An Introduction to MF.beta4 via Examples

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`MF.beta4` is an R package for measuring ecosystem multifunctionality and assessing BEF relationships. The measures are illustrated by using ecosystem function and biodiversity data collected in a total of 209 plots in six European countries (the FunDivEUROPE dataset). All data are available from the Dryad repository; see Ratcliffe et al. (2017b) and Scherer-Lorenzen et al. (2023) for details. The software was originally developed for the Beta4 project (Müller et al. 2022) on the effect of enhancing the beta diversity between forest patches on ecosystem multifunctionality and forest resilience across spatial scales.

Based on a framework of Hill-Chao numbers of orders q = 0, 1 and 2, `MF.beta4` features the following multifunctionality measures for a single and multiple ecosystems; see Chao et al. (2023) for pertinent methodology and decomposition theory.

(1) Multifunctionality measures in a single ecosystem:

`MF.beta4` computes a class of weighted multifunctionality measures for given function weights. Multifunctionality measures that correct for strong correlations between ecosystem functions to avoid redundancy are also provided.

(2) Multifunctionality measures in multiple ecosystems:

For given function weights, `MF.beta4` computes the gamma multifunctionality of pooled ecosystems, the within-ecosystem component (alpha multifunctionality) and the among-ecosystem component (beta multifunctionality). The correlation between functions can also be corrected for.

Based on biodiversity and function data from ecosystems, this package also provides graphics for assessing biodiversity-ecosystem functioning (BEF) relationships across scales.

How to cite

If you publish your work based on the results from the MF.beta4 package, you should make references to the following methodology paper and the R package.

Chao, A., Chiu, C. H., Hu, K. H., van der Plas, F., Cadotte, M. W., Mitesser, O., et al. (2023). Hill-Chao numbers in multifunctionality allows decomposing gamma multifunctionality into alpha and beta components. To appear in Ecology Letters.

Chao, A., Liu, C. Y., and Hu, K. H. (2023). MF.beta4 package: measuring ecosystem multifunctionality and assessing BEF relationships. Available from CRAN.

SOFTWARE NEEDED TO RUN MF.beta4 IN R

- Required: R
- Suggested: RStudio IDE

HOW TO RUN MF.beta4:

The `MF.beta4` package can be downloaded from CRAN or Github MF.beta4_github using the following commands. For a first-time installation, an additional visualization extension package (`ggplot2`) must be installed and loaded.

```
## install MF.beta4 package from CRAN
# install.packages("MF.beta4")

## install the latest version from github
install.packages('devtools')
library(devtools)
install_github("AnneChao/MF.beta4")

## import packages
library(MF.beta4)
```

This package includes four functions, as listed below with default arguments. See package manual for the detailed description of each argument.

- **function_normalization**: transforms ecosystem function data to values between 0 and 1; other variables remain unchanged.

```
function_normalization(data, fun_cols = 1:ncol(data), negative = NULL, by_group = NULL)
```

- **MF1_single**: computes multifunctionality measures of orders q = 0, 1 and 2 for given function weights in a single ecosystem separately for two cases: (i) correlations between functions are not corrected for, and (ii) correlations between functions are corrected for.

```
MF1_single(func_data, species_data = NULL, weight = 1, q = c(0, 1, 2))
```

- **MF2_multiple**: computes alpha, beta and gamma multifuctionality measures of orders q = 0, 1 and 2 for given function weights in multiple ecosystems separately for two cases (i) correlations between functions are not corrected for, and (ii) correlations between functions are corrected for.

```
MF2_multiple(func_data, species_data = NULL, weight = 1, q = c(0, 1, 2), by_group = NULL)
```

- **MFggplot**: provides the graphical BEF relationships based on the output obtained from the function `MF1_single` or `MF2_multiple`.

```
MFggplot(output, model = "LMM.both", by_group = NULL, caption = "slope")
```

Data input format

Ecosystem function data The FunDivEurope data are used here to demonstrate the use of the four functions; see Ratcliffe et al. (2017a, b) and Scherer-Lorenzen et al. (2023) for the original datasets. There are three datasets provided with the package: raw ecosystem function dataset (`forest_function_data_raw`), normalized function dataset (`forest_function_data_normalized`), and biodiversity dataset (`forest_biodiversity_data`). The first dataset includes the raw values of 26 ecosystem functions collected from 209 plots in six European countries, representing six major European forest types: boreal forest (Finland, 28 plots); hemi-boreal (Poland, 43 plots); temperate deciduous (Germany, 38 plots); mountainous deciduous (Romania, 28 plots); thermophilous deciduous (Italy, 36 plots); and Mediterranean mixed (Spain, 36 plots). Each plot is designated as an ecosystem in assessing BEF relationships. See Table 1 of Ratcliffe et al. (2017a) for a description of the 26 functions, and Ratcliffe et al. (2017a) and Scherer-Lorenzen et al. (2023) for data details of the original datasets.

In addition to row name (plot/ecosystem id) and column name (plot information and function names), the data in the file `forest_function_data_raw` are input as a data.frame with 209 plots (rows) and 32 columns. The first 5 columns show the relevant plot information, followed by 26 raw ecosystem functions (in consecutive columns from 6 to 31). An additional column "country" for each plot is added (as column 32) as a stratification/group variable because function normalization and relevant decomposition analyses will be performed within each country. For each missing value of functions in the original dataset, the mean of the given function within the country was imputed. Thus, the raw ecosystem function dataset provided with the package is slightly different from the original one.

Run the following code for the data `forest_function_data_raw` to view the first ten rows and five columns (columns 1:3, 6 and 7); columns 6 and 7 show respectively the first two raw ecosystem functions (earthworm_biomass and fine_woody_debris) :

```r
data("forest_function_data_raw")
head(cbind(forest_function_data_raw[1:3], round(forest_function_data_raw[6:7], 3)), 10)
```

```
#>       plotid target_species_richness composition earthworm_biomass fine_woody_debris
#> FIN01  FIN01                       2   Piab.Pisy             0.000               171
#> FIN02  FIN02                       2     Be.Piab             0.465               110
#> FIN03  FIN03                       2     Be.Piab             0.626                81
#> FIN04  FIN04                       2     Be.Piab             0.000                82
#> FIN05  FIN05                       2     Be.Pisy             0.928                38
#> FIN06  FIN06                       1        Piab             0.000                75
#> FIN07  FIN07                       1          Be            49.672                44
#> FIN08  FIN08                       1          Be            28.013                38
#> FIN09  FIN09                       1        Pisy             0.204                65
#> FIN10  FIN10                       1        Piab             0.000               136
```

To meaningfully quantify multifunctionality in a ecosystem based on multiple functions, all function values should be first normalized to the range [0, 1]. Proper normalization can be performed by using `function_normalization` provided in the package. In the FunDivEUROPE data, the forests in the six countries represent different ecosystems, all functions were thus normalized within a country, by specifying the argument `by_group = "country"`. Because different transformations are applied to positive and negative functionality, it is required to specify negative functionality in the argument `"negative"`. In the raw function dataset, there are 26 ecosystem functions (in consecutive columns from 6 to 31). Among them, two are negative functionality: `"soil_cn_ff_10"` and `"wue"`, and others are positive functionality. Run the following code to view the first ten rows and five columns (columns 1:3, 6 and 7); columns 6 and 7 show respectively the normalized values of the first two ecosystem functions (earthworm_biomass and fine_woody_debris):

```
data("forest_function_data_raw")
normalized_forest_function_data <- function_normalization(data = forest_function_data_raw,
                    fun_cols = 6:31, negative = c("soil_cn_ff_10","wue"), by_group = "country")
head(cbind(normalized_forest_function_data[1:3], round(normalized_forest_function_data[6:7], 3)), 10)
```

```
#>       plotid target_species_richness composition earthworm_biomass fine_woody_debris
#> FIN01  FIN01                       2   Piab.Pisy             0.000             0.416
#> FIN02  FIN02                       2     Be.Piab             0.009             0.238
#> FIN03  FIN03                       2     Be.Piab             0.013             0.152
#> FIN04  FIN04                       2     Be.Piab             0.000             0.155
#> FIN05  FIN05                       2     Be.Pisy             0.019             0.026
#> FIN06  FIN06                       1        Piab             0.000             0.135
#> FIN07  FIN07                       1          Be             1.000             0.044
#> FIN08  FIN08                       1          Be             0.564             0.026
#> FIN09  FIN09                       1        Pisy             0.004             0.106
#> FIN10  FIN10                       1        Piab             0.000             0.314
```

This normalized dataset is exactly the same as the dataset `forest_function_data_normalized` provide with the package.

Biodiversity data The `forest_biodiversity_data` consist of three columns: the "plotID" column includes the name of ecosystems/plots, the "species" column includes species names, and the "abundance" column includes the corresponding species abundance (basal area as a proxy of species abundance),in addition to row and column names; see Scherer-Lorenzen et al. (2023) for the original data. Because missing values of "basal area" in the original dataset were imputed by the mean of the same species within the country, and basal areas were combined for two species (Betula pendula and Betula pubescens), the dataset provided with the package is slightly different from the original dataset.

Run the following code to view the first ten rows of the biodiversity data:

```
data("forest_biodiversity_data")
head(forest_biodiversity_data,10)
```

```
#> # A tibble: 10 x 3
#> # Groups:   plotID [5]
#>    plotID species          abundance
#>    <chr>  <chr>                <dbl>
#>  1 FIN01  Picea.abies          1.84
#>  2 FIN01  Pinus.sylvestris     0.535
#>  3 FIN02  Betula.pendula       1.18
#>  4 FIN02  Picea.abies          0.408
#>  5 FIN03  Betula.pendula       1.09
#>  6 FIN03  Picea.abies          0.215
#>  7 FIN04  Betula.pendula       0.662
#>  8 FIN04  Picea.abies          1.14
#>  9 FIN05  Betula.pendula       0.423
#> 10 FIN05  Pinus.sylvestris     1.25
```

Computing multifunctionality in a single ecosystem

Based on normalized function data, `MF1_single()` computes multifunctionality measures of orders q = 0, 1 and 2 for given function weights in a single ecosystem separately for two cases: (i) correlations between functions are not corrected for, and (ii) correlations between functions are corrected for.

When `species_data = NULL` (i.e., biodiversity data are not provided), `MF1_single()` only computes multifunctionality measures of orders q = 0, 1 and 2 for each plot. When biodiversity data are specified (`species_data = forest_biodiversity_data`), tree species diversity values for q = 0, 1 and 2 are also computed.

Run the following code to view the first ten rows of the output:

```
data("forest_function_data_normalized")
data("forest_biodiversity_data")
output1 <- MF1_single(func_data = forest_function_data_normalized[,6:31],weight = 1,
           species_data = forest_biodiversity_data)
```

```
#>    plotID             Type Order.q   qMF Species.diversity
#> 1   FIN01 corr_uncorrected   q = 0 10.71              2.00
#> 2   FIN01 corr_uncorrected   q = 1 10.03              1.70
#> 3   FIN01 corr_uncorrected   q = 2  9.58              1.53
#> 4   FIN01   corr_corrected   q = 0 10.35              2.00
#> 5   FIN01   corr_corrected   q = 1  9.70              1.70
#> 6   FIN01   corr_corrected   q = 2  9.28              1.53
#> 7   FIN02 corr_uncorrected   q = 0  9.32              2.00
#> 8   FIN02 corr_uncorrected   q = 1  8.36              1.77
#> 9   FIN02 corr_uncorrected   q = 2  7.64              1.62
#> 10  FIN02   corr_corrected   q = 0  9.02              2.00
```

The above output includes the ID of plot (`plotID`), `Type` (corr_uncorrected and corr_corrected), the diversity order (`Order.q`), the multifunctionality measure of order q (`qMF`) and tree species diversity (`Species.diversity`).

Computing alpha, beta and gamma multifunctionality for any pair of plots within a country

`MF2_multiple()` computes alpha, beta and gamma multifunctionality measures of orders q = 0, 1 and 2 for given function weights in multiple ecosystems separately for two cases: (i) correlations between functions are not corrected for, and (ii) correlations between functions are corrected for. The decomposition of mltifunctionality measure of order q is based on all pairs of plots separately within each country. The alpha scale refers to individual plots, whereas the gamma scale refers to the two collective plots.

When `species_data = NULL` (i.e., biodiversity data are not provided), `MF2_multiple` computes alpha, beta, and gamma multifunctionality values for q = 0, 1 and 2 for all pairs of plots within each country. When biodiversity data are specified (`species_data = forest_biodiversity_data`), tree species diversity values for q = 0, 1 and 2 are also computed.

Due to sparse data in Finland (with richness levels of only one or two species in 90% of plots), data from Finland are excluded from following computation. Run the following code to view the first ten rows of the output:

```
data("forest_function_data_normalized")
data("forest_biodiversity_data")
forest_function_data_normalized <- forest_function_data_normalized %>% filter(country != "FIN")
forest_biodiversity_data <- forest_biodiversity_data[-(1:48),]
output2 = MF2_multiple(func_data = forest_function_data_normalized[,6:32],
                      species_data = forest_biodiversity_data,
                      weight = 1,
                      by_group = "country")
```

```
#>              plotID country Order.q             Type Scale  qMF Species.diversity
#> 1  GER01 vs. GER02     GER   q = 0 corr_uncorrected Gamma 9.26             1.000
#> 2  GER01 vs. GER02     GER   q = 0 corr_uncorrected Alpha 9.26             1.000
#> 3  GER01 vs. GER02     GER   q = 0 corr_uncorrected  Beta 1.00             1.000
#> 4  GER01 vs. GER02     GER   q = 0   corr_corrected Gamma 8.98             1.000
#> 5  GER01 vs. GER02     GER   q = 0   corr_corrected Alpha 8.98             1.000
#> 6  GER01 vs. GER02     GER   q = 0   corr_corrected  Beta 1.00             1.000
#> 7  GER01 vs. GER02     GER   q = 1 corr_uncorrected Gamma 7.95             1.000
#> 8  GER01 vs. GER02     GER   q = 1 corr_uncorrected Alpha 7.84             0.999
#> 9  GER01 vs. GER02     GER   q = 1 corr_uncorrected  Beta 1.01             1.001
#> 10 GER01 vs. GER02     GER   q = 1   corr_corrected Gamma 7.77             1.000
```

The above output includes the combinations of two plots (`plotID`), `Country` of the two plots, `Type` (corr_uncorrected or corr_corrected), `Scale` (gamma, alpha or beta), the diversity order (`Order.q`), multifunctionality value of order q (`qMF`) and the corresponding gamma/alpha/beta species diversity (`Species.diversity`).

NOTE: Because the total number of pair plots is huge, it is very time consuming to obtain the numerical output and graphical displays from running the above code. Users can simply select part of the data to quickly view/obtain the output. See later part for a simple example based on only 18 plots from Germany and Italy.

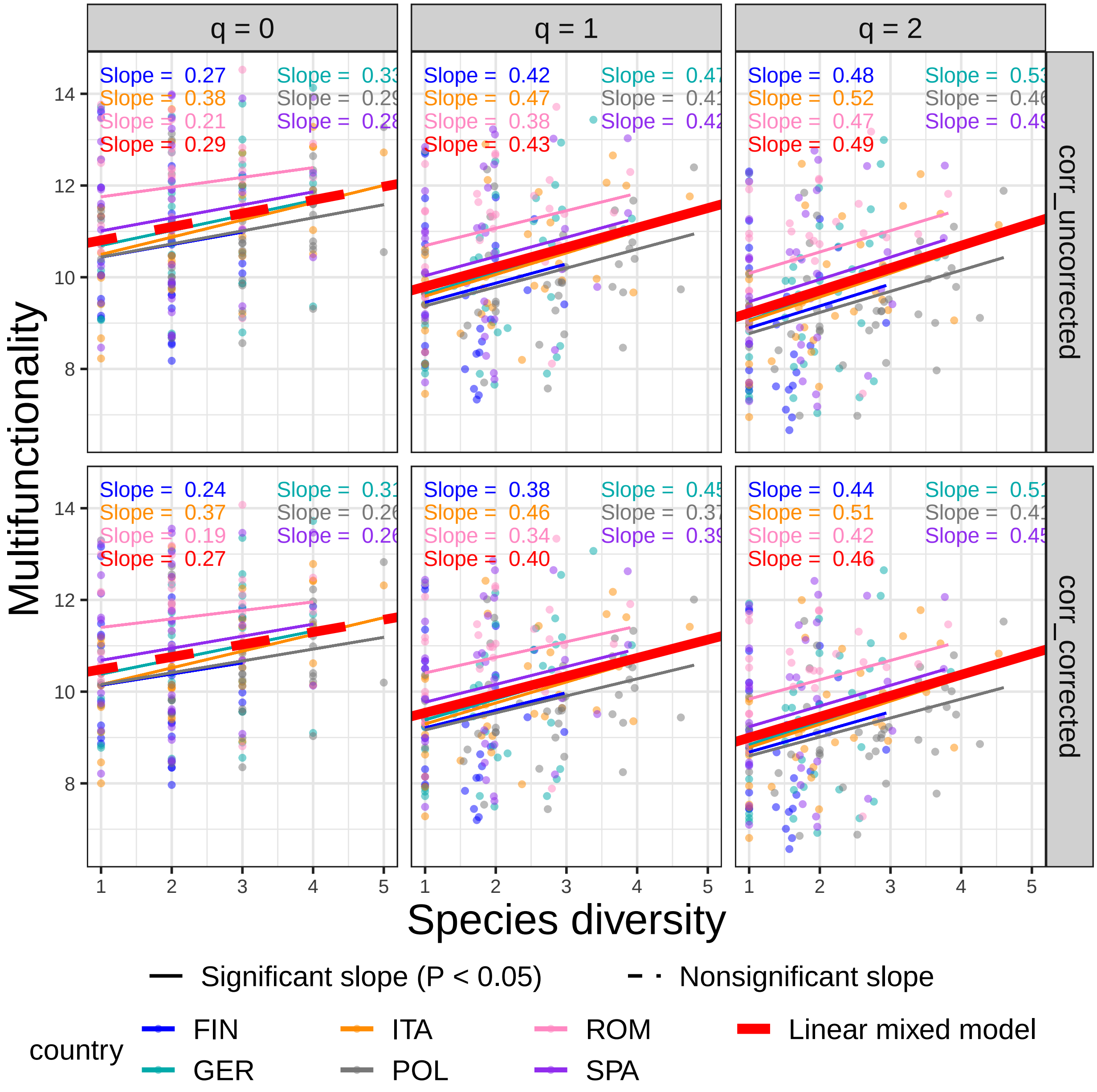
Assessing BEF Relationships by MFggplot()

Function `MFggplot()` provides the graphical BEF relationships based on the output from the function `MF1_single` or `MF2_multiple`.

Within-plot BEF relationship For an MF1_single object of given individual function weights, function `MFggplot` plots the BEF relationship between multifunctionality of order q (= 0, 1 and 2) and species diversity of the same order q for two cases: (i) correlations between functions are not corrected for. (ii) correlations between functions are corrected for. The fitted lines for the chosen model are also shown in the figure.

Below we demonstrate how to reveal BEF relationships under the most useful linear mixed-effects model (`model = "LMM.both"`). Under the model, for each value of q, the relationship between tree species diversity and multifunctionality is modeled using a linear mixed-effects model with random slopes and random intercepts for each country. To fit a linear mixed-effect model, the stratification/group variable must be specified (e.g., `by_group = "country"` in the following code). If `by_group = NULL`, one can only fit linear model (`model = "lm"`). Run the following code to reveal the overall fixed-effect slopes (bold red lines) and each country's relationships (thin lines) estimated from the same linear mixed model. All the fitted results and the associated test of significance for the overall slopes and R-squared were based on the output using the function “lmer” in the R packages “lme4” and “lmerTest”.

```r
data("forest_function_data_normalized")
output1 <- data.frame(output1, country=rep(forest_function_data_normalized$country, each = 6))
MFggplot(output1, model = "LMM.both", by_group = "country", caption = "slope")
```

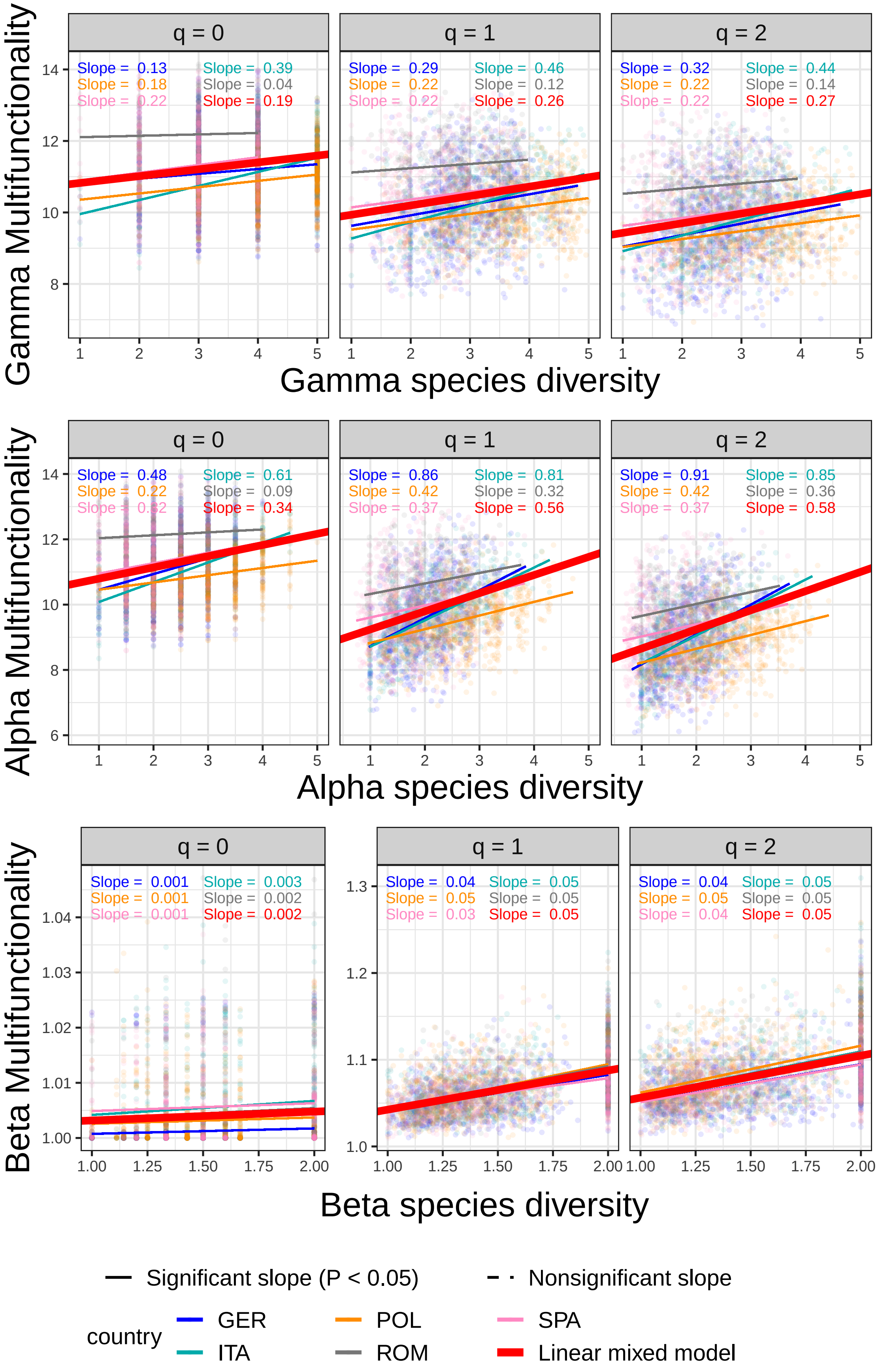


BEF relationships at gamma, alpha and beta scales For an MF2_multiple object of given individual function weights, function `MFggplot` plots the BEF relationship between alpha/beta/gamma multifunctionality of order q (= 0, 1 and 2) and the corresponding alpha/beta/gamma species diversity of the same order q for two cases: (i) correlations between functions are not corrected for. (ii) correlations between functions are corrected. The fitted lines for the chosen model are also shown in the figure.

By default, the BEF relationship for each scale is modeled using a linear mixed model with random slopes and random intercepts for each country. Run the following code to obtain the BEF graphical relationships when correlations are not corrected for. (Data from Finland are not considered in the plots, as explained earlier. See the package manual for a simple example where the code for plotting BEF relationships based on 18 plots from Germany and Italy is available.)

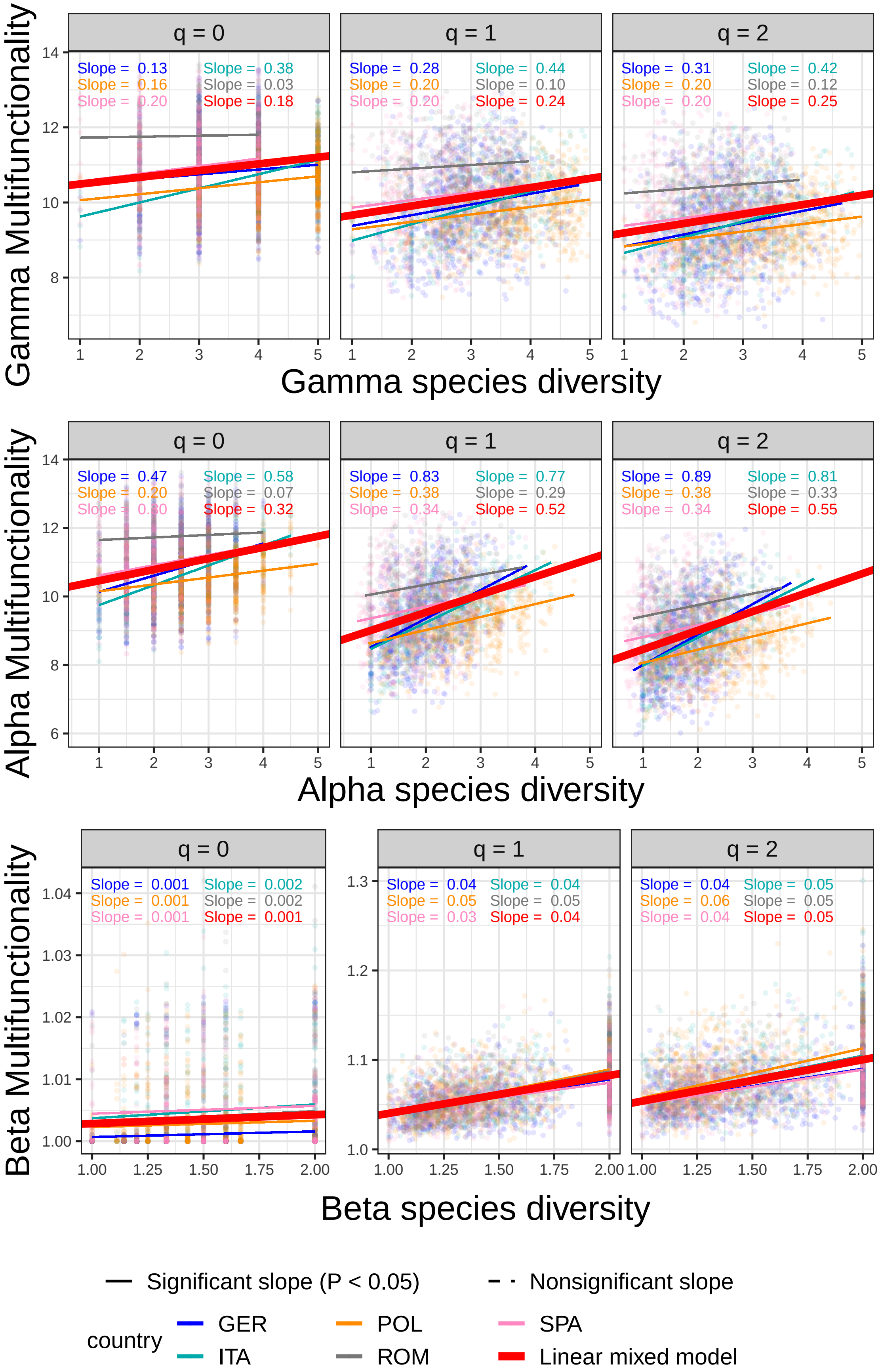
```
figure_LMM <- MFggplot(output2, model = "LMM.both", by_group = "country", caption = "slope")
```

```
figure_LMM$corr_uncorrected$ALL
```


Gamma Multifunctionality
q = 0
Slope = 0.13
Slope = 0.18
Slope = 0.22
Slope = 0.39
Slope = 0.04
Slope = 0.19
q = 1
Slope = 0.29
Slope = 0.22
Slope = 0.22
Slope = 0.46
Slope = 0.12
Slope = 0.26
q = 2
Slope = 0.32
Slope = 0.22
Slope = 0.22
Slope = 0.44
Slope = 0.14
Slope = 0.27
14
12
10
8
1
2
3
4
5
Gamma species diversity
Alpha Multifunctionality
q = 0
Slope = 0.48
Slope = 0.22
Slope = 0.32
Slope = 0.61
Slope = 0.09
Slope = 0.34
q = 1
Slope = 0.86
Slope = 0.42
Slope = 0.37
Slope = 0.81
Slope = 0.32
Slope = 0.56
q = 2
Slope = 0.91
Slope = 0.42
Slope = 0.37
Slope = 0.85
Slope = 0.36
Slope = 0.58
14
12
10
8
6
1
2
3
4
5
Alpha species diversity
Beta Multifunctionality
q = 0
Slope = 0.001
Slope = 0.001
Slope = 0.001
Slope = 0.003
Slope = 0.002
Slope = 0.002
1.04
1.03
1.02
1.01
1.00
q = 1
Slope = 0.04
Slope = 0.05
Slope = 0.03
Slope = 0.05
Slope = 0.05
Slope = 0.05
1.3
1.2
1.1
1.0
q = 2
Slope = 0.04
Slope = 0.05
Slope = 0.04
Slope = 0.05
Slope = 0.05
Slope = 0.05
1.00
1.25
1.50
1.75
2.00
Beta species diversity
Significant slope (P < 0.05)
Nonsignificant slope
country
GER
ITA
POL
ROM
SPA
Linear mixed model

The BEF graphical relationships when correlations are corrected for are shown below.

```
figure_LMM$corr_corrected$ALL
```


Gamma Multifunctionality
q = 0
Slope = 0.13
Slope = 0.16
Slope = 0.20
Slope = 0.38
Slope = 0.03
Slope = 0.18
q = 1
Slope = 0.28
Slope = 0.20
Slope = 0.20
Slope = 0.44
Slope = 0.10
Slope = 0.24
q = 2
Slope = 0.31
Slope = 0.20
Slope = 0.20
Slope = 0.42
Slope = 0.12
Slope = 0.25
14
12
10
8
1
2
3
4
5
Gamma species diversity
Alpha Multifunctionality
q = 0
Slope = 0.47
Slope = 0.20
Slope = 0.30
Slope = 0.58
Slope = 0.07
Slope = 0.32
q = 1
Slope = 0.83
Slope = 0.38
Slope = 0.34
Slope = 0.77
Slope = 0.29
Slope = 0.52
q = 2
Slope = 0.89
Slope = 0.38
Slope = 0.34
Slope = 0.81
Slope = 0.33
Slope = 0.55
14
12
10
8
6
1
2
3
4
5
Alpha species diversity
Beta Multifunctionality
q = 0
Slope = 0.001
Slope = 0.001
Slope = 0.001
Slope = 0.002
Slope = 0.002
Slope = 0.001
1.04
1.03
1.02
1.01
1.00
q = 1
Slope = 0.04
Slope = 0.05
Slope = 0.03
Slope = 0.04
Slope = 0.05
Slope = 0.04
1.3
1.2
1.1
1.0
q = 2
Slope = 0.04
Slope = 0.06
Slope = 0.04
Slope = 0.05
Slope = 0.05
Slope = 0.05
1.00
1.25
1.50
1.75
2.00
Beta species diversity
Significant slope (P < 0.05)
Nonsignificant slope
country
GER
ITA
POL
ROM
SPA
Linear mixed model

NOTE: Because the total number of pair plots is huge, it is very time consuming to obtain the BEF graphical relationships from running the above code for alpha/beta/gamma scales. Users can use partial data to quickly view the graphical results; see below for an example.

Computing multifunctionality in a single ecosystem for partial data

Here we only use the first 18 plots from Germany and the last 18 plots from Italy for illustration. Run the following code to view the first ten rows of the output:

```
data("forest_function_data_raw")
data("forest_biodiversity_data")
GER_ITA_forest_function_raw <- filter(forest_function_data_raw,
                                      country=="GER"|country=="ITA")[c(1:18,57:74),]
GER_ITA_forest_function_normalized <- function_normalization(data = GER_ITA_forest_function_raw,
                                                             fun_cols = 6:31,
                                                             negative = c("soil_cn_ff_10","wue"),
                                                             by_group = "country")
GER_ITA_forest_biodiversity <- forest_biodiversity_data[c(49:82,181:229),]
output3 <- MF1_single(func_data = GER_ITA_forest_function_normalized[,6:31], weight = 1,
                      species_data = GER_ITA_forest_biodiversity)
```

```
#>    plotID             Type Order.q  qMF Species.diversity
#> 1   GER01 corr_uncorrected   q = 0 9.99                 1
#> 2   GER01 corr_uncorrected   q = 1 8.70                 1
#> 3   GER01 corr_uncorrected   q = 2 7.99                 1
#> 4   GER01   corr_corrected   q = 0 9.33                 1
#> 5   GER01   corr_corrected   q = 1 8.26                 1
#> 6   GER01   corr_corrected   q = 2 7.64                 1
#> 7   GER02 corr_uncorrected   q = 0 9.20                 1
#> 8   GER02 corr_uncorrected   q = 1 8.02                 1
#> 9   GER02 corr_uncorrected   q = 2 7.47                 1
#> 10  GER02   corr_corrected   q = 0 8.62                 1
```

Computing alpha, beta and gamma multifunctionality for partial data

Here we only use the first 18 plots from Germany and the last 18 plots from Italy for illustration. Run the following code to view the first ten rows of the output:

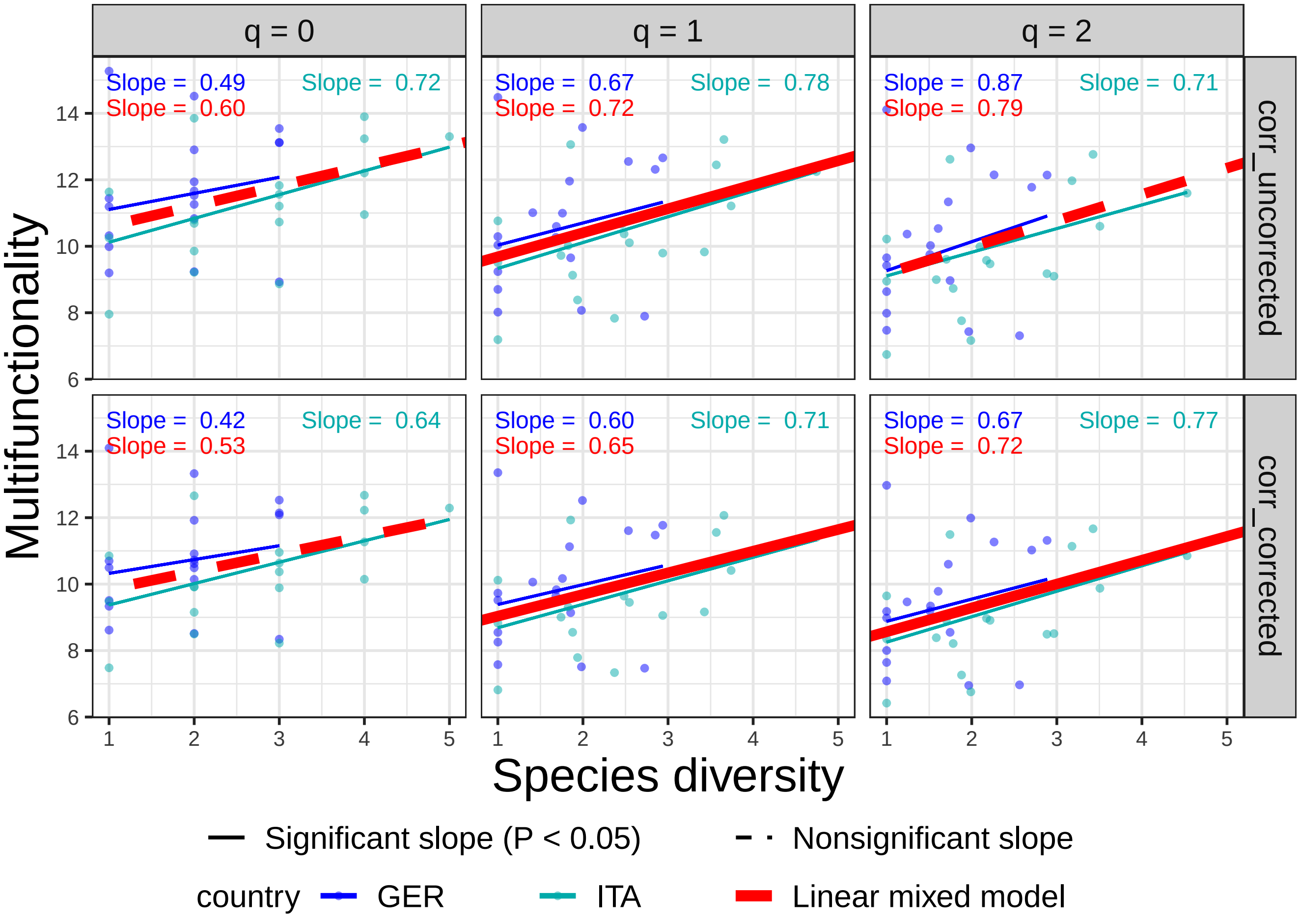
```
data("forest_function_data_raw")
data("forest_biodiversity_data")
GER_ITA_forest_function_raw <- filter(forest_function_data_raw,
                                      country=="GER"|country=="ITA")[c(1:18,57:74),]
GER_ITA_forest_function_normalized <- function_normalization(data = GER_ITA_forest_function_raw,
                                                             fun_cols = 6:31,
                                                             negative = c("soil_cn_ff_10","wue"),
                                                             by_group = "country")
GER_ITA_forest_biodiversity <- forest_biodiversity_data[c(49:82,181:229),]
output4 <- MF2_multiple(func_data = GER_ITA_forest_function_normalized[,6:32],
                        species_data = GER_ITA_forest_biodiversity,
                        weight=1,
                        by_group = "country")
```

```
#>               plotID country Order.q              Type Scale  qMF Species.diversity
#> 1  GER01 vs. GER02     GER   q = 0 corr_uncorrected Gamma 9.59             1.000
#> 2  GER01 vs. GER02     GER   q = 0 corr_uncorrected Alpha 9.59             1.000
#> 3  GER01 vs. GER02     GER   q = 0 corr_uncorrected  Beta 1.00             1.000
#> 4  GER01 vs. GER02     GER   q = 0   corr_corrected Gamma 8.96             1.000
#> 5  GER01 vs. GER02     GER   q = 0   corr_corrected Alpha 8.96             1.000
#> 6  GER01 vs. GER02     GER   q = 0   corr_corrected  Beta 1.00             1.000
#> 7  GER01 vs. GER02     GER   q = 1 corr_uncorrected Gamma 8.36             1.000
#> 8  GER01 vs. GER02     GER   q = 1 corr_uncorrected Alpha 8.18             0.999
#> 9  GER01 vs. GER02     GER   q = 1 corr_uncorrected  Beta 1.02             1.001
#> 10 GER01 vs. GER02     GER   q = 1   corr_corrected Gamma 7.91             1.000
```

Assessing BEF Relationships by MFggplot()

Within-plot BEF relationship for partial data Run the following code to obtain the within-plot BEF graphical relationships based on 18 plots from Germany and Italy when correlations are not corrected for and corrected for.

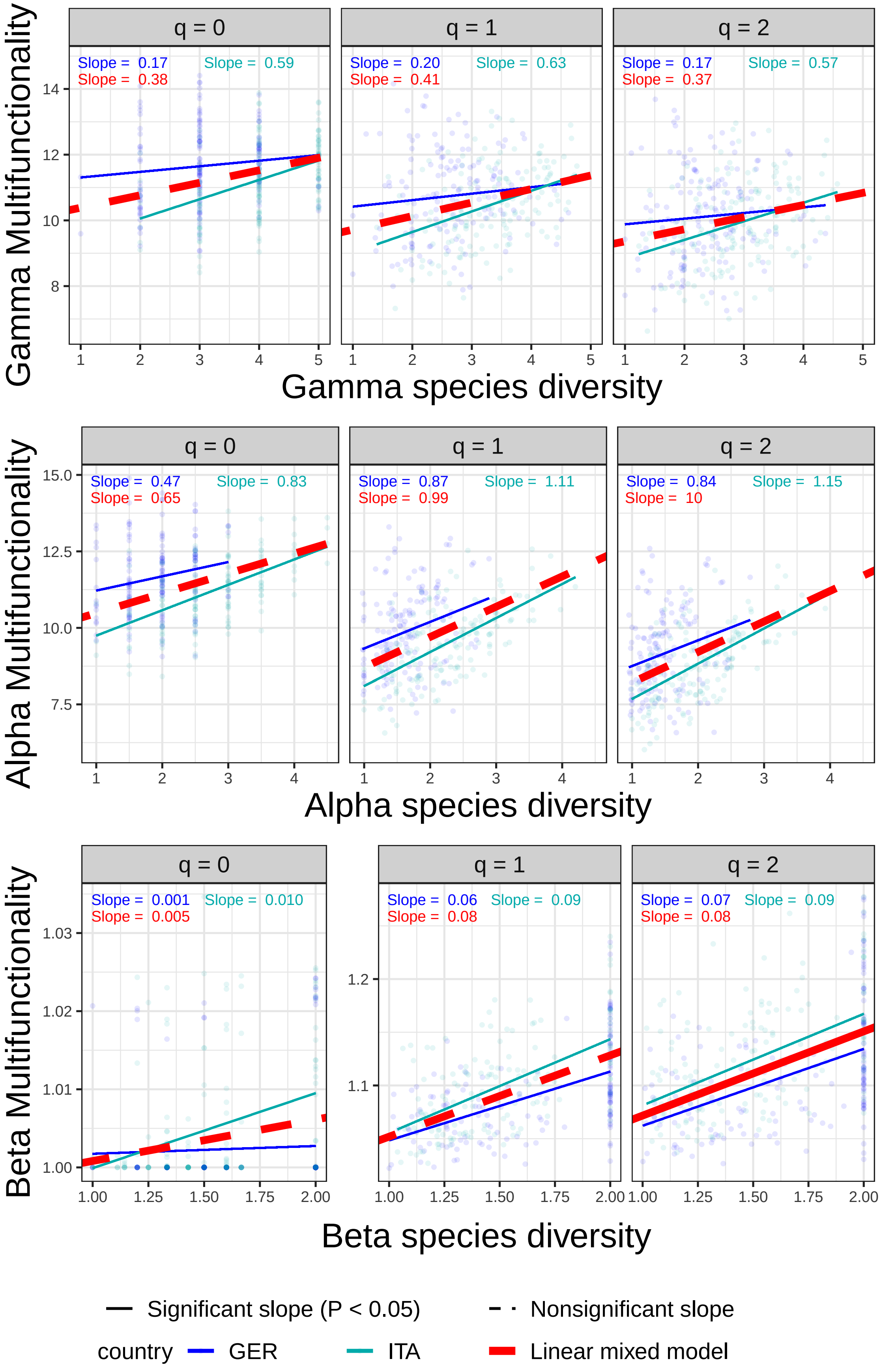
```
output3 <- data.frame(output3, country=rep(GER_ITA_forest_function_normalized$country, each = 6))
MFggplot(output3, model = "LMM.both", by_group="country", caption = "slope")
```



BEF relationships at gamma, alpha and beta scales for partial data Run the following code to obtain the BEF graphical relationships in 18 plots from Germany and Italy when correlations are not corrected for.

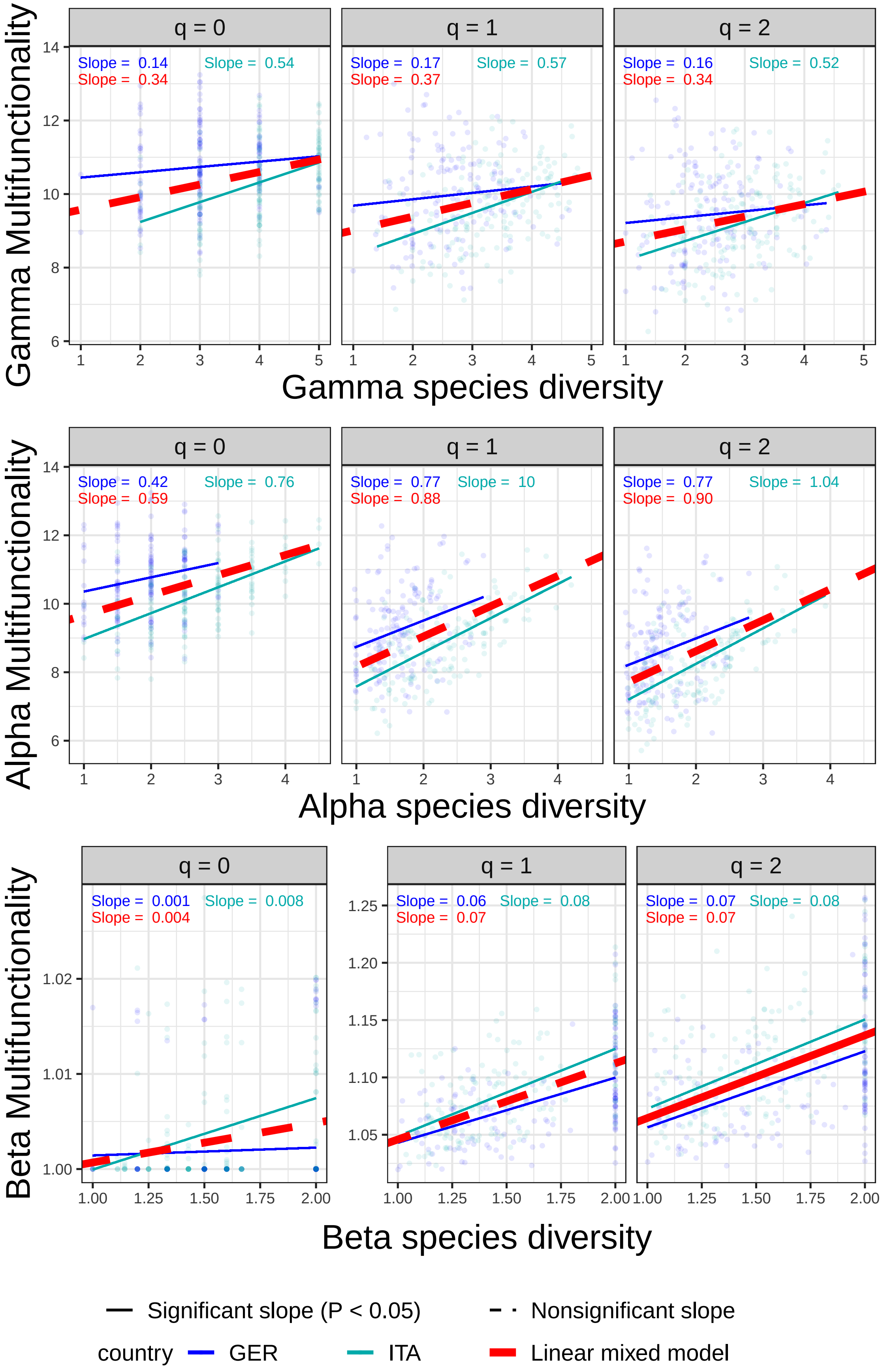
```
figure_LMM_GER_ITA <- MFggplot(output4, model = "LMM.both", by_group = "country", caption = "slope")
```

```
figure_LMM_GER_ITA$corr_uncorrected$ALL
```


Gamma Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.17
Slope = 0.38
Slope = 0.59
Slope = 0.20
Slope = 0.41
Slope = 0.63
Slope = 0.17
Slope = 0.37
Slope = 0.57
14
12
10
8
1
2
3
4
5
Gamma species diversity
Alpha Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.47
Slope = 0.65
Slope = 0.83
Slope = 0.87
Slope = 0.99
Slope = 1.11
Slope = 0.84
Slope = 10
Slope = 1.15
15.0
12.5
10.0
7.5
1
2
3
4
Alpha species diversity
Beta Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.001
Slope = 0.005
Slope = 0.010
Slope = 0.06
Slope = 0.08
Slope = 0.09
Slope = 0.07
Slope = 0.08
Slope = 0.09
1.03
1.02
1.01
1.00
1.2
1.1
1.00
1.25
1.50
1.75
2.00
Beta species diversity
Significant slope (P < 0.05)
Nonsignificant slope
country
GER
ITA
Linear mixed model

The BEF graphical relationships based on 18 plots from Germany and Italy when correlations are corrected for are shown below.

```
figure_LMM_GER_ITA$corr_corrected$ALL
```


Gamma Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.14
Slope = 0.34
Slope = 0.54
Slope = 0.17
Slope = 0.37
Slope = 0.57
Slope = 0.16
Slope = 0.34
Slope = 0.52
14
12
10
8
6
1
2
3
4
5
Gamma species diversity
Alpha Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.42
Slope = 0.59
Slope = 0.76
Slope = 0.77
Slope = 0.88
Slope = 10
Slope = 0.77
Slope = 0.90
Slope = 1.04
14
12
10
8
6
1
2
3
4
Alpha species diversity
Beta Multifunctionality
q = 0
q = 1
q = 2
Slope = 0.001
Slope = 0.004
Slope = 0.008
Slope = 0.06
Slope = 0.07
Slope = 0.08
Slope = 0.07
Slope = 0.07
Slope = 0.08
1.02
1.01
1.00
1.25
1.20
1.15
1.10
1.05
1.00
1.25
1.50
1.75
2.00
Beta species diversity
Significant slope (P < 0.05)
Nonsignificant slope
country
GER
ITA
Linear mixed model

References

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