

# Introduction to FestR

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This package is based on the [MCMCglmm package](#) and runs a MCMCglmm analysis on multiple trees using the [MulTree package](#).

## Installation

To install FestR its dependency [MulTree package](#) must first be installed directly from GitHub using the following:

```
if(!require(devtools)) install.packages("devtools")
install_github("TGuillaume/mulTree", ref = "master")
```

Following this you can then install FestR directly from GitHub using the following:

```
install_github("healyke/FestR", ref = "master")
```

And load in the data

```
library(mulTree)
library(FestR)
```

## Read in the data

```
#read in the data
mydata<-read.csv(file=system.file("extdata", "FestR_data.csv", package = "FestR"),
  header=T, stringsAsFactors = F)

# re-order it into species
mydata <- mydata[order(mydata$species),]

#read in the phylogentic information
#first the mammal trees
mammal_trees <- read.tree(system.file("extdata", "3firstFritzTrees.tre", package = "FestR"))
#than the bird trees
bird_trees <- read.tree(system.file("extdata", "3firstJetzTrees.tre", package = "FestR"))

#combine them together using the tree.bind function from the mulTree package
combined_trees<-tree.bind(x = mammal_trees, y = bird_trees, sample = 2, root.age = 250)
```

## Testing the new data: `set.tef.est`

In order to estimate a trophic enrichment factor for a new species we need to check that the species is already present in our phylogeny and check what data is available for the new species.

This data set.tef.est checks for includes:

tissue type (“blood”, “claws”, “collagen”, “feather”, “hair”, “kidney”, “liver”, “milk”, “muscle”),

habitat (“terrestrial”, “marine”),

diet.type (“carnivore”, “herbivore”, “omnivore”, “pellet”),

and the isotopic ratios of the food sources for carbon

(source.iso.13C)

and nitrogen

(source.iso.15N).

```
#####function that checks the dat for some species we want to estimate TEF for
new.data.test <- setTefEst(species = "Meles_meles",
                           habitat = "terrestrial",
                           taxonomic.class = "mammalia",
                           tissue = "blood",
                           diet.type = "omnivore",
                           source.iso.13C = c(-24.1),
                           source.iso.15N = c(7.0),
                           tree = combined_trees)
```

```
## Meles_meles present in phylogeny
```

If the species is not in the phylogeny already such as the Komodo dragon (*Varanus komodoensis*), or we are missing on of the values, in this case diet.type we get warning messages to indicate what is missing from our data.

```
## Varanus_komodoensis not present in phylogeny
```

Note that future veriosn of FestR will allow the analysis to be run with missing data for isotopic ratio, diet.type and habitat.

## Formating the new data: `tef.mul.clean`

We now need to format the data by combining both the isotpic data already avialbe within the package and the data from the new species and matching these species to the included phylogeny. We also include what isotope we want to estimate a trophic discrimination value for (either “carbon” or “nitrogen”).

```
## The following taxa were dropped from the analysis:
```

```
## Tachyglossus_aculeatus Zaglossus_bruijni Zaglossus_bartoni Ornithorhynchus_anatinus Anomalurus_beec
```