Package: stability (via r-universe)

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Type Package

Title Stability Analysis of Genotype by Environment Interaction (GEI)

Version 0.5.0

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Description Functionalities to perform Stability Analysis of Genotype by Environment Interaction (GEI) to identify superior and stable genotypes under diverse environments. It performs Eberhart & Russel's ANOVA (1966) (<doi:10.2135/cropsci1966.0011183X000600010011x>), Finlay and Wilkinson (1963) Joint Linear Regression (<doi:10.1071/AR9630742>), Wricke (1962, 1964) Ecovalence, Shukla's stability variance parameter (1972) (<doi:10.1038/hdy.1972.87>) and Kang's (1991) (<doi:10.2134/agronj1991.00021962008300010037x>) simultaneous selection for high yielding and stable parameter.

Depends R (>= 3.1)

Imports dplyr, ggplot2, ggfortify, lme4, magrittr, matrixStats, reshape2, rlang, scales, stats, tibble, tidyr

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URL `https://github.com/myaseen208/stability`, `https://myaseen208.github.io/stability/`

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

Note Department of Mathematics and Statistics, University of Agriculture Faisalabad, Faisalabad-Pakistan.

Repository https://myaseen208.r-universe.dev

RemoteUrl https://github.com/myaseen208/stability

RemoteRef HEAD

RemoteSha bc1dc470c4cb188b32715d46e341059ac3fe2e5a

Contents

`add_anova` *Additive ANOVA for Genotypes by Environment Interaction (GEI) model*

Description

Additive ANOVA for Genotypes by Environment Interaction (GEI) model

Usage

```
add_anova(.data, .y, .rep, .gen, .env)

## Default S3 method:
add_anova(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
YieldANOVA <-
     add_anova(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
YieldANOVA
```

`ammi` *Additive Main Effects and Multiplicative Interaction (AMMI)*

Description

Performs Additive Main Effects and Multiplicative Interaction (AMMI) Analysis for Genotypes by Environment Interaction (GEI)

Usage

```
ammi(.data, .y, .rep, .gen, .env)

## Default S3 method:
ammi(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Stability Measures

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.ammi <-
     ammi(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
Yield.ammi
```

`ammi_biplot` *Additive Main Effects and Multiplicative Interaction (AMMI) Biplot*

Description

Plots Additive Main Effects and Multiplicative Interaction (AMMI) for Genotypes by Environment Interaction (GEI)

Usage

```
ammi_biplot(.data, .y, .rep, .gen, .env)

## Default S3 method:
ammi_biplot(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Stability Measures

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
     ammi_biplot(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
```

`er_anova` *Eberhart & Russel's Model ANOVA*

Description

ANOVA of Eberhart & Russel's Model

Usage

```
er_anova(.data, .y, .rep, .gen, .env)

## Default S3 method:
er_anova(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.er_anova <-
         er_anova(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
          )
Yield.er_anova
```

`ge_data` *Data for Genotypes by Environment Interaction (GEI)*

Description

`ge_data` is used for performing Genotypes by Environment Interaction (GEI) Analysis.

Usage

```
data(ge_data)
```

Format

A `data.frame` 1320 obs. of 6 variables.

Details

- Gen Genotype
- Institute Institute
- Rep Replicate
- Block Block
- Env Environment
- Yield Yield Response

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
```

`ge_effects` *Genotype by Environment Interaction Effects*

Description

Calcuates Genotype by Environment Interaction Effects

Usage

```
ge_effects(.data, .y, .gen, .env)

## Default S3 method:
ge_effects(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Effects

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.Effects <-
              ge_effects(
                .data  = ge_data
               , .y    = Yield
               , .gen  = Gen
               , .env  = Env
               )
names(Yield.Effects)

Yield.Effects$ge_means
Yield.Effects$ge_effects
Yield.Effects$gge_effects
```

`ge_means` *Genotype by Environment Interaction Means and Ranks*

Description

Calcuates Genotype by Environment Interaction Means along with their Ranks

Usage

```
ge_means(.data, .y, .gen, .env)

## Default S3 method:
ge_means(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Means and Ranks

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)

Yield.ge_means <-
          ge_means(
                .data  = ge_data
              , .y     = Yield
              , .gen   = Gen
              , .env   = Env
              )

Yield.ge_means$ge_means
Yield.ge_means$ge_ranks
Yield.ge_means$g_means
Yield.ge_means$e_means
```

`gge_biplot` *Genotype plus Genotypes by Environment (GGE) Interaction Biplot*

Description

Plots Genotype plus Genotypes by Environment (GGE) Interaction Biplot for Genotypes by Environment Interaction (GEI)

Usage

```
gge_biplot(.data, .y, .rep, .gen, .env)

## Default S3 method:
gge_biplot(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Stability Measures

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
     gge_biplot(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
```

`indiv_anova` *Individual ANOVA for Each Environment*

Description

Individual ANOVA for Each Environment

Usage

```
## Default S3 method:
indiv_anova(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)
3. Ghulam Murtaza (<`gmurtaza208@gmail.com`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.indiv_anova <-
         indiv_anova(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
          )
Yield.indiv_anova
```

`stability` *Stability Analysis of Genotype by Environment Interaction (GEI)*

Description

The `stability` package provides functionalities to perform Stability Analysis of Genotype by Environment Interaction (GEI) to identify superior and stable genotypes under diverse environments. It performs Eberhart & Russel's ANOVA (1966), Finlay and Wilkinson (1963) Joint Linear Regression, Wricke (1962, 1964) Ecovalence, Shukla's stability variance parameter (1972) and Kang's (1991) simultaneous selection for high yielding and stable parameter.

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)
3. Ghulam Murtaza (<`gmurtaza208@gmail.com`>)

`stab_asv` *Additive Main Effects and Multiplicative Interacion Stability Value*

Description

Additive ANOVA for Genotypes by Environment Interaction (GEI) model

Usage

```
stab_asv(.data, .y, .rep, .gen, .env)

## Default S3 method:
stab_asv(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
YieldASV <-
     stab_asv(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
YieldASV
```

`stab_dist` *Stability Distance in AMMI*

Description

Stability Distance of Genotypes in Additive ANOVA for Genotypes by Environment Interaction (GEI) model

Usage

```
stab_dist(.data, .y, .rep, .gen, .env, .m = 2)

## Default S3 method:
stab_dist(.data, .y, .rep, .gen, .env, .m = 2)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor
`.m`	No of PCs retained

Value

Stability Distance

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

Examples

```
data(ge_data)
YieldDist <-
     stab_dist(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
          , .m    = 2
      )
YieldDist
```

`stab_fox` *Stability Fox Function*

Description

Performs a stability analysis based on the criteria of Fox et al. (1990), using the statistical "TOP third" only. In Fox function, a stratified ranking of the genotypes at each environment separately is done. The proportion of locations at which the genotype occurred in the top third are expressed in TOP output.

Usage

```
stab_fox(.data, .y, .rep, .gen, .env)

## Default S3 method:
stab_fox(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

1. Fox, P.N. and Skovmand, B. and Thompson, B.K. and Braun, H.J. and Cormier, R. (1990). Yield and adaptation of hexaploid spring triticale. *Euphytica*, **47**, 57-64.

Examples

```
data(ge_data)
YieldFox <-
     stab_fox(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
YieldFox
```

`stab_kang` *Stability Kang Function*

Description

Performs a stability analysis based on the Kang (1988) criteria. Kang nonparametric stability (ranksum) uses both "trait single value" and stability variance (Shukla, 1972), and the genotype with the lowest ranksum is commonly the most favorable one.

Usage

```
stab_kang(.data, .y, .rep, .gen, .env)

## Default S3 method:
stab_kang(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

1. Kang, M.S. (1988). A rank-sum method for selecting high-yielding, stable corn genotypes. *Cereal Research Communications*, **16**, 1-2.
2. Shukla, G.K. (1972). Some aspects of partitioning genotype environmental components of variability. *Heredity*, **29**, 237-245.

Examples

```
data(ge_data)
YieldKang <-
     stab_kang(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
      )
YieldKang
```

`stab_masv` *Modified Additive Main Effects and Multiplicative Interacion Stability Value*

Description

Additive ANOVA for Genotypes by Environment Interaction (GEI) model

Usage

```
stab_masv(.data, .y, .rep, .gen, .env, .m = 2)

## Default S3 method:
stab_masv(.data, .y, .rep, .gen, .env, .m = 2)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor
`.m`	No of PCs retained

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
YieldMASV <-
     stab_masv(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
          , .m    = 2
      )
YieldMASV
```

`stab_measures` *Stability Measures for Genotypes by Environment Interaction (GEI)*

Description

Stability Measures for Genotypes by Environment Interaction (GEI)

Usage

```
stab_measures(.data, .y, .gen, .env)

## Default S3 method:
stab_measures(.data, .y, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Stability Measures

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.StabMeasures <- stab_measures(
                .data  = ge_data
              , .y     = Yield
              , .gen   = Gen
              , .env   = Env
              )
Yield.StabMeasures
```

`stab_par` *Stability Parameters for Genotypes by Environment Interaction (GEI)*

Description

Stability Parameters for Genotypes by Environment Interaction (GEI)

Usage

```
stab_par(.data, .y, .rep, .gen, .env, alpha = 0.1, .envCov = NULL)

## Default S3 method:
stab_par(.data, .y, .rep, .gen, .env, alpha = 0.1,
  .envCov = NULL)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor
`alpha`	Level of Significance, default is 0.1
`.envCov`	Environmental Covariate, default is NULL

Value

Stability Parameters

Author(s)

1. Muhammad Yaseen (`<myaseen208@gmail.com>`)
2. Kent M. Edkridge (`<keskridge1@unl.edu>`)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.StabPar <-
   stab_par(
            .data   = ge_data
          , .y      = Yield
          , .rep    = Rep
          , .gen    = Gen
          , .env    = Env
          , alpha   = 0.1
          , .envCov = NULL
)

Yield.StabPar
```

`stab_reg` *Individual Regression for each Genotype*

Description

Individual Regression for each Genotype in Genotypes by Environment Interaction (GEI)

Usage

```
stab_reg(.data, .y, .rep, .gen, .env)

## Default S3 method:
stab_reg(.data, .y, .rep, .gen, .env)
```

Arguments

`.data`	data.frame
`.y`	Response Variable
`.rep`	Replication Factor
`.gen`	Genotypes Factor
`.env`	Environment Factor

Value

Additive ANOVA

Author(s)

1. Muhammad Yaseen (<`myaseen208@gmail.com`>)
2. Kent M. Edkridge (<`keskridge1@unl.edu`>)

References

Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

Examples

```
data(ge_data)
Yield.StabReg <-
        stab_reg(
            .data = ge_data
          , .y    = Yield
          , .rep  = Rep
          , .gen  = Gen
          , .env  = Env
          )
```

```
Yield.StabReg
```

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