Package 'growthfd'

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Title Fitting FPCA-based growth curve model

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Description
This package provides a method for fiting an FPCA-based growth curve model described in the paper stated bellow. 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/

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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:

`growthfd` *Fit a FPCA Growth Curve Model to a population*

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)
```

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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 *Gather selected columns*

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.interpolateNAs *Estimate NA values*

Description

Interpolates missing values using spline method. Interpolates data from the 'value' column and join them as the 'valuei' column.

Usage

```
growthfd.bgs.interpolateNAs(gatheredData)
```

Arguments

gatheredData	Data in gathered form

Value

Interpolated data

`growthfd.bgs.measurementsAge` *List ages of measurements*

Description

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

Usage

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

Value

Vector of ages

`growthfd.bgs.resample` *Resample the data*

Description

Resample the data without NA values to fine grid.

Usage

```
growthfd.bgs.resample(interpolatedData)
```

Arguments

`interpolatedData`	Data to be resampled.

Value

Resampled data

growthfd.evaluate — *Generate a Discrete Growth Curve*

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 — *Fit a FPCA Growth Curve Model to measurements of a single individual*

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 *Standardized model scores*

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 *Plot a Growth Curve*

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 *Compute residuals*

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 *Generate a Curve Function*

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 *Time warping function*

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 *Inverse time warping function*

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 *FPCA model for girls*

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` *FPCA model for boys*

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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