

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/>

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foreach,
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R topics documented:

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growthfd	<i>Fit a FPCA Growth Curve Model to a population</i>
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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.apvs

Find apvs on growth curves

Description

This function finds ages of maximal growth velocity on the velocity curves.

Usage

```
growthfd.bgs.apvs(age, velocity)
```

Arguments

age	Vector of ages
velocity	Matrix of velocity curves
ids	Vector of individuals' ids
limits	List of limits

Value

Vector of apv values

`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.eval`*Evaluate general fda splines*

Description

This function evaluates non monotone fda splines.

Usage

```
growthfd.bgs.eval(fda, age, deriv = 0)
```

Arguments

<code>fda</code>	Fda object
<code>age</code>	Vector of ages to be evaluated
<code>deriv</code>	Derivative of the curve

Value

Matrix of evaluated points

`growthfd.bgs.evalMonotone`*Evaluate monotone fda splines*

Description

This function evaluates the set of monotone splines.

Usage

```
growthfd.bgs.evalMonotone(fda, age, deriv = 0)
```

Arguments

<code>fda</code>	Fda object
<code>age</code>	Vector of ages to be evaluated
<code>deriv</code>	Derivative of the curve

Value

Matrix of evaluated points

`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 = "vysk", age = NULL)
```

Arguments

<code>data</code>	BGS data
<code>prefix</code>	Columns prefix
<code>age</code>	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.invertTw` *Compute inverse time-warping functions*

Description

Computes inverse for given functions.

Usage

```
growthfd.bgs.invertTw(age, tw)
```

Arguments

`age` Vector of ages
`tw` Fda object containing the time-warping functions

Value

Fda object containing the inverse functions

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.plotAll *Plot curves in one figure*

Description

Plots all curves from given matrix into a single figure.

Usage

```
growthfd.bgs.plotAll(age, values, xlimit = NULL, ylimit = NULL)
```

Arguments

age	Vector of ages
values	Matrix containing curves as columns
xlimit	Limits for the x axis
ylimit	Limits for the y axis

Value

GGPlot2 plot

`growthfd.bgs.plotIndividuals`*Plot all individual curves to pdf*

Description

Plots value, velocity and acceleration curves together with apvs and measured data points into separate figure for each individual. All plots are stored into a single pdf file, one figure per page.

Usage

```
growthfd.bgs.plotIndividuals(  
  age,  
  ids,  
  apvs,  
  values,  
  vel,  
  acc,  
  data,  
  filename = "plots.pdf"  
)
```

Arguments

age	Vector of ages
ids	Vector containing ids
apvs	Vector containing apv for each individual
values	Matrix with acceleration curves
vel	Matrix with velocity curves
data	Matrix with original data points
filename	File name of the output pdf

`growthfd.bgs.registerCurvesToApvs`*Register curves to the apvs*

Description

Calculates the time warping functions with respect to the supplied apvs and the growth curves for the final refinement.

Usage

```
growthfd.bgs.registerCurvesToApvs(fdaObject, apvs)
```

Arguments

fdaObject	Fda object containing the curves
apvs	Vector containing the respective apvs

Value

FDA object containing the time warping functions

growthfd.bgs.resample *Resample the data*

Description

Resamples the data without NA values to fine grid.

Usage

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

Arguments

interpolatedData	Data to be resampled.
------------------	-----------------------

Value

Resampled data

growthfd.bgs.smooth *Fit the monotone spline*

Description

This function fit the monotone splines to the data.

Usage

```
growthfd.bgs.smooth(
  resampledData,
  monotone = T,
  norder = 6,
  Lfdobj = 3,
  lambda = 0.05
)
```

Arguments

resampledData	Data to be interpolated by monotone fda splines
---------------	---

Value

Object with fitted splines

Examples

```
data <- read.table("D:/Growth/playground/data/bgs_07.txt", header=TRUE, sep="\t", na.strings="NA", dec=".")
data <- data[!(data$id %in% growthfd.bgs.dropoutsIds.Height()) & data$sex == "1",]
gather <- growthfd.bgs.gather(data)
interp <- growthfd.bgs.interpolateNAs(gather)
resampled <- growthfd.bgs.resample(interp)
smoothed <- growthfd.bgs.smooth(resampled)

age <- seq(10, 18, 0.05)
m<-growthfd.bgs.evalMonotone(smoothed,age,1)
apvs<-growthfd.bgs.apvs(age,m)

age <- seq(0, 18, 0.05)
ids <- unique(data$id)
values <- growthfd.bgs.evalMonotone(smoothed,age)
vel <- growthfd.bgs.evalMonotone(smoothed,age,1)
acc <- growthfd.bgs.evalMonotone(smoothed,age,2)
growthfd.bgs.plotIndividuals(age, ids, apvs, values, vel, acc, gather)
growthfd.bgs.plotAll(age,acc, ylimit = c(-25, 25))

smoothed2 <- growthfd.bgs.smooth(resampled, F)
m2<-growthfd.bgs.eval(smoothed2$fd,age)
values2 <- growthfd.bgs.eval(smoothed2$fd,age)
vel2 <- growthfd.bgs.eval(smoothed2$fd,age,1)
acc2 <- growthfd.bgs.eval(smoothed2$fd,age,2)
growthfd.bgs.plotIndividuals(age, ids, apvs, values2, vel2, acc2, gather, filename = "plots2.pdf")

resampled3 <- values
dim(resampled3) <- c(prod(dim(values)), 1)
resampled3 <- cbind(rep(ids, each=dim(values)[1]), rep(age, dim(values)[2]), resampled3[,1])
colnames(resampled3) <- colnames(resampled)
smoothed3 <- growthfd.bgs.smooth(resampled3, F)
m3<-growthfd.bgs.eval(smoothed3$fd,age)
values3 <- growthfd.bgs.eval(smoothed3$fd,age)
vel3 <- growthfd.bgs.eval(smoothed3$fd,age,1)
acc3 <- growthfd.bgs.eval(smoothed3$fd,age,2)
growthfd.bgs.plotIndividuals(age, ids, apvs, values3, vel3, acc3, gather, filename = "plots3.pdf")

tw <- growthfd.bgs.registerCurvesToApvs(smoothed, apvs)
reged<-fda::register.newfd(smoothed$yhatfd, tw)
fda::register.newfd(accelfdUN, regListLM$warpdfd)

reged.bak<-fda::register.newfd(smoothed$yhatfd, tw)
tw.bak <- tw
```

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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