

# Analysis of arthropod communities in Hawaii using METE Theory

## Setup

```
library(meteR)
library(ggplot2)
library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
# load data
load("../data/arth.rda")

# create column for abundance, each row is an individual, therefore abundance = 1
arth$abundance <- 1

# create column for metabolic rates, assuming 3/4 scaling
arth$metabolic_rate <- arth$individual_biomass_g^0.75

# make sites factors with levels following chronosequence
arth$site <- factor(arth$site, levels = c("VO", "LA", "KH", "MO", "KA"))
```

## Calculate Deviation from METE

```
# holds deviation from METE
arth_meter <- group_by(arth, site, tree) |>
  summarise(llz = {
    arth_esf <- meteESF(spp = species_code,
                          abund = abundance,
                          power = metabolic_rate)

    arth_sad <- sad(arth_esf)
    logLikZ(arth_sad)$z
  }) |>
  ungroup()
```



Visualizing deviations from METE across chronosequence

### How do METE and the real data differ

Which one over-predicts rarity?

Comparing deviations from METE with potential explanatory variables

## Single island endemism

```
# hold data on proportion of endemics
arth_end <- group_by(arth, site, tree, species_binom) |>
  summarise(spp_end = any(endemic_status == "Endemic"),
            spp_abund = sum(abundance),
            spp_metab = sum(metabolic rate)) |>
```

```

ungroup() |>
group_by(site, tree) |>
summarise(spp_prop_end = mean(spp_end),
           ind_prop_end = sum(spp_end * spp_abund / sum(spp_abund)),
           met_prop_end = sum(spp_end * spp_metab / sum(spp_metab))) |>
ungroup()

```

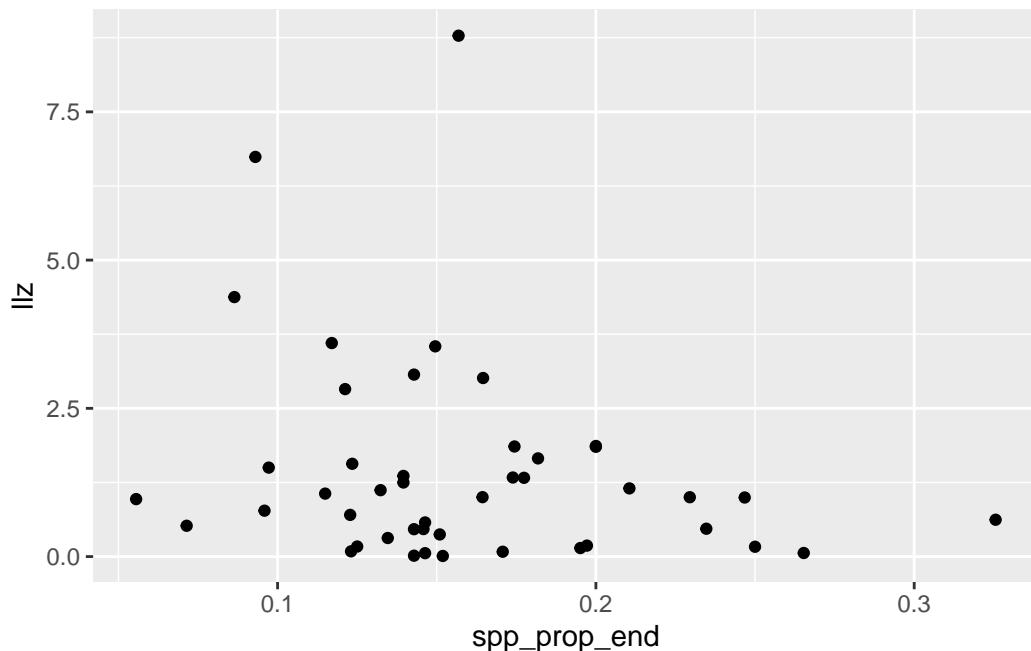
`summarise()` has grouped output by 'site', 'tree'. You can override using the `.`groups` argument.  
`summarise()` has grouped output by 'site'. You can override using the `.`groups` argument.

```
dat <- full_join(arth_meter, arth_end)
```

Joining with `by = join\_by(site, tree)`

```
ggplot(dat, aes(spp_prop_end, llz)) +
geom_point()
```

Don't know how to automatically pick scale for object of type <logLik>. Defaulting to continuous.



```
mean(unique(arth[, c("species_binom", "endemic_status")])[ , 2] == "Endemic")
```

```
[1] 0.1905537
```

```
arth[, c("species_binom", "endemic_status")] |>  
  unique() |>  
  select(2) |>  
  (function(y) y == "Endemic")() |>  
  mean()
```

```
[1] 0.1905537
```

```
arth_2_meter <- ungroup(arth_meter)  
arth_2_meter$site <- factor(arth_2_meter$site, levels = c("VO", "LA", "KH", "MO", "KA"))
```