Package: RHC (via r-universe)

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Type Package

Title Rangeland Health and Condition

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Description The evaluation criteria of rangeland health, condition and landscape function analysis based on species diversity and functional diversity of rangeland plant communities.

License GPL (>= 2)

Depends R (>= 3.5.0), permute, lattice, ade4, geometry

Imports vegan, FD, randomForest, stats, ggplot2, gridExtra

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`canopy_oc_file` *Canopy - oc Data*

Description

A dataset containing canopy cover information.

Usage

```
data(canopy_oc_file)
```

`plot_RHC` *Create Evaluation Criteria Plots*

Description

This function creates plots to compare evaluation criteria of landscape function analysis (LFA), rangeland health and condition.

Usage

```
plot_RHC(evaluation.criteria, selected_columns = NULL, ncol = 4)
```

Arguments

`evaluation.criteria`	A data frame containing standardized data from the first function.
`selected_columns`	A vector of column indices specifying which criteria to plot. If NULL, all columns will be plotted.
`ncol`	Number of columns for arranging the plots. Default is 4.
`plot_RHC`	A function that takes standardized data and generates evaluation plots for different criteria of landscape function analysis (LFA), rangeland health and condition.

Details

The function takes the output from RHC_function and creates evaluation plots for different criteria.

Value

A list of evaluation criteria(attributes) plots.

Examples

```
data(canopy_oc_file)
data(trait_file)
final_data_st <- prepare_RHC_data(canopy_oc_file, trait_file)
evaluation.criteria <- RHC_function(final_data_st)
# Plot all columns
plots_all <- plot_RHC(evaluation.criteria, ncol = 4)
# Plot specific columns
selected_columns <- c(4, 8)
plots_selected <- plot_RHC(evaluation.criteria, selected_columns, ncol = 2)
```

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plot_samples *Plot Samples*

Description

This function creates graphs for the inputs of the RHC_function model.

Arguments

final_data_st	A data frame containing standardized data from the first function.
row_indices	A vector of row indices specifying which rows to use for creating sample plots.
plot_title_prefix	A prefix for the plot titles (default is "Sample").
ncol	Number of columns for arranging the plots. Default is 3.

Details

The function takes input data and specific row indices, creates sample charts, and returns the plots.

Value

A list of sample charts.

Examples

```
data(canopy_oc_file)
data(trait_file)
final_data_st <- prepare_RHC_data(canopy_oc_file, trait_file)
row_indices <- 1:17
plots.samples <- plot_samples(final_data_st, row_indices, plot_title_prefix = "Sample", ncol = 3)
```

prepare_RHC_data *Prepare Input Data*

Description

This function prepares input data for the evaluation criteria of landscape function analysis (LFA), rangeland health and condition.

Usage

```
prepare_RHC_data(canopy_oc_file, trait_file)
```

Arguments

canopy_oc_file	A data frame containing canopy cover and soil organic carbon data.
trait_file	A data frame containing plant species trait data.

Details

The function takes canopy cover, soil organic carbon (OC), and plant species trait data, and returns standardized data.

Note: The first row of the input data matrix (canopy_oc_file) must be the reference sample, and the second column must contain the OC data, and the canopy cover must be entered as a relative value.

Value

A standardized data frame for further analysis using Min-Max Normalization.

Examples

```
data(canopy_oc_file)
data(trait_file)
final_data_st <- prepare_RHC_data(canopy_oc_file, trait_file)
```

RHC_function *Rangeland Health, Condition*

Description

This function calculates attributes of landscape function analysis (LFA), rangeland health and condition.

Usage

```
RHC_function(final_data_st)
```

Arguments

`final_data_st` A data frame containing standardized data from the first function.

Details

The function takes standardized data, performs predictions using pre-trained models, and returns the results.

Value

The attributes of landscape function analysis (LFA), rangeland health and condition.

Examples

```
data(canopy_oc_file)
data(trait_file)
final_data_st <- prepare_RHC_data(canopy_oc_file, trait_file)
evaluation.criteria <- RHC_function(final_data_st)
```

`trait_file` *Trait Data*

Description

A dataset containing trait information.

Usage

```
data(trait_file)
```

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