Package 'novelforestSG'

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Title Data for Lai et al. (2021) Appl. Veg. Sci.

Version 1.2.1

Description The dataset and model used in Lai et al. (2021)
Decoupled responses of native and exotic tree diversities to
distance from old-growth forest and soil phosphorous in
novel secondary forests. Applied Vegetation Science, 24, e12548.

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URL https://hrlai.github.io/novelforestSG/,

https://github.com/hrlai/novelforestSG,

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BugReports https://github.com/hrlai/novelforestSG/issues

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

Depends R (>= 2.10)

Suggests brms (>= 2.10.0), testthat

NeedsCompilation no

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R topics documented:

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backtransform   *Backtransform Scaled Predictors*

Description

Backtransform scaled predictors in `novelforest_data` to their original scales. This is done by first back-scaling to the log-scale, and then backtranformed to the original scale (the predictors were log-transformed as described in Lai et al. 2021).

Usage

```
backtransform(data = novelforest_data)
```

Arguments

data   Defaults to the data object in `novelforest`, but could also be another `data.frame` with the same predictor names, should you wish to (back)scale and (back)center using the same means and standard deviations for any reason.

Value

A backtransformed `data.frame` with predictors at their original scales.

References

Lai, H.R., Tan, G.S.Y., Neo, L., Kee, C.Y., Yee, A.T.K., Tan, H.T.W. and Chong, K.Y. (2021) Decoupled responses of native and exotic tree diversities to distance from old-growth forest and soil phosphorous in novel secondary forests. *Applied Vegetation Science*, 24, e12548. doi: 10.1111/ avsc.12548

Examples

```
# argument could be left blank
dat <- backtransform()
head(dat)
```

---

download_model *Download Model Fitted to the* novelforest *Data*

Description

Download the brms model fitted to the novelforest data (Lai et al. 2021). The model object is too large (16.5 MB) to be included with the package, so the function downloads the model from the development GitHub website. The generalised linear mixed-effect model was fitted via brms::brm so this package is recommended to properly view the model object.

Usage

```
download_model(save_to = NULL)
```

Arguments

save_to   Path and name of the file where the R object is saved to. Defaults to NULL, which does not save the model object locally.

Value

A brms model output of class brmsfit, which is a list containing the input data and other slots that store the model components.

References

Lai, H.R., Tan, G.S.Y., Neo, L., Kee, C.Y., Yee, A.T.K., Tan, H.T.W. and Chong, K.Y. (2021) Decoupled responses of native and exotic tree diversities to distance from old-growth forest and soil phosphorous in novel secondary forests. *Applied Vegetation Science*, 24, e12548. doi: 10.1111/avsc.12548

See Also

brms::brmsfit, brms::brm

Examples

```
novelforest_model <- download_model()

# library(brms)  # recommended
summary(novelforest_model)
```

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novelforestSG	*novelforestSG*

Description

The dataset and model used in Lai et al. (2021) Decoupled responses of native and exotic tree diversities to distance from old-growth forest and soil phosphorous in novel secondary forests. *Applied Vegetation Science*.

Details

The main component of `novelforestSG` is the dataset, which can be accessed with `novelforest_data`. See `?novelforest_data` for more details.

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References

Lai, H.R., Tan, G.S.Y., Neo, L., Kee, C.Y., Yee, A.T.K., Tan, H.T.W. and Chong, K.Y. (2021) Decoupled responses of native and exotic tree diversities to distance from old-growth forest and soil phosphorous in novel secondary forests. *Applied Vegetation Science*, 24, e12548. doi: 10.1111/avsc.12548

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novelforest_data	*Novel Forest Dataset*

Description

The dataset used in Lai et al. (2021), who examined the diversity–environment relationships of native and exotic species in two types of post-cultivation novel secondary forests in Singapore.

Usage

```
novelforest_data
```

Format

A `data.frame` containing the following response variables:

SD_N_0 first-order native taxonomic diversity, i.e., species richness

SD_N_2 second-order native taxonomic diversity, i.e., inverse Simpson index

SD_E_0 first-order exotic taxonomic diversity

SD_E_2 second-order exotic taxonomic diversity

FD_N_0 first-order native functional diversity

FD_N_2 second-order native functional diversity

FD_E_0 first-order exotic functional diversity

FD_E_2 second-order exotic functional diversity,

and the following explanatory variables (and measurement units if you backtransform them using `backtransform`):

dist Distance to old-growth forests (m)

size Patch area (km^2)

nitrogen Total soil nitrogen (mg/kg)

phosphorous Total extractable soil phosphorous (mg/kg)

potassium Total extractable soil potassium (mg/kg)

patch Forest patch ID

Note that all explanatory variables were log-transformed and standardised to zero mean and unit standard deviations. Use `backtransform` to obtain the variables in their original scales. See Lai et al. (2021) for more details on model building and data collection.

References

Lai, H.R., Tan, G.S.Y., Neo, L., Kee, C.Y., Yee, A.T.K., Tan, H.T.W. and Chong, K.Y. (2021) Decoupled responses of native and exotic tree diversities to distance from old-growth forest and soil phosphorous in novel secondary forests. *Applied Vegetation Science*, 24, e12548. doi: 10.1111/avsc.12548

See Also

backtransform

Examples

```
# To access the dataset
head(novelforest_data)
```

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