

# Package: NPStability (via r-universe)

May 22, 2026

**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

**Author** Prakash Kumar [aut, cre], Himadri Sekhar Roy [aut], Ranjit Kumar Paul [aut], Md. Yeasin [aut], Sunil Kumar Yadav [aut], Amrit Kumar Paul [aut]

**Maintainer** Prakash Kumar <prakash289111@gmail.com>

**Repository** <https://cran.r-universe.dev>

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**RemoteRef** HEAD

**RemoteSha** 959fc5ae154bd8dd8025cad72c836cadde8560a3

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

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### Description

Compute Rank-based Stability Index (RSI)

### Usage

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

### Arguments

<code>data</code>	A data frame with genotype, environment, and response columns.
<code>y</code>	Response variable column.
<code>gen</code>	Genotype column.
<code>env</code>	Environment column.
<code>rep</code>	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)
```

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example_data	<i>Example genotype x environment dataset</i>
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**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

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rsi_biplot	<i>Create GGE-style biplot annotated by RSI</i>
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**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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