

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

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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, μ is the grand mean, α_i is the genotype deviation from the grand mean, β_j is the environment deviation, N is the total number of interaction principal components (IPCs), λ_n is the singular value for IPC n and correspondingly λ_n^2 is its eigen value, γ_{in} is the eigenvector value for i th genotype, δ_{jn} is the eigenvector value for j th environment and ρ_{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'} \left \lambda_n^{0.5} \gamma_{in} \right $ $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) |
| $AV_{(AMGE)}$ | NA | $AV_{AMGE} = \sum_{j=1}^E \sum_{n=1}^{N'} \lambda_n \gamma_{in} \delta_{jn} $ | Zali et al. (2012) |
| D_a | NA | <p>The unsquared Euclidean distance from the origin of significant IPC axes (D) in the AMMI model.</p> $D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$ | Annicchiarico (1997) |

| AMMI stability parameter | function | Details | Reference |
|---|------------------------------------|---|---|
| AMMI statistic coefficient or AMMI distance or AMMI stability index D_z | NA | The distance of IPC point with origin in space. (AMMI stability index) | Zhang et al. (1998) |
| | | $D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$ | |
| 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> | | Zali et al. (2012) |
| | | $MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} \times PC_n\right)^2 + (PC_{N'})^2}$ | |
| Absolute value of the relative contribution IPCs to the interaction Za | NA | | Zali et al. (2012) |
| | | $Za = \sum_{i=1}^{N'} \theta_n \gamma_{in} $ | |
| Stability measure based on fitted AMMI model FA | NA | | Raju (2002); Zali et al. (2012) |
| | | $FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$ | |

| AMMI stability parameter | function | Details | Reference |
|--|----------|--|--|
| FP | NA | 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 λ_1^2 will be same for all the genotypes, the absolute value of γ_{i1} alone is sufficient for comparison. So this is also equivalent to the comparison based on biplot with first IPC axis.</p> | | | |
| B | NA | Equivalent to FA , when 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> | | | |
| $W_{(AMMI)}$ | NA | Equivalent to FA , when all the IPC axes in the AMMI model are considered for computation. | Wricke (1962); Raju (2002); Zali et al. (2012) |
| $W_{AMMI} = \sum_{n=1}^N \lambda_n^2 \gamma_{in}^2$ <p>Equivalent to Wricke's ecovalence.</p> | | | |
| AMMI Stability Index (ASI) | NA | $ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$ | Jambhulkar et al. (2014); Jambhulkar et al. (2015); Jambhulkar et al. (2017) |

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); λ_n is the singular value for IPC n and correspondingly λ_n^2 is its eigen value; γ_{in} is the eigenvector value for i th genotype; δ_{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; θ_n is the percentage sum of squares explained by n th principal component interaction effect; and E is the number of environments.

Yield Stability Index

The most stable genotype need not necessarily be the high yielding genotype. As we need to select the the most stable and highest yielding genotypes, Yield stability index (*YSI*) was proposed (Farshadfar et al. (2011), Jambhulkar et al. (2017)). *YSI* 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.

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

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

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] readxl_1.1.0      AMMISbP_0.0.0.9000 agricolae_1.2-8
```

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

```
[1] httr_1.3.1          jsonlite_1.5        splines_3.5.1
[4] gtools_3.5.0        shiny_1.0.5          Rdpack_0.7-0
[7] assertthat_0.2.0    xmlparsedata_1.0.1   expm_0.999-2
[10] sp_1.2-7            highr_0.6           pandor_0.6.1
[13] cellranger_1.1.0    remotes_1.1.1.9000   yaml_2.1.19
[16] LearnBayes_2.15.1   pillar_1.2.2         backports_1.1.2
[19] lattice_0.20-35     goodpractice_1.0.2   digest_0.6.15
[22] promises_1.0.1      htmltools_0.3.6      httpuv_1.4.1
[25] Matrix_1.2-14       clisymbols_1.2.0     klaR_0.6-14
[28] devtools_1.13.5     bibtex_0.4.2         rcmdcheck_1.2.1
[31] questionr_0.6.2     gmodels_2.16.2       xtable_1.8-2
[34] processx_3.1.0      gdata_2.18.0         later_0.7.1
[37] tibble_1.4.2        combinat_0.0-8       withr_2.1.2
```

| | | |
|----------------------------|--------------------|-------------------|
| [40] lazyeval_0.2.1 | magrittr_1.5 | crayon_1.3.4 |
| [43] mime_0.5 | deldir_0.1-15 | memoise_1.1.0 |
| [46] evaluate_0.10.1 | fs_1.2.3 | nlme_3.1-137 |
| [49] MASS_7.3-50 | xml2_1.2.0 | praise_1.0.0 |
| [52] tools_3.5.1 | hunspell_2.9 | cyclocomp_1.1.0 |
| [55] gbRd_0.4-11 | stringr_1.3.0 | cluster_2.0.7-1 |
| [58] callr_2.0.4 | pkgdown_1.1.0.9000 | rex_1.1.2 |
| [61] compiler_3.5.1 | covr_3.0.1 | tinytex_0.5 |
| [64] rlang_0.2.1 | debugme_1.1.0 | grid_3.5.1 |
| [67] rstudioapi_0.7.0-9000 | miniUI_0.1.1 | rmarkdown_1.10 |
| [70] boot_1.3-20 | roxygen2_6.0.1 | AlgDesign_1.1-7.3 |
| [73] R6_2.2.2 | knitr_1.20 | commonmark_1.5 |
| [76] rprojroot_1.3-2 | spdep_0.7-7 | lintr_1.0.2 |
| [79] desc_1.2.0 | stringi_1.1.7 | whoami_1.1.2 |
| [82] Rcpp_0.12.16 | spData_0.2.8.3 | coda_0.19-1 |

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