Indian J. Genet., 79(2) 460-466 (2019)
DOI: 10.31742/IJGPB.79.2.10

ammistability: R package for ranking genotypes based on stability parameters derived from AMMI model

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(Received: December 2018; Revised: April 2019; Accepted: May 2019)

Abstract

Selection of genotype for target environment is affected by genotype-by-environment interactions (GEI) and AMMI model is widely used tool to analyse GEI. AMMI does not quantify stability measure making it difficult to rank genotypes. To overcome this lacuna AMMI model output is used to quantify stability measures and rank genotypes. Of several stability measures available in literature, only AMMI stability value (ASV) is implemented in package 'agricole' and others have not been implemented in any other R packages. '*ammistability*' uses output from 'AMMI' function in 'agricolae' package and computes various stability parameters for AMMI model. Further, genotypes are ranked on the basis of simultaneous selection of yield and stability (SSI). Package also helps to study association among several stability measures.

Key words: AMMI, ammistability, GEI, R package

Introduction

In plant breeding programs, genotypes are selected based on their yield and adaptability over multiple environments. The breeder's selection process is hindered by genotype-by-environment interactions (GEI), which are detected by studying the responses of genotypes when tested in multiple environments. The additive main effects and multiplicative interaction (AMMI) model (Gauch 1988, 1992) is one of the most widely used tools to analyse and structure GEI. It interprets genotype (G) and environment (E) as additive effect using two-way ANOVA by least squares and genotype × environment interaction (G×E) as multiplicative effect by applying singular value decomposition (SVD) on the residuals from ANOVA. This technique can readily identify cultivars with wide adaptability (suitable for several environments) and specific adaptability (suitable for target environment). Nevertheless, the AMMI model does not quantify any stability measures, which are necessary for ranking the genotypes. To overcome this problem several stability measures have been proposed which are derived from the AMMI model output and subsequently can be employed to quantify the stability and rank the genotypes.

Stability *per se* is not a desirable selection criterion, because most stable genotypes would not necessarily give the best yield performance; hence, simultaneous consideration of grain yield and stability parameter as a single non-parametric index is more useful (Farshadfar et al. 2011). Two approaches for simultaneous selection index for yield and stability (SSI) have been proposed namely, (1) Weighted family of selection indices (Rao and Prabhakaran 2005) and (2) Genotype selection index or Yield stability index (Farshadfar 2008).

The statistical programming language R (R core team, 2018) is one of the most popular tools in academia today owing to its flexibility, broad range of application and an exhaustive library of add-on packages (Tippman 2015). One such package — 'agricolae' (de Mendiburu 2015) can be used for fitting an AMMI model using the 'AMMI' function and subsequently the fitted model is used to compute a stability measure — AMMI stability value (ASV) (Purchase 1997; Purchase et al. 1999, 2000) and an index combining yield and stability — Yield stability index (Farshadfar 2008) using the 'index.AMMI' function. However, there are several other stability measures available in literature, which have not been

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Published by the Indian Society of Genetics & Plant Breeding, A-Block, F2, First Floor, NASC Complex, IARI P.O., Pusa Campus, New Delhi 110 012; Online management by www.isgpb.org; indianjournals.com

implemented in any R package. In this note, we introduce 'ammistability' package (Additive Main effects and Multiplicative Interactions Stability Parameters) which aims to fill the gap between the existing R packages and the current need in quantitative genetic data analysis.

Materials and methods

The 'ammistability' package is written entirely in R (R core team 2018). It requires the standard R ($\geq$ 3.0.1) installations and attached dependent packages such as agricolae (de Mendiburu 2015), ggcorrplot (Kassambara 2018) and ggplot2 (Wickam 2016). The package 'ammistability' uses the output generated from 'AMMI' function available in 'agricolae' package and computes various stability parameters from AMMI model. Further using these computed stability parameters, genotypes were ranked on the basis SSI according to the method of Rao and Prabhakaran (2005) or Farshadfar (2008). The details about AMMI stability parameters/indices implemented in package 'ammistability' are described in Table 1. A wrapper function has also been written which facilitates the simultaneous computation of multiple AMMI stability parameters along with the corresponding SSIs. It also computes the correlation among indices and visualizes the results as a correlogram (Fig. 1a, 1b, 1g) implemented using the package 'ggcorrplot' (Kassambara 2018). Moreover, the ranks are visualised as slopegraphs (Fig. 1e, 1f) or heatmaps (Fig. 1c, 1d) implemented using the 'ggplot2' package (Wickam 2016).

Among different stability parameters derived from AMMI, ASV (Purchase 1997; Purchase et al. 1999, 2000) is the most popular. It considers the first two interaction principal components (IPCs) for computation. The 'index.AMMI' function in 'agricolae' implements this and Zali et al. (2012) further extended it as Modified AMMI Stability value (MASV) which considers all the significant IPCs for computation. However, in both these cases, formula used for AMMI stability value (ASV) was found to be erroneous and different from that of the original authors. Hence in 'ammistability' the corrected version of MASV has been implemented based on the original formula (See Table 1). The correct version of ASV can computed by using the 'MASV.AMMI' function in 'ammistability' keeping the argument 'n' as 2 (indicates that only the first two IPCs are to be considered for computation).

In addition, we have also proposed a new stability parameter, the Modified AMMI stability Index (MASI) (Ajay et al. 2018a) implemented as 'MASI.AMMI' function which is a modified version of AMMI stability index (ASI) (Jambulkar et al. 2014, 2015, 2017). Unlike ASI which considers only first two IPCs, MASI will consider all significant IPCs for calculating the stability parameter.

The package has been published in CRAN (Ajay et al. 2018b) under GNU Public License v3 and distributed with a tutorial (vignette). All the functions have been extensively documented in the help files with examples. A website with package, help files and the tutorial is also hosted in github at https://ajaygpb.github.io/ammistability/ and is free to download.

Usage scenario

To illustrate the utility and features of the package 'ammistability' we have used dataset 'plrv' available in the 'agricolae' package. It consists yield data of 28 genotypes evaluated in 6 different environments with three replications. Before proceeding with analysis using 'ammistability' package, the AMMI model has to be generated using the 'AMMI' function of 'agricolae' with the following code.

```
# Load agricolae package
library(agricolae)

# Load example data
data(plrv)

# Fit AMMI model
model <- with (plrv, AMMI (Locality,
Genotype, Rep, Yield,
                console = FALSE))
```

The output 'model' thus generated is used by package 'ammistability' for computing various stability parameters. After calculating stability parameter, SSI is computed according to the methods specified in the argument 'ssi.method'. With method = "rao", SSI is calculated as proposed by Rao and Prabhakaran (2005) and with method = "farshadfar" SSI is calculated according to Farshadfar et al. (2008). By default, the package considers all significant IPCs for computing stability parameters (except for ASI.AMMI) and the SSI computation method as "farshadfar". If desired users can specify number of principal components to be included and SSI method to be used. The 'MASI.AMMI' function is illustrated below for different criterion and all other functions can be worked out

Table 1. AMMI stability parameters/indices implemented in ammistability

Function	AMMI stability parameter	Description	References
AMGE.AMMI	Sum across environments of GEI modelled by AMMI(AMGE)	$AGME = \sum_{j=1}^{E} \sum_{n=1}^{N'} \lambda_n \gamma_{in} \delta_{jn}$	Sneller et al. (1997)
ASI.AMMI	AMMI stability Index	$ASI = \sqrt{[PC_1^2 \times \theta_1^2] + [PC_2^2 \times \theta_2^2]}$	(Jambhulkar et al. 2014); (Jambhulkar et al. 2015); (Jambhulkar et al. 2017)
ASTAB.AMMI	AMMI Based StabilityParameter (ASTAB)	$ASTAB = \sum_{n=1}^{N'} \lambda_n \gamma_{in}^2$	Rao and Prabhakaran (2005)
AVAMGE.AMMI	Sum Across Environments of Absolute Value of Genotype-Environment Interaction Modelled by AMMI	$AV_{(AMGE)} = \sum_{j=1}^{E} \sum_{n=1}^{N'} \lvert \lambda_n \gamma_{in} \delta_{jn} \rvert$	Zali et al. (2012)
DA.AMMI	Annicchiarico's Dparameter (Da)	$D_a = \sqrt{\sum_{n=1}^{N'} (\lambda_n \gamma_{in})^2}$	Annicchiarico (1997)
DZ.AMMI	Zhang's D parameter orAMMI statistic coefficient or AMMI distance or AMMI stability index (Dz)	$D_z = \sqrt{\sum_{n=1}^{N'} \gamma_{in}^2}$	(Zhang et al. 1998)
EV.AMMI	Averages of the squaredeigenvector values EV	$EV = \sqrt{\sum_{n=1}^{N'} \frac{\gamma_{in}^2}{N'}}$	Zobel (1994)
FA.AMMI	Stability measure basedon fitted AMMI model (FA)	$B = \sum_{n=1}^{2} \lambda_n^2 \gamma_{in}^2$	(Raju 2002; Zali et al. 2012)
	FP	Equivalent to FA, when only the first IPC axis is considered for computation. $FP = \lambda_1^2 \gamma_{i1}^2$ As λ_1 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.	
	B	Equivalent to FA, when only the first two IPC axes are considered for computation.	

Table 1. *Contd ....*

Function	AMMI stability parameter	Description	References
		$B=\sum_{n=1}^{2}\lambda_n^2\gamma_{in}^2$	
		Stability comparisons based on this measure will be equivalent to the comparisons based on biplot with first two IPC axes.	
	W(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)
MASI.AMMI	Modified AMMI stability Index (MASI)	$MASI=\sqrt{\sum_{n=1}^{N'}PC_2^n\times\theta_n^2}$	Ajay et al. 2018a
MASV.AMMI	Modified AMMI stability Value (MASV)	$MASV=\sqrt{\sum_{n=1}^{N-2}\left(\frac{SSIPC_n}{SSIPC_{n+1}}\times PC_n\right)^2+(PC_{N'})^2}$	(Zali et al. 2012)
SIPC.AMMI	Sums of the absolutevalue of the IPC scores (SIPC)	$SIPC=\sum_{n=1}^{N'}\lvert\lambda_n^{0.5}\gamma_{in}\rvert$	(Sneller et al. 1997)
Za.AMMI	Absolute value of therelative contribution of IPCs to the interaction Za	$Za=\sum_{i=1}^{N'}\lvert\theta_n\gamma_{in}\rvert$	(Zali et al. 2012)
agricolae:: index.AMMI and MASV. AMMI (with argument n = 2)	AMMI stability value (ASV)	$ASV=\sqrt{\left(\frac{SSIPC_1}{SSIPC_2}\times PC_1\right)^2+(PC_2)^2}$	(Purchase 1997; Purchase et al. 1999; Purchase et al. 2000)

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 i^{th} genotype; δ_{jn} is the eigenvector value for the j^{th} environment; $SSIPC_1$, $SSIPC_2$, ..., $SSIPC_n$ are the sum of squares of the 1st, 2nd, …, and n^{th} IPC; PC_n, PC_1, PC_2, ..., PC_n are the scores of 1st, 2nd, …, and n^{th} IPC; θ_n is the percentage sum of squares explained by th principal component interaction effect; and E is the number of environments.

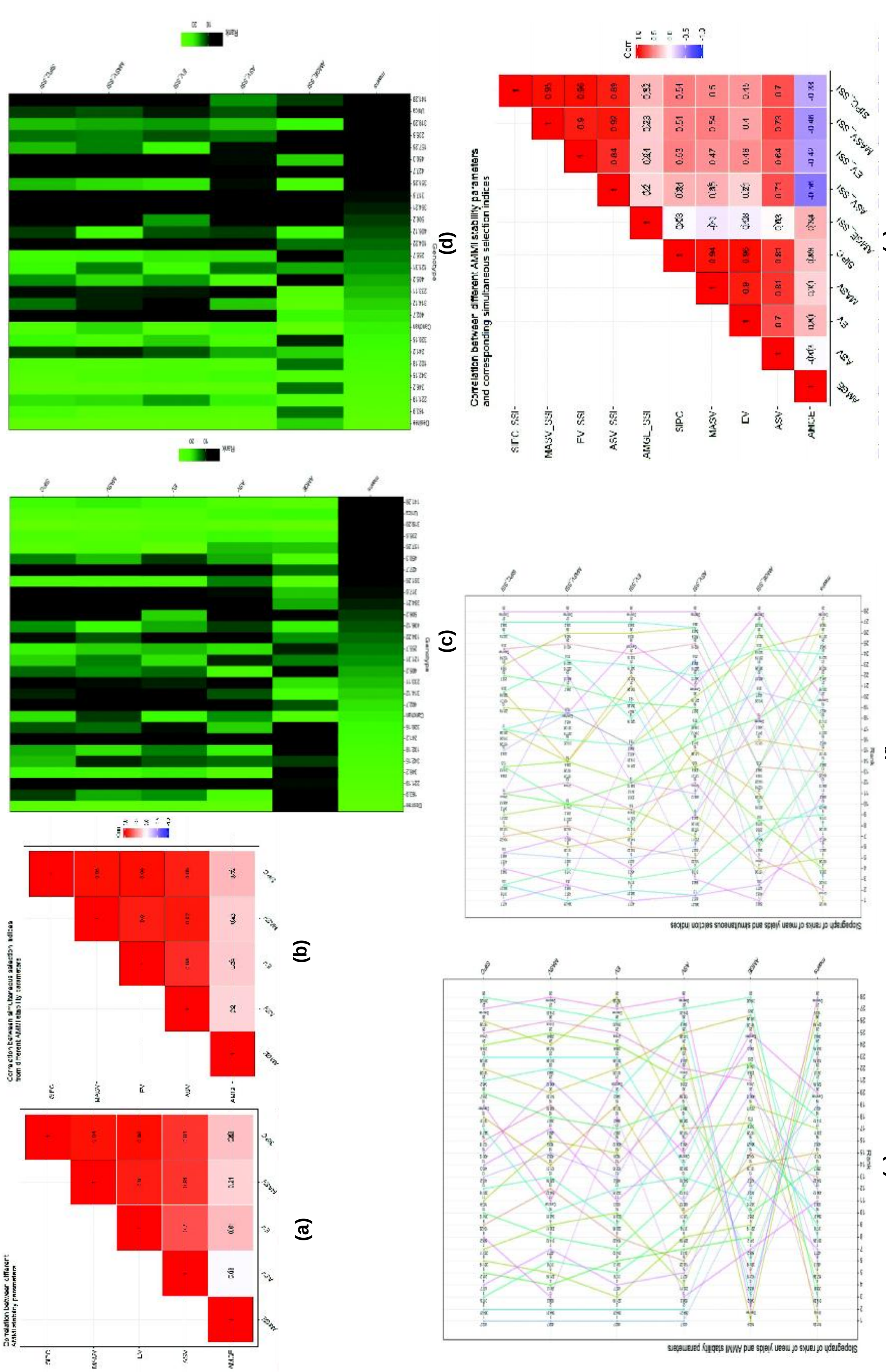

Fig. 1: Correlogram and slopegraph outputs from 'ammistability' wrapper function. a) Correlogram of stability parameters; b) Correlogram of simultaneous selection indices; c) Heatmap of stability parameters and d) Heatmap of simultaneous selection indices; e) Slopegraph of stability parameters; f) Slopegraph of simultaneous selection indices; g) Correlogram of stability parameters and simultaneous selection indices

similarly.

```
# Load ammistability package library
(ammistability)

# 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)
```

When only two principal components are found significant in data, then ASI.AMMI will give identical results as MASI.AMMI.

```
a <- ASI.AMMI(model)
b <- MASI.AMMI(model, n = 2)

identical(a$ASI, b$MASI)
```

The use of the wrapper function ‘ammistability’ which computes multiple stability parameters at a time, computes and visualizes correlation between them and plots slopegraph and heatmaps for visual comparison of ranks are illustrated by the following code.

```
library(agricolae)
data(plrv)

model <- with(plrv, AMMI(Locality,
Genotype, Rep, Yield, console = FALSE))

Fm1 <- 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)
```

Various plots generated by this wrapper function for the dataset ‘plrv’ are presented in Fig. 1. Further examples are available in the help documentation and the tutorial (vignette). They are also available in the associated website https://ajaygpb.github.io/ammistability/.

```
# Get help
?ASTAB.AMMI
?DZ.AMMI

# Open vignette
browseVignettes(package
= ‘ammistability’)
```

Ranking genotypes based on yield as well as stability in multi-environment-trials is essential as it can assist breeders in choosing best genotype for a location. *Ammistability* facilitates simultaneous computation of multiple AMMI stability parameters along with the corresponding SSIs, correlogram and slopegraphs.

Authors’ contribution

Conceptualization of research (BCA); Designing of the experiments (BCA, RAF); Contribution of experimental materials (BCA, JA, RAF); Execution of field/lab experiments and data collection (BCA, JA, RAF); Analysis of data and interpretation (BCA, JA); Preparation of manuscript (BCA, JA).

Declaration

The authors declare no conflict of interest.

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