

# Package ‘InfDim’

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**Type** Package

**Title** Infine-dimensional model (IDM) to analyse phenotypic variation in growth trajectories.

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**Description** This package contains functions to perform calculations of the infine-dimensional model (IDM) and to produce 95% confidence intervals around the model elements through bootstrapping.

**License** GPL (>= 2)

**LazyLoad** yes

**LazyData** yes

**ZipData** no

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**NeedsCompilation** no

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InfDim-package	<i>Infine-dimensional model (IDM) to analyse phenotypic variation in growth trajectories.</i>
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## Description

This package contains functions to perform calculations of the infine-dimensional model (IDM) and to produce confidence intervals around the model elements via bootstrapping.

## Details

Package:	InfDim
Type:	Package
Version:	1.0
Date:	2011-03-23
License:	GPL (>= 2)
LazyLoad:	yes

The package contains two mains functions, IDM and IDM.bootCI. The former calculates IDM elements based on data on ages at which growth trajectory has been evaluated and covariances of the sizes at ages. The latter functions requires raw growth data as an input and, in addition to IDM elements, produces CIs around them via bootstrap sampling.

## Author(s)

Anna Kuparinen and Mats Björklund Maintainer: Anna Kuparinen (anna.kuparinen@gmail.com)

## References

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

Kuparinen A, Björklund M (2011) Theory put into practice: an R implementation of the infinite-dimensional model. *Ecological Modelling* (in press).

## See Also

[IDM](#), [IDM.bootCI](#)

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adjust                    *A generic function to scale the values of a vector between -1 and 1.  
This function is a subfunction of [IDM](#).*

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### Description

A generic function to scale the values of a vector between -1 and 1. The function is used in the IDM calculation, to scale a vector of ages at which size has been measured.

### Usage

```
adjust(age)
```

### Arguments

age                    A numeric vector containing ages to be scaled between -1 and 1.

### Author(s)

Anna Kuparinen and Mats Björklund

### References

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

### See Also

[IDM](#), [IDM.bootCI](#)

### Examples

```
# The function is currently defined as
function(age){
  u=-1
  v=1
  n=length(age)
  amin=min(age)
  amax=max(age)

  temp=u+(v-u)/(amax-amin)*(age-amin)
  return(temp)
}
```

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fish	<i>Stickleback growth data</i>
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**Description**

The data gives lengths (mm) of 53 female stickleback measured at the age of 17, 45, 80 and 115 days.

**Usage**

```
fish
```

**Format**

A dataframe with 53 observations of four variables:

fish[,1] Length at age at 17 days

fish[,2] Length at age at 45 days

fish[,3] Length at age at 80 days

fish[,4] Length at age at 115 days

**References**

Kuparinen A, Björklund M (2011) Theory put into practice: an R implementation of the infinite-dimensional model. *Ecological Modelling* (in press)

**See Also**

[IDM.bootCI](#)

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IDM	<i>Infinite-dimensional model (IDM)</i>
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**Description**

A function to calculate infinite-dimensional model (IDM) elements as implemented by Kirkpatrick et al. (1990).

**Usage**

```
IDM(P, age)
```

**Arguments**

P Covariance matrix for sizes-at-ages.

age A numeric vector of ages at which sizes were measured. Ages must be positive values given in an ascending order.

## Details

The IDM model detects alternative patterns of growth (i.e. shapes of the growth trajectory) present in a population, as well as the amounts of phenotypic variation accounted for by each of the growth patterns, by decomposing a covariance matrix of size over a set of ages. For further details about the model formulation and its use, see Kirkpatrick et al. (1990) and Kuparinen and Björklund (in press).

## Value

The function returns a list of eigenvalues, eigenvectors, growth trajectories (each trajectory is given as a column in the trajectory matrix), and percentages of variation accounted for by each growth trajectory.

## Author(s)

Anna Kuparinen and Mats Björklund

## References

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

Kuparinen A, Björklund M (2011) Theory put into practice: an R implementation of the infinite-dimensional model. *Ecological Modelling* (in press).

## See Also

[IDM.bootCI](#).

## Examples

```
#This example utilizes data given in Kirkpatrick et al. (1990).
myage=c(2,3,4)
myP=matrix(c(436.0,522.3,424.2,522.3,808.0,664.7,424.2,664.7,558.0),nrow=3,ncol=3,byrow=TRUE)

out=IDM(P=myP,age=myage)

#Growth patterns (i.e. trajectories)
out$Trajectories

#Proportions of variation accounted for by each growth trajectory
out$Percent.trajectory
```

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`IDM.bootCI`*Infinite dimensional model (IDM) with bootstrapping*

---

**Description**

A function to calculate infinite-dimensional model (IDM) elements, as implemented by Kirkpatrick et al. (1990), and to estimate error ranges for the model outputs via bootstrapping.

**Usage**

```
IDM.bootCI(data, age, nboot)
```

**Arguments**

<code>data</code>	A matrix containing growth trajectories of individuals (rows) measured at fixed times (columns). Missing values are not allowed.
<code>age</code>	A numeric vector of ages at which sizes were measured. Ages must be positive values given in an ascending order.
<code>nboot</code>	number of bootstrap iterations.

**Details**

For calculation of IDM elements, `IDM.bootCI` calls `IDM` function. Bootstrapping is performed by resampling the growth trajectory data with replacing, and IDM elements are calculated for every resampled dataset. Confidence intervals are then obtained as 0.25 and 0.975 quantiles.

**Value**

The function returns as a list eigenvalues, growth trajectories (each trajectory is given as a column in the trajectory matrix), and percentages of variation accounted for by each growth trajectory, as well as boundaries for 95 percentage confidence intervals (CI) for each output element.

**Author(s)**

Anna Kuparinen and Mats Björklund

**References**

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

Kuparinen A, Björklund M (2011) Theory put into practice: an R implementation of the infinite-dimensional model. *Ecological Modelling* (in press).

**See Also**

[IDM](#).

**Examples**

```

#a built-in dataset fish is used. This data gives sizes of 53 female stickleback measured at the age of 17, 45, 80
age=c(17,45,80,115)
P=cov(fish)

out=IDM.bootCI(data=fish,age=age,nboot=1000)

#Growth patterns (i.e. trajectories)
out$Trajectories

#Percentages of variation accounted for by each growth trajectory
out$Percent.trajectory

#figure showing first two trajectories and percentages of variations accounted for by each trajectory.
par(mfrow=c(3,1),mar=c(5,4,0.5,0.5),oma=c(0.5,0.5,0.5,0.5))
barplot(out$Percent.trajectory,ylim=c(0,105),las=1,names.arg=c("1","2","3","4"), ylab="Percentage of variation")
lines(c(0.65,0.65),c(out$Percent.trajectory2.5CI[1],out$Percent.trajectory97.5CI[1]))
lines(c(1.9,1.9),c(out$Percent.trajectory2.5CI[2],out$Percent.trajectory97.5CI[2]))
lines(c(3.15,3.15),c(out$Percent.trajectory2.5CI[3],out$Percent.trajectory97.5CI[3]))
lines(c(4.4,4.4),c(out$Percent.trajectory2.5CI[4],out$Percent.trajectory97.5CI[4]))
text(0.18,100,"a",cex=1.4)
box(which="plot")

plot(age,out$Trajectories97.5CI[,1],type="l",lty=2,ylim=c(-1,1),las=1,ylab="Trajectory value",xlab="Age (days)")
lines(age,out$Trajectories2.5CI[,1],lty=2)
lines(age,out$Trajectories[,1],lty=1)
abline(h=0,lty=1)
text(17,0.9,"b",cex=1.4)

plot(age,out$Trajectories97.5CI[,2],type="l",lty=2,ylim=c(-1,1),las=1,ylab="Trajectory value",xlab="Age (days)")
lines(age,out$Trajectories2.5CI[,2],lty=2)
lines(age,out$Trajectories[,2],lty=1)
abline(h=0,lty=1)
text(17,0.9,"c",cex=1.4)

```

p.function

*A generic function to calculate Legendre polynomials***Description**

The function calculates the value of  $j$ :th normalized Legendre polynomial at  $x$ . This function is a subfunction of [IDM](#).

**Usage**

```
p.function(j, x)
```

**Arguments**

j                    an integer giving the rank of the polynomial  
 x                    numeric value between -1 and 1

**Author(s)**

Anna Kuparinen and Mats Björklund

**References**

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

**See Also**

[IDM](#), [IDM.bootCI](#)

**Examples**

```
# The function is currently defined as
function(j,x){

  temp1=1/(2^j)*sqrt((2*j+1)/2)
  jj=floor(j/2)

  temp2=0
  for(i in 0:jj){
    temp2b=(-1)^i*factorial(j)/(factorial(i)*factorial(j-i))*factorial(2*j-2*i)/(factorial(j)*factorial(2*j-2*i-j))
    temp2=temp2+temp2b
  }
  return(temp1*temp2)
}
```

---

psii

*A generic function to produce a matrix of Legendre polynomials for IDM calculation*

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**Description**

The function creates an n times n matrix, each row of the matrix replicating Legendre polynomials for the corresponding value of the re-scaled age vector the length of which is n. This function is a subfunction of [IDM](#).

**Usage**

psii(adjusted\_age)



**Arguments**

adjusted\_age    The vector of ages scaled to range from -1 to 1.

**Details**

For further details, see Kirkpatrick et al. 1990.

**Value**

A n times n matrix of Legendre polynomials, value replicated at each row being the polynomials at the corresponding age.

**Author(s)**

Anna Kuparinen and Mats Björklund

**References**

Kirkpatrick M, Lofsvold D, Bulmer M (1990) Analysis of the inheritance, selection and evolution of growth trajectories. *Genetics* 124:979-993.

**See Also**

[IDM](#), [IDM.bootCI](#)

**Examples**

```
# The function is defined as
function(adjusted_age){
  n=length(adjusted_age)

  adjust_temp=rep(adjusted_age,each=n)
  j_temp=rep(0:(n-1),n)

  psii_elements=rep(NA,n*n)
  for(i in 1:(n*n)){
    psii_elements[i]=p.function(j=j_temp[i],x=adjust_temp[i])
  }
  psii_temp=matrix(psii_elements,byrow=T,nrow=n,ncol=n)
  return(psii_temp)
}
```

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