The **AMMIStbP** package: A brief introduction

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The package `AMMIStbP` 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 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 `AMMIStbP` 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 ($SIPC$)	`SIPC.AMMI`	$SIPC = \sum_{n=1}^{N'} \left\lvert \lambda_n^{0.5} \gamma_{in} \right\rvert$ $SIPC = \sum_{n=1}^{N'} \lvert IPC_n \rvert$	Sneller et al. (1997)
Averages of the squared eigenvector values EV	`EV.AMMI`	$EV = \sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}$	Zobel (1994)
Sum across environments of GEI modelled by AMMI $AMGE$	`AMGE.AMMI`	$AMGE = \sum_{j=1}^{E} \sum_{n=1}^{N'} \lambda_n \gamma_{in} \delta_{jn}$	Sneller et al. (1997)
$AV_{(AMGE)}$	`NA`	$AV_{AMGE} = \sum_{j=1}^{E} \sum_{n=1}^{N'} \lvert \lambda_n \gamma_{in} \delta_{jn} \rvert$	Zali et al. (2012)
D_a	`NA`	The unsquared Euclidean distance from the origin of significant IPC axes (D) in the AMMI model. $D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$	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) $$D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$$	Zhang et al. (1998)
AMMI stability value (ASV)	`agricolae::index.AMMI`	Distance from the coordinate point to the origin in a two dimensional scattergram generated by plotting of IPC1 score against IPC2 score. $$ASV = \sqrt{\left(\frac{SSIPC_1}{SSIPC_2} \times PC_1\right)^2 + (PC_2)^2}$$	Purchase (1997); Purchase et al. (1999); Purchase et al. (2000)
Modified AMMI stability value (ASV)	`MASV.AMMI`	$$MASV = \sqrt{\sum_{n=1}^{N'-1} \left(\frac{SSIPC_n}{SSIPC_{n+1}} \times PC_n\right)^2 + (PC_{N'})^2}$$	Zali et al. (2012)
Absolute value of the relative contribution IPCs to the interaction Za	`NA`	$$Za = \sum_{i=1}^{N'} \lvert\theta_n \gamma_{in}\rvert$$	Zali et al. (2012)
Stability measure based on fitted AMMI model FA	`NA`	$$FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$$	Raju (2002); Zali et al. (2012)

AMMI stability parameter	function	Details	Reference
FP	`NA`	Equivalent to FA, when only the first IPC axis is considered for computation. $$FP = \lambda_1^2 \gamma_{i1}^2$$ As λ_1^2 will be same for all the genotypes, the absolute value of $gamma_{i1}$ alone is sufficient for comparison. So this is also equivalent to the comparison based on biplot with first IPC axis.	Raju (2002); Zali et al. (2012)
B	`NA`	Equivalent to FA, when the first two IPC axes are considered for computation. $$B = \sum_{n=1}^{2} \lambda_n^2 \gamma_{in}^2$$ Stability comparisons based on this measure will be equivalent to the comparisons based on biplot with first two IPC axes.	Raju (2002); Zali et al. (2012)
$W_{(AMMI)}$	`NA`	Equivalent to FA, when all the IPC axes in the AMMI model are considered for computation. $$W_{AMMI} = \sum_{n=1}^{N} \lambda_n^2 \gamma_{in}^2$$ Equivalent to Wricke's ecovalence.	Wricke (1962); Raju (2002); Zali et al. (2012)
AMMI Stability Index (ASI)	`NA`	$$ASI = \sqrt{\left[PC_1^2 \times \theta_1^2\right] + \left[PC_2^2 \times \theta_2^2\right]}$$	Jambhulkar et al. (2014); Jambhulkar et al. (2015); Jambhulkar et al. (2017)

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), N' is the number of significant IPCAs (number of IPC that were retained in the AMMI model via F tests), λ_n is the 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.

$SSIPC_1$, $SSIPC_2$, $\cdots$, $SSIPC_n$ are the sum of squares of the 1^{st}, 2^{nd}, $\ldots$, and n^{th} IPC. PC_1, PC_2, $\cdots$, PC_n are the scores of 1^{st}, 2^{nd}, $\ldots$, and n^{th} IPC.

θ_n is the percentage IPC sum of squares (IPCSS) explained by the interaction effect.

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.

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  stringi_1.1.7

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      expm_0.999-2          xmlparsedata_1.0.1
[10] sp_1.2-7              highr_0.6             pander_0.6.1
[13] cellranger_1.1.0      yaml_2.1.19           remotes_1.1.1.9000
[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] gdata_2.18.0          processx_3.1.0        later_0.7.1
[37] tibble_1.4.2          combinat_0.0-8        withr_2.1.2
[40] agricolae_1.2-8       lazyeval_0.2.1        magrittr_1.5
[43] crayon_1.3.4          mime_0.5              deldir_0.1-15
[46] memoise_1.1.0         evaluate_0.10.1       fs_1.2.3
[49] nlme_3.1-137          MASS_7.3-50           xml2_1.2.0
```

```
[52] praise_1.0.0          tools_3.5.1           hunspell_2.9
[55] cyclocomp_1.1.0       gbRd_0.4-11           stringr_1.3.0
[58] cluster_2.0.7-1       callr_2.0.4           rex_1.1.2
[61] compiler_3.5.1        pkgdown_1.1.0.9000    covr_3.0.1
[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            whoami_1.1.2          Rcpp_0.12.16
[82] spData_0.2.8.3        coda_0.19-1
```

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