

fit_hmsc_model.R

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fit_hmsc_model	<i>Fit HMSC Model</i>
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Description

Fits a Hierarchical Modelling of Species Communities (HMSC) model to community and abiotic data.

Usage

```
fit_hmsc_model(  
  data_community = NULL,  
  data_abiotic = NULL,  
  error_family = c("normal", "binomial"),  
  fit_model = TRUE,  
  n_chains = 20,  
  n_samples = 10000,  
  n_thin = 5,  
  n_transient = 2500,  
  n_parallel = 20,  
  n_samples_verbose = 500  
)
```

Arguments

- | | |
|----------------|--|
| data_community | A data frame containing community data. Must have the same row names as 'data_abiotic'. |
| data_abiotic | A data frame containing abiotic data. Must have the same row names as 'data_community'. |
| error_family | A character string specifying the error family. Options are "normal" or "binomial" (default: "normal"). |
| fit_model | Logical. If 'TRUE', the model is fitted; otherwise, only the model object is returned (default: 'TRUE'). |

<code>n_chains</code>	Number of MCMC chains (default: 20).
<code>n_samples</code>	Number of MCMC samples (default: 10,000).
<code>n_thin</code>	Thinning interval for MCMC samples (default: 5).
<code>n_transient</code>	Number of transient iterations (default: 2,500).
<code>n_parallel</code>	Number of parallel chains (default: 20).
<code>n_samples_verbose</code>	Verbosity interval for MCMC sampling (default: 500).

Details

Validates input data, ensures compatibility between community and abiotic data, and fits an HMSC model using the specified parameters. If `'error_family'` is "binomial", the community data is converted to binary presence/absence data, and the error family is set to "probit".

Value

If `'fit_model'` is `'TRUE'`, returns a fitted HMSC model object. Otherwise, returns an unfitted HMSC model object.

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