

# make\_hmsc\_model.R

May 15, 2025

## Contents

make_hmsc_model . . . . .	1
---------------------------	---

<b>Index</b>	<b>2</b>
--------------	----------

---

make_hmsc_model	<i>Make HMSC Model</i>
-----------------	------------------------

---

## Description

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

## Usage

```
make_hmsc_model(  
  data_to_fit = NULL,  
  sel_formula = NULL,  
  random_structure = NULL,  
  error_family = c("normal", "binomial")  
)
```

## Arguments

data_to_fit	A list containing the community and abiotic data to fit the model.
random_structure	A list containing the random structure for the model, including the study design and random levels.
error_family	A character string specifying the error family. Options are "normal" or "binomial" (default: "normal").

## Details

If 'error\_family' is "binomial", the community data is converted to binary presence/absence data, and the error family is set to "probit".

## Value

returns an unfitted HMSC model object.

# Index

`make_hmsc_model`, [1](#)