

# Package ‘shapes’

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**Title** Statistical shape analysis

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**Author** Ian Dryden

**Description** Routines for the statistical analysis of shapes. In particular, the package provides routines for procrustes analysis, displaying shapes and principal components, testing for mean shape difference, thin-plate spline transformation grids and edge superimposition methods.

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**Depends** scatterplot3d, rgl

**License** GPL-2

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bookstein2d	<i>Bookstein's baseline registration for 2D data</i>
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---

## Description

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

## Usage

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

## Arguments

A	a $k \times 2 \times n$ real array, or $k \times n$ 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 l1, l2
bshpv	the $k \times n \times 2$ array of Bookstein shape variables, including the baseline

## Author(s)

Ian Dryden

## References

- Dryden, I.L. and Mardia, K.V. (1998) *Statistical Shape Analysis*. Wiley, Chichester. Chapter 2.
- Bookstein, F. L. (1986) Size and shape spaces for landmark data in two dimensions (with discussion). *Statistical Science*, 1:181-242.

## Examples

```
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

- Free, S.L., O'Higgins, P., Maudgil, D.D., Dryden, I.L., Lemieux, L., Fish, D.R. and Shorvon, S.D. (2001). Landmark-based morphometrics of the normal adult brain using MRI. *Neuroimage*, 13, 801-813.

## Examples

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

---

`digit3.dat`*Digit 3 data*

---

**Description**

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

**Usage**

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

**Format**

An array of dimension 6 x 2 x 30

**Source**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p318

**References**

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

Data from Cath Anderson

**Examples**

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

---

`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)
```

---

gorf.dat	<i>Female gorilla data</i>
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---

**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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p317

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, Journal of Human Evolution, 24, 183-205.

**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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p317

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, Journal of Human Evolution, 24, 183-205.

**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)
```

---

macf.dat

*Female macaque data*

---

**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

**Source**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p16

**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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p16

**References**

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

**Examples**

```
data (macm.dat)
plotshapes (macm.dat)
```

---

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**

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, *Journal of Human Evolution*, 24, 183-205.

**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**

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, *Journal of Human Evolution*, 24, 183-205.

**References**

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

**Examples**

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

---

plotshapes	<i>Plot configurations</i>
------------	----------------------------

---

**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

**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**

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, *Journal of Human Evolution*, 24, 183-205.

**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**

O'Higgins, P. and Dryden, I. L. (1993). Sexual dimorphism in hominoids: further studies of craniofacial shape differences in Pan, Gorilla, Pongo, *Journal of Human Evolution*, 24, 183-205.

**References**

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

**Examples**

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

---

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, tangentresiduals = TRUE, proc.output=FALSE,
distances=TRUE, pcaoutput=TRUE, alpha=0, affine=FALSE, expomap=FALSE)
```

**Arguments**

<code>x</code>	Input $k \times m \times n$ real array, (or $k \times n$ 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.
<code>scale</code>	Logical quantity indicating if scaling is required
<code>reflect</code>	Logical quantity indicating if reflection is required
<code>eigen2d</code>	Logical quantity indicating if complex eigenanalysis should be used to calculate Procrustes mean for the particular 2D case when <code>scale=TRUE</code> , <code>reflect=FALSE</code>
<code>tol1</code>	Tolerance for optimal rotation for the iterative algorithm: tolerance on the mean sum of squares (divided by size of mean squared) between successive iterations
<code>tol2</code>	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
<code>tangentresiduals</code>	Logical quantity indicating if Procrustes residuals should be used for analysis. If <code>tangentresiduals=TRUE</code> for the shape ( <code>scale=TRUE</code> ) case these are approximate tangent space coordinates, and for the size-and-shape ( <code>scale=FALSE</code> ) case these are exact tangent space coordinates. If <code>tangentresiduals=FALSE</code> then the partial tangent shape coordinates (see <code>tan</code> below).
<code>proc.output</code>	Logical quantity indicating if printed output during the iterations of the Procrustes GPA algorithm should be given
<code>distances</code>	Logical quantity indicating if shape distances and sizes should be calculated
<code>pcaoutput</code>	Logical quantity indicating if PCA should be carried out
<code>alpha</code>	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 $\alpha \neq 0$ .
<code>affine</code>	Logical. If <code>TRUE</code> then only the affine subspace of shape variability is considered.
<code>expomap</code>	Logical. If <code>TRUE</code> then the exponential map tangent co-ordinates are used instead of the the partial tangent shape co-ordinates

**Value**

A list with components

<code>k</code>	no of landmarks
<code>m</code>	no of dimensions ( $m$ -D dimension configurations)
<code>n</code>	sample size
<code>mshape</code>	Procrustes mean shape. Note this is unit size if complex eigenanalysis used, but on the scale of the data if iterative GPA is used.
<code>tan</code>	If <code>tangentresiduals=TRUE</code> this is the $mk \times n$ matrix of Procrustes residuals $X_i \hat{P} - \bar{X}$ , where $\bar{X} = \text{mean}(X_i \hat{P})$ . If <code>approx tangent=FALSE</code> this is the $km \times n$ matrix of partial Procrustes tangent shape coordinates with pole given by the preshape of the Procrustes mean

rotated	the $k \times m \times n$ array of full 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 $\tan$ . 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.
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	root mean square (r.m.s.) of $\rho$
rmsdl	r.m.s. of full Procrustes distances to the mean shape $d_F$

**Author(s)**

Ian Dryden, with input from Mohammad Faghihi and Alfred Kume

**References**

- Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester.
- Goodall, C.R. (1991). Procrustes methods in the statistical analysis of shape (with discussion). Journal of the Royal Statistical Society, Series B, 53: 285-339.
- Gower, J.C. (1975). Generalized Procrustes analysis, Psychometrika, 40, 33–50.
- Kent, J.T. (1994). The complex Bingham distribution and shape analysis, Journal of the Royal Statistical Society, Series B, 56, 285-299.
- Ten Berge, J.M.F. (1977). Orthogonal Procrustes rotation for two or more matrices. Psychometrika, 42, 267-276.

**See Also**

procOPA,riemdist,shapepca,testmeanshapes

**Examples**

```
#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 <- procGPA(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 <- procGPA(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 $\text{trace}(\text{Ahat} - \text{Bhat})^2$

**Author(s)**

Ian Dryden

**References**

Dryden, I.L. and Mardia, K.V. (1998). Statistical shape analysis. Wiley, Chichester.

**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)
plot(A,xlim=c(-2000,3000),ylim=c(-2000,3000),xlab=" ",ylab=" ")
```

```

lines(A[c(1:12,1),])
points(out$Bhat)
lines(out$Bhat[c(1:12,1),],lty=2)
title("Match adult onto juvenile")
#match A onto B
out<-procOPA(B,A)
#rotation angle
print(atan2(out$R[1,2],out$R[1,1])*180/pi)
#scale
print(out$s)
plot(B,xlim=c(-2000,3000),ylim=c(-2000,3000),xlab=" ",ylab=" ")
lines(B[c(1:12,1),],lty=2)
points(out$Bhat)
lines(out$Bhat[c(1:12,1),])
title("Match juvenile onto adult")

```

---

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, p
```

### Arguments

<code>x</code>	Input $k \times m \times n$ real array, where $k$ is the number of points, $m$ is the number of dimensions, and $n$ is the sample size.
<code>fixcovmatrix</code>	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. <code>fixcovmatrix=diag(8)</code> for the identity matrix with 8 landmarks.
<code>initial</code>	The initial value of the estimated covariance matrix. "Identity" - identity matrix, "Rawdata" - based on sample variance of the raw landmarks. Also, could be a $k \times k$ symmetric positive definite matrix.
<code>maxiterations</code>	The maximum number of iterations for estimating the covariance matrix
<code>scale</code>	Logical quantity indicating if scaling is required
<code>prior</code>	Indicates the type of prior. "Exponential" is exponential for the inverse eigenvalues. "Identity" is an inverse Wishart with the identity matrix as parameters.
<code>diagonal</code>	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:  $\Sigma_{k \times l \times m}$  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 $m \times k \times n$ matrix of Procrustes residuals $X_i^{\wedge} P - \bar{X}$ .
rotated	the $k \times m \times n$ array of weighted Procrustes rotated data
pcar	the columns are eigenvectors (PCs) of the sample covariance Sv of tan
pcasd	the square roots of eigenvalues of Sv 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

- Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester.
- Goodall, C.R. (1991). Procrustes methods in the statistical analysis of shape (with discussion). Journal of the Royal Statistical Society, Series B, 53: 285-339.

### 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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p313

**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	<i>Large T2 mouse vertebrae data</i>
-----------	--------------------------------------

---

**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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p313

**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	<i>Small T2 mouse vertebrae data</i>
-----------	--------------------------------------

---

**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**

Dryden, I.L. and Mardia, K.V. (1998). Statistical Shape Analysis, Wiley, Chichester. p313

## 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)
```

---

resampletest	<i>Tests for mean shape difference using complex arithmetic, including bootstrap and permutation tests.</i>
--------------	---

---

## 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 Sw is a singular within group covariance matrix, it is replaced by Sw + 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 x m x n1 array of data, where k is the number of landmarks and n1 is the sample size. (Alternatively a k x n1 complex matrix for 2D) |
| B | The random sample for group 3: k x m x n2 array of data, where k is the number of landmarks and n2 is the sample size. (Alternatively a k x n2 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	<i>lambda_min</i> statistic
lambda.pvalue	p-value for <i>lambda_min</i> test based on resampling
lambda.table.pvalue	p-value for <i>lambda_min</i> test based on the asymptotic chi-squared distribution (large n1,n2)
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 $F$ 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

- Amaral, G.J.A., Dryden, I.L. and Wood, A.T.A. (2007) Pivotal bootstrap methods for  $k$ -sample problems in directional statistics and shape analysis. *Journal of the American Statistical Association*. 102, 695-707.
- Dryden, I.L. and Mardia, K.V. (1998) *Statistical Shape Analysis*, Wiley, Chichester. Chapter 7.
- Goodall, C. R. (1991). Procrustes methods in the statistical analysis of shape (with discussion). *Journal of the Royal Statistical Society, Series B*, 53: 285-339.

**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**

```
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**

Kendall, D. G. (1984). Shape manifolds, Procrustean metrics and complex projective spaces, Bulletin of the London Mathematical Society, 16, 81-121.

**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, 0, -90 ) )
```

---

schizophrenia.dat *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

An array of dimension 13 x 2 x 28

### Source

Bookstein, F. L. (1996). Biometrics, biomathematics and the morphometric synthesis, *Bulletin of Mathematical Biology*, 58, 313–365.

### References

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

### Examples

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

shapepca

*Principal components analysis for shape***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=
```

**Arguments**

proc	List given by the output from <code>procGPA()</code>
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. <code>joinline=c(1:n,1)</code> 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 then open a new RGL window, if FALSE then 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

**References**

Dryden, I.L. and Mardia, K.V. (1998) Statistical Shape Analysis. Wiley, Chichester.

**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)
```

---

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**

<code>x</code>	An array of size $k \times 3 \times n$ , where $k$ is the number of landmarks and $n$ is the number of observations
<code>loop</code>	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.
<code>type</code>	Type of plot: "p" points, "dots" dots (quicker for large plots), "l" dots and lines though landmarks 1:k if 'joinline' not stated
<code>color</code>	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**

Dryden, I.L. and Mardia, K.V. (1998) *Statistical Shape Analysis*. Wiley, Chichester.

**Examples**

```
data(dna.dat)
shapes3d(dna.dat)
```

---

sooty.dat

*Sooty mangabey data*


---

**Description**

Sooty mangabey data skull data. 12 landmarks in 2 dimensions, 2 individuals (juvenile and adult)

**Usage**

```
data(sooty.dat)
```

**Format**

An array of dimension 12 x 2 x 2

**Source**

Dryden, I.L. and Mardia, K.V. (1998). *Statistical Shape Analysis*, Wiley, Chichester. p17, 42

**References**

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

**Examples**

```
data(sooty.dat)
plotshapes(sooty.dat, joinline=c(1:12, 1))
```

---

testmeanshapes	<i>Tests for mean shape difference, including permutation and bootstrap tests</i>
----------------	---

---

## 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 the Procrustes residuals.

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  $H_0$  (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 = TRUE, 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 $\text{resamples} = 0$ then no resampling procedures are carried out, and the tabular p-values are given only.
replace	Logical. If $\text{replace} = \text{TRUE}$ then bootstrap resampling is carried out with replacement *within* each group. If $\text{replace} = \text{FALSE}$ 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
J	The James $T^2$ statistic
J.pvalue	p-value for the James $T^2$ test based on resampling
J.table.pvalue	p-value for the James $T^2$ test based on the null F distribution, assuming normality but unequal covariance matrices
G	The Goodall $F$ 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**

- Amaral, G.J.A., Dryden, I.L. and Wood, A.T.A. (2007) Pivotal bootstrap methods for  $k$ -sample problems in directional statistics and shape analysis. *Journal of the American Statistical Association*. 102, 695-707.
- Dryden, I.L. and Mardia, K.V. (1998) *Statistical Shape Analysis*, Wiley, Chichester. Chapter 7.
- Goodall, C. R. (1991). Procrustes methods in the statistical analysis of shape (with discussion). *Journal of the Royal Statistical Society, Series B*, 53: 285-339.

**See Also**

resampletest

**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
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**

```
tpsgrid(TT, YY, xbegin=-999, ybegin=-999, xwidth=-999, opt=1, ext=0.1, ngrid=22, ce
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

**Author(s)**

Ian Dryden

**References**

Bookstein, F.L. (1989). Principal warps: thin-plate splines and the decomposition of deformations, *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 11, 567–585.

Dryden, I.L. and Mardia, K.V. (1998) *Statistical Shape Analysis*. Wiley, Chichester. Chapter 10.

**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)")
```

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