Package ‘NPStability’

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Title Rank-Based Stability Index (RSI) for Genotype by Environment Studies

Version 0.1.0

Description Provides functions to compute the Rank-Based Stability Index (RSI) for genotype by environment interaction data, along with a genotype plus genotype-by-environment (GGE) style biplot visualization of stability.

Depends R (>= 4.0)

Imports dplyr, tidyr, rlang, ggplot2

Suggests knitr, rmarkdown

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.3.3

NeedsCompilation no

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Repository CRAN

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`compute_rsi` *Compute Rank-based Stability Index (RSI)*

Description

Compute Rank-based Stability Index (RSI)

Usage

```
compute_rsi(data, y, gen, env, rep = NULL)
```

Arguments

`data`	A data frame with genotype, environment, and response columns.
`y`	Response variable column.
`gen`	Genotype column.
`env`	Environment column.
`rep`	Optional replication column.

Value

A table containing RSI values for each genotype.

References

1. Kumar, P., Paul, A. K., Paul, R. K., Raju, B., Rathod, S., Ray, M., ... & Yeasin, M. (2024). A robust non-parametric stability measure to select stable genotypes. *The Indian Journal of Agricultural Sciences*, 94(9), 1007–1012. 2. Pour-Aboughadareh, A., Khalili, M., Poczai, P., & Olivoto, T. (2022). Stability Indices to Deciphering the Genotype-by-Environment Interaction (GEI) Effect: An Applicable Review for Use in Plant Breeding Programs. *Plants*, 11(3), 414.

Examples

```
library(NPStability)
library(dplyr)
data(example_data)
rsi_results <- compute_rsi(example_data, Yield, Gen, Env)
rsi_biplot <- rsi_biplot(example_data, Yield, Gen, Env, rsi_table = rsi_results)
```

`example_data` *Example genotype x environment dataset*

Description

A small dataset containing 4 genotypes tested in 2 environments with yield data.

Usage

```
example_data
```

Format

A data frame with 8 rows and 3 variables:

Gen	Genotype ID (factor)
Env	Environment (factor)
Yield	Yield values (numeric)

Source

Generated for demonstration purposes

`rsi_biplot` *Create GGE-style biplot annotated by RSI*

Description

Create GGE-style biplot annotated by RSI

Usage

```
rsi_biplot(data, y, gen, env, rsi_table = NULL)
```

Arguments

`data`	Data frame with genotype, environment, and response columns.
`y`	Response variable column.
`gen`	Genotype column.
`env`	Environment column.
`rsi_table`	Optional RSI table from compute_rsi().

Value

A ggplot object of the biplot.

Examples

```
library(NPStability)
data(example_data)
rsi_results <- compute_rsi(example_data, Yield, Gen, Env)
rsi_biplot(example_data, Yield, Gen, Env, rsi_table = rsi_results)
```

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