

# 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.

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---

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)
```

---

growthfd.apv	<i>Compute apv of model instance</i>
--------------	--------------------------------------

---

**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	<i>Register a velocity curve at population apv</i>
-------------------------	--

---

**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	<i>Find apvs on growth curves</i>
-------------------	-----------------------------------

---

**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	<i>List ids of individuals to be dropped from height modeling</i>
---------------------------------	---

---

**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	<i>Evaluate general fda splines</i>
-------------------	-------------------------------------

---

**Description**

This function evaluates non monotone fda splines.

**Usage**

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

**Arguments**

fda	Fda object
age	Vector of ages to be evaluated
deriv	Derivative of the curve

**Value**

Matrix of evaluated points

---

growthfd.bgs.evalMonotone	<i>Evaluate monotone fda splines</i>
---------------------------	--------------------------------------

---

**Description**

This function evaluates the set of monotone splines.

**Usage**

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

**Arguments**

fda	Fda object
age	Vector of ages to be evaluated
deriv	Derivative of the curve

**Value**

Matrix of evaluated points

---

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

**Arguments**

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

**Value**

Gathered data

---

growthfd.bgs.interpolateNAs	<i>Estimate NA values</i>
-----------------------------	---------------------------

---

**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.model	Create FPCA growth model
--------------------	--------------------------

---

**Description**

Creates FPCA growth model from fda objects of growth functions registered on apv and inverse time warping functions.

**Usage**

```
growthfd.bgs.model(amplitude, itw, nharm = 6)
```

**Arguments**

itw	Fda object of inverse time warping functions
nharm	Number of harmonic functions for each fpca
amplitude	Fda object of registered growth functions

**Value**

FPCA growth model

---

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
xlim	Limits for the x axis
ylim	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.

Computes the time-warping functions based on landmark-based registration apv and atf points to the population means

### Usage

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

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

**Arguments**

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

**Value**

FDA object containing the time warping functions  
 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",]
data <- data[!(data$id %in% growthfd.bgs.dropoutsIds.Height()),]
gather <- growthfd.bgs.gather(data)
interp <- growthfd.bgs.interpolateNAs(gather)
resampled <- growthfd.bgs.resample(interp)
#smoothed <- growthfd.bgs.smooth(resampled)
smoothed <- growthfd.bgs.smooth(resampled, F)

#age <- seq(10, 18, 0.05)
#m<-growthfd.bgs.evalMonotone(smoothed$fd,age,1)
#apvs<-growthfd.bgs.apvs(age,m)
#ids <- unique(data$id)

age <- seq(10, 18, 0.05)
m<-growthfd.bgs.eval(smoothed$fd,age,1)
apvs<-growthfd.bgs.apvs(age,m)
ids <- unique(data$id)

# Fix individuals with apv lower than 10
age <- seq(7, 18, 0.05)
m<-growthfd.bgs.evalMonotone(smoothed,age,1)
apvs.na <- which(is.na(apvs))
apvs[apvs.na]<-growthfd.bgs.apvs(age,m[,apvs.na])

#age <- seq(0, 18, 0.05)
#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))

age <- seq(0, 18, 0.05)
values <- growthfd.bgs.eval(smoothed$fd,age)
vel <- growthfd.bgs.eval(smoothed$fd,age,1)
acc <- growthfd.bgs.eval(smoothed$fd,age,2)
growthfd.bgs.plotIndividuals(age, ids, apvs, values, vel, acc, gather, 'plot_weight.pdf')

resampled.new <- values
dim(resampled.new) <- c(prod(dim(values)), 1)
resampled.new <- cbind(rep(ids, each=dim(values)[1]), rep(age, dim(values)[2]), resampled.new[,1])
colnames(resampled.new) <- colnames(resampled)
smoothed.new <- growthfd.bgs.smooth(resampled.new, F)

tw <- growthfd.bgs.registerCurvesToApvs(smoothed, apvs)
amp<-fda::register.newfd(smoothed.new$fd,tw)
itw <- growthfd.bgs.invertTw(age, tw)

model <- growthfd.bgs.model(amp, itw$fd)
```

```
plDf <- data.frame('phasePC1'=model$warppca$scores[,1], 'amplitudePC1'=model$growthfpcascores[,1], sex=fac
ggplot2::ggplot(data = plDf, ggplot2::aes(x=phasePC1, y=amplitudePC1, colour=sex)) +
  ggplot2::geom_point() +
  ggplot2::stat_ellipse(geom = "polygon", linetype = 2, ggplot2::aes(fill = sex), alpha = 0.15) +
  ggplot2::geom_rug() +
  ggplot2::stat_smooth(method = "lm", fullrange = TRUE) +
  ggplot2::scale_colour_manual(name = "Sex", values = c('blue', 'red'), labels=c('Male', 'Female')) +
  ggplot2::scale_fill_manual(name = "Sex", values = c('blue', 'red'), labels=c('Male', 'Female'))
```

---

growthfd.digits	<i>Preprocess a digit data</i>
-----------------	--------------------------------

---

## Description

Selects data with minimal count of measurements and convert them into a data frame.

## Usage

```
growthfd.digits(data, colName, minCount = 9, ncores = 4)
```

## Arguments

data	A csv table containing the measurements
colName	Name of the particular column with the length data
minCount	Minimal count of measurements
ncores	Number of cores used for parallelisation

## Value

Data frame with uniformly distributed data

## Examples

```
data <- read.csv2('D:/growth/digits/data_muzi_all.csv', sep=";")
interp <- growthfd.digits(data=data, colName='X1_2_sur', minCount=9, ncores=4)

resampled <- growthfd.bgs.resample(interp)
smoothed <- growthfd.bgs.smooth(resampled)

age <- seq(10, 18, 0.05)
m<-growthfd.bgs.evalMonotone(smoothed$fd,age,1)
apvs<-growthfd.bgs.apvs(age,m)
ids <- unique(data$id)

age <- seq(min(data$age), max(data$age), 0.05)
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, 'plot_X1_2_sur.pdf')
```

---

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.plotwarps	<i>Plot eigenwarps and eigenamplitudes of the model</i>
--------------------	---

---

**Description**

Plots the effects of individual parameters on the curve shape.

**Usage**

```
growthfd.plotwarps(model, deriv = 0, ylim = NULL)
```

**Arguments**

model	FPCA growth model
deriv	Derivation of the growth curve
ylim	Limits the scale of y axis

---

growthfd.RegVelocities	<i>Prepare data for velocity boxplots registered on apv</i>
------------------------	---

---

**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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