

Package ‘stability’

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Type Package

Title Stability Analysis of Genotype by Environment Interaction (GEI)

Version 0.2.0

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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

License GPL-2

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LazyData true

RoxygenNote 6.0.1

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add_anova	<i>Additive ANOVA for Genotypes by Environment Interaction (GEI) model</i>
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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)

Muhammad Yaseen (<myaseen208@gmail.com>)

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)

Muhammad Yaseen (<myaseen208@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.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)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

ANOVA of Eberhart & Russel's Model

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)

Muhammad Yaseen (<myaseen208@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.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)

Muhammad Yaseen (<myaseen208@gmail.com>)

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

Calculates 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)

Muhammad Yaseen (<myaseen208@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.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

Calculates 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)

Muhammad Yaseen (<myaseen208@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.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)

Muhammad Yaseen (<myaseen208@gmail.com>)

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
  )
```

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)

Muhammad Yaseen (<myaseen208@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.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)

Muhammad Yaseen (<myaseen208@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.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)

Muhammad Yaseen (<myaseen208@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.StabReg <-
  stab_reg(
    .data = ge_data
    , .y   = Yield
    , .rep = Rep
    , .gen = Gen
    , .env = Env
  )

Yield.StabReg
```

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