The **ammistability** package: A brief introduction

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Overview

The package `ammistability` is .....

Installation

The package can be installed using the following functions:

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

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

Then the package can be loaded using the function

```
library(ammistability) # 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 the ith genotype in the jth 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 nth IPC and correspondingly λ_n^2 is its eigen value, γ_{in} is the eigenvector value for ith genotype, δ_{jn} is the eigenvector value for the jth environment and ρ_{ij} is the residual.

AMMI stability parameters

The details about AMMI stability parameters/indices implemented in `ammistability` are described in Table 1.

Table 1 : AMMI stability parameters/indices implemented in `ammistability`.

AMMI stability parameter	function	Details	Reference
Sums of the absolute value of the IPC scores ($SIPC$)	`SIPC.AMMI`	$SIPC = \sum_{n=1}^{N'} \left\lvert \lambda_n^{0.5} \gamma_{in} \right\rvert$ $SIPC = \sum_{n=1}^{N'} \lvert PC_n \rvert$	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)
$AV_{(AMGE)}$	`AVAMGE.AMMI`	$AV_{(AMGE)} = \sum_{j=1}^{E} \sum_{n=1}^{N'} \lvert \lambda_n \gamma_{in} \delta_{jn} \rvert$	Zali et al. (2012)
Annicchiarico's D parameter (D_a)	`DA.AMMI`	The unsquared Euclidean distance from the origin of significant IPC axes in the AMMI model. $D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$	Annicchiarico (1997)
Zhang's D parameter or AMMI statistic coefficient or AMMI distance or AMMI stability index (D_z)	`DZ.AMMI`	The distance of IPC point from origin in space. $D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$	Zhang et al. (1998)

AMMI stability parameter	function	Details	Reference
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 of IPCs to the interaction Za	`ZA.AMMI`	$$Za = \sum_{i=1}^{N'} \lvert\theta_n \gamma_{in}\rvert$$	Zali et al. (2012)
Stability measure based on fitted AMMI model FA	`FA.AMMI`	$$FA = \sum_{n=1}^{N'} \lambda_n^2 \gamma_{in}^2$$	Raju (2002); Zali et al. (2012)
FP	`FA.AMMI`	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 γ_{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	`FA.AMMI`	Equivalent to FA, when only 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)

AMMI stability parameter	function	Details	Reference
$W_{(AMMI)}$	`FA.AMMI`	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)	`ASI.AMMI`	$$ASI = \sqrt{\left[PC_1^2 \times \theta_1^2\right] + \left[PC_2^2 \times \theta_2^2\right]}$$	Jambhulkar et al. (2014); Jambhulkar et al. (2015); Jambhulkar et al. (2017)
Modified AMMI Stability Index ($MASI$)	`MASI.AMMI`	$$MASI = \sqrt{\sum_{n=1}^{N'} PC_n^2 \times \theta_n^2}$$	
AMMI Based Stability Parameter ($ASTAB$)	`ASTAB.AMMI`	$$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$$	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); λ_n is the 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; δ_{jn} is the eigenvector value for the jth environment; $SSIPC_1$, $SSIPC_2$, $\cdots$, $SSIPC_n$ are the sum of squares of the 1st, 2th, ..., and nth IPC; PC_1, PC_2, $\cdots$, PC_n are the scores of 1st, 2th, ..., and nth IPC; θ_n is the percentage sum of squares explained by nth 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 ith 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 ith genotype to the mean stability information of the genotypes under test.

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

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

Table 2 : α and corresponding weights (w_1 and w_2)

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

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

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

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 `ammistability`. Further, for each of the stability parameter functions, the simultaneous selection index is also computed by either of these functions as specifiend by the argument `ssi.method`.

Examples

Citing `ammistability`

```
To cite the R package 'ammistability' in publications use:

  Ajay B. C., J. Aravind, and R. Abdul Fiyaz (2018).
  ammistability: Additive Main Effects and Multiplicative
  Interaction Model Stability Parameters. R package version
  0.0.0.9000, https://ajaygpb.github.io/ammistability/.

A BibTeX entry for LaTeX users is

  @Manual{,
    title = {ammistability: Additive Main Effects and Multiplicative Interaction Model Stability Parame
    author = {{Ajay Basapura Chandrashekar} and {J. Aravind} and {R. Abdul Fiyaz}},
    year = {2018},
    note = {R package version 0.0.0.9000},
    note = {https://ajaygpb.github.io/ammistability/},
  }

This free and open-source software implements academic research by
the authors and co-workers. If you use it, please support the
project by citing the package.
```

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] ammistability_0.0.0.9000 agricolae_1.2-8
[3] stringi_1.2.4            readxl_1.1.0

loaded via a namespace (and not attached):
 [1] splines_3.5.1         gtools_3.8.1          shiny_1.1.0
 [4] assertthat_0.2.0      expm_0.999-2          sp_1.3-1
 [7] highr_0.7             pander_0.6.2          cellranger_1.1.0
[10] yaml_2.2.0            LearnBayes_2.15.1     backports_1.1.2
```

```
[13] pillar_1.3.0          lattice_0.20-35       glue_1.3.0
[16] digest_0.6.15         promises_1.0.1        colorspace_1.3-2
[19] htmltools_0.3.6       httpuv_1.4.5          Matrix_1.2-14
[22] plyr_1.8.4            klaR_0.6-14           pkgconfig_2.0.1
[25] devtools_1.13.6       ggcorrplot_0.1.1      questionr_0.6.3
[28] gmodels_2.18.1        purrr_0.2.5           xtable_1.8-2
[31] scales_0.5.0          processx_3.1.0        gdata_2.18.0
[34] later_0.7.3           tibble_1.4.2          combinat_0.0-8
[37] ggplot2_3.0.0         withr_2.1.2           lazyeval_0.2.1
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[43] deldir_0.1-15         evaluate_0.11         memoise_1.1.0
[46] fs_1.2.4              nlme_3.1-137          MASS_7.3-50
[49] xml2_1.2.0            tools_3.5.1           stringr_1.3.1
[52] munsell_0.5.0         cluster_2.0.7-1       bindrcpp_0.2.2
[55] callr_2.0.4           compiler_3.5.1        pkgdown_1.1.0.9000
[58] rlang_0.2.1           debugme_1.1.0         grid_3.5.1
[61] rstudioapi_0.7.0-9000 miniUI_0.1.1.1        rmarkdown_1.10
[64] boot_1.3-20           gtable_0.2.0          roxygen2_6.0.1
[67] AlgDesign_1.1-7.3     R6_2.2.2              knitr_1.20
[70] dplyr_0.7.6           rprojroot_1.3-2       bindr_0.1.1
[73] commonmark_1.5        spdep_0.7-7           Rcpp_0.12.18
[76] spData_0.2.9.0        tidyselect_0.2.4      coda_0.19-1
```

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