

Package ‘ammistability’

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Type Package

Title Additive Main Effects and Multiplicative Interaction Model Stability Parameters

Version 0.1.4

Description Computes various stability parameters from Additive Main Effects and Multiplicative Interaction (AMMI) analysis results such as Modified AMMI Stability Value (MASV), Sums of the Absolute Value of the Interaction Principal Component Scores (SIPC), Sum Across Environments of Genotype-Environment Interaction Modelled by AMMI (AMGE), Sum Across Environments of Absolute Value of Genotype-Environment Interaction Modelled by AMMI (AV_(AMGE)), AMMI Stability Index (ASI), Modified ASI (MASI), AMMI Based Stability Parameter (ASTAB), Annicchiarico's D Parameter (DA), Zhang's D Parameter (DZ), Averages of the Squared Eigenvector Values (EV), Stability Measure Based on Fitted AMMI Model (FA), Absolute Value of the Relative Contribution of IPCs to the Interaction (Za). Further calculates the Simultaneous Selection Index for Yield and Stability from the computed stability parameters. See the vignette for complete list of citations for the methods implemented.

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Encoding UTF-8

Depends R (>= 3.5.0)

VignetteBuilder knitr

RoxygenNote 7.2.3

Imports agricolae,
ggcorrplot,
ggplot2,
methods,
reshape2,
stats,
Rdpack,
mathjaxr

Suggests knitr,
rmarkdown,
pander,
XML,
httr,
RCurl

RdMacros Rdpack,
mathjaxr

URL <https://github.com/ajaygpb/ammistability/>
<https://CRAN.R-project.org/package=ammistability>
<https://ajaygpb.github.io/ammistability/>
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BugReports <https://github.com/ajaygpb/ammistability/issues>

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AMGE . AMMI	<i>Sum Across Environments of GEI Modelled by AMMI</i>
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Description

AMGE.AMMI computes the Sum Across Environments of Genotype-Environment Interaction (GEI) Modelled by AMMI (AMGE) (Sneller et al. 1997) considering all significant interaction principal components (IPCs) in the AMMI model. Using AMGE, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

AMGE.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)

Arguments

model	The AMMI model (An object of class AMMI generated by AMMI).
n	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
alpha	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
ssi.method	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Sum Across Environments of GEI Modelled by AMMI (*AMGE*) (Sneller et al. 1997) is computed as follows:

$$AMGE = \sum_{j=1}^E \sum_{n=1}^{N'} \lambda_n \gamma_{in} \delta_{jn}$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for i th genotype; and δ_{jn} is the eigenvector value for the j th environment.

Value

A data frame with the following columns:

AMGE	The AMGE values.
SSI	The computed values of simultaneous selection index for yield and stability.
rAMGE	The ranks of AMGE values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Sneller CH, Kilgore-Norquest L, Dombek D (1997). "Repeatability of yield stability statistics in soybean." *Crop Science*, **37**(2), 383–390.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
AMGE.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
AMGE.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
AMGE.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
AMGE.AMMI(model, ssi.method = "rao", a = 0.43)
```

ammistability

Estimate multiple AMMI model Stability Parameters

Description

ammistability computes multiple stability parameters from an AMMI model. Further, the corresponding Simultaneous Selection Indices for Yield and Stability (SSI) are also calculated according to the argument `ssi.method`. From the results, correlation between the computed indices will also be computed. The resulting correlation matrices will be plotted as correlograms. For visual comparisons of ranks of genotypes for different indices, slopegraphs and heatmaps will also be generated by this function.

Usage

```
ammistability(
  model,
  n,
  alpha = 0.05,
  ssi.method = c("farshadfar", "rao"),
  a = 1,
  AMGE = TRUE,
```

```

    ASI = TRUE,
    ASV = TRUE,
    ASTAB = TRUE,
    AVAMGE = TRUE,
    DA = TRUE,
    DZ = TRUE,
    EV = TRUE,
    FA = TRUE,
    MASI = TRUE,
    MASV = TRUE,
    SIPC = TRUE,
    ZA = TRUE,
    force.grouping = TRUE,
    line.size = 1,
    line.alpha = 0.5,
    line.col = NULL,
    point.size = 1,
    point.alpha = 0.5,
    point.col = NULL,
    text.size = 2
  )

```

Arguments

model	The AMMI model (An object of class AMMI generated by AMMI).
n	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
alpha	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
ssi.method	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).
AMGE	If TRUE, computes AMGE (see Details). Default is TRUE.
ASI	If TRUE, computes ASI (see Details). n = 2 will be used in this case. Default is TRUE.
ASV	If TRUE, computes ASV (see Details). n = 2 will be used in this case. Default is TRUE.
ASTAB	If TRUE, computes ASTAB (see Details). Default is TRUE.
AVAMGE	If TRUE, computes AVAMGE (see Details). Default is TRUE.
DA	If TRUE, computes DA (see Details). Default is TRUE.
DZ	If TRUE, computes DZ (see Details). Default is TRUE.
EV	If TRUE, computes EV (see Details). Default is TRUE.
FA	If TRUE, computes FA (see Details). Default is TRUE.
MASI	If TRUE, computes MASI (see Details). Default is TRUE.
MASV	If TRUE, computes MASV (see Details). Default is TRUE.
SIPC	If TRUE, computes SIPC (see Details). Default is TRUE.
ZA	If TRUE, computes ZA (see Details). Default is TRUE.

<code>force.grouping</code>	If TRUE, genotypes will be considered as a grouping variable for plotting the slopegraphs. (Each genotype will be represented by a different colour in the slopegraphs). Default is TRUE.
<code>line.size</code>	Size of lines plotted in the slopegraphs. Must be numeric.
<code>line.alpha</code>	Transparency of lines plotted in the slopegraphs. Must be numeric.
<code>line.col</code>	Default is TRUE. Overrides colouring by <code>force.grouping</code> argument.
<code>point.size</code>	Size of points plotted in the slopegraphs. Must be numeric.
<code>point.alpha</code>	Transparency of points plotted in the slopegraphs. Must be numeric.
<code>point.col</code>	Default is TRUE. Overrides colouring by <code>force.grouping</code> argument.
<code>text.size</code>	Size of text annotations plotted in the slopegraphs. Must be numeric.

Details

ammistability computes the following stability parameters from an AMMI model.

Sum Across Environments of GEI Modelled by AMMI (AMGE) Sneller et al. (1997)

AMMI Stability Index (ASI) Jambhulkar et al. (2014); Jambhulkar et al. (2015); Jambhulkar et al. (2017)

AMMI Stability Value (ASV) Purchase (1997); Purchase et al. (1999); Purchase et al. (2000)

AMMI Based Stability Parameter (ASTAB) Rao and Prabhakaran (2005)

Sum Across Environments of Absolute Value of GEI Modelled by AMMI (AVAMGE) Zali et al. (2012)

Annicchiarico's D Parameter (DA) Annicchiarico (1997)

Zhang's D Parameter (DZ) Zhang et al. (1998)

Averages of the Squared Eigenvector Values (EV) Zobel (1994)

Stability Measure Based on Fitted AMMI Model (FA) Raju (2002)

Modified AMMI Stability Index (MASI) Ajay et al. (2018)

Modified AMMI Stability Value (MASV) Zali et al. (2012); Ajay et al. (2019)

Sums of the Absolute Value of the IPC Scores (SIPC) Sneller et al. (1997)

Absolute Value of the Relative Contribution of IPCs to the Interaction (Za) Zali et al. (2012)

Value

A list with the following components:

Details	A data frame indicating the stability parameters computed and the method used for computing the SSI.
Stability Parameters	A data frame of computed stability parameters.
Simultaneous Selection Indices	A data frame of computed SSIs.
SP Correlation	A data frame of correlation between stability parameters.
SSI Correlation	A data frame of correlation between SSIs.
SP and SSI Correlation	A data frame of correlation between stability parameters and SSIs.

SP Correlogram	Correlogram of stability parameters.
SSI Correlogram	Correlogram of SSIs.
SP and SSI Correlogram	Correlogram of stability parameters and SSIs.
SP Slopegraph	Slopegraph of stability parameter ranks.
SSI Slopegraph	Slopegraph of SSI ranks.
SP Heatmap	Heatmap of stability parameter ranks.
SSI Heatmap	Heatmap of SSI ranks.

References

- Ajay BC, Aravind J, Abdul Fiyaz R, Bera SK, Kumar N, Gangadhar K, Kona P (2018). “Modified AMMI Stability Index (MASI) for stability analysis.” *ICAR-DGR Newsletter*, **18**, 4–5.
- Ajay BC, Aravind J, Fiyaz RA (2019). “ammistability: R package for ranking genotypes based on stability parameters derived from AMMI model.” *Indian Journal of Genetics and Plant Breeding (The)*, **79**(2), 460–466.
- Annicchiarico P (1997). “Joint regression vs AMMI analysis of genotype-environment interactions for cereals in Italy.” *Euphytica*, **94**(1), 53–62.
- Jambhulkar NN, Bose LK, Pande K, Singh ON (2015). “Genotype by environment interaction and stability analysis in rice genotypes.” *Ecology, Environment and Conservation*, **21**(3), 1427–1430.
- Jambhulkar NN, Bose LK, Singh ON (2014). “AMMI stability index for stability analysis.” In Mohapatra T (ed.), *CRRI Newsletter, January-March 2014*, volume 35(1), 15. Central Rice Research Institute, Cuttack, Orissa.
- Jambhulkar NN, Rath NC, Bose LK, Subudhi HN, Biswajit M, Lipi D, Meher J (2017). “Stability analysis for grain yield in rice in demonstrations conducted during rabi season in India.” *Oryza*, **54**(2), 236–240.
- Purchase JL (1997). *Parametric analysis to describe genotype \times environment interaction and yield stability in winter wheat*. Ph.D. Thesis, University of the Orange Free State.
- Purchase JL, Hatting H, van Deventer CS (1999). “The use of the AMMI model and AMMI stability value to describe genotype \times environment interaction and yield stability in winter wheat (*Triticum aestivum* L.).” In *Proceedings of the Tenth Regional Wheat Workshop for Eastern, Central and Southern Africa, 14-18 September 1998*. University of Stellenbosch, South Africa.
- Purchase JL, Hatting H, van Deventer CS (2000). “Genotype \times environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance.” *South African Journal of Plant and Soil*, **17**(3), 101–107.
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Sneller CH, Kilgore-Norquest L, Dombek D (1997). "Repeatability of yield stability statistics in soybean." *Crop Science*, **37**(2), 383–390.

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype \times environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136.

Zhang Z, Lu C, Xiang Z (1998). "Analysis of variety stability based on AMMI model." *Acta Agronomica Sinica*, **24**(3), 304–309.

Zobel RW (1994). "Stress resistance and root systems." In *Proceedings of the Workshop on Adaptation of Plants to Soil Stress. 1-4 August, 1993. INTSORMIL Publication 94-2*, 80–99. Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln.

See Also

[AMMI](#), [AMGE.AMMI](#), [ASI.AMMI](#), [ASTAB.AMMI](#), [AMGE.AMMI](#), [DA.AMMI](#), [DZ.AMMI](#), [EV.AMMI](#), [FA.AMMI](#), [MASV.AMMI](#), [SIPC.AMMI](#), [ZA.AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

ammistability(model, AMGE = TRUE, ASI = FALSE, ASV = TRUE, ASTAB = FALSE,
               AVAMGE = FALSE, DA = FALSE, DZ = FALSE, EV = TRUE,
               FA = FALSE, MASI = FALSE, MASV = TRUE, SIPC = TRUE,
               ZA = FALSE)
```

ASI.AMMI

AMMI Stability Index

Description

ASI.AMMI computes the AMMI Stability Index (ASI) (Jambhulkar et al. 2014; Jambhulkar et al. 2015; Jambhulkar et al. 2017) considering the first two interaction principal components (IPCs) in the AMMI model. Using ASI, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
ASI.AMMI(model, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The AMMI Stability Index (*ASI*) (Jambhulkar et al. 2014; Jambhulkar et al. 2015; Jambhulkar et al. 2017) is computed as follows:

$$ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$$

Where, PC_1 and PC_2 are the scores of 1st and 2nd IPCs respectively; and θ_1 and θ_2 are percentage sum of squares explained by the 1st and 2nd principal component interaction effect respectively.

Value

A data frame with the following columns:

ASI	The ASI values.
SSI	The computed values of simultaneous selection index for yield and stability.
rASI	The ranks of ASI values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Jambhulkar NN, Bose LK, Pande K, Singh ON (2015). “Genotype by environment interaction and stability analysis in rice genotypes.” *Ecology, Environment and Conservation*, **21**(3), 1427–1430.

Jambhulkar NN, Bose LK, Singh ON (2014). “AMMI stability index for stability analysis.” In Mohapatra T (ed.), *CRRI Newsletter, January-March 2014*, volume 35(1), 15. Central Rice Research Institute, Cuttack, Orissa.

Jambhulkar NN, Rath NC, Bose LK, Subudhi HN, Biswajit M, Lipi D, Meher J (2017). “Stability analysis for grain yield in rice in demonstrations conducted during rabi season in India.” *Oryza*, **54**(2), 236–240.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
```

```

model$biplot

# GxE matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default ssi.method (farshadfar)
ASI.AMMI(model)

# With ssi.method = "rao"
ASI.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
ASI.AMMI(model, ssi.method = "rao", a = 0.43)

```

ASTAB.AMMI

AMMI Based Stability Parameter

Description

ASTAB.AMMI computes the AMMI Based Stability Parameter (ASTAB) (Rao and Prabhakaran 2005) considering all significant interaction principal components (IPCs) in the AMMI model. Using ASTAB, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
ASTAB.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The AMMI Based Stability Parameter value (*ASTAB*) (Rao and Prabhakaran 2005) is computed as follows:

$$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for i th genotype.

Value

A data frame with the following columns:

ASTAB	The ASTAB values.
SSI	The computed values of simultaneous selection index for yield and stability.
rASTAB	The ranks of ASTAB values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Rao AR, Prabhakaran VT (2005). "Use of AMMI in simultaneous selection of genotypes for yield and stability." *Journal of the Indian Society of Agricultural Statistics*, **59**, 76–82.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
ASTAB.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
ASTAB.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
ASTAB.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
ASTAB.AMMI(model, ssi.method = "rao", a = 0.43)
```

AVAMGE.AMMI	<i>Sum Across Environments of Absolute Value of GEI Modelled by AMMI</i>
-------------	--

Description

AVAMGE.AMMI computes the Sum Across Environments of Absolute Value of GEI Modelled by AMMI (AVAMGE) (Zali et al. 2012) considering all significant interaction principal components (IPCs) in the AMMI model. Using AVAMGE, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
AVAMGE.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Sum Across Environments of Absolute Value of GEI Modelled by AMMI ($AV_{(AMGE)}$) (Zali et al. 2012) is computed as follows:

$$AV_{(AMGE)} = \sum_{j=1}^E \sum_{n=1}^{N'} |\lambda_n \gamma_{in} \delta_{jn}|$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for i th genotype; and δ_{jn} is the eigenvector value for the j th environment.

Value

A data frame with the following columns:

AVAMGE	The AVAMGE values.
SSI	The computed values of simultaneous selection index for yield and stability.
rAVAMGE	The ranks of AVAMGE values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype \times environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
AVAMGE.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
AVAMGE.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
AVAMGE.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
AVAMGE.AMMI(model, ssi.method = "rao", a = 0.43)
```

DA.AMMI

Annicchiarico's D Parameter

Description

DA.AMMI computes the Annicchiarico's D Parameter values (D_a) (Annicchiarico 1997) considering all significant interaction principal components (IPCs) in the AMMI model. It is the unsquared Euclidean distance from the origin of significant IPC axes in the AMMI model. Using D_a , the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
DA.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Annicchiarico's D Parameter value (D_a) (Annicchiarico 1997) is computed as follows:

$$D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for i th genotype.

Value

A data frame with the following columns:

DA	The DA values.
SSI	The computed values of simultaneous selection index for yield and stability.
rDA	The ranks of DA values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Annicchiarico P (1997). "Joint regression vs AMMI analysis of genotype-environment interactions for cereals in Italy." *Euphytica*, **94**(1), 53–62.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# GxE matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
DA.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
DA.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
DA.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
DA.AMMI(model, ssi.method = "rao", a = 0.43)
```

DZ.AMMI

Zhang's D Parameter

Description

DZ.AMMI computes the Zhang's D Parameter values or AMMI statistic coefficient or AMMI distance or AMMI stability index (D_z) (Zhang et al. 1998) considering all significant interaction principal components (IPCs) in the AMMI model. It is the distance of IPC point from origin in space. Using D_z , the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
DZ.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.

alpha	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
ssi.method	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Zhang's D Parameter value (D_z) (Zhang et al. 1998) is computed as follows:

$$D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); and γ_{in} is the eigenvector value for i th genotype.

Value

A data frame with the following columns:

DZ	The DZ values.
SSI	The computed values of simultaneous selection index for yield and stability.
rDZ	The ranks of DZ values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Zhang Z, Lu C, Xiang Z (1998). "Analysis of variety stability based on AMMI model." *Acta Agronomica Sinica*, **24**(3), 304–309.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
```



```

model$biplot

# GxE matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
DZ.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
DZ.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
DZ.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
DZ.AMMI(model, ssi.method = "rao", a = 0.43)

```

EV.AMMI

*Averages of the Squared Eigenvector Values***Description**

EV.AMMI computes the Sums of the Averages of the Squared Eigenvector Values (EV) (Zobel 1994) considering all significant interaction principal components (IPCs) in the AMMI model. Using EV, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
EV.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Averages of the Squared Eigenvector Values (*EV*) (Zobel 1994) is computed as follows:

$$EV = \sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); and γ_{in} is the eigenvector value for i th genotype.

Value

A data frame with the following columns:

EV	The EV values.
SSI	The computed values of simultaneous selection index for yield and stability.
rEV	The ranks of EV values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Zobel RW (1994). "Stress resistance and root systems." In *Proceedings of the Workshop on Adaptation of Plants to Soil Stress. 1-4 August, 1993. INTSORMIL Publication 94-2*, 80–99. Institute of Agriculture and Natural Resources, University of Nebraska-Lincoln.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
EV.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
EV.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
EV.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
EV.AMMI(model, ssi.method = "rao", a = 0.43)
```

Description

FA.AMMI computes the Stability Measure Based on Fitted AMMI Model (FA) (Raju 2002) considering all significant interaction principal components (IPCs) in the AMMI model. Using FA, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
FA.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Stability Measure Based on Fitted AMMI Model (*FA*) (Raju 2002) is computed as follows:

$$FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for i th genotype.

When N' is replaced by 1 (only first IPC axis is considered for computation), then the parameter *FP* can be estimated (Zali et al. 2012).

$$FP = \lambda_1^2 \gamma_{i1}^2$$

When N' is replaced by 2 (only first two IPC axes are considered for computation), then the parameter *B* can be estimated (Zali et al. 2012).

$$B = \sum_{n=1}^2 \lambda_n^2 \gamma_{in}^2$$

When N' is replaced by N (All the IPC axes are considered for computation), then the parameter estimated is equivalent to Wricke's ecovalence ($W_{(AMMI)}$) (Wricke 1962; Zali et al. 2012).

$$W_{(AMMI)} = \sum_{n=1}^N \lambda_n^2 \gamma_{in}^2$$

Value

A data frame with the following columns:

FA	The FA values.
SSI	The computed values of simultaneous selection index for yield and stability.
rFA	The ranks of FA values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Raju BMK (2002). “A study on AMMI model and its biplots.” *Journal of the Indian Society of Agricultural Statistics*, **55**(3), 297–322.

Wricke G (1962). “On a method of understanding the biological diversity in field research.” *Zeitschrift für Pflanzenzüchtung*, **47**, 92–146.

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). “Evaluation of genotype \times environment interaction in chickpea using measures of stability from AMMI model.” *Annals of Biological Research*, **3**(7), 3126–3136.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
FA.AMMI(model)
```

```
# With n = 4 and default ssi.method (farshadfar)
FA.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
FA.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
FA.AMMI(model, ssi.method = "rao", a = 0.43)
```

MASI.AMMI

Modified AMMI Stability Index

Description

MASI.AMMI computes the Modified AMMI Stability Index (MASI) (Ajay et al. 2018) from a modified formula of AMMI Stability Index (ASI) (Jambhulkar et al. 2014; Jambhulkar et al. 2015; Jambhulkar et al. 2017). Unlike ASI, MASI calculates stability value considering all significant interaction principal components (IPCs) in the AMMI model. Using MASI, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
MASI.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Modified AMMI Stability Index (*MASI*) (Ajay et al. 2018) is computed as follows:

$$MASI = \sqrt{\sum_{n=1}^{N'} PC_n^2 \times \theta_n^2}$$

Where, PC_n are the scores of n th IPC; and θ_n is the percentage sum of squares explained by the n th principal component interaction effect.

Value

A data frame with the following columns:

MASI	The MASI values.
SSI	The computed values of simultaneous selection index for yield and stability.
rMASI	The ranks of MASI values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Ajay BC, Aravind J, Abdul Fiyaz R, Bera SK, Kumar N, Gangadhar K, Kona P (2018). “Modified AMMI Stability Index (MASI) for stability analysis.” *ICAR-DGR Newsletter*, **18**, 4–5.

Jambhulkar NN, Bose LK, Pande K, Singh ON (2015). “Genotype by environment interaction and stability analysis in rice genotypes.” *Ecology, Environment and Conservation*, **21**(3), 1427–1430.

Jambhulkar NN, Bose LK, Singh ON (2014). “AMMI stability index for stability analysis.” In Mohapatra T (ed.), *CRRI Newsletter, January-March 2014*, volume 35(1), 15. Central Rice Research Institute, Cuttack, Orissa.

Jambhulkar NN, Rath NC, Bose LK, Subudhi HN, Biswajit M, Lipi D, Meher J (2017). “Stability analysis for grain yield in rice in demonstrations conducted during rabi season in India.” *Oryza*, **54**(2), 236–240.

See Also

[AMMI](#), [ASI.AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
MASI.AMMI(model)
```

```
# With n = 4 and default ssi.method (farshadfar)
MASI.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
MASI.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
MASI.AMMI(model, ssi.method = "rao", a = 0.43)

# ASI.AMMI same as MASI.AMMI with n = 2

a <- ASI.AMMI(model)
b <- MASI.AMMI(model, n = 2)

identical(a$ASI, b$MASI)
```

MASV.AMMI

*Modified AMMI Stability Value***Description**

MASV.AMMI computes the Modified AMMI Stability Value (MASV) (Zali et al. 2012; Ajay et al. 2019) (Please see **Note**) from a modified formula of AMMI Stability Value (ASV) (Purchase 1997). This formula calculates AMMI stability value considering all significant interaction principal components (IPCs) in the AMMI model. Using MASV, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
MASV.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Modified AMMI Stability Value (*MASV*) (Ajay et al. 2019) is computed as follows:

$$MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} \times PC_n \right)^2 + (PC_{N'})^2}$$

Where, $SSIPC_1, SSIPC_2, \dots, SSIPC_n$ are the sum of squares of the 1st, 2nd, ..., and n th IPC; and PC_1, PC_2, \dots, PC_n are the scores of 1st, 2nd, ..., and n th IPC.

Value

A data frame with the following columns:

MASV	The MASV values.
SSI	The computed values of simultaneous selection index for yield and stability.
rMASV	The ranks of MASV values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

Note

In Zali et al. (2012), the formula for both AMMI stability value (ASV) was found to be erroneous, when compared with the original publications (Purchase 1997; Purchase et al. 1999; Purchase et al. 2000).

ASV (Zali et al. 2012)

$$ASV = \sqrt{\left(\frac{SSIPC_1}{SSIPC_2}\right) \times (PC_1)^2 + (PC_2)^2}$$

ASV (Purchase 1997; Purchase et al. 1999; Purchase et al. 2000)

$$ASV = \sqrt{\left(\frac{SSIPC_1}{SSIPC_2} \times PC_1\right)^2 + (PC_2)^2}$$

The authors believe that the proposed Modified AMMI stability value (MASV) in Zali et al. (2012) is also erroneous and have implemented the corrected one in MASV.AMMI (Ajay et al. 2019).

MASV (Zali et al. 2012)

$$MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}}\right) \times (PC_n)^2 + (PC_{N'})^2}$$

References

- Ajay BC, Aravind J, Fiyaz RA, Kumar N, Lal C, Gangadhar K, Kona P, Dagla MC, Bera SK (2019). "Rectification of modified AMMI stability value (MASV)." *Indian Journal of Genetics and Plant Breeding (The)*, **79**, 726–731.
- Purchase JL (1997). *Parametric analysis to describe genotype \times environment interaction and yield stability in winter wheat*. Ph.D. Thesis, University of the Orange Free State.
- Purchase JL, Hatting H, van Deventer CS (1999). "The use of the AMMI model and AMMI stability value to describe genotype \times environment interaction and yield stability in winter wheat (*Triticum aestivum* L.)." In *Proceedings of the Tenth Regional Wheat Workshop for Eastern, Central and Southern Africa, 14-18 September 1998*. University of Stellenbosch, South Africa.

Purchase JL, Hatting H, van Deventer CS (2000). “Genotype \times environment interaction of winter wheat (*Triticum aestivum* L.) in South Africa: II. Stability analysis of yield performance.” *South African Journal of Plant and Soil*, **17**(3), 101–107.

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). “Evaluation of genotype \times environment interaction in chickpea using measures of stability from AMMI model.” *Annals of Biological Research*, **3**(7), 3126–3136.

See Also

[AMMI](#), [index.AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
MASV.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
MASV.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
MASV.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
MASV.AMMI(model, ssi.method = "rao", a = 0.43)
```

rankdf

Ranks in a data.frame

Description

Ranks in a data.frame

Usage

```
rankdf(df, increasing = NULL, decreasing = NULL, ...)
```

Arguments

<code>df</code>	A data frame.
<code>increasing</code>	A character vector of column names of the data frame to be ranked in increasing order.
<code>decreasing</code>	A character vector of column names of the data frame to be ranked in decreasing order.
<code>...</code>	Additional arguments to be passed on to <code>rank()</code> .

Value

A data frame with the ranks computed in the columns specified in arguments `increasing` and `decreasing`.

Examples

```
library(agricolae)
data(soil)

dec <- c("pH", "EC")
inc <- c("CaCO3", "M0", "CIC", "P", "K", "sand",
        "slime", "clay", "Ca", "Mg", "K2", "Na", "Al_H", "K_Mg", "Ca_Mg",
        "B", "Cu", "Fe", "Mn", "Zn")

soilrank <- rankdf(soil, increasing = inc, decreasing = dec)
soilrank
```

rankslopegraph

Rank Slopegraph

Description

Create a slopegraph or bump chart from a data frame of ranks.

Usage

```
rankslopegraph(
  df,
  names,
  group,
  force.grouping = TRUE,
  line.size = 1,
  line.alpha = 0.5,
  line.col = NULL,
  point.size = 1,
  point.alpha = 0.5,
  point.col = NULL,
  text.size = 2,
  legend.position = "bottom"
)
```

Arguments

<code>df</code>	A data frame of records.
<code>names</code>	The name of the column having the names of the records.
<code>group</code>	Optional. The name of the column with a grouping variable.
<code>force.grouping</code>	If TRUE, the column specified in the argument <code>names</code> will be considered as a grouping variable for plotting the slopegraphs. (Each record will be represented by a different colour). Default is TRUE.
<code>line.size</code>	Size of lines plotted. Must be numeric.
<code>line.alpha</code>	Transparency of lines plotted. Must be numeric.
<code>line.col</code>	Default is TRUE. Overrides colouring by <code>force.grouping</code> argument.
<code>point.size</code>	Size of points plotted. Must be numeric.
<code>point.alpha</code>	Transparency of points plotted. Must be numeric.
<code>point.col</code>	Default is TRUE. Overrides colouring by <code>force.grouping</code> argument.
<code>text.size</code>	Size of text annotations plotted. Must be numeric.
<code>legend.position</code>	Position of the legend in the plot.

Value

The slopegraph as a ggplot2 grob.

References

Tufte ER (1986). *The Visual Display of Quantitative Information*. Graphics Press, Cheshire, CT, USA. ISBN 0-9613921-0-X.

Examples

```
library(agricolae)
data(soil)

dec <- c("pH", "EC")
inc <- c("CaCO3", "M0", "CIC", "P", "K", "sand",
        "slime", "clay", "Ca", "Mg", "K2", "Na", "Al_H", "K_Mg", "Ca_Mg",
        "B", "Cu", "Fe", "Mn", "Zn")

soilrank <- rankdf(soil, increasing = inc, decreasing = dec)
soilrank
soilslopeg <- rankslopegraph(soilrank, names = "place")
soilslopeg
```

Description

SIPC.AMMI computes the Sums of the Absolute Value of the IPC Scores (ASI) (Sneller et al. 1997) considering all significant interaction principal components (IPCs) in the AMMI model. Using SIPC, the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
SIPC.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Sums of the Absolute Value of the IPC Scores (*SIPC*) (Sneller et al. 1997) is computed as follows:

$$SIPC = \sum_{n=1}^{N'} |\lambda_n^{0.5} \gamma_{in}|$$

OR

$$SIPC = \sum_{n=1}^{N'} |PC_n|$$

Where, N' is the number of significant IPCs (number of IPC that were retained in the AMMI model via F tests); λ_n is the singular value for n th IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for i th genotype; and PC_1, PC_2, \dots, PC_n are the scores of 1st, 2nd, ..., and n th IPC.

The closer the SIPC scores are to zero, the more stable the genotypes are across test environments.

Value

A data frame with the following columns:

SIPC	The SIPC values.
SSI	The computed values of simultaneous selection index for yield and stability.
rSIPC	The ranks of SIPC values.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Sneller CH, Kilgore-Norquest L, Dombek D (1997). “Repeatability of yield stability statistics in soybean.” *Crop Science*, **37**(2), 383–390.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
SIPC.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
SIPC.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
SIPC.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
SIPC.AMMI(model, ssi.method = "rao", a = 0.43)
```

Description

SSI computes the Simultaneous Selection Index for Yield and Stability (SSI) according to the methods specified in the argument method.

Usage

```
SSI(y, sp, gen, method = c("farshadfar", "rao"), a = 1)
```

Arguments

y	A numeric vector of the mean yield/performance of genotypes.
sp	A numeric vector of the stability parameter/index of the genotypes.
gen	A character vector of the names of the genotypes.
method	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See Details).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See Details).

Details

The SSI according to Rao and Prabhakaran (2005) (I_i) is computed as follows:

$$I_i = \frac{\bar{Y}_i}{\bar{Y}_{..}} + \alpha \frac{\frac{1}{SP_i}}{\frac{1}{T} \sum_{i=1}^T \frac{1}{SP_i}}$$

Where SP_i is the stability measure of the i th genotype under AMMI procedure; \bar{Y}_i is mean performance of i th genotype; $\bar{Y}_{..}$ is the overall mean; T is the number of genotypes under test and α is the ratio of the weights given to the stability components (w_2) and yield (w_1) with a restriction that $w_1 + w_2 = 1$. The weights can be specified as required.

α	w_1	w_2
1.00	0.5	0.5
0.67	0.6	0.4
0.43	0.7	0.3
0.25	0.8	0.2

The SSI proposed by Farshadfar (2008) is called the Genotype stability index (GSI) or Yield stability index (YSI) (Farshadfar et al. 2011) and is computed by summation of the ranks of the stability index/parameter and the ranks of the mean yields.

$$GSI = YSI = R_{SP} + R_Y$$

Where, R_{SP} is the stability parameter/index rank of the genotype and R_Y is the mean yield rank of the genotype.

Value

A data frame with the following columns:

SP	The stability parameter values.
SSI	The computed values of simultaneous selection index for yield and stability.
rSP	The ranks of the stability parameter.
rY	The ranks of the mean yield of genotypes.
means	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Farshadfar E (2008). "Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat." *Pakistan Journal of biological sciences*, **11**(14), 1791.

Farshadfar E, Mahmodi N, Yaghotipoor A (2011). "AMMI stability value and simultaneous estimation of yield and yield stability in bread wheat (*Triticum aestivum* L.)." *Australian Journal of Crop Science*, **5**(13), 1837–1844.

Rao AR, Prabhakaran VT (2005). "Use of AMMI in simultaneous selection of genotypes for yield and stability." *Journal of the Indian Society of Agricultural Statistics*, **59**, 76–82.

See Also

[AMGE.AMMI](#), [ASI.AMMI](#), [ASTAB.AMMI](#), [AVAMGE.AMMI](#), [DA.AMMI](#), [DZ.AMMI](#), [EV.AMMI](#), [FA.AMMI](#), [MASV.AMMI](#), [SIPC.AMMI](#), [ZA.AMMI](#)

Examples

```
library(agricolae)
data(plrv)
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console=FALSE))

yield <- aggregate(model$means$Yield, by= list(model$means$GEN),
  FUN=mean, na.rm=TRUE)[,2]
stab <- DZ.AMMI(model)$DZ
genotypes <- rownames(DZ.AMMI(model))

# With default ssi.method (farshadfar)
SSI(y = yield, sp = stab, gen = genotypes)

# With ssi.method = "rao"
SSI(y = yield, sp = stab, gen = genotypes, method = "rao")

# Changing the ratio of weights for Rao's SSI
SSI(y = yield, sp = stab, gen = genotypes, method = "rao", a = 0.43)
```

ZA.AMMI

*Absolute Value of the Relative Contribution of IPCs to the Interaction***Description**

ZA.AMMI computes the Absolute Value of the Relative Contribution of IPCs to the Interaction (Z_a) (Zali et al. 2012) considering all significant interaction principal components (IPCs) in the AMMI model. Using Z_a , the Simultaneous Selection Index for Yield and Stability (SSI) is also calculated according to the argument `ssi.method`.

Usage

```
ZA.AMMI(model, n, alpha = 0.05, ssi.method = c("farshadfar", "rao"), a = 1)
```

Arguments

<code>model</code>	The AMMI model (An object of class AMMI generated by AMMI).
<code>n</code>	The number of principal components to be considered for computation. The default value is the number of significant IPCs.
<code>alpha</code>	Type I error probability (Significance level) to be considered to identify the number of significant IPCs.
<code>ssi.method</code>	The method for the computation of simultaneous selection index. Either "farshadfar" or "rao" (See SSI).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See SSI).

Details

The Absolute Value of the Relative Contribution of IPCs to the Interaction (Z_a) (Zali et al. 2012) is computed as follows:

$$Z_a = \sum_{i=1}^{N'} |\theta_n \gamma_{in}|$$

Where, N' is the number of significant IPCAs (number of IPC that were retained in the AMMI model via F tests); γ_{in} is the eigenvector value for i th genotype; and θ_n is the percentage sum of squares explained by the n th principal component interaction effect..

Value

A data frame with the following columns:

<code>Za</code>	The Z_a values.
<code>SSI</code>	The computed values of simultaneous selection index for yield and stability.
<code>rZa</code>	The ranks of Z_a values.
<code>rY</code>	The ranks of the mean yield of genotypes.
<code>means</code>	The mean yield of the genotypes.

The names of the genotypes are indicated as the row names of the data frame.

References

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype \times environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136.

See Also

[AMMI](#), [SSI](#)

Examples

```
library(agricolae)
data(plrv)

# AMMI model
model <- with(plrv, AMMI(Locality, Genotype, Rep, Yield, console = FALSE))

# ANOVA
model$ANOVA

# IPC F test
model$analysis

# Mean yield and IPC scores
model$biplot

# G×E matrix (deviations from mean)
array(model$genXenv, dim(model$genXenv), dimnames(model$genXenv))

# With default n (N') and default ssi.method (farshadfar)
ZA.AMMI(model)

# With n = 4 and default ssi.method (farshadfar)
ZA.AMMI(model, n = 4)

# With default n (N') and ssi.method = "rao"
ZA.AMMI(model, ssi.method = "rao")

# Changing the ratio of weights for Rao's SSI
ZA.AMMI(model, ssi.method = "rao", a = 0.43)
```

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