Package ‘shapes’

July 6, 2016

Title Statistical Shape Analysis
Date 2016-7-6
Version 1.1-13
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Description Routines for the statistical analysis of landmark shapes, including Procrustes analysis, graphical displays, principal components analysis, permutation and bootstrap tests, thin-plate spline transformation grids and comparing covariance matrices.
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Imports scatterplot3d, rgl, MASS
Depends R (>= 2.10)
License GPL-2
URL http://www.maths.nottingham.ac.uk/~ild/shapes
NeedsCompilation no
Repository CRAN
Date/Publication 2016-07-06 14:56:49

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apes

Great ape data

Description

Great ape skull landmark data. 8 landmarks in 2 dimensions, 167 individuals
Usage
data(apes)

Format
apes$x : An array of dimension 8 x 2 x 167
apes$group : Species and sex of each specimen: "gorf" 30 female gorillas, "gorm" 29 male gorillas,
"pamf" 26 female chimpanzees, "pamm" 28 male chimpanzees, "pongof" 24 female orang utans,
"pongom" 30 male orang utans.

Source

References
Data from Paul O'Higgins (Hull-York Medical School)

Examples
data(apes)
par(mfrow=c(1,2))
plotshapes(apes$x[,apes$group=="gorf"],symbol="f")
plotshapes(apes$x[,apes$group=="gorm"],symbol="m")

Description
Carries out Bookstein's baseline registration and calculates a mean shape

Usage
bookstein2d(A,l1=1,l2=2)

Arguments
A a k x 2 x n real array, or k x n complex matrix, where k is the number of landmarks, n is the number of observations
l1 l1: an integer : l1 is sent to (-1/2,0) in the registration
l2 l2: an integer : l2 is sent to (1/2,0) in the registration
Value

A list with components:

- k : number of landmarks
- n : sample size
- mshape : Bookstein mean shape with baseline 1, 12
- bshpv : the k x n x 2 array of Bookstein shape variables, including the baseline

Author(s)

Ian Dryden

References


Examples

```r
data(gorf.dat)
data(gorm.dat)

bookf<-bookstein2d(gorf.dat)
bookm<-bookstein2d(gorm.dat)

plotshapes(bookf$mshape,bookm$mshape,joinline=c(1,6,7,8,2,3,4,5,1))
```

brains: Brain landmark data

Description

24 landmarks located in 58 adult healthy brains

Usage

data(brains)

Format

A list with components:

- brains$x : An array of dimension 24 x 3 x 58 containing the landmarks in 3D
- brains$sex : Sex of each volunteer (m or f)
- brains$age : Age of each volunteer
- brains$handed : Handedness of each volunteer (r or l)
- brains$grp : group label: 1= right-handed males, 2=left-handed males, 3=right-handed females, 4=left-handed females
References

Examples
data(brains)
# plot first three brains
shapes3d(brains$x[,1:3])

centroid.size  Centroid size

Description
Calculate centroid size from a configuration or a sample of configurations.

Usage
centroid.size(x)

Arguments
x
For a single configuration k x m matrix or complex k-vector
For a sample of configurations k x m x n array or k x n complex matrix

Value
Centroid size(s)

Author(s)
Ian Dryden

References

Examples
data(mice)
centroid.size(mice$x[,1])
Cortical surface data

Description

Cortical surface data, from MR scans. Axial slice outlines with 500 points on each outline. 68 individuals.

Usage

data(cortical)

Format

cortical$age (age) cortical$group (Control, Schizophrenia) cortical$sex (1 = male, 2 = female) cortical$symm (a symmetry measure from the original 3D cortical surface)
cortical$x (500 x, y coordinates of an axial slice through the cortical surface intersecting the anterior and posterior commissures)
cortical$r (500 radii from equal angular polar coordinates)

Source


References

Original MR data from Sean Flynn (UBC) in collaboration with Bert Park (Nottingham).

Examples

data(cortical)
plotshapes(cortical$x)
**digit3.dat**

**Digit 3 data**

**Description**

Handwritten digit ‘3’ data. 13 landmarks in 2 dimensions, 30 individuals

**Usage**

```r
data(digit3.dat)
```

**Format**

An array of dimension 13 x 2 x 30

**Source**


**References**

http://www.maths.nott.ac.uk/personal/ild/bookdata/digit3.dat

Data from Cath Anderson

**Examples**

```r
data(digit3.dat)
k<-dim(digit3.dat)[1]
n<-dim(digit3.dat)[3]
plotshapes(digit3.dat, joinline=c(1:13))
```

---

**distcov**

*Compute a distance between two covariance matrices*

**Description**

Compute a distance between two covariance matrices, with non-Euclidean options.

**Usage**

```r
distcov(S1, S2, method="Riemannian", alpha=1/2)
```
Arguments

S1
Input a covariance matrix (square, symmetric, positive definite)

S2
Input another covariance matrix of the same size

method
The type of distance to be used: "Procrustes": Procrustes size-and-shape metric, "ProcrustesShape": Procrustes metric with scaling, "Riemannian": Riemannian metric, "Cholesky": Cholesky based distance, "Power": Power Euclidean, with power alpha, "Euclidean": Euclidean metric, "LogEuclidean": Log-Euclidean metric, "RiemannianLe": Another Riemannian metric.

alpha
The power to be used in the power Euclidean metric

Value
The distance

Author(s)
Ian Dryden

References

See Also
estcov

Examples

A <- diag(5)
B <- A + 0.1*matrix(rnorm(25),5,5)
S1<-A
S2<- B

distcov(S1,S2,method="Procrustes")

dna.dat DNA data

Description
Part of a 3D DNA molecule moving in time, k = 22 atoms, 30 time points
Usage

data(dna.dat)

Format

An array of dimension 22 x 3 x 30

Examples

data(dna.dat)
plotshapestime3d(dna.dat)

---

**estcov**

*Weighted Frechet mean of covariance matrices*

**Description**

Computes the weighted Frechet means of an array of covariance matrices, with different options for the covariance metric. Also carries out principal co-ordinate analysis of the covariance matrices.

**Usage**

`estcov(S, method="Riemannian", weights=1, alpha=1/2, MDSk=2)`

**Arguments**

- **S**
  Input an array of covariance matrices of size k x k x n where each matrix is square, symmetric and positive definite.

- **method**
  The type of distance to be used: "Procrustes": Procrustes size-and-shape metric, "ProcrustesShape": Procrustes metric with scaling, "Riemannian": Riemannian metric, "Cholesky": Cholesky based distance, "Power": Power Euclidean, with power alpha, "Euclidean": Euclidean metric, "LogEuclidean": Log-Euclidean metric, "RiemannianLe": Another Riemannian metric.

- **weights**
  The weights to be used for calculating the mean. If weights=1 then equal weights are used, otherwise the vector must be of length n.

- **alpha**
  The power to be used in the power Euclidean metric.

- **MDSk**
  The number of MDS components in the principal co-ordinate analysis.

**Value**

A list with values

- **mean**
  The weighted mean covariance matrix.

- **sd**
  The weighted standard deviation.

- **pco**
  Principal co-ordinates (from multidimensional scaling with the metric).

- **eig**
  The eigenvalues from the principal co-ordinate analysis.
Author(s)
Ian Dryden

References

See Also
distcov

Examples

```r
S <- array(0,c(5,5,10))
for (i in 1:10){
tem <- diag(5)+1*matrix(rnorm(25),5,5)
S[,]<- tem
}
estcov(S, method="Procrustes")
```

---

**frechet**

**Mean shape estimators**

**Description**
Calculation of different types of Frechet mean shapes, or the isotropic offset Gaussian MLE mean shape

**Usage**

```r
frechet(x, mean="intrinsic")
```

**Arguments**

- `x` 
  Input k x m x n real array, where k is the number of points, m is the number of dimensions, and n is the sample size.

- `mean` 
  Type of mean shape. The Frechet mean shape is obtained by minimizing sum $d(x_i,\mu)^2$ with respect to $\mu$. Different estimators are obtained with different choices of distance $d$. "intrinsic" intrinsic mean shape ($d = \rho =$ Riemannian distance); "partial.procrustes" partial Procrustes ($d = 2\sin(\rho/2)$); "full.procrustes" full Procrustes ($d = \sin(\rho)$); $h$ (positive real number) M-estimator ($d^2 = (1 - \cos^2(2h)\rho)/h$) Kent (1992); "mle" - isotropic offset Gaussian MLE of Mardia and Dryden (1989)
Value

A list with components

mshape  Mean shape estimate
var  Minimized Frechet variance (not available for MLE)
kappa  (if available) The estimated kappa for the MLE
code  Code from optimization, as given by function nlm - should be 1 or 2
gradient  Gradient from the optimization, as given by function nlm - should be close to zero

Author(s)

Ian Dryden

References


See Also

procGPA

Examples

# 2D example : female and male Gorillas (cf. Dryden and Mardia, 1998)
data(gorf.dat)
frechet(gorf.dat[,1:4],mean="intrinsic")

Electrophoresis gel data

Description

Electrophoresis gel data. 10 invariant spots have been picked out by an expert on two electrophoretic gels.
Usage

data(gels)

Format

An array of dimension 10 x 2 x 2

Source


References

Data from Chris Glasbey (BioSS)

Examples

data(gels)
plotshapes(gels)

gorf.dat

Female gorilla data

Description

Female gorilla skull data. 8 landmarks in 2 dimensions, 30 individuals

Usage

data(gorf.dat)

Format

An array of dimension 8 x 2 x 30

Source


References

http://www.maths.nott.ac.uk/personal/ild/bookdata/gorf.dat
Data from Paul O’Higgins (Hull-York Medical School)
Examples

data(gorf.dat)
plotshapes(gorf.dat)

---

gorm.dat  Male gorilla data

Description

Male gorilla skull data. 8 landmarks in 2 dimensions, 29 individuals

Usage

data(gorm.dat)

Format

An array of dimension 8 x 2 x 29

Source


References

http://www.maths.nott.ac.uk/personal/ild/bookdata/gorm.dat

Data from Paul O’Higgins (Hull-York Medical School)

Examples

data(gorm.dat)
plotshapes(gorm.dat)
groupstack

Combine two or more groups of configurations

Description

Combine two or more groups of configurations and create a group label vector. (Maximum 8 groups).

Usage

\texttt{groupstack(A1, A2, A3=0, A4=0, A5=0, A6=0, A7=0, A8=0)}

Arguments

- A1: Input $k \times m \times n$ real array of the Procrustes transformed configurations, where $k$ is the number of points, $m$ is the number of dimensions, and $n$ is the sample size.
- A2: Input $k \times m \times n$ real array of the Procrustes original configurations, where $k$ is the number of points, $m$ is the number of dimensions, and $n$ is the sample size.
- A3: Optional array
- A4: Optional array
- A5: Optional array
- A6: Optional array
- A7: Optional array
- A8: Optional array

Value

A list with components

- $x$: The combined array of all configurations
- groups: The group labels (integers)

Author(s)

Ian Dryden

References


See Also

procGPA
Examples

#2D example: female and male Gorillas (cf. Dryden and Mardia, 1998)

data(gorf.dat)
data(gorm.dat)
groupstack(gorf.dat,gorm.dat)

Human movement data

Description

Human movement data. 4 landmarks in 2 dimensions, 5 individuals observed at 10 times.

Usage

data(humanmove)

Format

humanmove: An array of landmark configurations 4 x 2 x 10 x 5

Source


References

Data from James Richardson.

Examples

data(humanmove)
#plotshapes(humanmove[,]1)
#for (i in 2:5){
  #for (j in 1:4){
    #for (k in 1:10){
      #points(humanmove[j,k,i],col=i)
    #}
  #}
#}
**Description**

Male and female macaque skull data. 7 landmarks in 3 dimensions, 18 individuals (9 males, 9 females)

**Usage**

data(macaques)

**Format**

macaques$x : An array of dimension 7 x 3 x 18  
macaques$group : A factor indicating the sex ('m' for male and 'f' for female)

**Source**


**References**

Data from Paul O'Higgins (Hull-York Medical School)

**Examples**

```r
data(macaques)  
shapes3d(macaques$x[,1])
```

---

**Description**

Female macaque skull data. 7 landmarks in 3 dimensions, 9 individuals

**Usage**

data(macf.dat)

**Format**

An array of dimension 7 x 3 x 9
macm.dat

Source


References

Data from Paul O’Higgins (Hull-York Medical School)

Examples

data(macf.dat)
plotshapes(macf.dat)

---

macm.dat  Male macaque data

Description

Male macaque skull data. 7 landmarks in 3 dimensions, 9 individuals

Usage

data(macm.dat)

Format

An array of dimension 7 x 3 x 9

Source


References

Data from Paul O’Higgins (Hull-York Medical School)

Examples

data(macm.dat)
plotshapes(macm.dat)
T2 mouse vertebrae data

Description

T2 mouse vertebrae data - 6 landmarks in 2 dimensions, in 3 groups (30 Control, 23 Large, 23 Small mice). The 6 landmarks are obtained using a semi-automatic method at points of high curvature. This particular strain of mice is the ‘QE’ strain. In addition pseudo-landmarks are given around each outlines.

Usage

data(mice)

Format

mice$x : An array of dimension 6 x 2 x 76 of the two dimensional co-ordinates of 6 landmarks for each of the 76 mice.

mice$group : Group labels. "c" Control, "l" Large, "s" Small mice

mice$outlines : An array of dimension 60 x 2 x 76 containing the 6 landmarks and 54 pseudo-landmarks, with 9 pseudo-landmarks approximately equally spaced between each pair of landmarks.

Source


References


Data from Paul O’Higgins (Hull-York Medical School) and David Johnson (Leeds)

Examples

data(mice)
plotshapes(mice$x,symbol=as.character(mice$group),joinline=c(1,6,2:5,1))
**panf.dat**

*Female chimpanzee data*

**Description**

Female chimpanzee skull data. 8 landmarks in 2 dimensions, 26 individuals

**Usage**

data(panf.dat)

**Format**

An array of dimension 8 x 2 x 26

**Source**


**References**

Data from Paul O'Higgins (Hull-York Medical School)

**Examples**

data(panf.dat)
plotshapes(panf.dat)

---

**panm.dat**

*Male chimpanzee data*

**Description**

Male chimpanzee skull data. 8 landmarks in 2 dimensions, 28 individuals

**Usage**

data(panm.dat)

**Format**

An array of dimension 8 x 2 x 28
Source


References

Data from Paul O’Higgins (Hull-York Medical School)

Examples

data(panm.dat)
plotshapes(panm.dat)

Description

Plots configurations. Either one or two groups of observations can be plotted on the same scale.

Usage

plotshapes(A, B = 0, joinline = c(1, 1), orthproj=c(1,2), color=1, symbol=1)

Arguments

A k x m x n array, or k x m matrix for first group
B k x m x n array, or k x m matrix for 2nd group (can be missing)
joinline A vector stating which landmarks are joined up by lines, e.g. joinline=c(1:n,1) will start at landmark 1, join to 2, .... join to n, then re-join to landmark 1.
orthproj A vector stating which two orthogonal projections will be used. For example, for m=3 dimensional data: X-Y projection given by c(1,2) (default), X-Z projection given by c(1,3), Y-Z projection given by c(2,3).
color Colours for points. Can be a vector, e.g. 1:k gives each landmark a different colour for the specimens
symbol Plotting symbols. Can be a vector, e.g. 1:k gives each landmark a different symbol for the specimens

Value

Just graphical output

Author(s)

Ian Dryden
pongof.dat

See Also

shapepca, tpsgrid

Examples

data(gorf.dat)
data(gorm.dat)
plotshapes(gorf.dat, gorm.dat, joinline=c(1,6,7,8,2,3,4,5,1))
data(macm.dat)
data(macf.dat)
plotshapes(macm.dat, macf.dat)

pongof.dat    Female orang utan data

Description

Female orang utan skull data. 8 landmarks in 2 dimensions, 30 individuals

Usage

data(pongof.dat)

Format

An array of dimension 8 x 2 x 30

Source


References

Data from Paul O’Higgins (Hull-York Medical School)

Examples

data(pongof.dat)
plotshapes(pongof.dat)
**pongom.dat**  
*Male orang utan data*

**Description**

Male orang utan skull data. 8 landmarks in 2 dimensions, 30 individuals

**Usage**

`data(pongom.dat)`

**Format**

An array of dimension 8 x 2 x 30

**Source**


**References**

Data from Paul O’Higgins (Hull-York Medical School)

**Examples**

`data(pongom.dat)`  
`plotshapes(pongom.dat)`

---

**procdist**  
*Procrustes distance*

**Description**

Calculates different types of Procrustes shape or size-and-shape distance between two configurations

**Usage**

`procdist(x, y, type="full", reflect=FALSE)`
procGPA

Arguments

x  
k x m matrix (or complex k-vector for 2D data) where k = number of landmarks and m = no of dimensions

y  
k x m matrix (or complex k-vector for 2D data)

type  
string indicating the type of distance; "full" full Procrustes distance, "partial" partial Procrustes distance, "Riemannian" Riemannian shape distance, "sizeand-shape" size-and-shape Riemannian/Procrustes distance

reflect  
Logical. If reflect = TRUE then reflection invariance is included.

Value

The distance between the two configurations.

Author(s)

Ian Dryden

References


See Also

procOPA, procGPA

Examples

data(gorf.dat)
data(gorm.dat)

gorf<-procGPA(gorf.dat)
gorm<-procGPA(gorm.dat)
distfull<-procdist(gorf$mshape,gorm$mshape)
cat("Full Procrustes distance between mean shapes is ",distfull," \n")

---

procGPA  Generalised Procrustes analysis

Description

Generalised Procrustes analysis to register landmark configurations into optimal registration using translation, rotation and scaling. Reflection invariance can also be chosen, and registration without scaling is also an option. Also, obtains principal components, and some summary statistics.

Usage

procGPA(x, scale = TRUE, reflect = FALSE, eigen2d = FALSE,

tol1 = 1e-05, tol2 = tol1, tangentcoords = "residual", proc.output=FALSE,

distances=TRUE, pcaoutput=TRUE, alpha=0, affine=FALSE)
Arguments

- **x**: Input k x m x n real array, (or k x n complex matrix for m=2 is OK), where k is the number of points, m is the number of dimensions, and n is the sample size.
- **scale**: Logical quantity indicating if scaling is required
- **reflect**: Logical quantity indicating if reflection is required
- **eigen2d**: Logical quantity indicating if complex eigenanalysis should be used to calculate Procrustes mean for the particular 2D case when scale=TRUE, reflect=FALSE
- **tol1**: Tolerance for optimal rotation for the iterative algorithm: tolerance on the mean sum of squares (divided by size of mean squared) between successive iterations
- **tol2**: Tolerance for rescale/rotation step for the iterative algorithm: tolerance on the mean sum of squares (divided by size of mean squared) between successive iterations
- **tangentcoords**: Type of tangent coordinates. If (SCALE=TRUE) the options are "residual" (Procrustes residuals, which are approximate tangent coordinates to shape space), "partial" (Kent’s partial tangent co-ordinates), "expomap" (tangent coordinates from the inverse of the exponential map, which are the similar to "partial" but scaled by (rho/sin(rho)) where rho is the Riemannian distance to the pole of the projection. If (SCALE=FALSE) then all three options give the same tangent coordinates to size-and-shape space, which is simply the Procrustes residual X^P - mu.
- **proc.output**: Logical quantity indicating if printed output during the iterations of the Procrustes GPA algorithm should be given
- **distances**: Logical quantity indicating if shape distances and sizes should be calculated
- **pcaoutput**: Logical quantity indicating if PCA should be carried out
- **alpha**: The parameter alpha used for relative warps analysis, where alpha is the power of the bending energy matrix. If alpha = 0 then standard Procrustes PCA is carried out. If alpha = 1 then large scale variations are emphasized, if alpha = -1 then small scale variations are emphasised. Requires m=2 and m=3 dimensional data if alpha $!=$ 0.
- **affine**: Logical. If TRUE then only the affine subspace of shape variability is considered.

Value

A list with components

- **k**: no of landmarks
- **m**: no of dimensions (m-D dimension configurations)
- **n**: sample size
- **mshape**: Procrustes mean shape. Note this is unit size if complex eigenanalysis used, but on the scale of the data if iterative GPA is used.
- **tan**: The tangent shape (or size-and-shape) coordinates
- **rotated**: the k x m x n array of full Procrustes rotated data
**procGPA**

The columns are eigenvectors (PCs) of the sample covariance $S_v$ of the square roots of eigenvalues of $S_v$ using $\tan$. If alpha $\neq 0$ then it is the percent of non-affine variation of the relative warp scores. If affine is TRUE it is the percentage of total shape variability of each affine component.

- **pca**: the centroid sizes of the configurations
- **pcasd**: standardised PC scores (each with unit variance) using $\tan$
- **rawscores**: raw PC scores using $\tan$
- **rho**: Kendall’s Riemannian distance rho to the mean shape
- **rmsrho**: root mean square (r.m.s.) of rho
- **rmsd1**: r.m.s. of full Procrustes distances to the mean shape $d_F$
- **GSS**: Minimized Procrustes sum of squares

**Author(s)**

Ian Dryden, with input from Mohammad Faghihi and Alfred Kume

**References**


**See Also**

 procOPA, riemdist, shapepca, testmeanshapes

**Examples**

```r
# 2D example: female and male Gorillas (cf. Dryden and Mardia, 1998)

data(gorf.dat)
data(gorm.dat)

plotshapes(gorf.dat, gorm.dat)
n1<-dim(gorf.dat)[3]
n2<-dim(gorm.dat)[3]
k<-dim(gorf.dat)[1]
m<-dim(gorf.dat)[2]
gor.dat<-array(0, c(k,2,n1+n2))
```
gor.dat[,1:n1]<-gorf.dat
gor.dat[,,(n1+1):(n1+n2)]<-gorm.dat

gor<-procOPA(gor.dat)
shapepca(gor,type="r",mag=3)
shapepca(gor,type="v",mag=3)

gor.gp<-c(rep("f",times=30),rep("m",times=29))
x<-cbind(gor$size,gor$rho,gor$scores[,1:3])
pairs(x,panel=function(x,y) text(x,y,gor.gp),
label=c("s","rho","score 1","score 2","score 3"))

#################################################################
#3D example

data(macm.dat)
out<-procOPA(macm.dat, scale=FALSE)

par(mfrow=c(2,2))
plot(out$rawscores[,1],out$rawscores[,2],xlab="PC1",ylab="PC2")
title("PC scores")
plot(out$rawscores[,2],out$rawscores[,3],xlab="PC2",ylab="PC3")
plot(out$rawscores[,1],out$rawscores[,3],xlab="PC1",ylab="PC3")
plot(out$size,out$rho,xlab="size",ylab="rho")
title("Size versus shape distance")

procOPA

Ordinary Procrustes analysis

Description

Ordinary Procrustes analysis: the matching of one configuration to another using translation, rotation and (possibly) scale. Reflections can also be included if desired. The function matches configuration B onto A by least squares.

Usage

procOPA(A, B, scale = TRUE, reflect = FALSE)

Arguments

A k x m matrix (or complex k-vector for 2D data), of k landmarks in m dimensions. This is the reference figure.

B k x m matrix (or complex k-vector for 2D data). This is the figure which is to be transformed.

scale logical indicating if scaling is required

reflect logical indicating if reflection is allowed
Value

A list with components:

- **R**: The estimated rotation matrix (may be an orthogonal matrix if reflection is allowed)
- **s**: The estimated scale matrix
- **Ahat**: The centred configuration A
- **Bhat**: The Procrustes registered configuration B
- **OSS**: The ordinary Procrustes sum of squares, which is $\|Ahat-Bhat\|^2$
- **rmsd**: $\text{rmsd} = \sqrt{\text{OSS}/(km)}$

Author(s)

Ian Dryden

References


See Also

procGPA, riemdist, tpsgrid

Examples

data(digit3.dat)
A<-digit3.dat[,1]
B<-digit3.dat[,2]
ans<-procOPA(A,B)
plotshapes(A,B,joinline=1:13)
plotshapes(ans$Ahat,ans$Bhat,joinline=1:13)

# Sooty mangabey data
data(sooty.dat)
A<-sooty.dat[,1]  # juvenile
B<-sooty.dat[,2]  # adult
par(mfrow=c(1,3))
par(pty="s")
plot(A,xlim=c(-2000,3000),ylim=c(-2000,3000),xlab="",ylab="")
lines(A[c(1:12,1),])
points(B)
lines(B[c(1:12,1),],lty=2)
title("Juvenile (--------) Adult ( - - - )")
# match B onto A
out<-procOPA(A,B)
# rotation angle
print(atan2(out$R[1,2],out$R[1,1])*180/pi)
# scale
print(out$s)
procWGPA

Weighted Procrustes analysis

Description

Weighted Procrustes analysis to register landmark configurations into optimal registration using translation, rotation and scaling. Registration without scaling is also an option. Also, obtains principal components, and some summary statistics.

Usage

procWGPA(x, fixcovmatrix=FALSE, initial="Identity", maxiterations=10, scale=TRUE, reflect=FALSE, prior="Exponential", diagonal=TRUE, sampleweights="Equal")

Arguments

x 
Input k x m x n real array, where k is the number of points, m is the number of dimensions, and n is the sample size.

fixcovmatrix 
If FALSE then the landmark covariance matrix is estimated. If a fixed covariance matrix is desired then the value should be given here, e.g. fixcovmatrix=diag(8) for the identity matrix with 8 landmarks.

initial 
The initial value of the estimated covariance matrix. "Identity" - identity matrix, "Rawdata" - based on sample variance of the raw landmarks. Also, could be a k x k symmetric positive definite matrix.

maxiterations 
The maximum number of iterations for estimating the covariance matrix,

scale 
Logical quantity indicating if scaling is required,

reflect 
Logical quantity indicating if reflection invariance is required,

prior 
Indicates the type of prior. "Exponential" is exponential for the inverse eigenvalues. "Identity" is an inverse Wishart with the identity matrix as parameters.
**diagW GPA**

**diagonal**
Logical. Indicates if the diagonal of the landmark covariance matrix (only) should be used. Diagonal matrices can lead to some landmarks having very small variability, which may or may not be desirable.

**sampleweights**
Gives the weights of the observations in the sample, rather than the landmarks. This is a fixed quantity. "Equal" indicates that all observations in the sample have equal weight. The weights do not need to sum to 1.

**Details**

The factored covariance model is assumed: \( \Sigma_k \times I_m \) with \( \Sigma_k \) being the covariance matrix of the landmarks, and the cov matrix at each landmark is the identity matrix.

**Value**

A list with components

- \( k \) no of landmarks
- \( m \) no of dimensions (m-D dimension configurations)
- \( n \) sample size
- \( mshape \) Weighted Procrustes mean shape.
- \( tan \) This is the mk x n matrix of Procrustes residuals \( X_i^P - \text{Xbar} \).
- \( rotated \) the k x m x n array of weighted Procrustes rotated data
- \( pcar \) the columns are eigenvectors (PCs) of the sample covariance \( S_v \) of \( tan \)
- \( pcasd \) the square roots of eigenvalues of \( S_v \) using \( tan \) (s.d.'s of PCs)
- \( percent \) the percentage of variability explained by the PCs using \( tan \)
- \( size \) the centroid sizes of the configurations
- \( scores \) standardised PC scores (each with unit variance) using \( tan \)
- \( rawscores \) raw PC scores using \( tan \)
- \( rho \) Kendall's Riemannian distance rho to the mean shape
- \( rmsrho \) r.m.s. of rho
- \( rmsd1 \) r.m.s. of full Procrustes distances to the mean shape \( d_F \)
- \( Sigmak \) Estimate of the sample covariance matrix of the landmarks

**Author(s)**

Ian Dryden

**References**


See Also

procGPA

Examples

#2D example : female Gorillas (cf. Dryden and Mardia, 1998)
data(gorf.dat)
gor<-procWGPA(gorf.dat,maxiterations=3)

qcet2.dat  Control T2 mouse vertabrae data

Description

T2 mouse vertebrae data - control group. 6 landmarks in 2 dimensions, 30 individuals

Usage

data(qcet2.dat)

Format

An array of dimension 6 x 2 x 30

Source


References

http://www.maths.nott.ac.uk/personal/ild/bookdata/qcet2.dat
Data from Paul O’Higgins (Hull-York Medical School) and David Johnson (Leeds)

Examples

data(qcet2.dat)
plotshapes(qcet2.dat)
**qlet2.dat**

*Large T2 mouse vertabrae data*

**Description**

T2 mouse vertebrae data - large group. 6 landmarks in 2 dimensions, 23 individuals

**Usage**

data(qlet2.dat)

**Format**

An array of dimension 6 x 2 x 23

**Source**


**References**

http://www.maths.nott.ac.uk/personal/ild/bookdata/qlet2.dat

Data from Paul O’Higgins (Hull-York Medical School) and David Johnson (Leeds)

**Examples**

data(qlet2.dat)
plotshapes(qlet2.dat)

---

**qset2.dat**

*Small T2 mouse vertabrae data*

**Description**

T2 mouse vertebrae data - small group. 6 landmarks in 2 dimensions, 23 individuals

**Usage**

data(qset2.dat)

**Format**

An array of dimension 6 x 2 x 23

**Source**

Rats

References

http://www.maths.nott.ac.uk/personal/ild/bookdata/qset2.dat

Data from Paul O’Higgins (Hull-York Medical School) and David Johnson (Leeds)

Examples

data(qset2.dat)
plotshapes(qset2.dat)

rats

Rat skulls data

Description

Rat skulls data, from X rays. 8 landmarks in 2 dimensions, 18 individuals observed at 7, 14, 21, 30, 40, 60, 90, 150 days.

Usage

data(rats)

Format

rats$x: An array of landmark configurations 144 x 2 x 2
rats$no: Individual rat number (note rats 3, 13, 20 missing due to incomplete data)
rats$time observed time in days

Source

Vilmann’s rat data set (Bookstein, 1991, Morphometric Tools for Landmark Data: Geometry and Biology, pp. 408-414)

References


Examples

data(rats)
plotshapes(rats$x, col=1:8)
resampletest  Tests for mean shape difference using complex arithmetic, including bootstrap and permutation tests.

---

Description

Carries out tests to examine differences in mean shape between two independent populations. For 2D data the methods use complex arithmetic and exploit the geometry of the shape space (which is the main use of this function). An alternative faster, approximate procedure using Procrustes residuals is given by the function ‘testmeanshapes’. For 3D data tests are carried out on the Procrustes residuals, which is an approximation suitable for small variations in shape.

Up to four test statistics are calculated:

- **lambda**: the asymptotically pivotal statistic $\lambda_{\min}$ from Amaral et al. (2007), equ.(14),(16) (m=2 only)
- **H**: Hotelling $T^2$ statistic (see Amaral et al., 2007, equ.(23), Dryden and Mardia, 1998, equ.(7.4))
- **J**: James’ statistic (see Amaral et al., 2007, equ.(24)) (m=2 only)
- **G**: Goodall’s F statistic (see Amaral et al., 2007, equ.(25), Dryden and Mardia, 1998, equ.(7.9))

p-values are given based on resampling as well as the usual table based p-values.

Note when the sample sizes are low (compared to the number of landmarks) some regularization is carried out. In particular if $S_w$ is a singular within group covariance matrix, it is replaced by $S_w + 0.000001$ (Identity matrix) and a ‘*’ is printed in the output.

Usage

```
resampletest(A, B, resamples = 200, replace = TRUE)
```

Arguments

- **A**: The random sample for group 1: $k \times m \times n_1$ array of data, where $k$ is the number of landmarks and $n_1$ is the sample size. (Alternatively a $k \times n_1$ complex matrix for 2D)
- **B**: The random sample for group 3: $k \times m \times n_2$ array of data, where $k$ is the number of landmarks and $n_2$ is the sample size. (Alternatively a $k \times n_2$ complex matrix for 2D)
- **resamples**: Integer. The number of resampling iterations. If resamples = 0 then no resampling procedures are carried out, and the tabular p-values are given only.
- **replace**: Logical. If replace = TRUE then for 2D data bootstrap resampling is carried out with replacement *within* each group. If replace = FALSE then permutation resampling is carried out (sampling without replacement in *pooled* samples).
Value

A list with components (or a subset of these)

- `lambda` $\lambda_{\text{min}}$ statistic
- `lambda.pvalue` p-value for $\lambda_{\text{min}}$ test based on resampling
- `lambda.table.pvalue` p-value for $\lambda_{\text{min}}$ test based on the asymptotic chi-squared distribution (large $n_1, n_2$)
- `H` The Hotelling $T^2$ statistic
- `H.pvalue` p-value for the Hotelling $T^2$ test based on resampling
- `H.table.pvalue` p-value for the Hotelling $T^2$ test based on the null F distribution, assuming normality and equal covariance matrices
- `J` The Hotelling $T^2$ statistic
- `J.pvalue` p-value for the Hotelling $T^2$ test based on resampling
- `J.table.pvalue` p-value for the Hotelling $T^2$ test based on the null F distribution, assuming normality and unequal covariance matrices
- `G` The Goodall $F_S$ statistic
- `G.pvalue` p-value for the Goodall test based on resampling
- `G.table.pvalue` p-value for the Goodall test based on the null F distribution, assuming normality and equal isotropic covariance matrices

Author(s)

Ian Dryden

References


See Also

testmeanshapes

Examples

#2D example: female and male Gorillas

data(gorf.dat)
data(gorm.dat)
#just select 3 landmarks and the first 10 observations in each group
select<-c(1,2,3)
A<-gorf.dat[select,,1:10]
B<-gorm.dat[select,,1:10]
resampletest(A,B,resamples=100)

---

**riemdist**

*Riemannian shape distance*

**Description**

Calculates the Riemannian shape distance $\rho$ between two configurations

**Usage**

```r
riemdist(x, y, reflect=FALSE)
```

**Arguments**

- **x**: k x m matrix (or complex k-vector for 2D data) where k = number of landmarks and m = no of dimensions
- **y**: k x m matrix (or complex k-vector for 2D data)
- **reflect**: Logical. If reflect = TRUE then reflection invariance is included.

**Value**

The Riemannian shape distance $\rho$ between the two configurations. Note $0 \leq \rho \leq \pi/2$ if no reflection invariance

**Author(s)**

Ian Dryden

**References**


**See Also**

procOPA, procGPA
Examples

    data(gorf.dat)
    data(gorm.dat)
    gorf<-procGPA(gorf.dat)
    gorm<-procGPA(gorm.dat)
    rho<--riemdist(gorf$mshape,gorm$mshape)
    cat("Riemannian distance between mean shapes is ",rho," \n")

rigidbody  Rigid body transformations

Description

Applies a rigid body transformations to a landmark configuration or array

Usage

    rigidbody(X,transx=0,transy=0,transz=0,thetax=0,thetay=0,thetaz=0)

Arguments

    X  k x m matrix, or k x m x n array where k = number of landmarks and m = no of
dimensions and n is no of specimens
    transx  negative shift in x-coordinates
    transy  negative shift in y-coordinates
    transz  negative shift in z-coordinates
    thetax  Rotation about x-axis in degrees
    thetay  Rotation about y-axis in degrees
    thetaz  Rotation about z-axis in degrees

Value

The transformed coordinates (X - trans) Rx Ry Rz

Author(s)

Ian Dryden

Examples

    data(gorf.dat)
    plotshapes(rigidbody(gorf.dat , 0, 0, 0, 0, -90 ))
Description

50 points on 24 sea sand and 25 river sand grain profiles in 2D. The original data were kindly provided by Professor Dietrich Stoyan (Stoyan and Stoyan, 1994; Stoyan, 1997). The 50 points on each outline were extracted at approximately equal arc-lengths by the method described in Kent et al. (2000, section 8.1)

Usage

data(sand)

Format

A list with components:

sea$x : An array of dimension 50 x 2 x 49 containing the 50 point co-ordinates in 2D for each grain

sea$group : The types of the sand grains: "sea", 24 particles from the Baltic Sea
"river", 25 particles from the Caucasian River Selenchuk

References


Examples

data(sand)

plotshapes(sand$x[,sand$group=="sea"],sand$x[,sand$group=="river"],joinline=c(1:50))
Bookstein’s schizophrenia data

Description

Bookstein’s schizophrenia data. 13 landmarks in 2 dimensions, 28 individuals. The first 14 individuals are controls. The last fourteen cases were diagnosed with schizophrenia. The landmarks were taken in the near midline from MR images of the brain: (1) splenium, posteriormost point on corpus callosum; (2) genu, anteriormost point on corpus callosum; (3) top of corpus callosum, uppermost point on arch of callosum (all three to an approximate registration on the diameter of the callosum); (4) top of head, a point relaxed from a standard landmark along the apparent margin of the dura; (5) tentorium of cerebellum at dura; (6) top of cerebellum; (7) tip of fourth ventricle; (8) bottom of cerebellum; (9) top of pons, anterior margin; (10) bottom of pons, anterior margin; (11) optic chiasm; (12) frontal pole, extension of a line from landmark 1 through landmark 2 until it intersects the dura; (13) superior colliculus.

Usage

data(schizophrenia.dat)

Format

schizophrenia$x : An array of dimension 13 x 2 x 28

schizophrenia$group : A factor of group labels ‘con’ for Controls and ‘scz’ for the schizophrenia patients.

Source


References

Data kindly provided by Fred Bookstein (University of Washington and University of Vienna)

Examples

data(schizophrenia)
plotshapes(schizophrenia$x,symbol=as.integer(schizophrenia$group))
**Description**

Bookstein’s schizophrenia data. 13 landmarks in 2 dimensions, 28 individuals. The first 14 individuals are controls. The last fourteen cases were diagnosed with schizophrenia. The landmarks were taken in the near midline from MR images of the brain: (1) splenium, posteriormost point on corpus callosum; (2) genu, anteriormost point on corpus callosum; (3) top of corpus callosum, uppermost point on arch of callosum (all three to an approximate registration on the diameter of the callosum); (4) top of head, a point relaxed from a standard landmark along the apparent margin of the dura; (5) tentorium of cerebellum at dura; (6) top of cerebellum; (7) tip of fourth ventricle; (8) bottom of cerebellum; (9) top of pons, anterior margin; (10) bottom of pons, anterior margin; (11) optic chiasm; (12) frontal pole, extension of a line from landmark 1 through landmark 2 until it intersects the dura; (13) superior colliculus.

**Usage**

```r
data(schizophrenia.dat)
```

**Format**

An array of dimension 13 x 2 x 28

**Source**


**References**

Data kindly provided by Fred Bookstein (University of Washington and University of Vienna)

**Examples**

```r
data(schizophrenia.dat)
k<-dim(schizophrenia.dat)[1]
n<-dim(schizophrenia.dat)[3]
plotshapes(schizophrenia.dat)
```
Description

Provides graphical summaries of principal components for shape.

Usage

shapepca(proc, pcno = c(1, 2, 3), type = "r", mag = 1, joinline = c(1, 1),
project=c(1,2),scores3d=FALSE,color=2,axes3=FALSE,rglopen=TRUE,zslice=0)

Arguments

proc       List given by the output from procGPA()
pcno       A vector of the PCs to be plotted
type       Options for the types of plot for the $m=2$ planar case: "r" : rows along PCs evaluated at $c = -3, 0, 3$ sd's along PC, "v" : vectors drawn from mean to $+3$ sd's along PC, "s" : plots along $c = -3, -2, -1, 0, 1, 2, 3$ superimposed, "m" : movie backward and forwards from $-3$ to $+3$ sd's along PC, "g" : TPS grid from mean to $+3$ sd's along PC.
mag        Magnification of the effect of the PC (scalar multiple of sd's)
joinline   A vector stating which landmarks are joined up by lines, e.g. joinline=c(1:n,1) will start at landmark 1, join to 2, ...., join to n, then re-join to landmark 1.
project    The default orthogonal projections if in higher than 2 dimensions
scores3d   Logical. If TRUE then a 3D scatterplot of the first 3 raw PC scores with labels in 'pcno' is given, instead of the default plot of the mean and PC vectors.
color      Color of the spheres used in plotting. Default color = 2 (red). If a vector is given then the points are colored in that order.
axes3      Logical. If TRUE then the axes are plotted in a 3D plot.
rglopen    Logical. If TRUE open a new RGL window, otherwise plot in current window.
zslice     For 3D case, type = "g" : the z co-ordinate(s) for the grid slice(s)

Details

The mean and PCs are plotted.

Value

No value is returned

Author(s)

Ian Dryden
shapes.cva

Canonical variate analysis for shapes

Description

Carry out canonical variate analysis for shapes (in two or more groups)

Usage

shapes.cva(X, groups, scale=TRUE, ncv=2)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>Input k x m x n real array of the configurations, where k is the number of points, m is the number of dimensions, and n is the sample size.</td>
</tr>
<tr>
<td>groups</td>
<td>The group labels</td>
</tr>
<tr>
<td>scale</td>
<td>Logical, indicating if Procrustes scaling should be carried out</td>
</tr>
<tr>
<td>ncv</td>
<td>Number of canonical variates to display</td>
</tr>
</tbody>
</table>

Value

A plot if ncv=2 or 3 and the Canonical Variate Scores

References


See Also

procGPA

Examples

# 2d example
data(gorf.dat)
data(gorm.dat)
gorf<-procGPA(gorf.dat)
gorm<-procGPA(gorm.dat)
shapepca(gorf,type="r",mag=3)
shapepca(gorf,type="v",mag=3)
shapepca(gorm,type="r",mag=3)
shapepca(gorm,type="v",mag=3)

# 3D example
# data(macm.dat)
# out<-procGPA(macm.dat)
# movie
# shapepca(out,pcno=1)
Author(s)
Ian Dryden

References

See Also
procGPA

Examples

#2D example: female and male apes (cf. Dryden and Mardia, 1998)

data(pongof.dat)
data(pongom.dat)
data(panm.dat)
data(panf.dat)

apes <- groupstack( pongof.dat, pongom.dat, panm.dat, panf.dat )

shapes.cva( apes$x, apes$groups)

shapes3d

Plot 3D data

Description
Plot the landmark configurations from a 3D dataset

Usage
shapes3d(x, loop=0, type="p", color = 2, joinline=c(1:1), axes3=FALSE, rglopen=TRUE)

Arguments

x An array of size k x 3 x n, where k is the number of landmarks and n is the
number of observations

loop gives the number of times an animated loop through the observations is
displayed (in order 1 to n). loop > 0 is suitable when a time-series of shapes is
available. loop = 0 gives a plot of all the observations on the same figure.

type Type of plot: 'p' points, "dots" dots (quicker for large plots), "l" dots and lines
though landmarks 1:k if 'joinline' not stated

color Colour of points (default color = 2 (red)). If a vector is given then the points are
coloured in that order.
**joinline**
Join the numbered landmarks by lines

**axes3**
Logical. If TRUE then plot the axes.

**rglopen**
Logical. If TRUE then open a new RGL window, if FALSE then plot in current window.

**Value**
None

**Author(s)**
Ian Dryden

**References**

**Examples**
```r
data(dna.dat)
shapes3d(dna.dat)
```

---

**shells**  
*Microfossil shell data*

**Description**
Microfossil shell data. Triangles from 21 individuals. Lohmann (1983) published 21 mean outlines of the microfossil which were based on random samples of organisms taken at different latitudes in the South Indian Ocean.

**Usage**
```r
data(shells)
```

**Format**
```r
shells$uv  
Scaled shape coordinates (Bookstein shape co-ordinates with base (0,0) and (1,0).  
shells$size  
Centroid size
```

**Source**

References

The data have been extracted from Fig. 7 of Bookstein (1986).

Examples

```r
data(shells)
plotshapes(shells$uv)
```

---

sooty  
Sooty mangabey data

Description

Sooty mangabey data skull data. 12 landmarks in 2 dimensions, 2 individuals (juvenile and male adult) followed by three individuals, female adult, male adult. The first entries are rotated, translated versions of the 3rd and 7th figure.

Usage

```r
data(sooty)
```

Format

An array of dimension 12 x 2 x 7

Source


References

Data from Paul O’Higgins (Hull-York Medical School)

Examples

```r
data(sooty)
plotshapes(sooty,joinline=c(1:12,1))
```
ssriemdist

Riemannian size-and-shape distance

Description

Calculates the Riemannian size-and-shape distance \( d_S \) between two configurations

Usage

ssriemdist(x, y, reflect=FALSE)

Arguments

- **x**: \( k \times m \) matrix (or complex \( k \)-vector for 2D data) where \( k \) = number of landmarks and \( m \) = no of dimensions
- **y**: \( k \times m \) matrix (or complex \( k \)-vector for 2D data)
- **reflect**: Logical. If \( \text{reflect} = \text{TRUE} \) then reflection invariance is included.

Value

The Riemannian size-and-shape distance \( \rho \) between the two configurations.

Author(s)

Ian Dryden

References


See Also

procOPA, procGPA

Examples

data(gorf.dat)
data(gorm.dat)
gorf<-procGPA(gorf.dat, scale=FALSE)
gorm<-procGPA(gorm.dat, scale=FALSE)
ds<-ssriemdist(gorf$mshape, gorm$mshape)
cat("Riemannian size-and-shape distance between mean size-and-shapes is ", ds, " \n")
Description

Steroid data. Between 42 and 61 atoms for each of 31 steroid molecules.

Usage

data(steroids)

Format

steroids$x : An array of dimension 61 x 3 x 31 of 3D co-ordinates of the 31 steroids. If a molecule has less than 61 atoms then the remaining co-ordinates are all zero.

steroids$sactivity : Activity class (‘1’ = high, ‘2’ = intermediate, and ‘3’ = low binding affinities to the corticosteroid binding globulin (CBG) receptor)

steroids$sradius : van der Waals radius (0 = missing value)

steroids$atom : atom type (0 = missing value)

steroids$charge : partial charge (0 = missing value)

steroids$snames : steroid names

Source

This particular version of the steroids data set of (x, y, z) atom co-ordinates and partial charges was constructed by Jonathan Hirst and James Melville (School of Chemistry, University of Nottingham). Also see Wagener, M., Sadowski, J., Gasteiger, J. (1995). J. Am. Chem. Soc., 117, 7769-7775. http://www2.ccc.uni-erlangen.de/services/steroids/

References


Examples

data(steroids)
 shapes3d(steroids$x[,1])
Description

Carries out tests to examine differences in mean shape between two independent populations, for $m=2$ or $m=3$ dimensional data. Tests are carried out using tangent co-ordinates.

H: Hotelling $T^2$ statistic (see Dryden and Mardia, 1998, equ.(7.4))

G: Goodall’s F statistic (see Dryden and Mardia, 1998, equ.(7.9))

J: James $T^2$ statistic (see Amaral et al., 2007)

p-values are given based on resampling (either a bootstrap test or a permutation test) as well as the usual table based p-values. Bootstrap tests involve sampling with replacement under H0 (as in Amaral et al., 2007).

Note when the sample sizes are low (compared to the number of landmarks) some minor regularization is carried out. In particular if $S_w$ is a singular within group covariance matrix, it is replaced by $S_w + 0.000001$ (Identity matrix) and a '*' is printed in the output.

Usage

testmeanshapes(A, B, resamples = 1000, replace = FALSE, scale = TRUE)

Arguments

A The random sample for group 1: $k \times m \times n_1$ array of data, where $k$ is the number of landmarks and $n_1$ is the sample size. (Alternatively a $k \times n_1$ complex matrix for 2D)

B The random sample for group 2: $k \times m \times n_2$ array of data, where $k$ is the number of landmarks and $n_2$ is the sample size. (Alternatively a $k \times n_2$ complex matrix for 2D)

resamples Integer. The number of resampling iterations. If resamples = 0 then no resampling procedures are carried out, and the tabular p-values are given only.

replace Logical. If replace = TRUE then bootstrap resampling is carried out with replacement *within* each group. If replace = FALSE then permutation resampling is carried out (sampling without replacement in *pooled* samples).

scale Logical. Whether or not to carry out Procrustes with scaling in the procedure.

Value

A list with components

H The Hotelling statistic (F statistic)

H.pvalue p-value for the Hotelling test based on resampling

H.table.pvalue p-value for the Hotelling test based on the null F distribution, assuming normality and equal covariance matrices
The James $T^2$ statistic

p-value for the James $T^2$ test based on resampling

p-value for the James $T^2$ test based on the null F distribution, assuming normality but unequal covariance matrices

The Goodall $F$ statistic

p-value for the Goodall test based on resampling

p-value for the Goodall test based on the null F distribution, assuming normality and equal isotropic covariance matrices

Author(s)

Ian Dryden

References


See Also

resampletest

Examples

#2D example : female and male Gorillas
data(gorf.dat)
data(gorm.dat)
A<-gorf.dat
B<-gorm.dat
testmeanshapes(A,B,resamples=100)
tpsgrid

Thin-plate spline transformation grids

Description

Thin-plate spline transformation grids from one set of landmarks to another.

Usage

```r
tpsgrid(TT, YY, xbegin=-999, ybegin=-999, xwidth=-999, opt=1, ext=0.1, ngrid=22,
        cex=1, pch=20, col=2, zslice=0, mag=1, axes3=FALSE)
```

Arguments

- **TT**: First object (source): (k x m matrix)
- **YY**: Second object (target): (k x m matrix)
- **xbegin**: lowest x value for plot: if -999 then a value is determined
- **ybegin**: lowest y value for plot: if -999 then a value is determined
- **xwidth**: width of plot: if -999 then a value is determined
- **opt**: Option 1: (just deformed grid on YY is displayed), option 2: both grids are displayed
- **ext**: Amount of border on plot in 2D case.
- **ngrid**: Number of grid points: size is ngrid * (ngrid - 1)
- **cex**: Point size
- **pch**: Point symbol
- **col**: Point colour
- **zslice**: For 3D case the scaled z co-ordinate(s) for the grid slice(s). The values are on a standardized scale as a proportion of height from the middle of the z-axis to the top and bottom. Values in the range -1 to 1 would be sensible.
- **mag**: Exaggerate effect (mag > 1). Standard effect has mag=1.
- **axes3**: Logical. If TRUE then the axes are plotted in a 3D plot.

Details

A square grid on the first configuration is deformed smoothly using a pair of thin-plate splines in 2D, or a triple of splines in 3D, to a curved grid on the second object. For 3D data the grid is placed at a constant z-value on the first figure, indicated by the value of zslice.

For 2D data the covariance function in the thin-plate spline is $\sigma(h) = |h|^2 \log |h|^2$ and in 3D it is given by $\sigma(h) = -|h|$.

Value

No returned value
transformations

Author(s)
Ian Dryden

References

See Also
procGPA

Examples

data(gorf.dat)
data(gorm.dat)

#TPS grid with shape change exaggerated (2x)
gorf<-procGPA(gorf.dat)
gorm<-procGPA(gorm.dat)
TT<-gorf$mshape
YY<-gorm$mshape
tpsgrid(TT,YY,mag=2)
title("TPS grid: Female mean (left) to Male mean (right)"

---

transformations Calculate similarity transformations

Description
Calculate similarity transformations between configurations in two arrays.

Usage
transformations(Xrotated,Xoriginal)

Arguments

Xrotated Input k x m x n real array of the Procrustes transformed configurations, where k is the number of points, m is the number of dimensions, and n is the sample size.

Xoriginal Input k x m x n real array of the Procrustes original configurations, where k is the number of points, m is the number of dimensions, and n is the sample size.
transformations

Value

A list with components

- translation: The translation parameters. These are the relative translations of the centroids of the individuals.
- scale: The scale parameters
- rotation: The rotation parameters. These are the rotations between the individuals after they have both been centred.

Author(s)

Ian Dryden

References


See Also

procGPA

Examples

#2D example: female and male Gorillas (cf. Dryden and Mardia, 1998)

data(gorf.dat)

Xorig <- forf.dat
Xrotated <- procGPA(gorf.dat)$rotated

transformations(Xrotated,Xorig)
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