Package 'RHC'

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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

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Contents

`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)
```

`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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