Package ‘novelforestSG’

July 22, 2025

Title Dataset from the Novel Forests of Singapore

Version 2.1.0

Description The raw 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`

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

Encoding UTF-8

LazyData true

RoxygenNote 7.3.0

Depends R (>= 3.5.0)

Suggests brms (>= 2.10.0), testthat

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-01-15 23:30:03 UTC

Contents

`download_model` *Download Model Fitted to* `novelforest_data`

Description

Download the `brms` model fitted to `novelforest_data` (Lai et al. 2021). The model object is too large (16.5 MB) to be included with the package, so this function downloads the model from the developmental GitHub website. The generalised linear mixed-effect model was fitted via `brms::brm` so this package is recommended to make full use of 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.

Notably, the `data` slot contains a `data.frame` with 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, brms::brmsfit, brms::brm

Examples

```
## Not run:
novelforest_model <- download_model()

# library(brms)  # recommended
summary(novelforest_model)

# to obtain input data
novelforest_model$data

## End(Not run)
```

`novelforestSG` *novelforestSG*

Description

Forest community data used in Lai et al. (2021); also comprised part of the raw data used in Neo et al. (2017).

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

Neo, L., Yee, A. T. K., Chong, K. Y., Kee, C. Y. and Tan, H. T. W. (2017). Vascular plant species richness and composition in two types of post-cultivation tropical secondary forest. *Applied Vegetation Science*, 20, 692-701. doi:10.1111/avsc.12322

`novelforest_data` *Novel Forest Raw Dataset*

Description

The raw data used in Lai et al. (2021) and Neo et al. (2017).

Usage

```
novelforest_data
```

Format

A list of four `data.frame`:

- **trees** a table of woody stems measured, with `treeID` as the unique identifier
- **pres** a table of presences of vascular plant species in each plot
- **plots** a table of the environmental measurements or landscape characteristics for each plot, with `plotID` as the unique identifier
- **patches** a table of the patches and their characteristics, with `patchID` as the unique identifier

With the following variables:

- **patch** Forest patch identifier
- **plot** Plot identifier
- **UID** Stem identifier
- **species** Species name following Chong et al. (2011)
- **stem** Indicator column denoting whether a stem is the main trunk (=1) of an individual tree, or otherwise (=0)

dbh_2011 Diameter-at-breast-height (cm) measured in year 2011.

canopy % Canopy cover

litter Leaf litter depth / cm

nitrogen Soil total Nitrogen /g^-1 kg^-1

phosphorous Soil extractable Phosphorous /mg^-1 kg^-1

potassium Soil extractable Potassium /mg^-1 kg^-1

dist Distance to nearest old-growth forest /km

type Type of forest; `ABA`: abandoned-land forest type, `WAS`: waste-woodland forest type

size Size (i.e., area) of forest patch /ha

See Lai et al. (2021) or Neo et al. (2017) for more detail on data collection.

References

Chong, K. Y., Tan, H. T. W. and Corlett, R. T. (2011). A summary of the total vascular plant flora of Singapore. *Gardens' Bulletin Singapore*, 63, 197-204.

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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Examples

```
# Tree community matrix (by stem counts)
comm_stem <- xtabs(~ plot + species, data = novelforest_data$trees)
comm_stem[1:10, 1:4]

# Species occurrence matrix (of all vascular plants)
comm_all <- xtabs(~ plot + species, data = novelforest_data$pres)
comm_all[1:10, 1:4]

# Reproduce (part of) the summary table (Appendix S2) in the supplementary
# material of Neo et al. (2017)
with(novelforest_data,
    apply(plots[3:8], 2,
        function(x) tapply(x, plots$patch, mean, na.rm = TRUE))
    )
```

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