

# Package ‘ammistability’

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**Type** Package

**Title** Additive Main Effects and Multiplicative Interaction Model Stability Parameters

**Version** 0.1.2

**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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**License** GPL-2 | GPL-3

**Encoding** UTF-8

**Depends** R (>= 3.5.0)

**VignetteBuilder** knitr

**RoxygenNote** 7.1.1

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

**Suggests** knitr,  
rmarkdown,  
pander

**RdMacros** Rdpack

**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

*Sum Across Environments of GEI Modelled by AMMI*

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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

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

## 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value;  $\gamma_{in}$  is the eigenvector value for  $i$ th genotype; and  $\delta_{jn}$  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. doi: [10.2135/cropsci1997.0011183X003700020013x](https://doi.org/10.2135/cropsci1997.0011183X003700020013x), <https://doi.org/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

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*Estimate multiple AMMI model Stability Parameters*


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## 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

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).
<code>AMGE</code>	If TRUE, computes AMGE (see <b>Details</b> ). Default is TRUE.
<code>ASI</code>	If TRUE, computes ASI (see <b>Details</b> ). n = 2 will be used in this case. Default is TRUE.
<code>ASV</code>	If TRUE, computes ASV (see <b>Details</b> ). n = 2 will be used in this case. Default is TRUE.
<code>ASTAB</code>	If TRUE, computes ASTAB (see <b>Details</b> ). Default is TRUE.
<code>AVAMGE</code>	If TRUE, computes AVAMGE (see <b>Details</b> ). Default is TRUE.
<code>DA</code>	If TRUE, computes DA (see <b>Details</b> ). Default is TRUE.
<code>DZ</code>	If TRUE, computes DZ (see <b>Details</b> ). Default is TRUE.
<code>EV</code>	If TRUE, computes EV (see <b>Details</b> ). Default is TRUE.
<code>FA</code>	If TRUE, computes FA (see <b>Details</b> ). Default is TRUE.
<code>MASI</code>	If TRUE, computes MASI (see <b>Details</b> ). Default is TRUE.
<code>MASV</code>	If TRUE, computes MASV (see <b>Details</b> ). Default is TRUE.
<code>SIPC</code>	If TRUE, computes SIPC (see <b>Details</b> ). Default is TRUE.
<code>ZA</code>	If TRUE, computes ZA (see <b>Details</b> ). 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, 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

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- 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://doi.org/10.1023/A:1002954824178), <https://link.springer.com/article/10.1023/A:1002954824178>.
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- Raju BMK (2002). "A study on AMMI model and its biplots." *Journal of the Indian Society of Agricultural Statistics*, **55**(3), 297–322.
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- 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. [http://www.crri.nic.in/CRRI\\_newsletter/crnl\\_jan\\_mar\\_14\\_web.pdf](http://www.crri.nic.in/CRRI_newsletter/crnl_jan_mar_14_web.pdf).
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- 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. doi: [10.5958/22495266.2017.00030.3](https://doi.org/10.5958/22495266.2017.00030.3), <https://doi.org/10.5958/2249-5266.2017.00030.3>.
- 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. doi: [10.5958/22495266.2017.00030.3](https://doi.org/10.5958/22495266.2017.00030.3), <https://doi.org/10.5958/2249-5266.2017.00030.3>.
- 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. <https://www.isgpb.org/article/ammistability-r-package-for-ranking-genotypes-b>

### 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)
```

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ASI.AMMI

*AMMI Stability Index*

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

### 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  $\theta_1$  and  $\theta_2$  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.), *CRRRI Newsletter, January-March 2014*, volume 35(1), 15. Central Rice Research Institute, Cuttack, Orissa. [http://www.crrri.nic.in/CRRRI\\_newsletter/crnl\\_jan\\_mar\\_14\\_web.pdf](http://www.crrri.nic.in/CRRRI_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](http://www.envirobiotechjournals.com/article_abstract.php?aid=6346&iid=200&jid=3).
- 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. doi: [10.5958/22495266.2017.00030.3](https://doi.org/10.5958/22495266.2017.00030.3), <https://doi.org/10.5958/2249-5266.2017.00030.3>.

**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

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

## 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value; and  $\gamma_{in}$  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)
```

## 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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

## 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value;  $\gamma_{in}$  is the eigenvector value for  $i$ th genotype; and  $\delta_{jn}$  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. <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

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

## 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value; and  $\gamma_{in}$  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. doi: [10.1023/A:1002954824178](https://doi.org/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

# 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, 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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

### 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  $\gamma_{in}$  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. <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

# 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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

### 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  $\gamma_{in}$  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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

### 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value; and  $\gamma_{in}$  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

- Wricke G (1962). "On a method of understanding the biological diversity in field research." *Zeitschrift für 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  $\times$  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) (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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

### Details

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

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

Where,  $PC_n$  are the scores of  $n$ th IPC; and  $\theta_n$  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**

- Jambhulkar NN, Bose LK, Singh ON (2014). “AMMI stability index for stability analysis.” In Mohapatra T (ed.), *CRRRI Newsletter, January-March 2014*, volume 35(1), 15. Central Rice Research Institute, Cuttack, Orissa. [http://www.crrri.nic.in/CRRRI\\_newsletter/crn1\\_jan\\_mar\\_14\\_web.pdf](http://www.crrri.nic.in/CRRRI_newsletter/crn1_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](http://www.envirobiotechjournals.com/article_abstract.php?aid=6346&iid=200&jid=3).
- 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. doi: [10.5958/22495266.2017.00030.3](https://doi.org/10.5958/22495266.2017.00030.3), <https://doi.org/10.5958/2249-5266.2017.00030.3>.
- 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.

**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 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**

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

**Details**

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

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

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

- 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. <http://scholar.ufs.ac.za:8080/xmlui/handle/11660/1966>.
- 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. doi: [10.1080/02571862.2000.10634878](https://doi.org/10.1080/02571862.2000.10634878), <https://doi.org/10.1080/02571862.2000.10634878>.



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. <http://eprints.icrisat.ac.in/id/eprint/7173>.

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. <http://www.isgpb.org/article/rectification-of-modified-ammi-stability-v>

## 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 <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

## Details

The Sums of the Absolute Value of the IPC Scores (*SIPC*) 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);  $\lambda_n$  is the singular value for  $n$ th IPC and correspondingly  $\lambda_n^2$  is its eigen value;  $\gamma_{in}$  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. doi: [10.2135/cropsci1997.0011183X003700020013x](https://doi.org/10.2135/cropsci1997.0011183X003700020013x), <https://doi.org/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 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 <b>Details</b> ).
a	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <b>Details</b> ).

**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  $\alpha$  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.

$\alpha$	$w_1$	$w_2$
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 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.
- 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**

<code>model</code>	The AMMI model (An object of class AMMI generated by <a href="#">AMMI</a> ).
<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 <a href="#">SSI</a> ).
<code>a</code>	The ratio of the weights given to the stability components for computation of SSI when method = "rao" (See <a href="#">SSI</a> ).

**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);  $\gamma_{in}$  is the eigenvector value for  $i$ th genotype; and  $\theta_n$  is the percentage sum of squares explained by the  $n$ th 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  $\times$  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)
```

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