Package 'AMMIStbP'

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Type Package

Title Additive Main Effects and Multiplicative Interaction Model Stability Parameters

Version 0.0.0.9000

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.

License GPL-2 | GPL-3

Encoding UTF-8

Depends R (>= 3.0.1)

VignetteBuilder knitr

RoxygenNote 6.0.1

Imports agricolae, ggcorrplot, Rdpack

Suggests knitr, rmarkdown, pander

RdMacros Rdpack

URL http://github.com/ajaygpb/AMMIStbp

BugReports http://github.com/ajaygpb/AMMIStbp/issues

R topics documented:

`AMGE.AMMI` *Sum Across Environments of GEI Modelled by AMMI*

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 ($AMGE$) 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 nth IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for ith genotype; and δjn is the eigenvector value for the jth 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. doi: 10.2135/cropsci1997.0011183X003700020013x.

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`.

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)
```

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`).
`point.col`	

Details

`ammistability` computes the following stability parameters from an AMMI model.

AMGE Sneller et al., 1997

ASI Jambhulkar et al., 2014; Jambhulkar et al., 2015; Jambhulkar et al., 2017

ASV Purchase 1997; Purchase et al., 1999; Purchase et al., 2000

ASTAB Rao and Prabhakaran, 2005

AVAMGE Zali et al., 2012

DA Annicchiarico, 1997

DZ Zhang, 1998

EV Zobel, 1994

FA Raju, 2002

MASI

MASV Zali et al., 2012

SIPC Sneller et al., 1997

ZA Zali et al., 2012

References

Zobel R (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.

Annicchiarico P (1997). "Joint regression vs AMMI analysis of genotype-environment interactions for cereals in Italy." *Euphytica*, **94**(1), 53–62. doi: 10.1023/A:1002954824178, https://link.springer.com/article/10.1023/A:1002954824178.

Purchase J (1997). *Parametric Analysis to Describe Genotype × Environment Interaction and Yield Stability in Winter Wheat*. PhD thesis, University of the Orange Free State. http://hdl.handle.net/11660/1966.

Sneller CH, Kilgore-Norquest L, Dombek D (1997). "Repeatability of yield stability statistics in soybean." *Crop Science*, **37**(2), 383–390. doi: 10.2135/cropsci1997.0011183X003700020013x.

Zhang Z, Lu C, Xiang Z (1998). "Analysis of variety stability based on AMMI model." *Acta Agronomica Sinica*, **24**(3), 304–309. http://zwxb.chinacrops.org/EN/Y1998/V24/I03/304.

Purchase J, Hatting H, Van Deventer C (1999). "The use of the AMMI model and AMMI stability value to describe genotype x 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, Deventer CSv (2000). "Genotype × 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. doi: 10.1080/02571862.2000.10634878.

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

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

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136. http://eprints.icrisat.ac.in/id/eprint/7173.

Jambhulkar NN, Bose LK, Singh ON (2014). "AMMI Stability Index for Stability Analysis." In Mohapatra T (ed.), *CRRI Newsletter, January-March 2014*, volume 35 number 1, 15. Central Rice Research Institute, Cuttack, Orissa. http://www.crri.nic.in/CRRI_newsletter/crnl_jan_mar_14_web.pdf.

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. http://www.envirobiotechjournals.com/article_abstract.php?aid=6346&iid=200&jid=3.

Jambhulkar N, Rath N, Bose L, Subudhi H, Biswajit M, Lipi D, Meher J, others (2017). "Stability analysis for grain yield in rice in demonstrations conducted during rabi season in India." *Oryza*, **54**(2), 236–240. doi: 10.5958/22495266.2017.00030.3.

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.AMMI

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

model	The AMMI model (An object of class AMMI generated by AMMI).
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 AMMI Stability Index (ASI) 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, Singh ON (2014). "AMMI Stability Index for Stability Analysis." In Mohapatra T (ed.), *CRRI Newsletter, January-March 2014*, volume 35 number 1, 15. Central Rice Research Institute, Cuttack, Orissa. http://www.crri.nic.in/CRRI_newsletter/crnl_jan_mar_14_web.pdf.

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. http://www.envirobiotechjournals.com/article_abstract.php?aid=6346&iid=200&jid=3.

Jambhulkar N, Rath N, Bose L, Subudhi H, Biswajit M, Lipi D, Meher J, others (2017). "Stability analysis for grain yield in rice in demonstrations conducted during rabi season in India." *Oryza*, **54**(2), 236–240. doi: 10.5958/22495266.2017.00030.3.

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 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

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 AMMI Based Stability Parameter value ($ASTAB$) 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 nth IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for ith 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 A, Prabhakaran V (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 *Sum Across Environments of Absolute Value of GEI Modelled by AMMI*

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

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 Absolute Value of GEI Modelled by AMMI ($AV_{(AMGE)}$) 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 nth IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for ith genotype; and δjn is the eigenvector value for the jth 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 × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136. http://eprints.icrisat.ac.in/id/eprint/7173.

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

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 Annicchiarico's D Parameter value (D_a) 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 nth IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for ith 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. doi: 10.1023/A:1002954824178, https://link.springer.com/article/10.1023/A:1002954824178.

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)
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, 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

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 Zhang's D Parameter value (D_z) 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 ith 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. http://zwxb.chinacrops.org/EN/Y1998/V24/I03/304.

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)
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

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 Averages of the Squared Eigenvector Values (EV) 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 ith 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 R (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)
```

FA.AMMI *Stability Measure Based on Fitted AMMI Model*

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

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 Stability Measure Based on Fitted AMMI Model (FA) 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 nth IPC and correspondingly λ_n^2 is its eigen value; and γ_{in} is the eigenvector value for ith 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

Wricke G (1962). "On a method of understanding the biological diversity in field research." *Zeitschrift fur Pflanzenzuchtung*, **47**, 92–146.

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

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136. http://eprints.icrisat.ac.in/id/eprint/7173.

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) 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

`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 Modified AMMI Stability Index ($MASI$) is computed as follows:

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

Where, PC_n are the scores of nth IPC; and θ_n is the percentage sum of squares explained by the nth 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.

See Also

AMMI, ASI, 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; Please see **Note**) from a modified formula of AMMI Stability Value (ASV) (Purchase et al. 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

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 Modified AMMI Stability Value ($MASV$) 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, $SSIPC_1$, $SSIPC_2$, $\cdots$, $SSIPC_n$ are the sum of squares of the 1st, 2nd, ..., and nth IPC; and PC_1, PC_2, $\cdots$, PC_n are the scores of 1st, 2nd, ..., and nth 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 erroneus, 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`.

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

Purchase J (1997). *Parametric Analysis to Describe Genotype × Environment Interaction and Yield Stability in Winter Wheat*. PhD thesis, University of the Orange Free State. http://hdl.handle.net/11660/1966.

Purchase J, Hatting H, Van Deventer C (1999). "The use of the AMMI model and AMMI stability value to describe genotype x 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, Deventer CSv (2000). "Genotype × 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. doi: 10.1080/02571862.2000.10634878.

Zali H, Farshadfar E, Sabaghpour SH, Karimizadeh R (2012). "Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136. http://eprints.icrisat.ac.in/id/eprint/7173.

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)
```

SIPC.AMMI *Sums of the Absolute Value of the IPC Scores*

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

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 Sums of the Absolute Value of the IPC Scores ($SIPC$) is computed as follows:

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

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 nth IPC and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for ith genotype; and PC_1, PC_2, $\cdots$, PC_n are the scores of 1st, 2nd, ..., and nth 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. doi: 10.2135/cropsci1997.0011183X003700020013x.

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)
```

SSI *Simultaneous Selection Indices for Yield and Stability*

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 paramter/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:

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

Where SP_i is the stability measure of the ith genotype under AMMI procedure; $\overline{Y}_i$ is mean performance of ith genotype; $\overline{Y}_{..}$ 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

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

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.

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 (Za) (Zali, 2012) considering all significant interaction principal components (IPCs) in the AMMI model. Using Za, 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

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 Absolute Value of the Relative Contribution of IPCs to the Interaction (Za) is computed as follows:

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

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 ith genotype; and θ_n is the percentage sum of squares explained by the nth principal component interaction effect..

Value

A data frame with the following columns:

Za	The Za values.
SSI	The computed values of simultaneous selection index for yield and stability.
rZa	The ranks of Za 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 × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research*, **3**(7), 3126–3136. http://eprints.icrisat.ac.in/id/eprint/7173.

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)
```

Index