</a> ).
<code>method</code>	character string, either <code>"REML"</code> or <code>"ML"</code> (default) (see <a href="#">nlme</a> ).
<code>na.action</code>	function for when the data contain NAs (see <a href="#">nlme</a> ).
<code>control</code>	list of control values for the estimation algorithm (see <a href="#">nlme</a> ).

## Details

**Start** is an initial estimation vector for fixed effect parameters, it is suggested that the initial values for `a`, `b`, `c` are 0, `mean(x)` and 0, respectively. Note that `a`, `b`, `c` are corresponding to  $\alpha_0$ ,  $\beta_0$  and  $-\beta_1$  in model (7) of Beath (2007). And if a covariate has both size and growth rate effect, this covariate should be in both `z` and `w` data.frame. One method for improving the initial guess for coefficients of fixed effects is to fit the model without random effects to the pooled data using a standard nonlinear least squares package. **bstart** allows the origin of `b` to be varied. Changing the original of `b` affects its random effect variance.

## Value

An object inheriting from class `gmusim` representing the nonlinear mixed-effects model fit, with all the components returned by `nlme` (see [nlmeObject](#) for a full description) plus the following components:

**bstart**: the value of arg `bstart`.

**call.gmusim**: the internal `gmusim_com` call that produced the object.

**fitnlme**: the function returning the predicted value of `y`.

**ns**: the `lm` object providing starting values for the B-spline curve.

**calindex**: `APHV`(age at `phv`), `PHV`(peak height velocity) and `HPHV`(height at `phv`).



**fitted.values:** a data frame, including expanded x, fitted values (y) for corresponding expanded x and id.

Generic functions such as print, plot, anova and summary can be used to show the results of the fit. The functions resid, coef, fitted, fixed.effects, random.effects, predict, getData, getGroups, getCovariate and getVarCov can be used to extract some of gmusim\_com's components.

### Author(s)

Zhiqiang Cao <zcaoae@connect.ust.hk>, Man-Yu Wong <mamywong@ust.hk>

### References

Beath KJ. Infant growth modelling using a shape invariant model with random effects. *Statistics in Medicine* 2007;26:2547-2564.

Cole TJ, Donaldson MD, Ben-Shlomo Y. SITAR—a useful instrument for growth curve analysis. *Int J Epidemiol* 2010;39:1558-66.

### See Also

[sitar](#), [gmusim](#), [gmusim\\_both](#), [gmusim\\_gr](#), [gmusim\\_size](#).

### Examples

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
id <- heights$id
men <- heights$men
df <- 5
#since negative value are censored, here use absolute value
z <- data.frame(z1=abs(men))
#generate assumed bmi at 6 years old for these 12 girls
set.seed(100)
bmi6 <- runif(12,min=16,max=26)
numid <- as.numeric(table(id))
bmi6 <- rep(bmi6,numid)
w <- data.frame(w1=bmi6)
p1 <- p2 <- 1
n <- length(x)
####Do not calculate phv, aphv and hphv
resu1 <- gmusim_com(x,y,z,w,p1,p2,n,id,df)
summary(resu1)
####Calculate phv, aphv and height at phv (hphv)
resu2 <- gmusim_com(x,y,z,w,p1,p2,n,id,df,cal=TRUE)
summary(resu2)
aphv <- resu2$calindex
fitted.values <- resu2$fitted.values
```

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gmusim_gr	<i>Fit a growth curve model using the Shape Invariant Model with random effects involved in time independent covariates affecting subject's growth rate.</i>
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## Description

The basis of the Shape Invariant Model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve. This function can deal with time independent covariates affecting subject's growth rate, note that every covariate in data.frame z only has growth rate effect.

## Usage

```
gmusim_gr(x, y, z, p, n, id, df, knots, len, cal = FALSE, fixed = random,
  random = "a+b+c", bounds = 0.04, start, bstart, verbose = FALSE,
  correlation = NULL, weights = NULL, subset = NULL, method = "ML",
  na.action = na.fail, control = nlmeControl(returnObject = TRUE))
```

## Arguments

x	vector of ages.
y	vector of measurements.
z	data.frame of time independent covariates.
p	number of columns in data.frame z.
n	length of x.
id	factor of subject identifiers.
df	degrees of freedom for cubic regression spline.
knots	vector of values for knots (default df quantiles of x distribution).
len	time (age) measures after extension for computing aphv, if it is missing, then it equals round(365*diff(range(x))); if cal=FALSE, it is useless.
cal	control for whether to calculate pv, apv and height at pv or not (default FALSE).
fixed	character string specifying a, b, c fixed effects (default random).
random	character string specifying a, b, c random effects (default "a+b+c").
bounds	span of x for regression spline, or fractional extension of range (default 0.04).
start	optional numeric vector of initial estimates for the fixed effects, or list of initial estimates for the fixed and random effects (see <a href="#">nlme</a> ).
bstart	optional starting value for fixed effect b, if it is missing, then it equals to mean(x) when calculating.
verbose	optional logical value to print information on the evolution of the iterative algorithm (see <a href="#">nlme</a> ).
correlation	optional corStruct object describing the within-group correlation structure (see <a href="#">nlme</a> ).
weights	optional varFunc object or one-sided formula describing the within-group heteroscedasticity structure (see <a href="#">nlme</a> ).

subset	optional expression indicating the subset of the rows of data that should be used in the fit (see <a href="#">nlme</a> ).
method	character string, either "REML" or "ML" (default) (see <a href="#">nlme</a> ).
na.action	function for when the data contain NAs (see <a href="#">nlme</a> ).
control	list of control values for the estimation algorithm (see <a href="#">nlme</a> ).

## Details

**Start** is an initial estimation vector for fixed effect parameters, it is suggested that the initial values for a, b, c are 0, mean(x) and 0, respectively. Note that a, b, c are corresponding to  $\alpha_0$ ,  $\beta_0$  and  $-\beta_1$  in model (7) of Beath (2007). One method for improving the initial guess for coefficients of fixed effects is to fit the model without random effects to the pooled data using a standard nonlinear least squares package. **bstart** allows the origin of b to be varied. Changing the original of b affects its random effect variance.

## Value

An object inheriting from class `gmusim` representing the nonlinear mixed-effects model fit, with all the components returned by `nlme` (see [nlmeObject](#) for a full description) plus the following components:

**bstart**: the value of arg `bstart`.

**call.gmusim**: the internal `gmusim_gr` call that produced the object.

**fitnlme**: the function returning the predicted value of y.

**ns**: the `lm` object providing starting values for the B-spline curve.

**calindex**: APHV(age at phv), PHV(peak height velocity) and HPHV(height at phv).

**fitted.values**: a data frame, including expanded x, fitted values (y) for corresponding expanded x and id.

Generic functions such as `print`, `plot`, `anova` and `summary` can be used to show the results of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, `random.effects`, `predict`, `getData`, `getGroups`, `getCovariate` and `getVarCov` can be used to extract some of `sitar_gr`'s components.

## Author(s)

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## References

Beath KJ. Infant growth modelling using a shape invariant model with random effects. *Statistics in Medicine* 2007;26:2547-2564.

Cole TJ, Donaldson MD, Ben-Shlomo Y. SITAR—a useful instrument for growth curve analysis. *Int J Epidemiol* 2010;39:1558-66.

## See Also

[sitar](#), [gmusim](#), [gmusim\\_both](#), [gmusim\\_com](#), [gmusim\\_size](#).

## Examples

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
men <- heights$men
id <- heights$id
df <- 5
#since negative value are censored, here use absolute value
z <- data.frame(z1=abs(men))
p <- 1
n <- length(x)
## Do not calculate phv, aphv and hphv
resu1 <- gmusim_gr(x,y,z,p,n,id,df)
summary(resu1)
## Calculate phv, aphv and height at phv (hphv)
resu2 <- gmusim_gr(x,y,z,p,n,id,df,cal=TRUE)
summary(resu2)
aphv <- resu2$calindex
fitted.values <- resu2$fitted.values
```

---

gmusim\_size

*Fit a growth curve model using the Shape Invariant Model with random effects involved in time independent covariates affecting subject's size.*

---

## Description

The basis of the Shape Invariant Model is that a population has a common characteristic curve or function, which by shifting and scaling can be made to have the form of any individual curve. This function can deal with time independent covariates affecting subject's size, note that every covariate in data.frame z only has size effect.

## Usage

```
gmusim_size(x, y, z, p, n, id, df, knots, len, cal = FALSE, fixed = random,
  random = "a+b+c", bounds = 0.04, start, bstart, verbose = FALSE,
  correlation = NULL, weights = NULL, subset = NULL, method = "ML",
  na.action = na.fail, control = nlmeControl(returnObject = TRUE))
```

## Arguments

x	vector of ages.
y	vector of measurements.
z	data.frame of time independent covariates.
p	number of columns in data.frame z.
n	length of x.
id	factor of subject identifiers.
df	degrees of freedom for cubic regression spline.
knots	vector of values for knots (default df quantiles of x distribution).

len	time (age) measures after extension for computing aphv, if it is missing, then it equals <code>round(365*diff(range(x)))</code> ; if <code>cal=FALSE</code> , it is useless.
cal	control for whether to calculate pv, apv and height at pv or not (default <code>FALSE</code> ).
fixed	character string specifying a, b, c fixed effects (default <code>random</code> ).
random	character string specifying a, b, c random effects (default <code>"a+b+c"</code> ).
bounds	span of x for regression spline, or fractional extension of range (default 0.04).
start	optional numeric vector of initial estimates for the fixed effects, or list of initial estimates for the fixed and random effects (see <a href="#">nlme</a> ).
bstart	optional starting value for fixed effect b, if it is missing, then it equals to <code>mean(x)</code> when calculating.
verbose	optional logical value to print information on the evolution of the iterative algorithm (see <a href="#">nlme</a> ).
correlation	optional <code>corStruct</code> object describing the within-group correlation structure (see <a href="#">nlme</a> ).
weights	optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure (see <a href="#">nlme</a> ).
subset	optional expression indicating the subset of the rows of data that should be used in the fit (see <a href="#">nlme</a> ).
method	character string, either <code>"REML"</code> or <code>"ML"</code> (default) (see <a href="#">nlme</a> ).
na.action	function for when the data contain NAs (see <a href="#">nlme</a> ).
control	list of control values for the estimation algorithm (see <a href="#">nlme</a> ).

## Details

**Start** is an initial estimation vector for fixed effect parameters, it is suggested that the initial values for a, b, c are 0, `mean(x)` and 0, respectively. Note that a, b, c are corresponding to  $\alpha_0$ ,  $\beta_0$  and  $-\beta_1$  in model (7) of Beath (2007). One method for improving the initial guess for coefficients of fixed effects is to fit the model without random effects to the pooled data using a standard nonlinear least squares package. **bstart** allows the origin of b to be varied. Changing the origin of b affects its random effect variance.

## Value

An object inheriting from class `gmusim` representing the nonlinear mixed-effects model fit, with all the components returned by `nlme` (see [nlmeObject](#) for a full description) plus the following components:

**bstart**: the value of arg `bstart`.

**call.gmusim**: the internal `gmusim_size` call that produced the object.

**fitnlme**: the function returning the predicted value of y.

**ns**: the `lm` object providing starting values for the B-spline curve.

**calindex**: APHV(age at phv), PHV(peak height velocity) and HPHV(height at phv).

**fitted.values**: a data frame, including expanded x, fitted values (y) for corresponding expanded x and id.

Generic functions such as `print`, `plot`, `anova` and `summary` can be used to show the results of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, `random.effects`, `predict`, `getData`, `getGroups`, `getCovariate` and `getVarCov` can be used to extract some of `gmusim_size`'s components.

**Author(s)**

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**References**

Beath KJ. Infant growth modelling using a shape invariant model with random effects. *Statistics in Medicine* 2007;26:2547-2564.

Cole TJ, Donaldson MD, Ben-Shlomo Y. SITAR—a useful instrument for growth curve analysis. *Int J Epidemiol* 2010;39:1558-66.

**See Also**

[sitar](#), [gmusim](#), [gmusim\\_both](#), [gmusim\\_com](#), [gmusim\\_gr](#).

**Examples**

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
men <- heights$men
id <- heights$id
df <- 5
#since negative value are censored, here use absolute value
z <- data.frame(z1=abs(men))
p <- 1
n <- length(x)
## Do not calculate phv, aphv and hphv
resu1 <- gmusim_size(x,y,z,p,n,id,df)
summary(resu1)
## Calculate phv, aphv and height at phv (hphv)
resu2 <- gmusim_size(x,y,z,p,n,id,df,cal=TRUE)
summary(resu2)
aphv <- resu2$calindex
fitted.values <- resu2$fitted.values
```

---

lim

---

*Linear interpolation method to calculate y value at time t0.*


---

**Description**

This function uses linear interpolation method to calculate corresponding y value at time t0.

**Usage**

```
lim(x, y, id, t0)
```

**Arguments**

x	vector of ages.
y	vector of measurements.
id	factor of subject identifiers.
t0	target age value.

**Details**

For each individual's measurements in growth data set, the first time measurement is usually not the same, people are interested in some measurement index of certain age, for example height of age 6 years old for each id. This function can help us compute corresponding measurement at interested age.

**Value**

a data frame including id and corresponding y value at t0.

**Author(s)**

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**Examples**

```
require(sitar)
data(heights)
x <- heights$age
h <- heights$height
id <- heights$id
## height at age 9
h9 <- lim(x,h,id,9)
```

---

predict.gmusim	<i>Predict the Shape Invariant Model with random effects involved in co-variates.</i>
----------------	---

---

**Description**

Predict method for gmusim objects, based on predict.lme.

**Usage**

```
## S3 method for class 'gmusim'
predict(object, newdata, level = 1, ...)
```

**Arguments**

object	an object inheriting from class gmusim.
newdata	an optional data frame to be used for obtaining the predictions. It requires named columns for x, z and for id if level = 1, matching the names in object. Note that values of covariates z should be centralized. By default their values are set to the mean so when level = 0 the prediction represents the mean curve. Note that factors are coded as instrumental variables for each level, corresponding to the fixed effect coefficients in the model, so their names need the level appending..
level	an optional integer giving the level of grouping to be used in obtaining the predictions, level 0 corresponding to the population predictions. Defaults to level 1.
...	other optional arguments, including na.action and naPattern.

**Details**

Note that if level = 1, this function calculates prediction for every measurement of individuals; if level = 0, it calculates mean value of individuals' measurements.

**Value**

A vector of the predictions.

**Author(s)**

Zhiqiang Cao <zcaoae@connect.ust.hk>, Man-Yu Wong <mamywong@ust.hk>

**Examples**

```
require(sitar)
data(heights)
x <- heights$age
y <- heights$height
men <- heights$men
id <- heights$id
df <- 5
#since negative value are censored, here use absolute value
z <- data.frame(z1=abs(men))
p <- 1
n <- length(x)
## fit sitar model with covariates
resu1 <- gmusim_both(x,y,z,p,n,id,df)
## predictions at level = 0
on.exit(detach(resu1))
eval(parse(text = "attach(resu1)"))
predict(resu1, newdata=data.frame(x=6:15,z1=rep(mean(men),10)), level=0)
## predictions at level = 1 for all subjects
newd <- data.frame(x=heights$age,z1=abs(men)-mean(abs(men)),id=id)
on.exit(detach(resu1))
eval(parse(text = "attach(resu1)"))
fitted.values <- predict(resu1, newdata=newd, level=1)
```



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