

# The **AMMIS**tb**P** package: A brief introduction

*Ajay B. C.<sup>1</sup>, J. Aravind<sup>2</sup>, R. Abdul Fiyaz<sup>3</sup> and S. K. Bera<sup>4</sup>*

*2018-07-19*

1. RRS, ICAR-Directorate of Groundnut Research, Anantapur.
  2. ICAR-National Bureau of Plant Genetic Resources, New Delhi.
  3. ICAR-Indian Institute of Rice Research, Hyderabad.
  4. ICAR-Directorate of Groundnut Research, Junagadh
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The package AMMIS**tb**P is .....

## Installation

The package can be installed using the following functions:

```
# Install from CRAN
install.packages('AMMIStbP', dependencies=TRUE)

# Install development version from Github
devtools::install_github("ajaygpb/AMMIStbP")
```

Then the package can be loaded using the function

```
library(AMMIStbP) # change eval
```

## AMMI

The AMMI equation

$$Y_{ij} = \mu + \alpha_i + \beta_j + \sum_{n=1}^N \lambda_n \gamma_{in} \delta_{jn} + \rho_{ij}$$

Where,  $Y_{ij}$  is the yield of  $i$ th genotype in  $j$ th environment,  $\mu$  is the grand mean,  $\alpha_i$  is the genotype deviation from the grand mean,  $\beta_j$  is the environment deviation,  $N$  is the total number of interaction principal components (IPCs),  $\lambda_n$  is the singular value for IPC  $n$  and correspondingly  $\lambda_n^2$  is its eigen value,  $\gamma_{in}$  is the eigenvector value for  $i$ th genotype,  $\delta_{jn}$  is the eigenvector value for  $j$ th environment and  $\rho_{ij}$  is the residual.

**AMMI stability parameters**

The details about AMMI stability parameters/indices implemented in **AMMIS**tbP**** are described in Table 1.

**Table 1 :** AMMI stability parameters/indices implemented in AMMIStbP.

AMMI stability parameter	function	Details	Reference
Sums of the absolute value of the IPC scores ( <i>SIPC</i> )	<code>SIPC.AMMI</code>	$SIPC = \sum_{n=1}^{N'}  \lambda_n^{0.5} \gamma_{in} $ $SIPC = \sum_{n=1}^{N'}  PC_n $	Sneller et al. (1997)
Averages of the squared eigenvector values <i>EV</i>	<code>EV.AMMI</code>	$EV = \sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}$	Zobel (1994)
Sum across environments of GEI modelled by AMMI ( <i>AMGE</i> )	<code>AMGE.AMMI</code>	$AMGE = \sum_{j=1}^E \sum_{n=1}^{N'} \lambda_n \gamma_{in} \delta_{jn}$	Sneller et al. (1997)
$AV_{(AMGE)}$	<code>AVAMGE.AMMI</code>	$AV_{(AMGE)} = \sum_{j=1}^E \sum_{n=1}^{N'}  \lambda_n \gamma_{in} \delta_{jn} $	Zali et al. (2012)
Annicchiarico's D parameter ( $D_a$ )	<code>DA.AMMI</code>	The unsquared Euclidean distance from the origin of significant IPC axes in the AMMI model.	Annicchiarico (1997)
		$D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$	
Zhang's D parameter or AMMI statistic coefficient or AMMI distance or AMMI stability index ( $D_z$ )	<code>DZ.AMMI</code>	The distance of IPC point from origin in space.	Zhang et al. (1998)
		$D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$	

AMMI stability parameter	function	Details	Reference
AMMI stability value (ASV)	<code>agricolae::index.AMMI</code>	Distance from the coordinate point to the origin in a two dimensional scattergram generated by plotting of IPC1 score against IPC2 score.	Purchase (1997); Purchase et al. (1999); Purchase et al. (2000)
$ASV = \sqrt{\left(\frac{SSIPC_1}{SSIPC_2} \times PC_1\right)^2 + (PC_2)^2}$			
Modified AMMI stability value (ASV)	<code>MASV.AMMI</code>	$MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} \times PC_n\right)^2 + (PC_{N'})^2}$	Zali et al. (2012)
Absolute value of the relative contribution of IPCs to the interaction $Za$	<code>ZA.AMMI</code>	$Za = \sum_{i=1}^{N'}  \theta_n \gamma_{in} $	Zali et al. (2012)
Stability measure based on fitted AMMI model $FA$	<code>FA.AMMI</code>	$FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$	Raju (2002); Zali et al. (2012)
$FP$	<code>FA.AMMI</code>	Equivalent to $FA$ , when only the first IPC axis is considered for computation.	Raju (2002); Zali et al. (2012)
$FP = \lambda_1^2 \gamma_{i1}^2$ <p>As <math>\lambda_1^2</math> will be same for all the genotypes, the absolute value of <math>\gamma_{i1}</math> alone is sufficient for comparison. So this is also equivalent to the comparison based on biplot with first IPC axis.</p>			
$B$	<code>FA.AMMI</code>	Equivalent to $FA$ , when only the first two IPC axes are considered for computation.	Raju (2002); Zali et al. (2012)
$B = \sum_{n=1}^2 \lambda_n^2 \gamma_{in}^2$ <p>Stability comparisons based on this measure will be equivalent to the comparisons based on biplot with first two IPC axes.</p>			

AMMI stability parameter	function	Details	Reference
$W_{(AMMI)}$	<b>FA.AMMI</b>	Equivalent to $FA$ , when all the IPC axes in the AMMI model are considered for computation.	Wricke (1962); Raju (2002); Zali et al. (2012)
$W_{(AMMI)} = \sum_{n=1}^N \lambda_n^2 \gamma_{in}^2$			
Equivalent to Wricke's ecovalence.			
AMMI Stability Index ( $ASI$ )	<b>ASI.AMMI</b>	$ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$	Jambhulkar et al. (2014); Jambhulkar et al. (2015); Jambhulkar et al. (2017)
AMMI Based Stability Parameter ( $ASTAB$ )	<b>ASTAB.AMMI</b>	$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$	Rao and Prabhakaran (2005)

↩

Where,  $N$  is the total number of interaction principal components (IPCs);  $N'$  is the number of significant IPCAs (number of IPC that were retained in the AMMI model via F tests);  $\lambda_n$  is the singular value for IPC  $n$  and correspondingly  $\lambda_n^2$  is its eigen value;  $\gamma_{in}$  is the eigenvector value for  $i$ th genotype;  $\delta_{jn}$  is the eigenvector value for  $j$ th environment;  $SSIPC_1, SSIPC_2, \dots, SSIPC_n$  are the sum of squares of the 1st, 2th,  $\dots$ , and  $n$ th IPC;  $PC_1, PC_2, \dots, PC_n$  are the scores of 1st, 2th,  $\dots$ , and  $n$ th IPC;  $\theta_n$  is the percentage sum of squares explained by  $n$ th principal component interaction effect; and  $E$  is the number of environments.

## Simultaneous Selection Indices for Yield and Stability

The most stable genotype need not necessarily be the highest yielding genotype. Hence, simultaneous selection indices (SSIs) have been proposed for the selection of stable as well as high yielding genotypes.

A family of simultaneous selection indices ( $I_i$ ) were proposed by Rao and Prabhakaran (2005) similar to those proposed by Bajpai and Prabhakaran (2000) by incorporating the AMMI Based Stability Parameter ( $ASTAB$ ) and Yield as components. These indices consist of yield component, measured as the ratio of the average performance of the  $i$ th genotype to the overall mean performance of the genotypes under test and a stability component, measured as the ratio of stability information ( $\frac{1}{ASTAB}$ ) of the  $i$ th genotype to the mean stability information of the genotypes under test.

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

Where  $ASTAB_i$  is the stability measure of the  $i$ th genotype under AMMI procedure;  $Y_i$  is mean performance of  $i$ th genotype;  $Y_{..}$  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 (Table 2).

**Table 2 :**  $\alpha$  and corresponding weights ( $w_1$  and  $w_2$ )

$\alpha$	$w_1$	$w_2$
1.00	0.5	0.5
0.67	0.6	0.4
0.43	0.7	0.3
0.25	0.8	0.2

In AMMISTbP, the above expression has been implemented for all the stability parameters ( $SP$ ) including  $ASTAB$ .

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

Genotype stability index ( $GSI$ ) (Farshadfar, 2008) or Yield stability index ( $YSI$ ) (Farshadfar et al., 2011; Jambhulkar et al., 2017) is a simultaneous selection index for yield and yield stability which is computed by summation of the ranks of the stability index/parameter and the ranks of the mean yields.  $YSI$  is computed for all the stability parameters/indices implemented in this package.

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

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

The function `SSI` implements both these indices in AMMISTbP. Further, for each of the stability parameter functions, the simultaneous selection index is also computed by either of these functions as specified by the argument `ssi.method`.

## Examples

### Citing AMMISbP

### Session Info

```
sessionInfo()
```

```
R version 3.5.1 (2018-07-02)
```

```
Platform: x86_64-w64-mingw32/x64 (64-bit)
```

```
Running under: Windows >= 8 x64 (build 9200)
```

```
Matrix products: default
```

```
locale:
```

```
[1] LC_COLLATE=English_India.1252 LC_CTYPE=English_India.1252
```

```
[3] LC_MONETARY=English_India.1252 LC_NUMERIC=C
```

```
[5] LC_TIME=English_India.1252
```

```
attached base packages:
```

```
[1] stats      graphics  grDevices  utils      datasets  methods    base
```

```
other attached packages:
```

```
[1] AMMISbP_0.0.0.9000 readxl_1.1.0      stringi_1.1.7
```

```
loaded via a namespace (and not attached):
```

```
[1] tinytex_0.5          gtools_3.5.0        pander_0.6.1
[4] splines_3.5.1        lattice_0.20-35      agricolae_1.2-8
[7] expm_0.999-2         miniUI_0.1.1         htmltools_0.3.6
[10] yaml_2.1.19          rlang_0.2.1          AlgDesign_1.1-7.3
[13] pillar_1.2.2         later_0.7.1          withr_2.1.2
[16] sp_1.2-7             questionr_0.6.2      stringr_1.3.0
[19] cellranger_1.1.0     combinat_0.0-8       commonmark_1.5
[22] devtools_1.13.5      evaluate_0.10.1     coda_0.19-1
[25] memoise_1.1.0        knitr_1.20           httpuv_1.4.1
[28] gbRd_0.4-11          spdep_0.7-7          highr_0.6
[31] Rcpp_0.12.16         xtable_1.8-2         promises_1.0.1
[34] backports_1.1.2      gdata_2.18.0         desc_1.2.0
[37] mime_0.5             deldir_0.1-15        klaR_0.6-14
[40] digest_0.6.15        gmodels_2.16.2      shiny_1.0.5
[43] grid_3.5.1           rprojroot_1.3-2      bibtex_0.4.2
[46] Rdpack_0.7-0         tools_3.5.1          LearnBayes_2.15.1
[49] magrittr_1.5         tibble_1.4.2         cluster_2.0.7-1
[52] crayon_1.3.4         MASS_7.3-50          Matrix_1.2-14
[55] xml2_1.2.0           spData_0.2.8.3       assertthat_0.2.0
[58] rmarkdown_1.10       roxygen2_6.0.1       rstudioapi_0.7.0-9000
[61] R6_2.2.2             boot_1.3-20          nlme_3.1-137
[64] compiler_3.5.1
```

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