

# 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)

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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

*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.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>
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---

**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      *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**

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.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)
```

---

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	<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>
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---

**Description**

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

**Usage**

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

**Arguments**

model	FPCA-based growth model
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**Value**

Matrix containing the scores

---

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

**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>
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---

**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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