

# Package ‘morphErr’

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**Title** Measurement Error Models for Morphometric Data

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**Description** Morphometric data collected on animal populations can be subject to measurement error, which leads to biased estimators using line-fitting techniques such as linear regression and reduced major axis. The models implemented in this package were described by Stevenson, Smit, and Setyawan (2026) [DOI:10.1214/26-AOAS2164](https://doi.org/10.1214/26-AOAS2164). They explicitly accommodate measurement error, allow for multivariate data, estimate relationships between dimensions, allow missing data, and provide tests for isometric relationships between dimensions. Morphometric data of the reef manta ray, collected in Raja Ampat, Indonesia, are included.

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|            |                                               |
|------------|-----------------------------------------------|
| boot.morph | <i>Bootstrapping for a Morphometric Model</i> |
|------------|-----------------------------------------------|

---

Description

Simulates bootstrap resamples and re-fits the original morphometric model to each one. The resulting object can be used as an argument for [summary.lme.morph\(\)](#) and [plot.lme.morph\(\)](#) to provide standard errors, confidence intervals, and p-values based on bootstrapping rather than asymptotic approximations.

Usage

```
boot.morph(object, B = 1000, control = NULL, progressbar = TRUE, n.cores = 1)
```

Arguments

|             |                                                                                                                                                |
|-------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| object      | An object of class <code>lme.morph</code> , returned by <a href="#">fit.morph()</a> .                                                          |
| B           | An integer, providing the number of bootstrap resamples.                                                                                       |
| control     | A list of control values for the estimation algorithm to replace the default values returned by the function <code>nlme::lmeControl()</code> . |
| progressbar | Logical. If TRUE a progress bar will be displayed.                                                                                             |
| n.cores     | Integer. The number of cores for parallel processing.                                                                                          |

Value

The original object, with additional bootstrapping information that can be used by [summary.lme.morph\(\)](#) and [plot.lme.morph\(\)](#)

## Examples

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Carrying out a parametric bootstrap.
fit.boot <- boot.morph(fit, B = 100)
## Standard errors based on a bootstrap will be a little different
## to those based on asymptotic approximations.
summary(fit)
summary(fit.boot)
```

---

|                   |                                                             |
|-------------------|-------------------------------------------------------------|
| extract.sim.morph | <i>Extract Results from a Morphometric Simulation Study</i> |
|-------------------|-------------------------------------------------------------|

---

## Description

Extracts results from each model fitted in a simulation study conducted using `sim.morph()`.

## Usage

```
extract.sim.morph(sim.res, FUN = summary, n.cores = 1)
```

## Arguments

|                      |                                                                                                                                               |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|
| <code>sim.res</code> | An object of class <code>lme.morph.sim</code> , returned by <code>sim.morph()</code>                                                          |
| <code>FUN</code>     | A function to apply to each model fit. Defaults to <code>summary.lme.morph()</code> , which extracts parameter estimates and standard errors. |
| <code>n.cores</code> | Integer. The number of cores for parallel processing.                                                                                         |

## Value

An array containing the results of applying `FUN` to each model fit.

## Examples

```
## Running a small simulation study.
sim.fits <- sim.morph(n.sims = 5,
  n.animals = 10,
  n.photos = 3,
  mus = c(315, 150, 100),
  sigmas = c(25, 15, 10),
  rhos = c(0.85, 0.80, 0.75),
  psis = c(10, 6, 4),
  phis = c(0.5, 0.4, 0.3),
  method = "REML",
  progressbar = FALSE,
  n.cores = 1)
```

```
## Extracting p-values from tests for isometry from each model
## fit.
iso.p <- function(x) summary(x, type = "isometric-pca")[, 3]
extract.sim.morph(sim.fits, FUN = iso.p)
```

fit.morph

*Fit Morphometric Model*

## Description

Fits the model described by Stevenson, Smit, and Setyawan (2026) to morphometric data.

## Usage

```
fit.morph(
  data,
  log.transform = FALSE,
  method = "REML",
  control = list(maxIter = 1e+05, msMaxIter = 1e+05)
)
```

## Arguments

|               |                                                                                                                                                             |
|---------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data          | A data frame containing the morphometric data. See the section below on the correct formatting of this argument.                                            |
| log.transform | Logical. If TRUE, the data are log-transformed prior to model fitting.                                                                                      |
| method        | A character string indicating the objective function used to fit the model. Either "ML" for maximum likelihood or "REML" for restricted maximum likelihood. |
| control       | A list of control values for the estimation algorithm to replace the default values returned by the function <code>nlme::lmeControl()</code> .              |

## Details

This is a special case of a linear mixed-effects model, and is fitted via a call to `nlme::lme()`. Some arguments of `fit.morph()` are directly passed to `nlme::lme()`.

## Value

An object of classes `lme.morph` (specific to this package) and `lme` (inherited from `nlme::lme()`). The object is the list returned by `nlme::lme()` with a couple of additional components.

Rather than inspecting the object directly, the best way to extract understandable output from the object is using the S3 methods `summary.lme.morph()`, `plot.lme.morph()`, and `predict.lme.morph()` via the generic functions `summary()`, `plot()`, and `predict()`. Other S3 methods for the `lme` class are available via `nlme`, such as `nlme::coef.lme()`.

## Log transformations

To fit a model to log-transformed measurement data, provide the untransformed measurements in the data argument and specify `log.transform = TRUE`. This will allow the S3 method `plot.lme.morph()` to plot the original data with back-transformed estimates, and the S3 method `summary.lme.morph()` to carry out the correct test for isometric growth.

## The data argument

The `manta` object is an example of a correctly formatted data argument. It must be a data frame with the following columns:

`animal.id` An individual identification number. Rows with the same `animal.id` correspond to measurements of the same individual manta ray.

`photo.id` A photo identification number. Rows with the same `photo.id` correspond to measurements taken from the same image.

`photo.id` An integer indicating the dimension the measurement is for.

`measurement` The corresponding measurement.

## References

Stevenson, B. C., Smit, E., and Setyawan, E. (2026) Measurement error models for morphometric data. *Annals of Applied Statistics*, **20**: 945–962.

## Examples

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Using maximum likelihood instead of REML.
fit <- fit.morph(manta, method = "ML")
```

---

manta

*Manta Ray Morphometric Data*


---

## Description

Data collected on a drone photogrammetry survey of the reef manta ray *Mobula alfredi* in Raja Ampat, Indonesia.

## Usage

```
manta
```

**Format**

manta:

A data frame with four columns:

animal.id An individual identification number. Rows with the same animal.id correspond to measurements of the same individual manta ray.

photo.id A photo identification number. Rows with the same photo.id correspond to measurements taken from the same image.

dim An integer indicating the dimension the measurement is for. Here, 1 is for disc width, 2 is for disc length, and 3 is for cranial width.

measurement The observed measurement value in centimetres.

---

plot.lme.morph

*Plot Morphometric Data and Estimated Relationships*

---

**Description**

An S3 method that plots morphometric data, estimated relationships between dimensions, or both, from a fitted model object returned by `fit.morph()`.

**Usage**

```
## S3 method for class 'lme.morph'
plot(
  x,
  dims = c(1, 2),
  type = "data",
  line.type = "lm",
  confints = !add,
  add = FALSE,
  reverse.axes = FALSE,
  plot.data = TRUE,
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL,
  ...
)
```

**Arguments**

|      |                                                                                                                                                                                     |
|------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x    | An object of class <code>lme.morph</code> , returned by <code>fit.morph()</code> .                                                                                                  |
| dims | An integer vector of length two, indicating which dimensions will appear on the x- and y-axes, respectively.                                                                        |
| type | A character string specifying the plot type. If "ratio", then the y-axis represents the ratio between measurements of the two dimensions. If "data", then the raw data are plotted. |

|                           |                                                                                                                                                                                                                                                                                                                               |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>line.type</code>    | A character string specifying the type of fitted line to overlay. If "lm", then a line with the same interpretation as linear regression is plotted. If "pca", then the reduced major axis (or principal component axis) summarising the relationship is plotted.                                                             |
| <code>confints</code>     | Logical. If TRUE, then confidence intervals are plotted.                                                                                                                                                                                                                                                                      |
| <code>add</code>          | Logical. If TRUE, then fitted lines are added to an existing plot.                                                                                                                                                                                                                                                            |
| <code>reverse.axes</code> | Logical. If TRUE, then a line of type "lm" will provide the expected value of the x-axis variable conditional on the y-axis variable, rather than the other way around. Only use <code>reverse.axes = TRUE</code> to add to an existing plot. For a new plot, simply reverse the order of the elements in <code>dims</code> . |
| <code>plot.data</code>    | Logical. If FALSE then the data are not plotted.                                                                                                                                                                                                                                                                              |
| <code>xlim, ylim</code>   | Limits for the axes.                                                                                                                                                                                                                                                                                                          |
| <code>xlab, ylab</code>   | Titles for the axes.                                                                                                                                                                                                                                                                                                          |
| <code>...</code>          | Additional arguments passed to <code>graphics::abline()</code> and <code>graphics::lines()</code> to modify the appearance of the fitted lines.                                                                                                                                                                               |

### Value

No return value. Called to produce a plot.

### Examples

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Plotting dimensions 1 and 2 with a fitted linear regression
## line.
plot(fit)
## Same again, but plotting the reduced major axis (or principal
## component axis) for dimensions 1 and 3.
plot(fit, dims = c(1, 3), line.type = "pca")
## A plot showing how the ratio between dimensions 2 and 3 changes
## with the size of dimension 3. Because the line is quite flat,
## it's plausible the relationship is isometric.
plot(fit, dims = c(3, 2), type = "ratio", line.type = "pca")
## On the other hand, the relationship between dimensions 1 and 2
## is clearly allometric.
plot(fit, dims = c(3, 1), type = "ratio", line.type = "pca")
```

### Description

Creates scatter plots of morphometric measurements, with options for different dimension combinations and plotting of ratios.

**Usage**

```
plotmorph(
  data,
  dims = c(1, 2),
  plot.data = TRUE,
  ratios = FALSE,
  xlim = NULL,
  ylim = NULL,
  xlab = NULL,
  ylab = NULL
)
```

**Arguments**

|                         |                                                                                                                  |
|-------------------------|------------------------------------------------------------------------------------------------------------------|
| <code>data</code>       | A data frame containing the morphometric data. See the section below on the correct formatting of this argument. |
| <code>dims</code>       | An integer vector of length two, indicating which dimensions will appear on the x- and y-axes, respectively.     |
| <code>plot.data</code>  | Logical. If FALSE, the plotting area is set up but points aren't plotted.                                        |
| <code>ratios</code>     | Logical. If TRUE, the y-axis represents the ratio between dimensions.                                            |
| <code>xlim, ylim</code> | Limits for the axes.                                                                                             |
| <code>xlab, ylab</code> | Titles for the axes.                                                                                             |

**Value**

No return value. Called to produce a plot.

**The data argument**

The `manta` object is an example of a correctly formatted data argument. It must be a data frame with the following columns:

`animal.id` An individual identification number. Rows with the same `animal.id` correspond to measurements of the same individual manta ray.

`photo.id` A photo identification number. Rows with the same `photo.id` correspond to measurements taken from the same image.

`photo.id` An integer indicating the dimension the measurement is for.

`measurement` The corresponding measurement.

**Examples**

```
## Plotting dimensions 1 and 2.
plotmorph(manta)
## Plotting dimensions 1 and 3.
plotmorph(manta, dims = c(1, 3))
## Plotting the ratio of dimension 2 divided by dimension 1 on the
## y-axis.
```

```
plotmorph(manta, dims = c(1, 2), ratios = TRUE)
```

---

|                   |                                              |
|-------------------|----------------------------------------------|
| predict.lme.morph | <i>Predict Measurements from True Values</i> |
|-------------------|----------------------------------------------|

---

## Description

Calculates model predictions for the true size of a dimension based on true values for any subset of the remaining dimensions. Predictions for multiple individuals are available from a single call to the function.

## Usage

```
## S3 method for class 'lme.morph'
predict(object, y.dim, newdata = NULL, type = c("lm", "pca"), ...)
```

## Arguments

|         |                                                                                                                                  |
|---------|----------------------------------------------------------------------------------------------------------------------------------|
| object  | An object of class <code>lme.morph</code> , returned by <code>fit.morph()</code> .                                               |
| y.dim   | Integer specifying which dimension to predict                                                                                    |
| newdata | A data frame of other dimensions to use for prediction. Column names must be of the form "dimX" where X is the dimension number. |
| type    | Either "lm" or "pca" for the type of prediction.                                                                                 |
| ...     | Additional arguments passed to methods                                                                                           |

## Details

This function computes estimated coefficients for the appropriate linear function (as per `summary.lme.morph()` with `type = "betas-lm"` or `type = "betas-pca"`), and then evaluates the function for the provided `newdata`. For `type = "pca"`, only a single column can be provided in `newdata`.

## Value

A matrix with estimated true sizes and standard errors. Note that these are standard errors, not prediction errors.

## Prediction functions in morphErr

There are three key differences between `predict.lme.morph()` and `predictblup()`.

- `predict.lme.morph()` only generates estimates for one dimension based on true values for other dimensions, whereas `predictblup()` can generate estimates from true values, observed values (i.e., subject to measurement error), or a combination of both.
- `predict.lme.morph()` can generate estimates for multiple individuals, whereas `predictblup()` only provides estimates for a single individual.
- `predict.lme.morph()` provides standard errors, but `predictblup()` does not.

**See Also**[predictblup\(\)](#)**Examples**

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Predicting dimension 2 for a single individual with a true value
## of 90 for dimension 3.
predict(fit, y.dim = 2, newdata = data.frame(dim3 = 90))
## Predicting dimension 1 from dimensions 2 and 3 for two
## individuals, one with true values of 130 and 60 for dimensions 2
## and 3, respectively, and one with true values of 140 and 70.
predict(fit, y.dim = 1, newdata = data.frame(dim2 = c(130, 140),
                                              dim3 = c(60, 70)))
```

predictblup

*Predict from Observed Measurements***Description**

Makes predictions for a single individual using the best linear unbiased predictor (BLUP).

**Usage**

```
predictblup(object, true = NULL, obs = NULL)
```

**Arguments**

|        |                                                                                                                                                                                     |
|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| object | An object of class <code>lme.morph</code> , returned by <a href="#">fit.morph()</a> .                                                                                               |
| true   | A vector of true dimension measurements, if available. Use NA for dimensions with unknown true measurements.                                                                        |
| obs    | A matrix of measurements observed with error, where each row represents measurements from one photograph. Use NA for dimensions with measurements that were not taken from a photo. |

**Details**

This function uses a BLUP to compute estimated true values for a single individual. A BLUP is computed by finding the mode of the multivariate probability density function of the true values, conditional on any provided values for true dimension sizes, dimension measurements observed with error, or a combination of both.

**Value**

A numeric vector of predictions for all dimensions.

### Prediction functions in morphErr

There are three key differences between `predict.lme.morph()` and `predictblup()`.

- `predict.lme.morph()` only generates estimates for one dimension based on true values for other dimensions, whereas `predictblup()` can generate estimates from true values, observed values (i.e., subject to measurement error), or a combination of both.
- `predict.lme.morph()` can generate estimates for multiple individuals, whereas `predictblup()` only provides estimates for a single individual.
- `predict.lme.morph()` provides standard errors, but `predictblup()` does not.

### See Also

`predict.lme.morph()`

### Examples

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Estimates for the true dimension sizes of an individual with a
## known true value for dimension 2 of 130, and observed
## measurements subject to error from two photographs. The first
## photograph has # observed measurements of 300 and 135 for
## dimensions 1 and 2, respectively, while the second photograph
## has observed # measurements of 290 and 140, respectively.
## Dimension 3 is not observed in any photograph.
predictblup(fit, true = c(NA, 130, NA), obs = rbind(c(300, 135, NA),
                                                    c(290, 140, NA)))
```

---

sim.measurements

*Simulate Morphometric Measurements*

---

### Description

Simulates morphometric data from a photogrammetry survey, with observations subject to measurement error, under the model described by Stevenson, Smit, and Setyawan (2026).

### Usage

```
sim.measurements(
  n.animals = NULL,
  n.photos = NULL,
  data = NULL,
  mus,
  sigmas,
  rhos,
  psis,
  phis,
```

```

    log.transform = FALSE
  )

```

### Arguments

|                            |                                                                                                                                                                                                                                                                                          |
|----------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>n.animals</code>     | Integer. The number of animals in the sample.                                                                                                                                                                                                                                            |
| <code>n.photos</code>      | Integer vector. If there are <code>n.animals</code> elements, each one specifies the number of photos for an individual. If there is one element, then that number of photos is used for all animals.                                                                                    |
| <code>data</code>          | A data frame with columns <code>animal.id</code> , <code>photo.id</code> , and <code>dim</code> , provided instead of <code>n.animals</code> and <code>n.photos</code> . This provides the user with full control over which dimensions are measured in which photos from which animals. |
| <code>mus</code>           | A vector with an element for each dimension, providing the means of the true dimension sizes in the population.                                                                                                                                                                          |
| <code>sigmas</code>        | A vector with an element for each dimension, providing the standard deviations for true dimension sizes in the population.                                                                                                                                                               |
| <code>rhos</code>          | A vector, with one element for each pair of dimensions, providing the pairwise correlations between true dimension sizes in the population. See 'Details' for the correct order for the correlations.                                                                                    |
| <code>psis</code>          | A vector with an element for each dimension, providing the standard deviations of measurement errors for the dimensions.                                                                                                                                                                 |
| <code>phis</code>          | A vector, with one element for each pair of dimensions, providing the pairwise correlations between measurement errors for the dimensions. See 'Details' for the correct order for the correlations.                                                                                     |
| <code>log.transform</code> | Logical. If TRUE, the parameters are considered to correspond to a model where the response was log-transformed. The data frame returned by this function will contain the back-transformed measurements.                                                                                |

### Details

For arguments `rhos` and `phis`, the elements must be ordered so that all  $m - 1$  correlations involving dimension 1 appear first in ascending numerical order, followed by all remaining  $m - 2$  correlations involving dimension 2, and so on, where  $\text{eqn}\{m\}$  is the number of dimensions.

For example, if  $m = 4$ , then the first three elements are the correlations between dimension 1 and dimensions 2, 3, and 4, respectively. The following two elements are correlations between dimension 2 and dimensions 3 and 4, respectively. The final element is the correlation between dimension 3 and 4.

### Value

A data frame with four columns:

|                          |                                                                                                                                   |
|--------------------------|-----------------------------------------------------------------------------------------------------------------------------------|
| <code>animal.id</code>   | An individual identification number. Rows with the same <code>animal.id</code> correspond to measurements of the same individual. |
| <code>photo.id</code>    | A photo identification number. Rows with the same <code>photo.id</code> correspond to measurements taken from the same image.     |
| <code>dim</code>         | An integer indicating the dimension the measurement is for.                                                                       |
| <code>measurement</code> | The observed measurement value.                                                                                                   |

## References

Stevenson, B. C., Smit, E., and Setyawan, E. (2026) Measurement error models for morphometric data. *Annals of Applied Statistics*, **20**: 945–962.

## See Also

`sim.morph()` to conduct a simulation study by simulating multiple data sets and fitting a model to each one.

## Examples

```
## Simulating data for ten animals, with two photos each, measuring
## three dimensions.
sim.data <- sim.measurements(n.animals = 10, n.photos = 2,
                             mus = c(315, 150, 100),
                             sigmas = c(25, 15, 10),
                             rhos = c(0.85, 0.80, 0.75),
                             psis = c(10, 6, 4),
                             phis = c(0.5, 0.4, 0.3))

head(sim.data)

## Simulating data for two animals, with different numbers of
## photos for each, and different measurements available from
## different photos.
data <- data.frame(animal.id = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2, 2),
                   photo.id = c(1, 1, 2, 2, 2, 1, 2, 3, 3, 4, 4),
                   dim = c(1, 3, 1, 2, 3, 1, 1, 1, 3, 2, 3))
sim.data <- sim.measurements(data = data,
                             mus = c(315, 150, 100),
                             sigmas = c(25, 15, 10),
                             rhos = c(0.85, 0.80, 0.75),
                             psis = c(10, 6, 4),
                             phis = c(0.5, 0.4, 0.3))

sim.data
```

---

sim.morph

---

*Conduct a Simulation Study for Morphometric Models*


---

## Description

Simulates multiple datasets and fits a model to each one.

## Usage

```
sim.morph(
  n.sims,
  n.animals = NULL,
  n.photos = NULL,
```

```

data = NULL,
mus,
sigmas,
rhos,
psis,
phis,
log.transform = FALSE,
method = "REML",
control = list(maxIter = 1e+05, msMaxIter = 1e+05),
progressbar = TRUE,
n.cores = 1
)

```

### Arguments

|               |                                                                                                                                                                                                                     |
|---------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| n.sims        | Integer. The number of data sets to simulate.                                                                                                                                                                       |
| n.animals     | Integer. The number of animals in the sample.                                                                                                                                                                       |
| n.photos      | Integer vector. If there are n.animals elements, each one specifies the number of photos for an individual. If there is one element, then that number of photos is used for all animals.                            |
| data          | A data frame with columns animal.id, photo.id, and dim, provided instead of n.animals and n.photos. This provides the user with full control over which dimensions are measured in which photos from which animals. |
| mus           | A vector with an element for each dimension, providing the means of the true dimension sizes in the population.                                                                                                     |
| sigmas        | A vector with an element for each dimension, providing the standard deviations for true dimension sizes in the population.                                                                                          |
| rhos          | A vector, with one element for each pair of dimensions, providing the pairwise correlations between true dimension sizes in the population. See 'Details' for the correct order for the correlations.               |
| psis          | A vector with an element for each dimension, providing the standard deviations of measurement errors for the dimensions.                                                                                            |
| phis          | A vector, with one element for each pair of dimensions, providing the pairwise correlations between measurement errors for the dimensions. See 'Details' for the correct order for the correlations.                |
| log.transform | Logical. If TRUE, the parameters are considered to correspond to a model where the response was log-transformed. The data frame returned by this function will contain the back-transformed measurements.           |
| method        | A character string indicating the objective function used to fit the model. Either "ML" for maximum likelihood or "REML" for restricted maximum likelihood.                                                         |
| control       | A list of control values for the estimation algorithm to replace the default values returned by the function <code>nlme::lmeControl()</code> .                                                                      |
| progressbar   | Logical. If TRUE a progress bar will be displayed.                                                                                                                                                                  |
| n.cores       | Integer. The number of cores for parallel processing.                                                                                                                                                               |

**Value**

An object of class `lme.morph.sim`. The best way to extract results from this object is to use `extract.sim.morph()`. See the example below.

**See Also**

`extract.sim.morph()` to extract results from the object returned by this function.

**Examples**

```
## Running a small simulation study.
sim.fits <- sim.morph(n.sims = 5,
  n.animals = 10,
  n.photos = 3,
  mus = c(315, 150, 100),
  sigmas = c(25, 15, 10),
  rhos = c(0.85, 0.80, 0.75),
  psis = c(10, 6, 4),
  phis = c(0.5, 0.4, 0.3),
  method = "REML",
  progressbar = FALSE,
  n.cores = 1)
## Extracting p-values from tests for isometry from each model
## fit.
iso.p <- function(x) summary(x, type = "isometric-pca")[, 3]
extract.sim.morph(sim.fits, FUN = iso.p)
```

---

summary.lme.morph

*Summarise Morphometric Model Fits*


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**Description**

An S3 method that creates summaries of fitted morphometric models. This function can provide different types of summaries including parameter estimates, beta coefficients, and tests for isometry.

**Usage**

```
## S3 method for class 'lme.morph'
summary(object, ..., type = "pars", y.dim, x.dim, level = 0.95)
```

**Arguments**

|                     |                                                                                                                                                                         |
|---------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>object</code> | An object of class <code>lme.morph</code> , returned by <code>fit.morph()</code> .                                                                                      |
| <code>...</code>    | Other parameters (for S3 generic compatibility).                                                                                                                        |
| <code>type</code>   | A character string specifying type of summary. Either "pars" (the default), "betas" "betas-lm", "betas-pca", or "isometric-pca". See 'Details' for further information. |

|       |                                                                                                               |
|-------|---------------------------------------------------------------------------------------------------------------|
| y.dim | An integer specifying the response dimension for when type is "betas", "betas-lm", or "betas-pca".            |
| x.dim | An integer vector specifying the explanatory dimensions for when type is "betas", "betas-lm", or "betas-pca". |
| level | The confidence level for any interval estimates.                                                              |

## Details

The following summaries are available with this method, controlled by the type argument:

type = "pars" Estimates and standard errors for the model parameters, including the vectors  $\mu$  for the means of the true dimension sizes,  $\sigma$  for the standard deviations for true dimension sizes,  $\rho$  for the correlations between true dimension sizes,  $\psi$  for the standard deviations in measurement errors for the dimensions, and  $\phi$  for the correlations between measurement errors for all pairs of dimensions.

type = "betas" or type = "betas-lm" Estimates and standard errors for coefficients of a linear combination that provides the expected value of one dimension (specified by y.dim) using any subset of the remaining dimensions (specified in the vector x.dim).

type = "betas-pca" An estimated intercept and slope for the reduced major axis (or principal component axis) summarising the relationship between the true values of dimensions specified by y.dim and x.dim.

type = "isometric-pca" Results for tests of the null hypotheses of isometric relationships between all pairs of dimensions. The p-values are obtained using normal approximations for the test statistics.

For models with log.transform = FALSE, the test statistic to test for isometric growth between dimensions  $p$  and  $q$  is  $\mu_p\sigma_q - \mu_q\sigma_p$ , which is equal to 0 under the null hypothesis.

For models with log.transform = TRUE, the test statistic is the slope for the reduced major axis (or principal component axis) summarising the relationship between the two dimensions, which is equal to 1 under the null hypothesis.

## Value

A matrix or data frame containing the requested summary.

## Examples

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Parameter estimates and standard errors.
summary(fit)
## Estimated coefficients for the linear combination that provides
## the expected value of the first dimension from only the second.
summary(fit, type = "betas-lm", y.dim = 1, x.dim = 2)
## Estimated coefficients for the linear combination that provides
## the expected value of the second dimension from both the first
## and third.
summary(fit, type = "betas-lm", y.dim = 2, x.dim = c(1, 3))
## Estimated intercept and slope for the reduced major axis (or
## principal component axis) summarising the relationship between
```

```
## the first and second dimensions.
summary(fit, type = "betas-pca", y.dim = 1, x.dim = 2)
## Tests for isometry between all pairs of dimensions.
summary(fit, type = "isometric-pca")
```

vcov.lme.morph

*Extract Variance-Covariance Matrix from Morphometric Model***Description**

An S3 method for extracting both parameter estimates and their variance-covariance matrix from a fitted morphometric model.

**Usage**

```
## S3 method for class 'lme.morph'
vcov(object, ...)
```

**Arguments**

|        |                                                  |
|--------|--------------------------------------------------|
| object | A fitted model of class "lme.morph"              |
| ...    | Other parameters (for S3 generic compatibility). |

**Value**

A list containing:

|        |                                     |
|--------|-------------------------------------|
| est    | Named vector of parameter estimates |
| varcov | Variance-covariance matrix          |

**Examples**

```
## Fitting model to manta ray data.
fit <- fit.morph(manta)
## Extracting variance-covariance matrix.
vcov(fit)
```

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