

Package ‘rYWAASB’

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Type Package

Title Simultaneous Selection of Trait and WAASB Index

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Maintainer Ali Arminian <abeyran@gmail.com>

Description Proposes a new ranking algorithm that utilizes a ‘Y*WAASB’ biplot generated from the ‘metan’ package. The aim of the package is to effectively distinguish the top-ranked genotypes. For a detailed explanation of the process of obtaining a ‘Y*WAASB’ biplot and the related data, please refer to the manual included in this package as well as the study by Olivoto & Lúcio (2020) <doi:10.1111/2041-210X.13384>. In this context, ‘WAASB’ refers to the ‘Weighted Average of Absolute Scores’ provided by Olivoto et al. (2019) <doi:10.2134/agronj2019.03.0220>, which quantifies the stability of genotypes across different environments using linear mixed-effect models. In order to run the package, it is necessary to extract the ‘WAASB’ coefficients using the ‘metan’ package.

License GPL-3

URL <https://github.com/abeyran/Stability1>

BugReports <https://github.com/abeyran/Stability1/issues>

Depends R (>= 3.5)

Imports ggplot2, graphics

Suggests car, metan, devtools, usethis, testthat, knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

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RoxygenNote 7.3.1

Language en-US

LazyData true

LazyLoad true

NeedsCompilation no

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bar_plot1	<i>Draw the first barplot of ranks of genotypes</i>
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Description

Proposes a new ranking algorithm that utilizes a "Y*WAASB" biplot generated from the 'metan' package. The aim of the package is to effectively distinguish the top-ranked genotypes. For a detailed explanation of the process of obtaining a "Y*WAASB" biplot and the related data, please refer to the manual included in this package as well as the study by Olivoto & Lúcio (2020) [doi:10.1111/2041210X.13384](https://doi.org/10.1111/2041210X.13384). In this context, "WAASB" refers to the "Weighted Average of Absolute Scores" provided by Olivoto et al. (2019) [doi:10.2134/agronj2019.03.0220](https://doi.org/10.2134/agronj2019.03.0220), which quantifies the stability of genotypes across different environments using linear mixed-effect models. In order to run the package, it is necessary to extract the "WAASB" coefficients using the 'metan' package.

Creates the bar plot for a new index for simultaneous selection of genotypes for trait and WAASB index.

Usage

```
bar_plot1(datap)
```

Arguments

datap	The data set
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Details

The bar_plot function creates the barplot of rank of genotypes

Author(s)

Ali Arminian (Ph.D.) Plant Geneticist and Breeder

Maintainer: Ali Arminian <abeyran@gmail.com>

References

- Olivoto, T., et al. (2019) Mean Performance and Stability in Multi-Environment Trials I: Combining Features of AMMI and BLUP Techniques. *Agronomy Journal*, 111, 1-12. <https://doi.org/10.2134/agronj2019.03.0220>
- H. Wickham. *ggplot2: Elegant Graphics for Data Analysis*. Springer-Verlag New York, 2016.

See Also

Useful links:

- <https://github.com/abeyran/Stability1>
- Report bugs at <https://github.com/abeyran/Stability1/issues>

Examples

```
data(maize)
bar_plot1(maize)
```

bar_plot2

Draw the second barplot of ranks of genotypes

Description

Proposes a new ranking algorithm that utilizes a "Y*WAASB" biplot generated from the 'metan' package. The aim of the package is to effectively distinguish the top-ranked genotypes. For a detailed explanation of the process of obtaining a "Y*WAASB" biplot and the related data, please refer to the manual included in this package as well as the study by Olivoto & Lúcio (2020) [doi:10.1111/2041210X.13384](https://doi.org/10.1111/2041210X.13384). In this context, "WAASB" refers to the "Weighted Average of Absolute Scores" provided by Olivoto et al. (2019) [doi:10.2134/agronj2019.03.0220](https://doi.org/10.2134/agronj2019.03.0220), which quantifies the stability of genotypes across different environments using linear mixed-effect models. In order to run the package, it is necessary to extract the "WAASB" coefficients using the 'metan' package.

Creates the bar plot for a new index for simultaneous selection of genotypes for trait and WAASB index.

Usage

```
bar_plot2(datap)
```

Arguments

datap The data set

Details

The bar_plot2 function creates the barplot of rank of genotypes

Author(s)

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References

Olivoto, T., et al. (2019) Mean Performance and Stability in Multi-Environment Trials I: Combining Features of AMMI and BLUP Techniques. *Agronomy Journal*, 111, 1-12. <https://doi.org/10.2134/agronj2019.03.0220>

See Also

Useful links:

- <https://github.com/abeyran/Stability1>
- Report bugs at <https://github.com/abeyran/Stability1/issues>

Examples

```
data(maize)
bar_plot2(maize)
```

data_ge	<i>Dataset2: a tibble containing ENV, GEN, REP variables and GY(grain yield) and HM traits from the metan package.</i>
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Description

Dataset2: a tibble containing ENV, GEN, REP variables and GY(grain yield) and HM traits from the metan package.

Usage

```
data(data_ge)
```

Format

A data.frame with 420 rows in and 5 columns.

ENV a character vector

GEN a character vector

REP a character vector

GY a numeric vector

HM a numeric vector

Examples

```
library(rYWAASB)
data(data_ge)
```

maize	<i>Dataset1: a tibble containing GEN, Trait and WAASB index columns.</i>
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Description

Dataset1: a tibble containing GEN, Trait and WAASB index columns.

Usage

```
data(maize)
```

Format

A data.frame with 20 observations (genotypes) in rows in and 2 columns of the trait and WAASB index values.

GEN a character vector

Y a numeric vector

WAASB a numeric vector

Examples

```
library(rYWAASB)
data(maize)

# ranking genotypes:
ranki(maize)

# first plot by ggplot2:
bar_plot1(maize)

# second plot by R:
bar_plot2(maize)
```

ranki	<i>Estimation of ranks</i>
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Description

Proposes a new ranking algorithm that utilizes a "Y*WAASB" biplot generated from the 'metan' package. The aim of the package is to effectively distinguish the top-ranked genotypes. For a detailed explanation of the process of obtaining a "Y*WAASB" biplot and the related data, please refer to the manual included in this package as well as the study by Olivoto & Lúcio (2020) [doi:10.1111/2041210X.13384](https://doi.org/10.1111/2041210X.13384). In this context, "WAASB" refers to the "Weighted Average of Absolute Scores" provided by Olivoto et al. (2019) [doi:10.2134/agronj2019.03.0220](https://doi.org/10.2134/agronj2019.03.0220), which quantifies the stability

of genotypes across different environments using linear mixed-effect models. In order to run the package, it is necessary to extract the "WAASB" coefficients using the 'metan' package.

Estimates a new index for simultaneous selection of genotypes for trait and WAASB index. This can be compared with WAASBY index of Olivoto (2019). We suggest users handle the missing data in inputs before considering analyses, due rank codes dose not implement a widespread algorithm to do this task.

Usage

```
ranki(datap)
```

Arguments

datap	The data set
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Details

The rank function estimates rank of genotypes

Author(s)

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References

Olivoto, T., et al. (2019). *Mean Performance and Stability in Multi-Environment Trials I: Combining Features of AMMI and BLUP Techniques*. Agronomy Journal, 111, 1-12. <https://doi.org/10.2134/agronj2019.03.0220>

See Also

Useful links:

- <https://github.com/abeyran/Stability1>
- Report bugs at <https://github.com/abeyran/Stability1/issues>

Examples

```
data(maize)  
ranki(maize)
```

Description

Proposes a new ranking algorithm that utilizes a "Y*WAASB" biplot generated from the 'metan' package. The aim of the package is to effectively distinguish the top-ranked genotypes. For a detailed explanation of the process of obtaining a "Y*WAASB" biplot and the related data, please refer to the manual included in this package as well as the study by Olivoto & Lúcio (2020) [doi:10.1111/2041210X.13384](https://doi.org/10.1111/2041210X.13384). In this context, "WAASB" refers to the "Weighted Average of Absolute Scores" provided by Olivoto et al. (2019) [doi:10.2134/agronj2019.03.0220](https://doi.org/10.2134/agronj2019.03.0220), which quantifies the stability of genotypes across different environments using linear mixed-effect models. In order to run the package, it is necessary to extract the "WAASB" coefficients using the 'metan' package.

Author(s)

Ali Arminian (Ph.D.), Plant Geneticist and Breeder

References

Olivoto, T., et al. (2019) Mean Performance and Stability in Multi-Environment Trials I: Combining Features of AMMI and BLUP Techniques. *Agronomy Journal*, 111, 1-12. <https://doi.org/10.2134/agronj2019.03.0220>

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