

Package ‘prWarp’

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Title Warping Landmark Configurations

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Description Compute bending energies, principal warps, partial warp scores, and the non-affine component of shape variation for 2D landmark configurations, as well as Mardia-Dryden distributions and self-similar distributions of landmarks, as described in Mitteroecker et al. (2020) <[doi:10.1093/sysbio/syaa007](https://doi.org/10.1093/sysbio/syaa007)>. Working examples to decompose shape variation into small-scale and large-scale components, and to decompose the total shape variation into outline and residual shape components are provided. Two landmark datasets are provided, that quantify skull morphology in humans and papionin primates, respectively from Mitteroecker et al. (2020) <[doi:10.5061/dryad.j6q573n8s](https://doi.org/10.5061/dryad.j6q573n8s)> and Grunstra et al. (2020) <[doi:10.5061/dryad.zkh189373](https://doi.org/10.5061/dryad.zkh189373)>.

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Author Anne Le Maitre [aut, cre] (<<https://orcid.org/0000-0003-2690-7367>>),
Silvester Bartsch [aut],
Nicole Grunstra [aut],
Philipp Mitteroecker [aut]

Maintainer Anne Le Maitre <anne.le.maitre@univie.ac.at>

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array.to.xxyy	<i>Convert (p x k x n) data array into 2D data matrix</i>
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Description

Convert a three-dimensional array of landmark coordinates into a two-dimensional matrix

Usage

```
array.to.xxyy(A)
```

Arguments

A A 3D array (p x k x n) containing landmark coordinates for a set of specimens

Value

Function returns a two-dimensional matrix of dimension (n x [p x k]), where rows represent specimens and columns represent variables. The p first columns correspond to X coordinates, etc.

See Also

[xxyy.to.array](#)

Examples

```
A <- array(rnorm(40), c(5, 2, 4)) # random 2D coordinates of 5 landmarks for 4 specimens
array.to.xxyy(A)
```

create.pw.be

*Principal warps***Description**

Computes the principal warps and the bending energy of a reference shape configuration, as well as the variance of the partial warps, the partial warp scores and the non-affine component of shape variation for 2D landmark coordinates (3D not implemented). Small-scale and large-scale components of shape variation can also be computed.

Usage

```
create.pw.be(A, M_ref, d = NULL)
```

Arguments

A	a $k \times 2 \times n$ array, where k is the number of 2D landmarks, and n is the sample size.
M_ref	a $k \times 2$ reference matrix (usually the sample mean shape), where k is the number of 2D landmarks
d	(optional) an integer value comprised between 1 and $(k-3)$ to compute small-scale shape components (between 1 and d) and large-scale shape components (between $d+1$ and $k-3$)

Value

A list containing the following named components:

bendingEnergy	the bending energy (the $(k-3)$ eigenvalues of the bending energy matrix)
principalWarps	the $k \times (k-3)$ matrix of principal warps (the k eigenvectors of the bending energy matrix)
partialWarpScores	the $n \times (2k-6)$ matrix of partial warp (the projection of the vectors of shape coordinates, expressed as deviations from the reference shape, onto the principal warps)
variancePW	the variance of the $(k-3)$ partial warps
Xnonaf	the $n \times 2k$ matrix of the non-affine component of shape variation
Xsmall	the $n \times 2k$ matrix of the small-scale shape variation (if d is provided)
Xlarge	the $n \times 2k$ matrix of the large-scale shape variation (if d is provided)

References

Bookstein FL. (1989). Principal Warps: Thin-plate splines and the decomposition of deformations. *IEEE Transactions on pattern analysis and machine intelligence* 11(6): 567–585. <https://ieeexplore.ieee.org/abstract/document/24792>

See Also

See [Createl](#) for the creation of the bending energy matrix

Examples

```
# 2D landmark coordinates
library("geomorph")
data("HomoMidSag") # dataset
n_spec <- dim(HomoMidSag)[1] # number of specimens
k <- dim(HomoMidSag)[2] / 2 # number of landmarks
homo_ar <- arrayspecs(HomoMidSag, k, 2) # create an array

# Procrustes registration
homo_gpa <- Morpho::procSym(homo_ar)
m_overall <- homo_gpa$rotated # Procrustes coordinates
m_mshape <- homo_gpa$mshape # average shape

# Computation of bending energy, partial warp scores etc.
homo_be_pw <- create.pw.be(m_overall, m_mshape)

# Partial warp variance as a function of bending energy
logInvBE <- log((homo_be_pw$bendingEnergy)^(-1)) # inverse log bending energy
logPWvar <- log(homo_be_pw$variancePW) # log variance of partial warps
mod <- lm(logPWvar ~ logInvBE) # linear regression
# Plot log PW variance on log BE^-1 with regression line
plot(logInvBE, logPWvar, col = "white", asp = 1,
main = "PW variance against inverse BE", xlab = "log 1/BE", ylab = "log PW variance")
text(logInvBE, logPWvar, labels = names(logPWvar), cex = 0.5)
abline(mod, col = "blue")
```

HomoMidSag

HomoMidSag dataset

Description

2D Cartesian coordinates of 87 landmarks quantifying the skull morphology along the midsagittal plane for 24 adult modern humans.

Usage

```
data(HomoMidSag)
```

Format

A data frame with 24 rows and 184 variables

References

Bartsch, Silvester (2019) The ontogeny of hominid cranial form: A geometric morphometric analysis of coordinated and compensatory processes. Master's thesis, University of Vienna.

Mitteroecker, Philipp et al. (2020) Morphometric variation at different spatial scales: coordination and compensation in the emergence of organismal form. *Systematic Biology*, 69(5): 913–926. doi: 10.1093/sysbio/syaa007

Mitteroecker, Philipp et al. (2020) Data form: Morphometric variation at different spatial scales: coordination and compensation in the emergence of organismal form. *Dryad Digital Repository*. doi: 10.5061/dryad.j6q573n8s

md.distri	<i>Mardia-Dryden distribution</i>
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Description

Create a matrix of 2D shape coordinates drawn from a Mardia-Dryden distribution (3D not implemented)

Usage

```
md.distri(M_ref, n, sd = 0.05)
```

Arguments

M_ref	a k x 2 refence matrix (usually the sample mean shape), where k is the number of 2D landmarks
n	the number of observations
sd	the standard deviation of the distribution (default = 0.02)

Value

the n x 2k matrix of shape coordinates drawn from a Mardia-Dryden distribution

Examples

```
# 2D landmark coordinates
library("geomorph")
data("HomoMidSag") # dataset
n_spec <- dim(HomoMidSag)[1] # number of specimens
k <- dim(HomoMidSag)[2] / 2 # number of landmarks
homo_ar <- arrayspecs(HomoMidSag, k, 2) # create an array

# Procrustes registration
homo_gpa <- Morpho::procSym(homo_ar)
m_mshape <- homo_gpa$mshape # average shape

# Mardia-Dryden distribution
```

```
Xmd <- md.distri(m_mshape, n = n_spec, sd = 0.005)
# Visualization
plot(Xmd[, 1:k], Xmd[, (k+1):(2*k)], asp = 1, las = 1, cex = 0.5,
main = "Mardia-Dryden distribution", xlab = "X", ylab = "Y")
```

papionin

papionin dataset

Description

2D Cartesian coordinates of 70 landmarks quantifying the skull morphology along the midsagittal plane for 67 adult modern primates (mostly papionins). The data correspond to a list with the 6 following elements:

Usage

```
data(papionin)
```

Format

A list of 6 elements.

Details

- **coords** The 3D array of landmark coordinates
- **species** The vector of species names
- **semi_lm** The vector of semilandmark numbers of the full dataset
- **curves** The list of curves for sliding semilandmarks of the full dataset
- **links** The matrix of links between landmarks for the full dataset
- **outline** A list of 4 elements for the analysis of the outline shape: **subset**, the landmark numbers for the subset; **semi_lm**, the vector of semilandmark numbers; **curves**, the list of curves for sliding semilandmarks; **links**, the matrix of links between landmarks for the full dataset.

References

Grunstra, Nicole D. S. et al. (2021) Detecting phylogenetic signal and adaptation in papionin cranial shape by decomposing variation at different spatial scales. *Systematic Biology*, 70(4): 694–706. doi: 10.1093/sysbio/syaa093

Grunstra, Nicole D. S. et al. (2020) Data form: Detecting phylogenetic signal and adaptation in papionin cranial shape by decomposing variation at different spatial scales. *Dryad Digital Repository*. doi: 10.5061/dryad.zkh189373

ssim.distri	<i>Self-similar distribution</i>
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Description

Create a matrix of 2D shape coordinates drawn from a self-similar distribution (3D not implemented)

Usage

```
ssim.distri(M_ref, n, sd = 0.02, f = 1)
```

Arguments

M_ref	a k x 2 reference matrix (usually the sample mean shape), where k is the number of 2D landmarks
n	the number of observations
sd	the standard deviation of the distribution (default = 0.02)
f	a scaling factor

Value

the n x 2k matrix of shape coordinates drawn from a self-similar distribution

Examples

```
# 2D landmark coordinates
library("geomorph")
data("HomoMidSag") # dataset
n_spec <- dim(HomoMidSag)[1] # number of specimens
k <- dim(HomoMidSag)[2] / 2 # number of landmarks
homo_ar <- arrayspecs(HomoMidSag, k, 2) # create an array

# Procrustes registration
homo_gpa <- Morpho::procSym(homo_ar)
m_mshape <- homo_gpa$mshape # average shape

# Self-similar distribution
Xdefl <- ssim.distri(m_mshape, n = n_spec, sd = 0.05, f = 1)
# Visualization
plot(Xdefl[, 1:k], Xdefl[, (k+1):(2*k)], asp = 1, las = 1, cex = 0.5,
main = "Self-similar distribution", xlab = "X", ylab = "Y")
```

tps.all	<i>Thin plate spline mapping (2D and 3D) for several sets of landmark coordinates</i>
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Description

Maps landmarks via thin plate spline based on a reference and a target configuration in 2D or in 3D. This function is an extension of the tps3d function for a set of specimens.

Usage

```
tps.all(X_array, REF_array, TAR_matrix)
```

Arguments

X_array	original coordinates - a 3D array (p x k x n) containing original landmark coordinates for a set of specimens
REF_array	reference coordinates (e.g., outline landmarks for all specimens) - a 3D array (p x k x n) containing reference landmark coordinates for a set of specimens
TAR_matrix	target coordinates (e.g., average outline landmarks) - a matrix (n x k) containing target landmark coordinates

Details

p is the number of landmark points, k is the number of landmark dimensions (2 or 3), and n is the number of specimens.

Value

Function returns a 3D array (p x k x n) containing the deformed input (original landmark set warped onto the target matrix).

References

Bookstein FL. (1989). Principal Warps: Thin-plate splines and the decomposition of deformations. *IEEE Transactions on pattern analysis and machine intelligence*, 11(6): 567–585. <https://ieeexplore.ieee.org/abstract/document/24792>

See Also

See [tps3d](#)

Examples

```

data("papionin") # load dataset
# Full dataset: 70 landmarks
papionin_ar <- papionin$coords
# Outline dataset: subset of 54 landmarks
outline_ar <- papionin_ar[papionin$outline$subset, , ]

# Subset: Macaca only
mac <- grep("Macaca", papionin$species) # genus Macaca
papionin_macaca <- papionin_ar[, , mac]
outline_macaca <- outline_ar[, , mac]

# Landmark sliding by minimizing bending energy + superimposition (GPA)
library("Morpho")
papionin_gpa <- procSym(papionin_macaca, SMvector = papionin$semi_lm,
  outlines = papionin$curves)
outline_gpa <- procSym(outline_macaca, SMvector = papionin$outline$semi_lm,
  outlines = papionin$outline$curves)

# Warping the slid landmarks of the full landmark dataset to the average outline shape
residual_shape <- tps.all(X_array = papionin_gpa$datalide,
  REF_array = outline_gpa$datalide,
  TAR_matrix = outline_gpa$mshape)

```

xxyy.to.array	<i>Convert landmark data matrix into array (p x k x n)</i>
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Description

Convert a matrix of landmark coordinates into a three-dimensional array

Usage

```
xxyy.to.array(M, p, k = 2)
```

Arguments

M	A matrix of dimension $n \times [p \times k]$ containing landmark coordinates for a set of specimens. Each row contains all landmark coordinates for a single specimen. The first columns correspond to the X coordinates for all landmarks, etc.
p	Number of landmarks
k	Number of dimensions (2 or 3)

Value

Function returns a 3D array ($p \times k \times n$), where p is the number of landmark points, k is the number of landmark dimensions (2 or 3), and n is the number of specimens. The third dimension of this array contains names for each specimen if specified in the original input matrix.

See Also[array.to.xyy](#)**Examples**

```
X <- matrix(rnorm(40), nrow = 4) # Random 2D coordinates of 5 landmarks for 4 specimens
xyy.to.array(X, 5, 2)
```

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