

Package ‘growthfd’

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Title Fitting FPCA-based growth curve model

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Description

This package provides a method for fitting an FPCA-based growth curve model described in the paper stated below. This research was funded by Technology Agency of the Czech Republic (Technologická agentura České republiky), grant number TL01000394.

Citation Kralik M., Klima O., Cuta M., Malina R., Koziel S., Polcerova L., Skultetyova A., Spanel M., Kukla L., Zemcik P. Estimating Growth in Height from Limited Longitudinal Growth Data Using Full-Curves Training Dataset: A Comparison of Two Procedures of Curve Optimization-Functional Principal Component Analysis and SITAR. Children, 2021, vol. 8, n. 10., pages 934-955.

URL <https://ondrej-klima.github.io/growthfd/>, <https://github.com/ondrej-klima/growthfd/>

License LGPL (>= 3)

Encoding UTF-8

RoxygenNote 7.1.2

Imports minpack.lm,
sitar (>= 1.2.0),
fda,
ggplot2,
parallel,
doParallel,
foreach,
flock,
MASS

Depends R (>= 2.10)

LazyData true

Suggests rmarkdown,
knitr

VignetteBuilder knitr

R topics documented:

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| | |
|----------|--|
| growthfd | <i>Fit a FPCA Growth Curve Model to a population</i> |
|----------|--|

Description

This function fits a model to the given measured data of a population.

Usage

```
growthfd(  
  data,  
  x,  
  y,  
  id,  
  model,  
  verbose = 1,  
  bounds = "negative",  
  filename = "",  
  startFromId = NULL,  
  parallel = F,  
  scores.filename = "parallel.txt"  
)
```

Arguments

| | |
|-----------------|---|
| data | Data frame containing age, height and id of individuals |
| x | Age at measured data points |
| y | Height at measured data points |
| id | Corresponding individual's id at measured data points |
| model | FPCA growth model to be fitted |
| verbose | Verbosity |
| bounds | Limitation of the interval for milestones estimation, 'negative' or 'inverse' |
| filename | File name for saving results after each individual |
| startFromId | Start the evaluation from this id |
| parallel | (Experimental) Parallel evaluation of the model fitting |
| scores.filename | File name for continuous saving of the scores |

Value

List containing individuals id and model

Examples

```
filename <- system.file("extdata", "data.csv", package="growthfd", mustWork=TRUE)
csv <- read.csv(filename)
d <- data.frame('id'=as.factor(csv[, 'id']), 'x'=csv[, 'age'], 'y'=csv[, 'height'])
fit<-growthfd(data=d, x=x, y=y, id=id, model=model.bgs.m)
```

growthfd.apv

Compute apv of model instance

Description

This function computes apv related to the certain instance of the model described by the given parameters.

Usage

```
growthfd.apv(model, par)
```

Arguments

| | |
|-------|---|
| model | FPCA growth model |
| par | Params of the model, corresponding to some individual |

Value

Age of maximum growth velocity

growthfd.ApvRegVelocity

Register a velocity curve at population apv

Description

This function registers a curve corresponding to the supplied parameters onto the population apv.

Usage

```
growthfd.ApvRegVelocity(model, par, verbose = F)
```

Arguments

| | |
|-------|--|
| model | FPCA growth model |
| par | Params of the model, corresponding to the individual |

Value

Velocity at apv data frame

Examples

```
filename <- system.file("extdata", "data.csv", package="growthfd", mustWork=TRUE)
csv <- read.csv(filename)
d <- data.frame('id'=as.factor(csv[, 'id']), 'x'=csv[, 'age'], 'y'=csv[, 'height'])
m <- d$id == 'John'
fit <- growthfd.fit(model.bgs.m, age=d$x[m], height=d$y[m])
data<-growthfd.ApvRegVelocity(model.bgs.m, fit$par)
```

growthfd.bgs.dropoutsIds.Height

List ids of individuals to be dropped from height modeling

Description

This function returns a vector containing ids of individuals with incomplete stature measurements.

Usage

```
growthfd.bgs.dropoutsIds.Height()
```

Value

Vector of ids

| | |
|---------------------|--------------------------------|
| growthfd.bgs.gather | <i>Gather selected columns</i> |
|---------------------|--------------------------------|

Description

Selects columns with given prefix for supplied ages and gathers them into a matrix together with id and sex data

Usage

```
growthfd.bgs.gather(data, prefix, age = NULL)
```

Arguments

| | |
|--------|-----------------------------------|
| data | BGS data |
| prefix | Columns prefix |
| age | Vector containing ages (optional) |

Value

Gathered data

| | |
|------------------------------|----------------------------------|
| growthfd.bgs.measurementsAge | <i>List ages of measurements</i> |
|------------------------------|----------------------------------|

Description

This function returns a vector of ages when the measurements were performed.

Usage

```
growthfd.bgs.measurementsAge()
```

Value

Vector of ages

| | |
|-------------------|---|
| growthfd.evaluate | <i>Generate a Discrete Growth Curve</i> |
|-------------------|---|

Description

This function evaluates a curve function for given ages. Depending on a degree of derivation, the function produces stature, velocity or acceleration curve.

Usage

```
growthfd.evaluate(x, par, model, deriv = 0)
```

Arguments

| | |
|-------|-------------------------|
| x | Ages to be evaluated |
| par | Parameters of the model |
| model | FPCA growth model |
| deriv | Path to the input file |

Value

Y-values of the evaluated curve

| | |
|--------------|---|
| growthfd.fit | <i>Fit a FPCA Growth Curve Model to measurements of a single individual</i> |
|--------------|---|

Description

This function fits a model to the given measured data of a single individual.

Usage

```
growthfd.fit(model, age, height, nprint = 1)
```

Arguments

| | |
|--------|-----------------------------------|
| model | FPCA growth model to be fitted |
| age | Age at measured data points |
| height | Height at at measured data points |
| nprint | Verbosity |

Value

An optimization result object

Examples

```

age <- c(6.9, 8.2, 10, 12.1)
height <- c(114, 122, 130, 141)
fit <- growthfd.fit(model.bgs.m, age=c(6.9, 8.2, 10, 12.1), height=c(114, 122, 130, 141))
x11()
growthfd.plot(model.bgs.m, fit$par)
points(age, height)
x11()
growthfd.plot(model.bgs.m, fit$par, from=0.5, deriv = 1)
x11()
growthfd.plot(model.bgs.m, fit$par, from=0.5, deriv = 2)

```

| | |
|--------------------|----------------------------------|
| growthfd.modelPars | <i>Standardized model scores</i> |
|--------------------|----------------------------------|

Description

This function returns model parameters for the individuals used for training the model.

Usage

```
growthfd.modelPars(model)
```

Arguments

| | |
|-------|-------------------------|
| model | FPCA-based growth model |
|-------|-------------------------|

Value

Matrix containing the scores

| | |
|---------------|----------------------------|
| growthfd.plot | <i>Plot a Growth Curve</i> |
|---------------|----------------------------|

Description

This function plots a stature, velocity or acceleration curve.

Usage

```
growthfd.plot(model, par, deriv = 0, from = 0, to = 18)
```

Arguments

| | |
|-------|-------------------------|
| model | FPCA growth model |
| par | Parameters of the model |
| deriv | Path to the input file |
| from | The lower age limit |
| to | The upper age limit |

```
growthfd.plot.ApvRegVelocity
```

Plot a velocity curve registered at apv

Description

This function plots a velocity curve, registered at population (model) apv in comparison with the mean curve.

Usage

```
growthfd.plot.ApvRegVelocity(data)
```

Arguments

model Data obtained using growthfd.ApvRegVelocity

Value

Velocity at apv plot

Examples

```
filename <- system.file("extdata", "data.csv", package="growthfd", mustWork=TRUE)
csv <- read.csv(filename)
d <- data.frame('id'=as.factor(csv[, 'id']), 'x'=csv[, 'age'], 'y'=csv[, 'height'])
m <- d$id == 'John'
fit <- growthfd.fit(model.bgs.m, age=d$x[m], height=d$y[m])
data<-growthfd.ApvRegVelocity(model.bgs.m, fit$par)
p<-growthfd.plot.ApvRegVelocity(data)
x11()
p
```

```
growthfd.plot.RegVelocities
```

Plot velocity boxplots registered on apv

Description

This function plots boxplots in time of measurements, after registration of the individual on population apv.

Usage

```
growthfd.plot.RegVelocities(populationData, individualData)
```

Arguments

populationData Data frame for population box plots
individualData Data frame for the individual

Value

GGPlot2 plot

Examples

```
filename <- system.file("extdata", "data.csv", package="growthfd", mustWork=TRUE)
csv <- read.csv(filename)
d <- data.frame('id'=as.factor(csv[, 'id']), 'x'=csv[, 'age'], 'y'=csv[, 'height'])
m <- d$id == 'John'
fit <- growthfd.fit(model.bgs.m, age=d$x[m], height=d$y[m])
b <- growthfd.RegVelocities(model.bgs.m, fit$par, d$x[m])
p<- growthfd.plot.RegVelocities(b$population, b$individual)
x11()
p
```

growthfd.RegVelocities

Prepare data for velocity boxplots registered on apv

Description

This function prepares data for boxplots in time of measurements, after registration of the individual on population apv.

Usage

```
growthfd.RegVelocities(model, par, ages, rndn = 0, verbose = F)
```

Arguments

| | |
|-------|--|
| model | Model |
| par | Parameters of the model fitted to the measurements |
| ages | Ages of measurements points |
| rndn | Count of random curves to be evaluated |

Value

Data frames for population and the individual

| | |
|--------------------|--------------------------|
| growthfd.residuals | <i>Compute residuals</i> |
|--------------------|--------------------------|

Description

This function computes residuals between measured stature data and data generated from the growth model.

Usage

```
growthfd.residuals(x, y, par, model)
```

Arguments

| | |
|-------|--|
| x | Vector with input ages |
| y | Vector with target height measurements |
| par | Parameters of the model |
| model | FPCA growth model |

Value

A vector of residuals

| | |
|--------------|----------------------------------|
| growthfd.std | <i>Generate a Curve Function</i> |
|--------------|----------------------------------|

Description

This function generates a growth curve function based on given model and parameters, describing the growth phase and amplitude.

Usage

```
growthfd.std(par, model)
```

Arguments

| | |
|-------|--------------------------------|
| par | Phase and amplitude parameters |
| model | FPCA growth model |

Value

FDA function object

| | |
|-----------------|------------------------------|
| growthfd.warpfd | <i>Time warping function</i> |
|-----------------|------------------------------|

Description

This function returns the time warping function corresponding to supplied model and particular parameters.

Usage

```
growthfd.warpfd(par, model)
```

Arguments

| | |
|-------|-------------------------|
| par | Parameters of the model |
| model | FPCA growth model |

| | |
|--------------------|--------------------------------------|
| growthfd.warpfdInv | <i>Inverse time warping function</i> |
|--------------------|--------------------------------------|

Description

This function returns the **inverse** time warping function corresponding to supplied model and particular parameters.

Usage

```
growthfd.warpfdInv(par, model)
```

Arguments

| | |
|-------|-------------------------|
| par | Parameters of the model |
| model | FPCA growth model |

| | |
|-------------|-----------------------------|
| model.bgs.f | <i>FPCA model for girls</i> |
|-------------|-----------------------------|

Description

Model trained using 167 female individuals from Brno Growth Study (BGS).

Usage

```
model.bgs.f
```

Format

An object of class `list` of length 3.

| | |
|-------------|----------------------------|
| model.bgs.m | <i>FPCA model for boys</i> |
|-------------|----------------------------|

Description

Model trained using 167 male individuals from Brno Growth Study (BGS).

Usage

```
model.bgs.m
```

Format

An object of class `list` of length 3.

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