Mean Performance and Stability in Multi-Environment Trials I: Combining Features of AMMI and BLUP Techniques

Article *in* Agronomy journal · July 2019

DOI: 10.2134/agronj2019.03.0220

CITATIONS
7

READS
466

6 authors, including:

Tiago Olivoto
Universidade Federal de Santa Maria
86 PUBLICATIONS **143** CITATIONS
SEE PROFILE

Alessandro Dal'Col Lúcio
Federal University of Santa Maria, Santa Maria, Brazil
250 PUBLICATIONS **1,393** CITATIONS
SEE PROFILE

José Antonio Gonzalez da Silva
Universidade Regional do Noroeste do Estado Estado do Rio Grande do Sul (UNIJUÍ)
222 PUBLICATIONS **957** CITATIONS
SEE PROFILE

Volmir Sergio Marchioro
Universidade Federal de Santa Maria
125 PUBLICATIONS **322** CITATIONS
SEE PROFILE

Mean performance and stability in multi-environment trials I:

Combining features of AMMI and BLUP techniques

Contents

This is the supplemental material for the article **Mean performance and stability in multi-environment trials I: Combining features of AMMI and BLUP techniques**. It has three main sections: The first section contains the supplemental tables; In the second one the supplemental figures; In the third and last section we introduce the `metan` (**m**ulti-**e**nvironment **t**rials **an**alysis) R package reproducing the examples shown in the manuscript using the *oat* dataset.

1 Supplemental Tables

A. C. Oliveira et al. (2012); A. C.O. Oliveira et al. (2012); Oliveira et al. (2011)

Table S 1: Code, commercial names, pedigree, release year and maturity range observed in the trials of the oat cultivars used in the study.

				Days from sowing to		
Code	Commercial name	Pedigree	Release year	Flowering	Maturation	Reference
G01	BARBARASUL	UPF 18 / CFT5	2007	69	107	NA
G02	BRISASUL	OR 2 / UPF 18	2007	75	108	(Oliveira et al., 2011)
G03	FAEM CARLASUL	UFRGS 10 / 90 SAT -285	2011	68	104	(Oliveira et al., 2012a)
G04	FAEM CHIARASUL	UFRGS 17 / UFRGS 10 // 90 SAT -28	2011	67	102	(Oliveira et al., 2012b)
G05	UPFA GAUDÉRIA	UPF 16 / CTC 5	2012	68	103	NA
G06	URS 21	UFRGS 10 x CTC 84B993	2001	67	103	NA
G07	URS CHARRUA	UFRGS 984126-1 / UFRGS 984109-7	2010	71	106	NA
G08	URS CORONA	UFRGS 987016-1 / UFRGS 970497-1	2012	68	104	NA
G09	URS TARIMBA	UFRGS 987016-1 / UFRGS 19	2009	68	102	NA
G10	URS TAURA	UFRGS 970216-2 / UFRGS 970461	2009	79	116	NA

Table S 2: Within-environments analysis of variance of 10 oat genotypes evaluated in 16 environments.

Environment	Mean Square			Mean (Mg/ha)	CV	h†
	Block	Genotype	Error			
WF 2010‡	0.065^{NS}	0.337^{NS}	0.144	2.521	15.055	0.573
WF 2011	0.698^{*}	0.207^{NS}	0.179	3.18	13.287	0.136
WF 2012	0.489^{NS}	0.335^{NS}	0.179	4.064	10.407	0.466
WF 2013	0.116^{NS}	0.531^{**}	0.138	3.675	10.095	0.741
WF 2014	0.067^{NS}	0.408^{NS}	0.231	2.507	19.173	0.433
WF 2015	0.166^{NS}	0.551^{***}	0.067	3.107	8.316	0.879
WF 2016	0.219^{NS}	0.526^{***}	0.066	3.911	6.587	0.874
WF 2017	0.16^{NS}	0.135^{NS}	0.058	2.663	9.081	0.565
NF 2010§	0.381^{*}	0.33^{**}	0.091	1.989	15.164	0.73
NF 2011	0.817^{***}	0.215^{***}	0.028	2.536	6.574	0.87
NF 2012	0.583^{*}	0.679^{***}	0.111	3.057	10.895	0.837
NF 2013	0.654^{***}	0.296^{***}	0.027	2.175	7.509	0.91
NF 2014	0.377^{*}	0.151^{NS}	0.105	1.368	23.678	0.305
NF 2015	0.092^{NS}	0.32^{***}	0.054	1.609	14.384	0.833
NF 2016	0.077^{NS}	0.713^{***}	0.099	2.91	10.833	0.861
NF 2017	0.428^{NS}	0.237^{NS}	0.150	1.713	22.601	0.368
DF¶	2	9	18.000	-	-	-

Note:

* Significant at $P < 0.05$.

** Significant at $P < 0.01$.

*** Significant at $P < 0.001$.

NS, nonsignificant.

*

† h, broad-sense heritability.

‡ WF, with fungicide.

§ NF, without fungicide.

¶ DF, degree of freedom.

Table S 3: Eigenvalues and explained variance proportion of the matrix with interaction effects estimated by mixed models for the experiment 1 (oat).

PCA axis	Eigenvalue	Proportion (%)	Accumulated (%)
1	1.840	32.489	32.489
2	1.518	26.789	59.278
3	0.957	16.896	76.174
4	0.521	9.200	85.375
5	0.384	6.774	92.149
6	0.222	3.916	96.065
7	0.106	1.871	97.936
8	0.084	1.488	99.424
9	0.033	0.576	100.000

Table S 4: Results for WAASB estimation of 10 oat genotypes assessed in 16 environmental environments (combinations of eight cultivation years and two fungicide manegements).

type	Code	R*	PC1†	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	W‡	PctW§	OrW¶	PctR	OrR	OrPCA	Wt.R**	Wt.W	WAASBY††	OrWA‡‡
Genotype	G1	2.624	0.110	0.230	-0.141	-0.119	0.110	-0.218	0.285	0.291	-0.163	0.159	94.44	2	22.039	6	5	65	35	47.38	4
Genotype	G2	2.703	0.063	0.103	0.837	0.022	0.262	-0.027	-0.100	0.069	0.046	0.213	76.62	6	36.879	4	2	65	35	50.79	3
Genotype	G3	2.941	-0.083	0.095	0.200	0.282	-0.251	-0.059	0.224	-0.331	-0.131	0.141	100.00	1	81.563	2	4	65	35	88.02	2
Genotype	G4	2.697	0.291	-0.411	-0.291	-0.032	0.414	-0.275	-0.027	-0.201	0.077	0.300	48.68	8	35.793	5	7	65	35	40.30	6
Genotype	G5	2.566	0.077	-0.329	-0.144	0.207	0.108	0.345	-0.198	0.064	-0.241	0.184	86.31	4	11.146	8	3	65	35	37.45	8
Genotype	G6	2.549	0.119	-0.151	-0.120	0.461	-0.131	0.142	0.140	0.166	0.247	0.163	93.11	3	8.095	9	6	65	35	37.85	7
Genotype	G7	2.710	0.669	0.017	0.024	-0.487	-0.297	0.190	0.004	-0.053	0.048	0.299	48.75	7	38.237	3	9	65	35	41.92	5
Genotype	G8	3.039	-0.020	0.442	-0.193	0.133	-0.262	-0.292	-0.352	0.038	0.007	0.206	78.97	5	100.000	1	1	65	35	92.64	1
Genotype	G9	2.574	-0.492	0.578	-0.236	-0.170	0.265	0.276	0.033	-0.104	0.082	0.402	15.54	9	12.666	7	8	65	35	13.67	9
Genotype	G10	2.506	-0.734	-0.574	0.064	-0.297	-0.219	-0.082	-0.009	0.061	0.028	0.450	0.00	10	0.000	10	10	65	35	0.00	10
WF§§	2010	2.521	0.233	0.167	0.247	0.002	0.024	-0.124	-0.067	-0.285	0.138	0.175	68.45	7	42.744	10	10	65	35	51.74	8
WF	2011	3.180	-0.225	-0.066	0.033	0.394	0.081	-0.081	0.087	-0.048	0.011	0.144	79.91	4	67.198	4	8	65	35	71.65	3
WF	2012	4.064	-0.230	0.204	0.309	-0.452	0.291	0.126	0.032	-0.027	-0.047	0.249	41.33	13	100.000	1	9	65	35	79.47	2
WF	2013	3.675	-0.637	0.036	0.116	0.058	-0.164	-0.179	-0.037	-0.063	-0.061	0.262	36.85	14	85.569	3	16	65	35	68.52	4
WF	2014	2.507	-0.532	0.087	-0.003	0.193	0.088	-0.128	-0.221	-0.022	0.059	0.230	48.23	11	42.241	11	15	65	35	44.34	11
WF	2015	3.107	0.175	-0.057	-0.751	-0.127	0.257	-0.112	-0.104	-0.103	0.034	0.236	46.14	12	64.498	5	7	65	35	58.07	6
WF	2016	3.911	0.114	0.443	-0.115	-0.076	-0.144	-0.379	-0.140	0.061	-0.120	0.211	55.35	10	94.294	2	3	65	35	80.66	1
WF	2017	2.663	-0.050	0.118	-0.081	-0.128	0.059	-0.092	0.220	-0.146	-0.213	0.088	100.00	1	48.031	8	2	65	35	66.22	5
NF¶¶	2010	1.989	0.134	-0.225	0.133	-0.366	-0.416	-0.206	-0.006	0.031	0.114	0.197	60.29	9	23.020	13	4	65	35	36.06	14
NF	2011	2.536	-0.157	-0.117	-0.233	0.052	-0.369	0.279	-0.079	-0.075	-0.161	0.166	71.69	5	43.327	9	5	65	35	53.25	7
NF	2012	3.057	0.289	-0.721	0.258	0.125	0.140	-0.211	-0.026	-0.119	-0.145	0.363	0.00	16	62.622	6	12	65	35	40.70	13
NF	2013	2.175	0.356	0.083	0.046	0.133	-0.049	-0.050	-0.015	0.228	-0.106	0.167	71.27	6	29.930	12	14	65	35	44.40	10
NF	2014	1.368	0.163	0.043	0.039	0.232	0.035	0.019	0.016	0.141	0.083	0.098	96.33	2	0.000	16	6	65	35	33.72	15
NF	2015	1.609	0.273	0.119	0.219	0.013	0.027	0.200	-0.389	-0.089	-0.087	0.178	67.49	8	8.911	15	11	65	35	29.41	16
NF	2016	2.910	0.331	0.537	0.064	0.244	-0.133	0.027	0.156	-0.185	-0.004	0.300	22.76	15	57.171	7	13	65	35	45.13	9
NF	2017	1.782	-0.008	-0.203	-0.169	-0.006	-0.227	0.104	0.026	-0.176	0.074	0.109	92.43	3	15.343	14	1	65	35	42.32	12

* R, response variable.

† PC, principal component axis.

‡ W, Weighted Average of the Absolute Scores considering the BLUP GE interaction matrix.

§ Pct, value in percentage related to stability (W) and response variable (R).

¶ Or, order (ranking) related to stability (W) or response variable (R).

** Wh, the weight used for stability (Wh.W) and response variable (Wh.R) for WAASBY estimation.

†† WAASBY, an index that consider both stability and response variable in the genotype ranking. Different weights can be used.

‡‡ OrWA, the order (ranking) related to WAASBY index.

§§ WF, with fungicide.

¶¶ NF, without fungicide.

Table S 5: Ranking of the 10 oat genotypes for grain yield, stability indexes, and simultaneous selection indexes.

	Yield	Stability indexes							Simultaneous selection indexes					
Genotype	GY*	IPCA1†	WAAS	WAASB‡	ASV§	SIPC¶	Za**	EV††	WAASY‡‡	WAASBY	ssiASV§§	ssiSIPC	ssiZa	ssiEV
G1	6	5	2	2	4	3	1	2	4	4	4	3	3	3
G2	4	2	6	6	1	6	6	6	3	3	2	4	4	4
G3	2	4	1	1	2	1	3	1	2	2	1	1	1	1
G4	5	7	7	8	7	7	7	7	6	8	6	7	7	6
G5	8	3	4	4	5	4	2	4	7	7	8	7	4	6
G6	9	6	3	3	3	2	5	3	8	6	6	5	8	6
G7	3	9	8	7	8	8	8	8	5	5	5	5	6	5
G8	1	1	5	5	6	5	4	5	1	1	3	2	1	2
G9	7	8	9	9	9	9	9	9	9	9	9	9	9	9
G10	10	10	10	10	10	10	10	10	10	10	10	10	10	10

* GY, grain yield.
† IPCA1, absolute values of the first principal component axis.
‡ WAAS and WAASB, weighted average of absolute scores.
§ ASV, AMMI stability value.
¶ SIPC, sums of the absolute value of the IPCA scores.
** Za, absolute value of the relative contribution of IPCAs to the interaction.
†† EV, averages of the squared eigenvector values.
‡‡ WAASY and WAASBY, simultaneous selection indexes using the using WAAS and WAASB, respectively.
§§ 'ssi', are the simultaneous selection indexes for each AMMI derived stability index.

Table S 6: Ranking of the 55 maize genotypes for grain yield, stability indexes, and simultaneous selection indexes.

	Yield	Stability indexes							Simultaneous selection indexes					
Genotype	GY*	IPCA1†	WAAS	WAASB‡	ASV§	SIPC¶	Za**	EV††	WAASY‡‡	WAASBY	ssiASV§§	ssiSIPC	ssiZa	ssiEV
G1	5	40	43	43	44	39	41	38	8	8	23	13	17	12
G2	4	54	54	54	54	54	54	54	32	29	29	32	32	33
G3	38	43	38	31	38	29	36	35	42	40	46	42	48	46
G4	3	21	47	47	42	46	47	49	9	9	18	19	22	25
G5	50	20	33	39	18	30	30	28	50	50	41	51	50	49
G6	1	46	50	49	45	52	51	53	1	2	19	25	27	26
G7	8	2	28	30	11	40	33	41	6	5	1	18	10	19
G8	19	18	46	45	43	48	46	47	34	34	34	42	38	41
G9	25	44	48	48	47	50	48	51	39	39	44	46	44	48
G10	16	23	32	29	37	34	32	33	18	17	27	22	19	19
G11	6	31	29	41	25	33	29	32	5	6	8	9	9	9
G12	17	7	11	8	12	16	12	21	12	12	7	7	5	9
G13	52	50	49	50	49	45	49	39	53	53	53	52	53	52
G14	29	3	2	2	5	1	2	2	13	15	10	5	6	5
G15	11	6	10	12	9	14	10	13	3	3	2	3	2	2
G16	43	32	22	18	22	21	22	15	43	42	40	40	38	33
G17	15	15	27	27	29	32	27	36	14	13	16	17	11	22
G18	26	1	6	5	14	7	6	18	17	19	13	7	8	13
G19	55	53	52	51	53	44	50	44	55	55	55	53	54	53
G20	30	29	41	34	21	47	43	42	35	31	25	48	44	43
G21	12	25	44	44	50	41	44	45	19	14	34	25	29	31
G22	39	8	30	38	3	37	34	43	40	44	14	47	44	51
G23	13	37	36	40	26	36	37	31	15	16	12	19	22	13
G24	7	27	37	37	28	38	38	30	7	7	11	14	15	7
G25	36	49	45	46	46	43	45	37	41	41	49	50	51	46
G26	35	42	14	6	34	11	14	9	23	21	42	15	21	13
G27	14	48	51	52	48	51	52	46	29	32	34	41	41	35
G28	40	41	25	26	36	23	25	20	38	38	46	39	38	35
G29	54	39	4	7	17	2	3	1	51	51	43	30	31	28
G30	18	16	21	20	13	24	24	26	21	20	8	11	11	13
G31	28	11	39	36	23	49	42	50	33	30	25	48	42	49
G32	20	4	40	32	40	42	40	40	28	27	33	38	35	35
G33	45	36	16	17	19	13	15	11	46	45	37	32	35	29
G34	27	35	19	16	30	15	16	8	22	22	28	11	14	6
G35	44	55	55	55	55	55	55	55	52	52	52	53	52	53

Table S 6: Ranking of the 55 maize genotypes for grain yield, stability indexes, and simultaneous selection indexes. *(continued)*

	Yield	Stability indexes							Simultaneous selection indexes					
Genotype	GY*	IPCA1†	WAAS	WAASB‡	ASV§	SIPC¶	Za**	EV††	WAASY‡‡	WAASBY	ssiASV§§	ssiSIPC	ssiZa	ssiEV
G36	23	5	15	25	2	26	19	34	20	23	4	19	11	31
G37	51	22	7	11	8	9	8	10	49	49	31	37	33	39
G38	47	9	1	1	1	3	1	3	36	37	21	22	19	21
G39	10	45	35	33	39	31	35	27	10	10	23	10	15	7
G40	53	52	53	53	52	53	53	52	54	54	54	55	55	55
G41	22	17	9	9	4	8	9	17	16	18	5	5	6	11
G42	33	28	18	19	31	17	17	12	26	26	37	22	22	17
G43	46	12	12	13	32	12	13	16	45	46	48	32	33	40
G44	41	13	5	10	6	5	5	7	30	35	20	15	17	18
G45	37	30	24	23	27	19	23	14	31	33	37	30	35	22
G46	2	47	23	21	41	18	21	23	2	1	15	2	3	3
G47	31	51	42	42	51	28	39	29	37	36	49	35	42	35
G48	32	14	17	15	16	22	18	19	24	25	21	27	22	22
G49	9	33	13	14	15	10	11	6	4	4	3	1	1	1
G50	48	34	31	28	35	25	28	24	48	48	51	45	49	43
G51	21	24	3	3	7	4	4	4	11	11	6	3	4	3
G52	24	10	26	24	20	35	26	48	25	24	16	35	22	43
G53	49	19	8	4	10	6	7	5	44	43	31	29	29	26
G54	34	38	20	22	24	20	20	22	27	28	29	27	28	29
G55	42	26	34	35	33	27	31	25	47	47	45	44	44	42

* GY, grain yield.
† IPCA1, absolute values of the first principal component axis.
‡ WAAS and WAASB, weighted average of absolute scores.
§ ASV, AMMI stability value.
¶ SIPC, sums of the absolute value of the IPCA scores.
** Za, absolute value of the relative contribution of IPCAs to the interaction.
†† EV, averages of the squared eigenvector values.
‡‡ WAASY and WAASBY, simultaneous selection indexes using the using WAAS and WAASB, respectively.
§§ 'ssi', are the simultaneous selection indexes for each AMMI derived stability index.

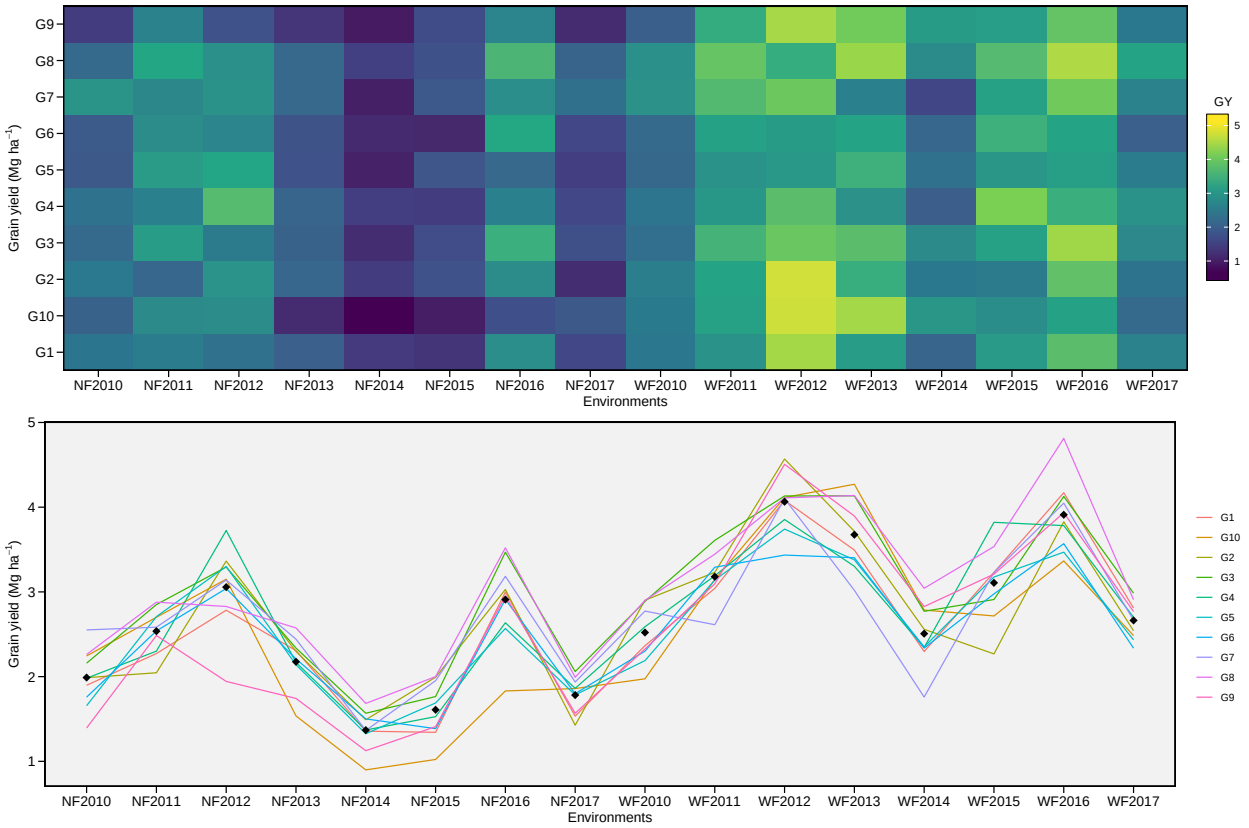


Figure S 1: Grain yield of the 10 oat genotypes observed in the 16 environments. Black rhombus show the mean of each environment

2 Supplemental figures

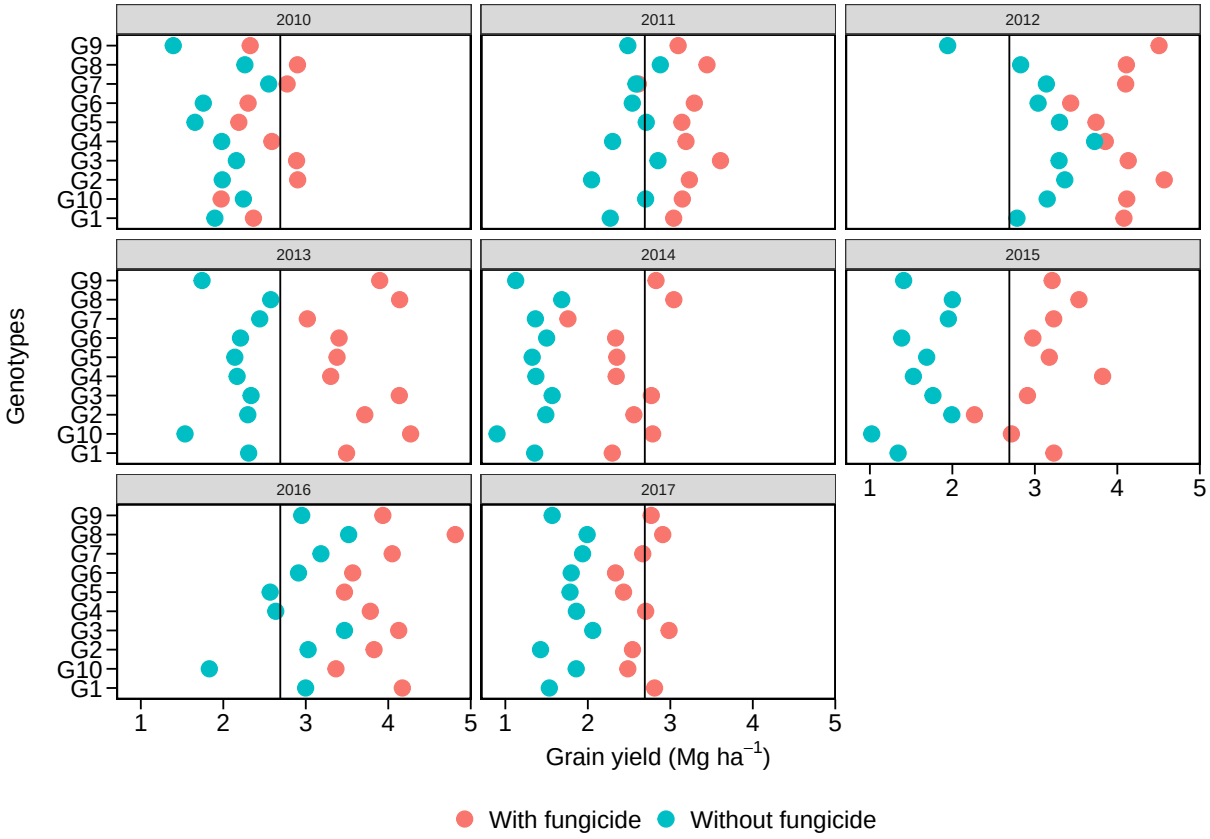


Figure S 2: Average values for grain yield for 10 oat genotypes growing in 16 environments (combination of fungicide management and growing year). Vertical lines within each plot shows the grand mean.

Figure S 3: Average values for grain yield for 10 oat genotypes growing in 16 environments (combination of fungicide management and growing year). Vertical lines within each plot shows the grand mean.

3 Supplemental R codes

The data set from experiment 1 (oat) is available in a public repository and was used in this material to reproduce the examples. Other replicated-based data can be used provided that the following columns are in the dataset: environment, genotype, block/replicate and response variable(s). By running the following code you will install and load the METAAB package (if it is still not installed) and download the dataset into a dataframe called `dataset`.

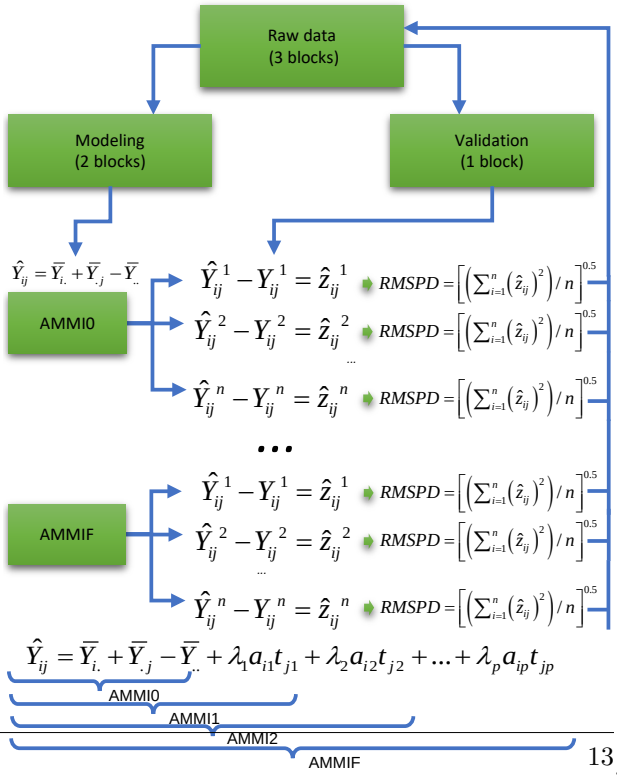
```
if (!require("devtools")) install.packages("devtools")
devtools::install_github("TiagoOlivoto/metan")
library(metan)

dataset = read.csv("https://data.mendeley.com/datasets/2sjz32k3s3/2/files/1561de7f-b8fd-4093-b4
```

The R packages kableExtra was used to produce this material.

```
library(kableExtra)
# Function to create the tables
print_table <- function(table,
                        fwidth = NULL,
                        options_styl = c("striped", "scale_down")){
kable(table,  align  = "l", booktabs = T,
      format = "latex", linesep = "", digits = 3) %>%
kable_styling(full_width = fwidth, latex_options = options_styl)
}
```

3.1 Predictive accuracy

The first steap in the article was to evaluate the predictive accucary of both AMMI and BLUP models. We will show in details how we can do that using the functions `cv_ammif()` and `cv_blup()` functions. The `cv_ammif()` function provides a complete cross-validation procedure for all member of AMMI model family (AMMI0-AMMIF) using replicate-based data, according to the side diagram:



Automatically the first validation is carried out considering the AMMIF (all possible axis used). Considering this model, the original data set is split up into two sets: training set and validation set. The training set has all combinations (genotype x environment) with $r-1$ replications. The validation set has one replication that were not included in the training set.

The splitting of the data set into training and validation sets depends on the design considered. For a Randomized Complete Block Design (default option) and the procedure we used in the article, completely blocks are randomly selected within environments, as suggested by Piepho (1994). The remaining block serves as validation data. If `design = "CRD"` is informed, thus declaring that a completely randomized design was used, single observations are randomized for each treatment (genotype-by-environment combination). This is the same procedure suggested by Gauch (1988). The estimated values for each member of the AMMI model family in each re-sampling cycle are compared with the observed values in the validation data. Then, the Root Mean Square Prediction Difference is computed as follows:

$$RMSPD = \left[\left(\sum_{i=1}^{n} (\hat{y}_{ij} - y_{ij})^2\right)/n\right]^{0.5}$$

where $\widehat{y}_{ij}$ is the model predicted value; and y_{ij} is the observed value in the validation set. The number of random selection of blocks/replicates (n) is defined in the argument `nboot`. At the end of the n cycles for all models, a list with all estimated RMSPD and the average of RMSPD is returned.

The function `cv_blup()` provides a cross-validation of replicate-based data using mixed models. By default, complete blocks are randomly selected for each environment. The procedure for computing the RSME is identical to the above function.

The following code computes the cross-validation of the oat data set that, for simplicity, we will use 200 re-sampling procedures. We suggest using a larger number, say, 1000.

```
# cross-validation for AMMI model family
AMMI_model <- cv_ammif(dataset,
                       resp = GY,
                       gen = GEN,
                       env = ENV,
                       rep = BLOCK)

# cross-validation for BLUP model
BLUP_model <- cv_blup(dataset,
                      resp = GY,
                      gen = GEN,
                      env = ENV,
                      rep = BLOCK)
```

3.1.1 Printing the means of RMSPD estimates

All outputs shown in tables were laid out using the R package kableExtra. The pdf file of this package can be found here..

```
bind <- bind_cv(AMMI_model, BLUP_model, bind = "means")
print_table(bind$RMSPD, fwidth = TRUE)
```

MODEL	mean	sd	se	Q2.5	Q97.5
BLUP_g_RCBD	0.412	0.023	0.002	0.370	0.455
AMMI3	0.422	0.022	0.002	0.376	0.461
AMMI4	0.424	0.023	0.002	0.382	0.464
AMMI2	0.424	0.023	0.002	0.376	0.464
AMMI5	0.428	0.022	0.002	0.384	0.463
AMMI6	0.429	0.021	0.002	0.385	0.464
AMMI7	0.431	0.021	0.001	0.390	0.470
AMMIF	0.431	0.023	0.002	0.383	0.468
AMMI8	0.432	0.024	0.002	0.381	0.473
AMMI1	0.440	0.024	0.002	0.395	0.483
AMMI0	0.442	0.026	0.002	0.394	0.494

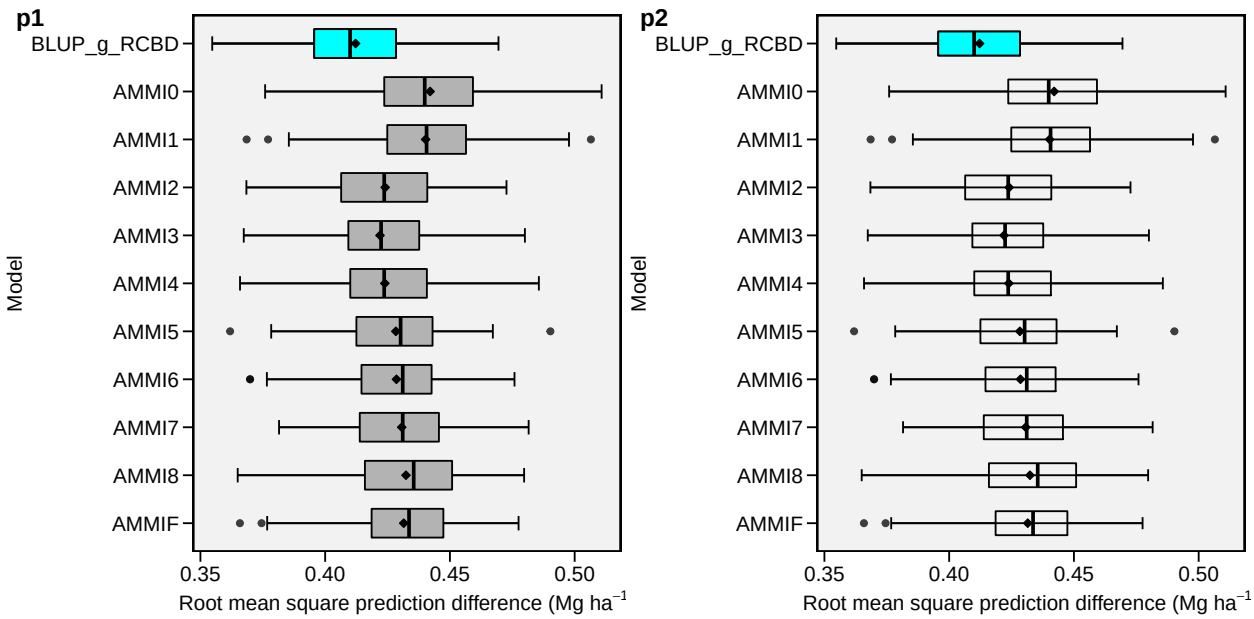
The results shown above are the means of the 200 RMSPD estimates for each tested model and are presented from the most accurate model (smallest RMSPD value) to the least accurate model (highest RMSPD value).

We can print the result from `RMSPDweat` in basically two distinct ways. First, printing the results in the R environment using `print(RMSPDweat)` (this is not a good idea since we probably will need work with these results). The second option is to export the results to an editable file, such as a .csv, or .xlsx file. We have R packages that facilitate this procedure. Let's do it. For example, to export the results to a .csv file, the command to be run is: `utils::write.csv(RMSPDweat, file = "myfile.csv")`. This command will create a .csv file called "myfile" in the R directory. To export the results to a .xlsx file, the package `xlsx` is needed. After properly installed, the command will be then `xlsx::write.xls(RMSPDweat, file = "myfile2.xlsx")`.

3.1.2 Plotting the RMSPD estimates

The values of the RMSPD estimates obtained in the cross-validation process may be plotted using the function`plot()` may be used.

```
# binding AMMI and BLUP RMSPDs
RMSPD_oat <- bind_cv(AMMI_model, BLUP_model)

# Plotting the RMSPD values
p1 <- plot(RMSPD_oat)
p2 <- plot(RMSPD_oat, width.boxplot = 0.5, col.boxplot = "transparent")
arrange_ggplot(p1, p2, labels = c("p1", "p2"))
```



Six statistics are shown in this boxplot. The mean (black rhombus), the median (black line), the lower and upper hinges that correspond sto the first and third quartiles (the 25th and 75th percentiles, respectively). The upper whisker extends from the hinge to the largest value no further than $1.5 \times IQR$ from the hinge (where IQR is the inter-quartile range). The lower whisker extends from the hinge to the smallest value at most $1.5 \times IQR$ of the hinge. Data beyond the end of the whiskers are considered outlying points. If the condition `violin = TRUE`, a violin plot is added along with the boxplot. A violin plot is a compact display of a continuous distribution displayed in the same way as a boxplot.

3.2 Estimating the response variable using the AMMI model

An interesting feature of `METAAB` package for traditional AMMI model estimation is the implementation of the S3 method `predict()`. The response variable of a two-way table (for example, the yield of m genotypes in n environments) may be estimated using the function `predict(model)`, where `model` is an object of class `waas`. This estimation is based on the number of multiplicative terms declared in the function. If `naxis = 0` is declared, only the main effects (AMMI0) are considered. In this case, the estimated mean will be the estimate from OLS estimation. If `naxis = 1`, the AMMI1 (with one multiplicative term) is used for estimating the response variable. If `naxis = min(gen-1;env-1)`, the AMMIF is fitted. A summary of all possible AMMI models is presented below.

Member of AMMI family	Espected response of the i-th genotype in the jth environment
AMMI0	$\hat{y}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{..}$
AMMI1	$\hat{y}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{..} + \lambda_1 a_{i1} t_{j1}$
AMMI2	$\hat{y}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{..} + \lambda_1 a_{i1} t_{j1} + \lambda_2 a_{i2} t_{j2}$
...	
AMMIF	$\hat{y}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{..} + \lambda_1 a_{i1} t_{j1} + \lambda_2 a_{i2} t_{j2} + ... + \lambda_p a_{ip} t_{jp}$

The number of axes used in the estimation must be carefully chosen. Procedures based on postdictive success, such as Gollobs's test (Gollob 1968) or predictive success, such as cross-validation procedures (Piepho 1994) should be used. This package provides both. The `waas()` function compute traditional AMMI analysis showing the number of significant axes according Gollobs's test. On the other hand, `cv_ammif()` function provides a cross-validation, estimating the RMSPD for all AMMI model family based on re-sampling procedures, considering an completely randomized desing or a randomized complete block design.

- Estimating the yield of the 10 oat cultivars in 16 environments using 5 multiplicative terms.

```
AMMI_model <- dataset %>%  waas(ENV, GEN, BLOCK, GY, verbose = FALSE)
predictoat <- predict(AMMI_model, naxis = 5)

# printing the results
print_table(predictoat[[1]][1:10,])
```

ENV	GEN	Y	resOLS	Ypred	ResAMMI	YpredAMMI	AMMI0
NF2010	G1	1.898	-0.024	1.922	-0.09148	1.830	1.922
NF2010	G10	2.244	0.439	1.804	0.40405	2.208	1.804
NF2010	G2	1.988	-0.013	2.001	-0.03240	1.968	2.001
NF2010	G3	2.159	-0.080	2.239	-0.03960	2.199	2.239
NF2010	G4	1.981	-0.014	1.995	-0.07142	1.924	1.995
NF2010	G5	1.657	-0.207	1.864	-0.06381	1.800	1.864
NF2010	G6	1.758	-0.090	1.847	-0.13428	1.713	1.847
NF2010	G7	2.551	0.543	2.008	0.58685	2.595	2.008
NF2010	G8	2.262	-0.076	2.337	-0.14999	2.187	2.337
NF2010	G9	1.393	-0.478	1.872	-0.40792	1.464	1.872

Only the first ten values are shown. The following values are presented: **ENV** is the environment; **GEN** is the genotype; **Y** is the response variable; **resOLS** is the residual ($\hat{z}_{ij}$) estimated by the Ordinary Least Square (OLS), where $\hat{z}_{ij} = y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{ij}$; **Ypred** is the predicted value by OLS ($\hat{y}_{ij} = y_{ij} - \hat{z}_{ij}$); **ResAMMI** is the residual estimated by the AMMI model ($\hat{a}_{ij}$) considering the number of multiplicative terms informed in the function (in this case 5), where $\hat{a}_{ij} = \lambda_1\alpha_{i1}\tau_{j1} + ... + \lambda_5\alpha_{i5}\tau_{j5}$; **YpredAMMI** is the predicted value by AMMI model $\hat{ya}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{ij} + \hat{a}_{ij}$; and **AMMI0** is the predicted value when no multiplicative terms are used, i.e., $\hat{y}_{ij} = \bar{y}_{i.} + \bar{y}_{.j} - \bar{y}_{ij}$.

3.3 Estimating the WAAS index

The `waas()` function computes the **W**eighted **A**verage of **A**bsolute **S**cores considering (i) all principal component axes that were significant ($p < 0.05$ by default); or (ii) declaring a specific number of axes to be used, according to the following equation:

$$WAAS_i = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| / \sum_{k=1}^{p} EP_k$$

where $WAAS_i$ is the weighted average of absolute scores of the ith genotype; PCA_{ik} is the score of the ith genotype in the kth IPCA; and EP_k is the explained variance of the kth IPCA for $k = 1, 2, .., p$, considering p the number of significant PCAs, or a declared number of PCAs. The following functions may be used to do that.

3.3.1 Number of axes based on F-test

In this example only IPCAs with P-value < 0.05 will be considered in the WAAS estimation.

```
# Assuming equal weights for productivity and stability (default)
WAAS1 <-
  dataset %>%
  waas(ENV, GEN, BLOCK, GY, verbose = FALSE)
```

```
# printing the WAAS object
options(digits = 3)
print_table(WAAS1$GY$individual$individual)
```

ENV	MEAN	MSB	MSG	MSR	FCB	PRFB	FCG	PRFG	CV	h2	AS
NF2010	1.99	0.381	0.337	0.091	4.189	0.032	3.71	0.009	15.16	0.730	0.854
NF2011	2.54	0.817	0.215	0.028	29.370	0.000	7.72	0.000	6.58	0.870	0.933
NF2012	3.06	0.583	0.679	0.111	5.253	0.016	6.12	0.001	10.90	0.837	0.915
NF2013	2.17	0.654	0.296	0.027	24.491	0.000	11.09	0.000	7.51	0.910	0.954
NF2014	1.37	0.377	0.151	0.105	3.595	0.049	1.44	0.244	23.68	0.304	0.552
NF2015	1.61	0.092	0.320	0.054	1.717	0.208	5.98	0.001	14.38	0.833	0.913
NF2016	2.91	0.077	0.713	0.099	0.772	0.477	7.18	0.000	10.83	0.861	0.928
NF2017	1.78	0.103	0.131	0.075	1.373	0.279	1.73	0.153	15.40	0.423	0.650
WF2010	2.52	0.065	0.337	0.144	0.453	0.643	2.34	0.059	15.05	0.573	0.757
WF2011	3.18	0.697	0.207	0.179	3.907	0.039	1.16	0.376	13.29	0.136	0.369
WF2012	4.06	0.489	0.335	0.179	2.731	0.092	1.87	0.123	10.41	0.466	0.683
WF2013	3.67	0.116	0.531	0.138	0.846	0.445	3.86	0.007	10.10	0.741	0.861
WF2014	2.51	0.067	0.408	0.231	0.290	0.751	1.76	0.146	19.17	0.433	0.658
WF2015	3.11	0.166	0.550	0.067	2.481	0.112	8.24	0.000	8.32	0.879	0.937
WF2016	3.91	0.219	0.526	0.066	3.297	0.060	7.93	0.000	6.59	0.874	0.935
WF2017	2.66	0.160	0.135	0.059	2.733	0.092	2.30	0.063	9.08	0.565	0.752

The above table shows the within-environment ANOVA considering a fixed-effect model. For each environment the Mean Squares for block, genotypes and error are shown. Estimated F-value and the probability error are also shown for block and genotype effects. Some measures of experimental precision are calculated, namelly, coefficient of variation, $CV = (\sqrt{MS_{res}}/Mean) \times 100$; the heritability, $h2 = (MS_{gen} - MS_{res})/MS_{gen}$; the accuracy of selection, $As = \sqrt{h2}$; and the coefficient of determination (R2).

```
# printing the WAAS object
print_table(WAAS1$GY$anova) %>%
row_spec(9, bold = T) %>%
add_indent(c(5:13))
```

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)	Percent	Accumul
ENV	15	285.910	19.061	60.24	0.000	.	.
REP(ENV)	32	10.125	0.316	3.07	0.000	.	.
GEN	9	13.084	1.454	14.09	0.000	.	.
ENV:GEN	135	39.755	0.294	2.85	0.000	.	.
PC1	23	13.062	0.568	5.50	0.000	32.9	32.9
PC2	21	10.687	0.509	4.93	0.000	26.9	59.7
PC3	19	6.803	0.358	3.47	0.000	17.1	76.8
PC4	17	3.685	0.217	2.10	0.007	9.3	86.1
PC5	**15**	**2.670**	**0.178**	**1.72**	**0.047**	**6.7**	**92.8**
PC6	13	1.454	0.112	1.08	0.376	3.7	96.5
PC7	11	0.727	0.066	0.64	0.794	1.8	98.3
PC8	9	0.465	0.052	0.50	0.874	1.2	99.5
PC9	7	0.203	0.029	0.28	0.962	0.5	100
Residuals	288	29.725	0.103	NA	NA	.	.
Total	479	378.599	0.790	NA	NA	.	.

The above table is the traditional AMMI analysis. Nine principal component axes were fitted and five were significant at 5% probability error. Based on this result, the AMMI5 model would be the best model to predict the yield of the genotypes in the studied environments. This is confirmed by the cross-validation in section 3. The AMMI model with the smallest RMSPD was the AMMI5.

- printing the WAAS object

```
data <- WAAS1$GY$model[, c(1:3,13:17, 21:22)]
print_table(data)
```

type	Code	Y	WAAS	PctResp	PctWAAS	wRes	wWAAS	WAASY	OrWAASY
GEN	G1	2.62	0.188	22.04	95.3	50	50	58.7	3
GEN	G10	2.51	0.598	0.00	0.0	50	50	0.0	10
GEN	G2	2.70	0.282	36.89	73.4	50	50	55.2	4
GEN	G3	2.94	0.168	81.56	100.0	50	50	90.8	1
GEN	G4	2.70	0.388	35.80	48.8	50	50	42.3	7
GEN	G5	2.57	0.221	11.15	87.5	50	50	49.3	6
GEN	G6	2.55	0.207	8.11	90.8	50	50	49.5	5
GEN	G7	2.71	0.400	38.26	45.9	50	50	42.1	8
GEN	G8	3.04	0.249	100.00	81.1	50	50	90.6	2
GEN	G9	2.57	0.521	12.68	17.9	50	50	15.3	9
ENV	NF2010	1.99	0.256	23.02	60.3	50	50	41.7	15
ENV	NF2011	2.54	0.217	43.33	70.7	50	50	57.0	7
ENV	NF2012	3.06	0.482	62.62	0.0	50	50	31.3	16
ENV	NF2013	2.17	0.199	29.93	75.5	50	50	52.7	9
ENV	NF2014	1.37	0.112	0.00	98.9	50	50	49.5	11
ENV	NF2015	1.61	0.201	8.91	75.0	50	50	42.0	14
ENV	NF2016	2.91	0.373	57.17	29.1	50	50	43.1	13
ENV	NF2017	1.78	0.153	15.34	87.9	50	50	51.6	10
ENV	WF2010	2.52	0.208	42.75	73.2	50	50	58.0	6
ENV	WF2011	3.18	0.202	67.20	74.7	50	50	71.0	3
ENV	WF2012	4.06	0.327	100.00	41.4	50	50	70.7	4
ENV	WF2013	3.67	0.330	85.57	40.6	50	50	63.1	5
ENV	WF2014	2.51	0.292	42.24	50.6	50	50	46.4	12
ENV	WF2015	3.11	0.317	64.50	44.1	50	50	54.3	8
ENV	WF2016	3.91	0.237	94.30	65.4	50	50	79.8	1
ENV	WF2017	2.66	0.108	48.03	100.0	50	50	74.0	2

In this example, the scores of the nine PCAs were not shown. The output generated by the `waas()` function shows the following results: **type**, genotype (GEN) or environment (ENV); **Code**, the code attributed to each level of the factors; **Y**, the response variable (in this case the grain yield); **WAAS** the weighted average of the absolute scores, estimated with all significant IPCA; **PctWAAS** and **PctResp**, the rescaled variable for the WAAS and Y, respectively; **OrResp** and **OrWAAS**, the ranks attributed to the genotype and environment regarding the Y or WAAS, respectively; **WAASY** is the simultaneous selection index that weights between response variable and stability. In this case, considering equal weights for PctResp and PctWAAS, the WAASY for G1 would be then: $WAASY_{G1} = [(22.043 \times 50) + (100 \times 50)]/50 + 50 = 92.60$, which, with equal weights is equivalente to the aritmetic mean of pctResp and PctWAAS. Then the $OrWAASY$ is the rank for the WAASY value. The genotype (or environment) with the largest WAASY value has the first ranked. Please, refer to Estimating the WAASBY index for a detailed explanation.

3.3.2 Number of axes declared manually

The second option to compute the WAAS is by manually declaring a specific number of multiplicative terms. In this case, the number of terms declared is used independently of its significance. Let us, for the moment, assume that after a cross-validation procedure the AMMI7 was the most predictively accurate AMMI model and the researcher will use this model. The additional argument `naxis` in the function `waas()` is then used to overwrite the default chose of significant terms.

```
WAAS2 <-
  dataset %>%
  waas(ENV, GEN, BLOCK, GY, naxis = 7, verbose = FALSE)
```

The only difference in this output compared to those from section 5.1 is that here we declared that seven PCA axes should be used for computing the WAAS value. Thus, only the values of WAAS, OrWAAS, WAASY and OrWAASY may have significant changes.

3.4 Other AMMI-based stability indexes

The following AMMI-based stability indexes tested in the article may be computed using the function `AMMI_indexes()`:

- **AMMI stability value, ASV, (Purchase, Hatting, and Deventer 2000).**

$$ASV = \sqrt{\left[\frac{IPCA1_{ss}}{IPCA2_{ss}} \times (IPCA1_{score})\right]^2 + (IPCA2_{score})^2}$$

- **Sums of the absolute value of the IPCA scores**

$$SIPC_i = \sum_{k=1}^{P} \left|\lambda_k^{0.5}\, a_{ik}\right|$$

- **Averages of the squared eigenvector values**

$$EV_i = \sum_{k=1}^{P} a_{ik}^2/P$$

described by Sneller, Kilgore-Norquest, and Dombek (1997), where P is the number of IPCA retained via F-tests;

- **absolute value of the relative contribution of IPCAs to the interaction (Zali et al. 2012).**

$$Za_i = \sum_{k=1}^{P} \theta_k a_{ik}$$

where θ_k is the percentage sum of squares explained by the k-th IPCA. Simultaneous selection indexes (ssi), are computed by summation of the ranks of the ASV, SIPC, EV and Za indexes and the ranks of the mean yields (Farshadfar 2008), which results in ssiASV, ssiSIPC, ssiEV, and ssiZa, respectively.

```
stab_indexes <- AMMI_indexes(WAAS1)
print_table(stab_indexes$GY)
```

GEN	Y	Y_R	ASV	ASV_R	ASV_SSI	SIPC	SIPC_R	SIPC_SSI	EV	EV_R	EV_SSI	ZA	ZA_R	ZA_SSI	WAAS	WAAS_R	WAAS_SSI
G1	2.62	6	0.338	4	10	0.873	1	7	0.022	1	7	0.134	2	8	0.188	2	8
G10	2.51	10	1.314	10	20	2.329	10	20	0.173	10	20	0.408	10	20	0.598	10	20
G2	2.70	4	0.156	1	5	1.604	6	10	0.168	9	13	0.213	6	10	0.282	6	10
G3	2.94	2	0.169	2	4	1.082	3	5	0.049	3	5	0.128	1	3	0.168	1	3
G4	2.70	5	0.678	7	12	1.830	7	12	0.123	6	11	0.275	7	12	0.388	7	12
G5	2.57	8	0.421	5	13	1.056	2	10	0.037	2	10	0.159	4	12	0.221	4	12
G6	2.55	9	0.260	3	12	1.275	5	14	0.079	5	14	0.157	3	12	0.207	3	12
G7	2.71	3	1.016	8	11	1.883	8	11	0.162	8	11	0.282	8	11	0.400	8	11
G8	3.04	1	0.533	6	7	1.242	4	5	0.059	4	5	0.180	5	6	0.249	5	6
G9	2.57	7	1.045	9	16	2.113	9	16	0.128	7	14	0.359	9	16	0.521	9	16

3.5 Estimating the WAASB index

The `waasb()` function computes the **W**eighted **A**verage of **A**bsolute **S**cores from the singular value decomposition of the matrix of **B**LUPs for the GEI effects generated by an linear mixed-effect model as follows:

$$WAASB_i = \sum_{k=1}^{p} |IPCA_{ik} \times EP_k| / \sum_{k=1}^{p} EP_k$$

where $WAASB_i$ is the weighted average of absolute scores of the ith genotype; $IPCA_{ik}$ is the scores of the ith genotype in the kth IPCA; and EP_k is the explained variance of the kth PCA for $k = 1, 2, .., p$, $p = min(G - 1; E - 1)$.

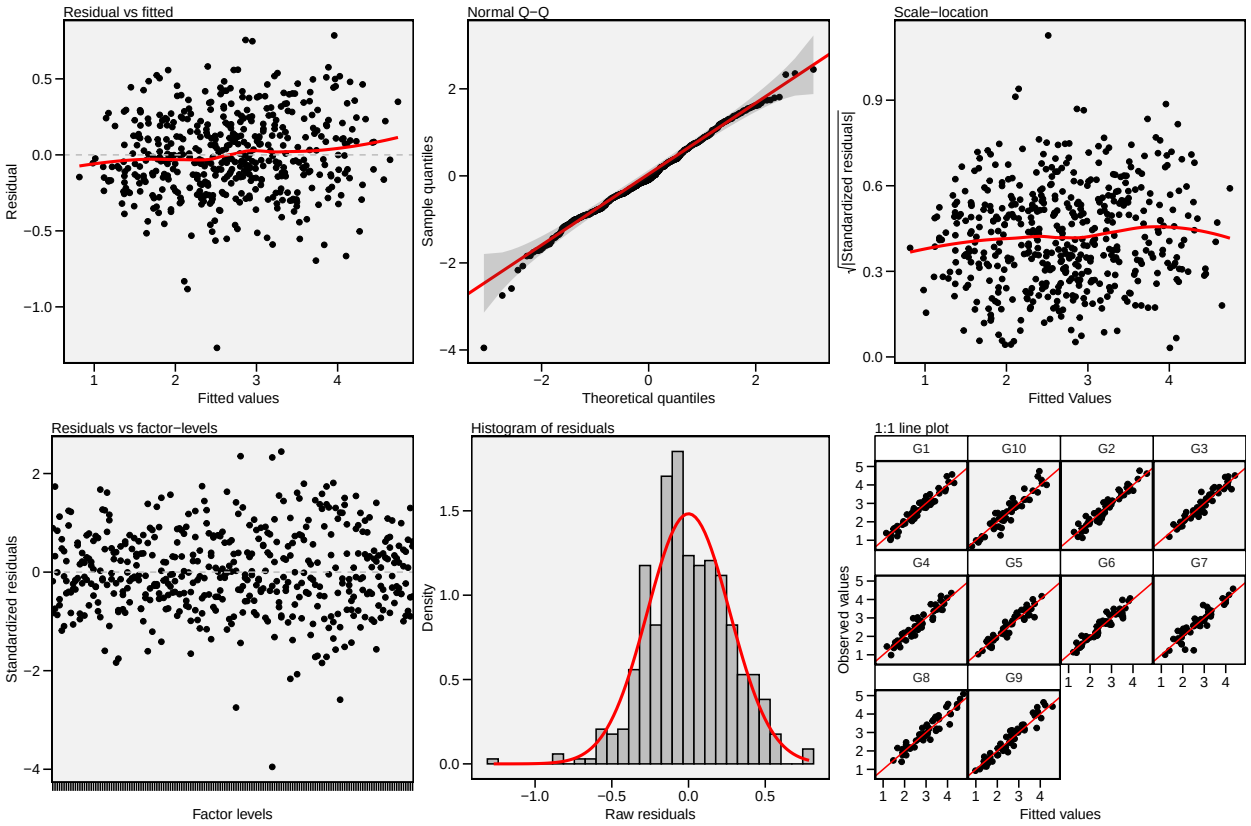
```
# Assuming equal weights for productivity and stability (default)
WAASB <-
  dataset %>%
  waasb(ENV, GEN, BLOCK, GY, wresp = 65)
```

```
All variables with significant (p < 0.05) genotype-vs-environment interaction
Done!
```

3.5.1 Diagnostic plot for residuals

The function `autoplot()` is used to generate diagnostic plots of residuals of the model. The normality of the random effects of genotype and interaction effects may be also obtained by using `type = "re"`.

```
plot(WAASB, which = c(1, 2, 3, 4, 5, 7), nrow = 2)
```



3.5.2 Printing the model outputs

3.5.2.1 Likelihood Ratio Tests

```
print_table(WAASB$GY$LRT, fwidth = TRUE)
```

model	npar	logLik	AIC	LRT	Df	Pr(>Chisq)
Complete	51	-260	623	NA	NA	NA
Genotype	50	-269	638	17.3	1	0
Gen:Env	50	-288	676	55.0	1	0

The output `LRT` contains the Likelihood Ratio Tests for genotype and genotype-vs-environment random effects.

3.5.2.2 Variance components and genetic parameters

```
print_table(WAASB$GY$ESTIMATES, fwidth = TRUE)
```

Parameters	Values
GEI variance	0.064
GEI (%)	33.360
Genotypic variance	0.024
Gen (%)	12.636
Residual variance	0.103
Res (%)	54.004
Phenotypic variance	0.191
Heritability	0.126
GEIr2	0.334
Heribatility of means	0.797
Accuracy	0.893
rge	0.382
CVg	5.775
CVr	11.939
CV ratio	0.484

In the output `ESTIMATES`, beyond the variance components for the declared random effects, some important parameters are also shown. **Heribatility** is the broad-sense heritability, h_g^2, estimated by $h_g^2 = \hat{\sigma}_g^2 \,/\, \left(\hat{\sigma}_g^2 + \hat{\sigma}_i^2 + \hat{\sigma}_e^2\right)$ where $\hat{\sigma}_g^2$ is the genotypic variance; $\hat{\sigma}_i^2$ is the genotype-by-environment interaction variance; and $\hat{\sigma}_e^2$ is the residual variance. **GEIr2** is the coefficient of determination of the interaction effects, r_i^2, estimated by $r_i^2 = \hat{\sigma}_i^2 \,/\, \left(\hat{\sigma}_g^2 + \hat{\sigma}_i^2 + \hat{\sigma}_e^2\right)$; **Heribatility of means** is the heribability on the mean basis, h_{gm}^2, estimated by $h_{gm}^2 = \hat{\sigma}_g^2 \,/\, \left[\hat{\sigma}_g^2 + \hat{\sigma}_i^2 \,/e + \hat{\sigma}_e^2 \,/\,(eb)\right]$, where e and b are the number of environments and blocks, respectively; **Accuracy** is the accuracy of selection, Ac, estimated by $Ac = \sqrt{h_{gm}^2}$; **rge** is the genotype-environment correlation, r_{ge}, estimated by $r_{ge} = \hat{\sigma}_g^2 \,/\, \left(\hat{\sigma}_g^2 + \hat{\sigma}_i^2\right)$; **CVg** is the the genotypic coefficient of variation, estimated by $\left(\sqrt{\hat{\sigma}_g^2}/\mu\right) \times 100$, where μ is the grand mean; **CVr** is the residual coefficient of variation, estimated by $\left(\sqrt{\hat{\sigma}_e^2}/\mu\right) \times 100$; **CV ratio** is the ratio between genotypic and residual coefficient of variation.

3.5.2.3 Some useful information

```
print_table(WAASB$GY$Details, fwidth = TRUE)
```

Parameters	Values
Ngen	10
Nenv	16
OVmean	2.6909
Min	0.899 (G10 in NF2014)
Max	4.812 (G8 in WF2016)
MinENV	NF2014 (1.368)
MaxENV	WF2012 (4.064)
MinGEN	G10 (2.506)
MaxGEN	G8 (3.039)

The following pieces of information are provided in `Details` output. **WgtResponse** is the weight

for the response variable in estimating WAASB; **WgtWAAS** is the weight for stability; **Ngen** is the number of genotypes; **Nenv** is the number of environments; **OVmean** is the overall mean; **Min** is the minimum value observed (returning the genotype and environment); **Max** is the maximum observed; **MinENV** is the environment with the lower mean; **MaxENV** is the environment with the largest mean observed; **MinGEN** is the genotype with the lower mean; **MaxGEN** is the genotype with the largest mean.

3.5.2.4 The WAASB object

```
data <- WAASB$GY$model[, c(1:3,13:17, 21:22)]
print_table(data)
```

type	Code	Y	WAASB	PctResp	PctWAASB	wRes	wWAASB	WAASBY	OrWAASBY
GEN	G1	2.62	0.159	22.04	94.4	65	35	47.4	4
GEN	G10	2.51	0.450	0.00	0.0	65	35	0.0	10
GEN	G2	2.70	0.213	36.89	76.6	65	35	50.8	3
GEN	G3	2.94	0.141	81.56	100.0	65	35	88.0	2
GEN	G4	2.70	0.300	35.80	48.7	65	35	40.3	6
GEN	G5	2.57	0.184	11.15	86.3	65	35	37.5	8
GEN	G6	2.55	0.163	8.11	93.1	65	35	37.9	7
GEN	G7	2.71	0.299	38.26	48.7	65	35	41.9	5
GEN	G8	3.04	0.206	100.00	79.0	65	35	92.6	1
GEN	G9	2.57	0.402	12.68	15.5	65	35	13.7	9
ENV	NF2010	1.99	0.197	23.02	60.3	65	35	36.1	14
ENV	NF2011	2.54	0.166	43.33	71.7	65	35	53.3	7
ENV	NF2012	3.06	0.363	62.62	0.0	65	35	40.7	13
ENV	NF2013	2.17	0.167	29.93	71.2	65	35	44.4	10
ENV	NF2014	1.37	0.098	0.00	96.3	65	35	33.7	15
ENV	NF2015	1.61	0.178	8.91	67.5	65	35	29.4	16
ENV	NF2016	2.91	0.300	57.17	22.8	65	35	45.1	9
ENV	NF2017	1.78	0.109	15.34	92.5	65	35	42.3	12
ENV	WF2010	2.52	0.175	42.75	68.4	65	35	51.7	8
ENV	WF2011	3.18	0.144	67.20	79.9	65	35	71.6	3
ENV	WF2012	4.06	0.249	100.00	41.3	65	35	79.5	2
ENV	WF2013	3.67	0.262	85.57	36.9	65	35	68.5	4
ENV	WF2014	2.51	0.230	42.24	48.2	65	35	44.3	11
ENV	WF2015	3.11	0.236	64.50	46.1	65	35	58.1	6
ENV	WF2016	3.91	0.211	94.30	55.4	65	35	80.7	1
ENV	WF2017	2.66	0.088	48.03	100.0	65	35	66.2	5

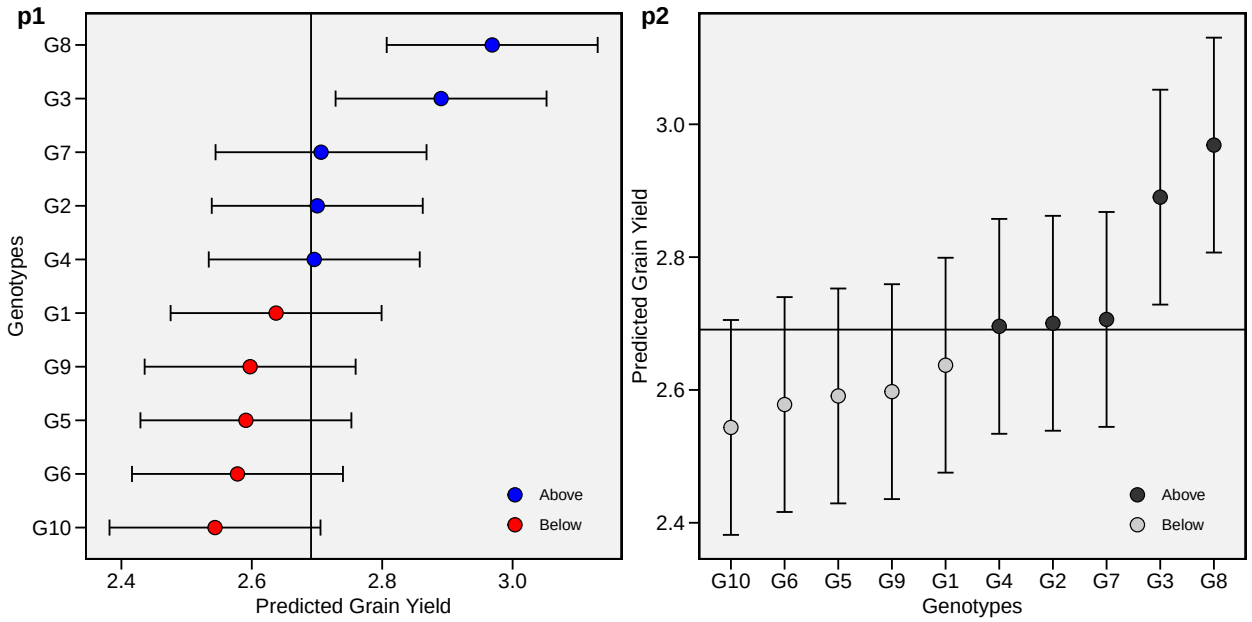
3.5.2.5 BLUP for genotypes

```
data <- WAASB$GY$blupGEN[1:10,]
print_table(data, fwidth = TRUE)
```

Rank	GEN	BLUPg	Predicted	LL	UL
1	G8	0.278	2.97	2.87	3.07
2	G3	0.199	2.89	2.79	2.99
3	G7	0.015	2.71	2.60	2.81
4	G2	0.010	2.70	2.60	2.80
5	G4	0.005	2.70	2.60	2.80
6	G1	-0.054	2.64	2.54	2.74
7	G9	-0.093	2.60	2.50	2.70
8	G5	-0.100	2.59	2.49	2.69
9	G6	-0.113	2.58	2.48	2.68
10	G10	-0.147	2.54	2.44	2.64

3.5.2.6 Plotting the BLUP for genotypes

```
# No file exported
p1 <- plot_blup(WAASB)
p2 <- plot_blup(WAASB,
                col.shape  =  c("gray20", "gray80")) + ggplot2::coord_flip()
arrange_ggplot(p1, p2, labels = c("p1", "p2"))
```



This output shows the predicted means for genotypes. **BLUPg** is the genotypic effect ($\hat{g}_i$) estimated by $\hat{g}_i = h^2_g(\bar{y}_{i.} - \bar{y}_{..})$ where h^2_g is the shrinkage effect for genotype. **Predicted** is the predicted mean estimated by $\hat{g}_i + \mu$ where μ is the grand mean. **LL** and **UL** are the lower and upper limits, respectively, estimated by $(\hat{g}_i + \mu) \pm CI$. CI is the confidence interval for BLUP prediction assuming a given probability error, where $CI = t \times \sqrt{((1 - Ac) \times \sigma^2_g)}$ where t is the Student's t value for a two-tailed t test at a given probability error; Ac is the accuracy of selection and σ^2_g is the genotypic variance.

3.5.2.7 BLUP for genotype-environment interaction

```
options(digits = 4)
data <- WAASB$GY$BLUPgge[1:10,]
print_table(data)
```

ENV	GEN	BLUPge	BLUPg	BLUPg+ge	Predicted	LL	UL
NF2010	G1	-0.024	-0.054	-0.078	1.911	1.810	2.012
NF2010	G10	0.261	-0.147	0.114	2.103	2.002	2.204
NF2010	G2	-0.007	0.010	0.003	1.991	1.891	2.092
NF2010	G3	-0.019	0.199	0.180	2.169	2.068	2.270
NF2010	G4	-0.008	0.005	-0.003	1.985	1.885	2.086
NF2010	G5	-0.151	-0.100	-0.251	1.738	1.637	1.839
NF2010	G6	-0.077	-0.113	-0.190	1.799	1.698	1.900
NF2010	G7	0.355	0.015	0.370	2.359	2.259	2.460
NF2010	G8	-0.003	0.278	0.275	2.263	2.163	2.364
NF2010	G9	-0.326	-0.093	-0.420	1.569	1.468	1.670

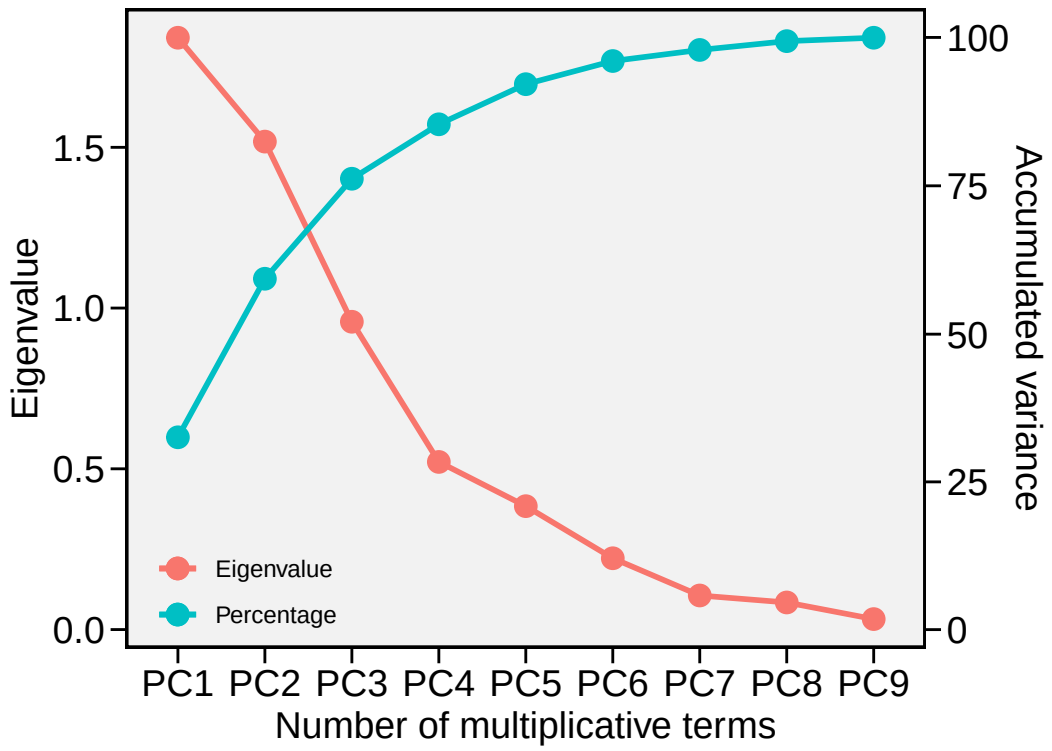
This output shows the predicted means for each genotype and environment combination. **BLUPg** is the genotypic effect described above. **BLUPge** is the genotypic effect of the ith genotype in the jth environment ($\hat{g}_{ij}$) estimated by $\hat{g}_{ij} = h^2_g(\bar{y}_{i.} - \bar{y}_{..}) + h^2_{ge}(y_{ij} - \bar{y}_{i.} - \bar{y}_{.j} + \bar{y}_{..})$, where h^2_{ge} is the shrinkage effect for the genotype-by-environment interaction; **BLUPg+ge** is $BLUP_g + BLUP_{ge}$; **Predicted** is the predicted mean ($\hat{y}_{ij}$) estimated by $\hat{y}_{ij} = \bar{y}_{.j} + BLUP_{g+ge}$.

3.5.3 Eigenvalues

```
print_table(WAASB$GY$PCA, fwidth = TRUE)
```

PC	Eigenvalue	Proportion	Accumulated
PC1	1.841	32.489	32.49
PC2	1.518	26.787	59.28
PC3	0.957	16.897	76.17
PC4	0.521	9.202	85.38
PC5	0.384	6.775	92.15
PC6	0.222	3.915	96.07
PC7	0.106	1.871	97.94
PC8	0.084	1.488	99.42
PC9	0.033	0.575	100.00

```
plot_eigen(WAASB, size.lab = 14, size.tex.lab = 14)
```



The above output shows the eigenvalues and the proportion of variance explained by each principal component axis of the BLUP interaction effects matrix.

3.5.4 Phenotypic means

```
data <- WAASB$GY$MeansGxE[1:10,]
print_table(data, fwidth = TRUE)
```

ENV	GEN	Y	envPC1	genPC1	nominal
NF2010	G1	1.898	0.134	0.110	1.912
NF2010	G10	2.244	0.134	-0.734	2.145
NF2010	G2	1.988	0.134	0.063	1.996
NF2010	G3	2.159	0.134	-0.083	2.148
NF2010	G4	1.981	0.134	0.291	2.020
NF2010	G5	1.657	0.134	0.078	1.667
NF2010	G6	1.758	0.134	0.119	1.774
NF2010	G7	2.551	0.134	0.669	2.641
NF2010	G8	2.262	0.134	-0.020	2.259
NF2010	G9	1.393	0.134	-0.492	1.327

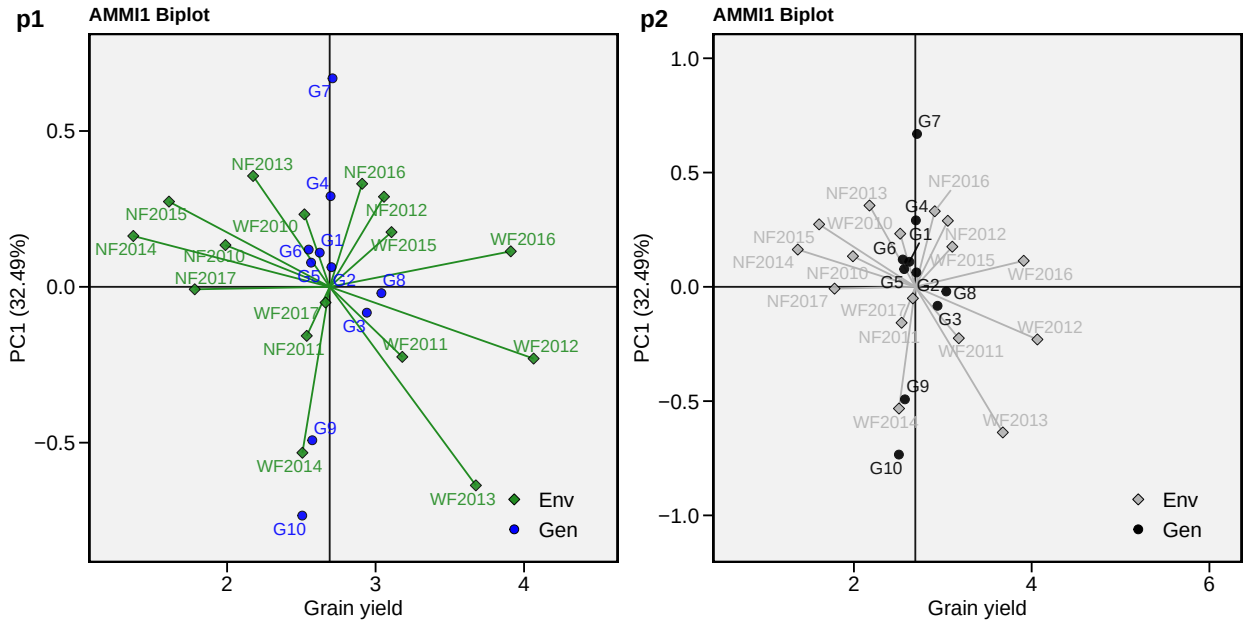
In this output, Y is the phenotypic mean for each genotype and environment combination (y_{ij}), estimated by $y_{ij} = \sum_k y_{ij}/B$ with $k = 1, 2, ...B$.

3.5.5 Biplots

We will show how biplots may be obtained for both traditional AMMI model, fitted by the function `waas()` and the mixed-effect model fitted by the function `waasb()`. Provided that an object of class "waas" or "WAASB" is available in the global environment, the graphics may be obtained using the function `plot_scores()`. To do that, we will revisit the previously fitted model `WAASB` . Please, refer to `?plot_scores` for more details. Four types of graphics can be generated: $1 = PC1 \times PC2$; $2 = GY \times PC1$; $3 = GY \times WAASB$; and 4 = a graphic with nominal yield as a function of the environment PCA1 scores.

3.5.5.1 biplot type 2: GY x PC1

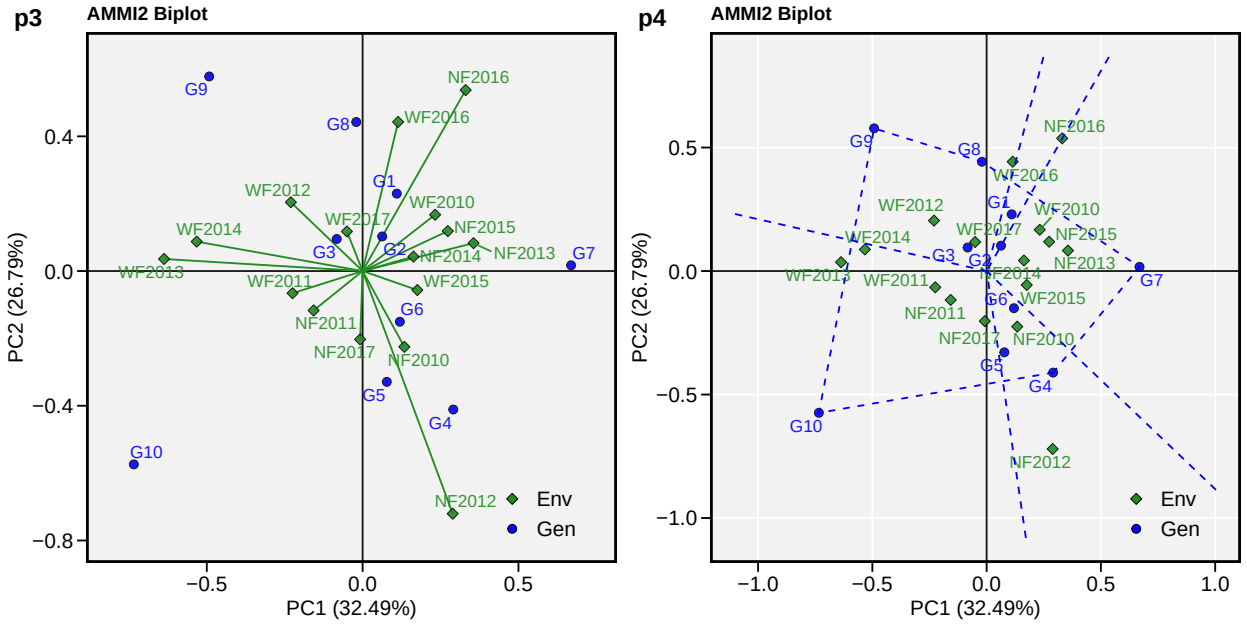
```
library(cowplot)
p1 <- plot_scores(WAASB)
p2 <- plot_scores(WAASB,
                  col.gen = "black",
                  col.env = "gray70",
                  col.segm.env = "gray70",
                  axis.expand = 1.5)
arrange_ggplot(p1, p2, labels = c("p1","p2"))
```



3.5.5.2 biplot type 1: PC1 x PC2

```
p3 = plot_scores(WAASB, type = 2)
p4 = plot_scores(WAASB,
                 type = 2,
                 polygon = TRUE,
                 col.segm.env = "transparent",
```

```
                  axis.expand = 1.5,
                  plot_theme = theme_metan(grid = "both"))

plot_grid(p3, p4, labels = c("p3","p4"))
```

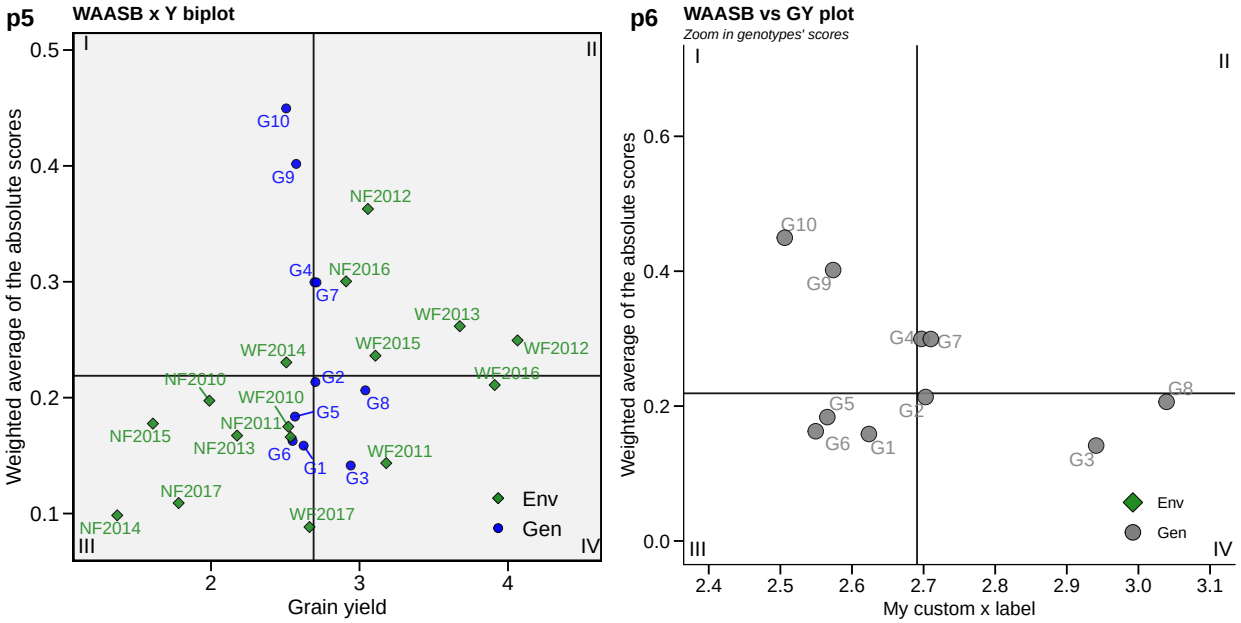


3.5.5.3 biplot type 3: GY x WAASB

The quadrants proposed in the following biplot represent the four classifications proposed here regarding the joint interpretation of productivity and stability. The genotypes or environments included in quadrant I can be considered unstable genotypes or environments with high discrimination ability, and with productivity below the grand mean. In quadrant II are included unstable genotypes, although with productivity above the grand mean. The environments included in this quadrant deserve special attention since, in addition to providing high magnitudes of the response variable, they present a good discrimination ability. Genotypes within quadrant III have low productivity, but can be considered stable due to the lower values of WAASB. The lower this value, the more stable the genotype can be considered. The environments included in this quadrant can be considered as poorly productive and with low discrimination ability. The genotypes within the quadrant IV are higly productive and broadly adapted due to the high magnitude of the response variable and high stability performance (lower values of WAASB).

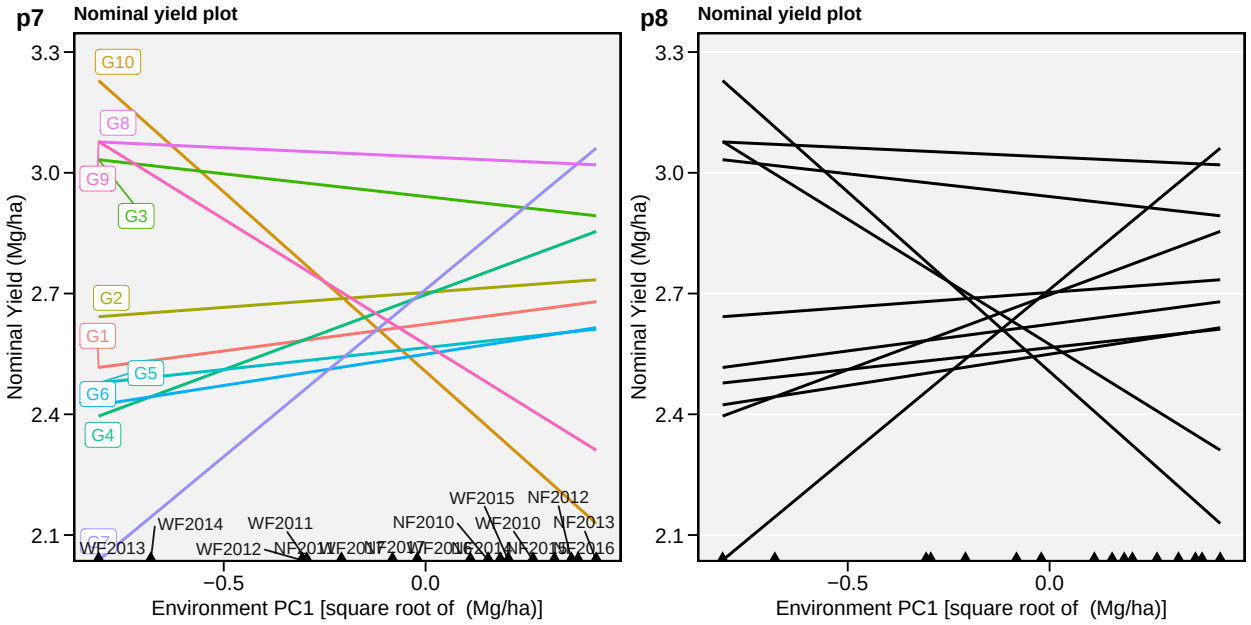
```
p5 <- plot_scores(WAASB, type = 3)
p6 <- plot_scores(WAASB,
                  type = 3,
                  x.lab = "My custom x label",
                  size.shape = 4, # Size of the shape point
                  col.gen = "gray50", # Color for genotypes
                  size.tex.pa = 4, # Size of the text
                  col.alpha.env = 0, # Transparency of environment's point
```

```
                  x.lim = c(2.4, 3.1), # Limits of x axis
                  x.breaks = seq(2.4, 3.1, by = 0.1), # Markers of x axis
                  y.lim = c(0, 0.7))+
  theme(legend.position = "none") +
  theme_metan_minimal() +
  ggtitle("WAASB vs GY plot", subtitle = "Zoom in genotypes' scores")
arrange_ggplot(p5, p6, labels = c("p5","p6"))
```



3.5.5.4 biplot type 4 : nominal yield and environment PCA1

```
p7 <- plot_scores(AMMI_model, type = 4)
p8 <- plot_scores(AMMI_model,
                  type = 4,
                  color = FALSE,
                  col.alpha.gen = 0,
                  col.alpha.env = 0,
                  plot_theme = theme_metan(grid = "y"))
arrange_ggplot(p7, p8, labels = c("p7","p8"))
```



3.6 The WAASBY index

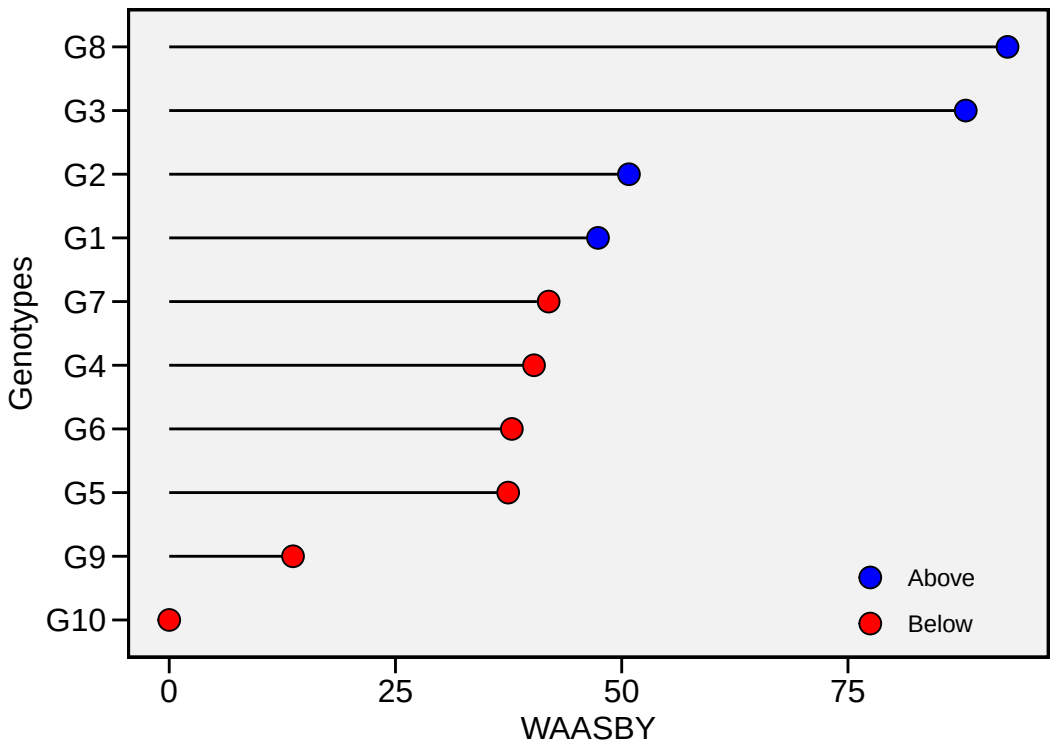
The functions `waasb()` considers both stability and productivity for genotype ranking considering the following model:

$$WAASBY_i = \frac{(rG_i \times \theta_Y) + (rW_i \times \theta_S)}{\theta_Y + \theta_S}$$

where $WAASBY_i$ is the superiority index for the i-th genotype that weights between performance and stability; rG_i and rW_i are the rescaled values (0-100) for GY and WAASB, respectively; θ_Y and θ_S are the weights for GY and WAASB, respectively.

This function provides the option of attributing weights for stability and productivity in genotype ranking by using the arguments wresp. For example, if the goal is to select genotypes with high yield (independently of the stability performance), then `wresp = 100` should be used. In this case, the ranking for WAASBY index will match perfectly with the ranking for the response variable. On the other hand, aiming at selecting high-stable genotypes (independently of the productivity), then `wresp = 0` should be used. In this case, the ranking for WAASBY index will match perfectly with the ranking for the WAASB index. Any value between 0 and 100 may be used in the argument wresp to weigh between mean performance and stability. In our example, the WAASBY index was calculated considering `wresp = 50`, that means equal weights for mean performance and stability. To plot the WAASBY values, the following code is used.

```
plot_waasby(WAASB)
```



3.6.1 Different scenarios of WAASBY estimation

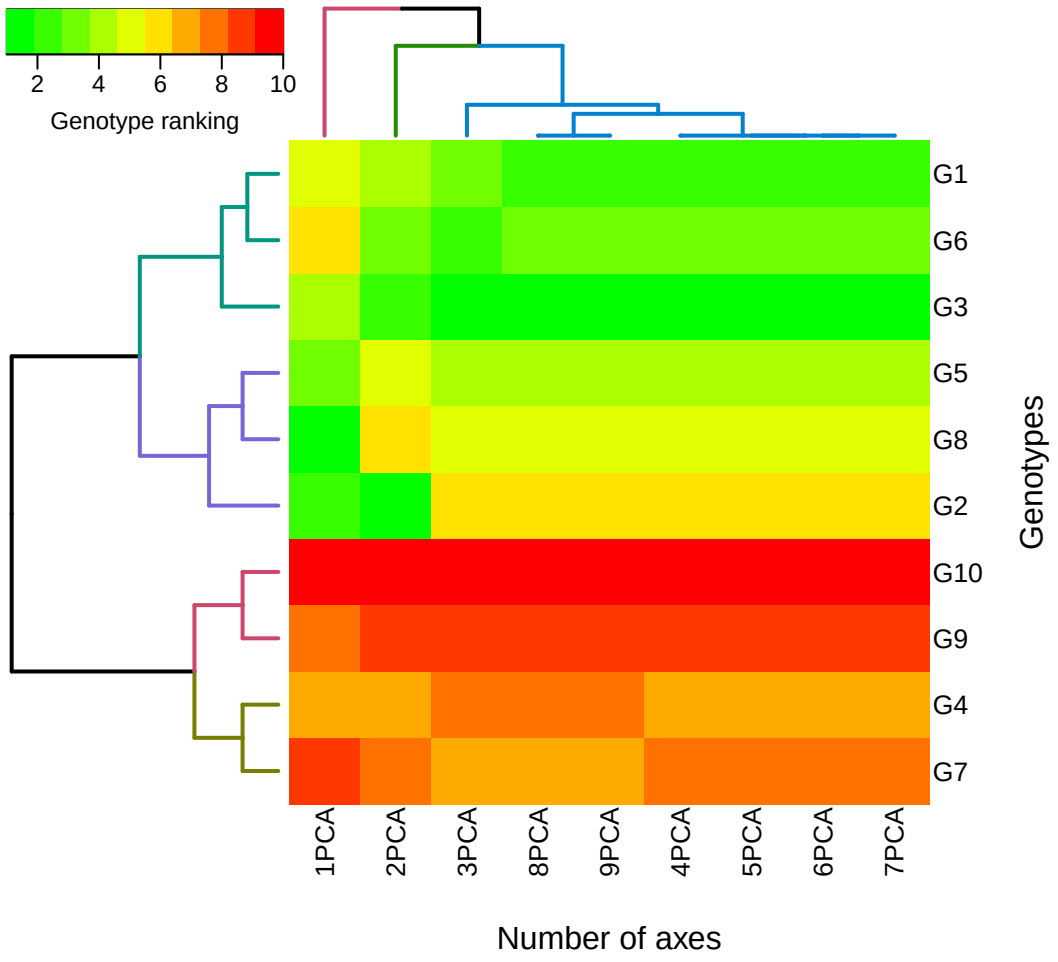
In the following example, we will apply the function `wsmp()` to the previously fitted model `WAASB` aiming at planning different scenarios of WAASBY estimation by changing the weights assigned to the stability and the mean performance. The number of scenarios is defined by the argument increment. By default, twenty-one different scenarios are computed. In this case, the the superiority index WAASBY is computed considering the following weights: stability (waasb or waas) = 100; mean performance = 0. In other words, only stability is considered for genotype ranking. In the next iteration, the weights becomes 95/5 (since increment = 5). In the third scenario, the weights become 90/10, and so on up to these weights become 0/100. In the last iteration, the genotype ranking for WAASY or WAASBY matches perfectly with the ranks of the response variable.

```
scenarios <- wsmp(WAASB)
```

The generic function plot is then used to plot the object. Two heatmaps are created. The first type of heatmap shows the genotype ranking depending on the number of principal component axes used for estimating the WAASB index. An euclidean distance-based dendrogram is used for grouping the genotype ranking for both genotypes and principal component axes. The second type of heatmap shows the genotype ranking depending on the WAASB/GY ratio. The ranks obtained with a ratio of 100/0 considers exclusively the stability for genotype ranking. On the other hand, a ratio of 0/100 considers exclusively the productivity for genotype ranking. Four clusters are estimated (1) unproductive and unstable genotypes; (2) productive, but unstable genotypes; (3) stable, but unproductive genotypes; and (4), productive and stable genotypes.

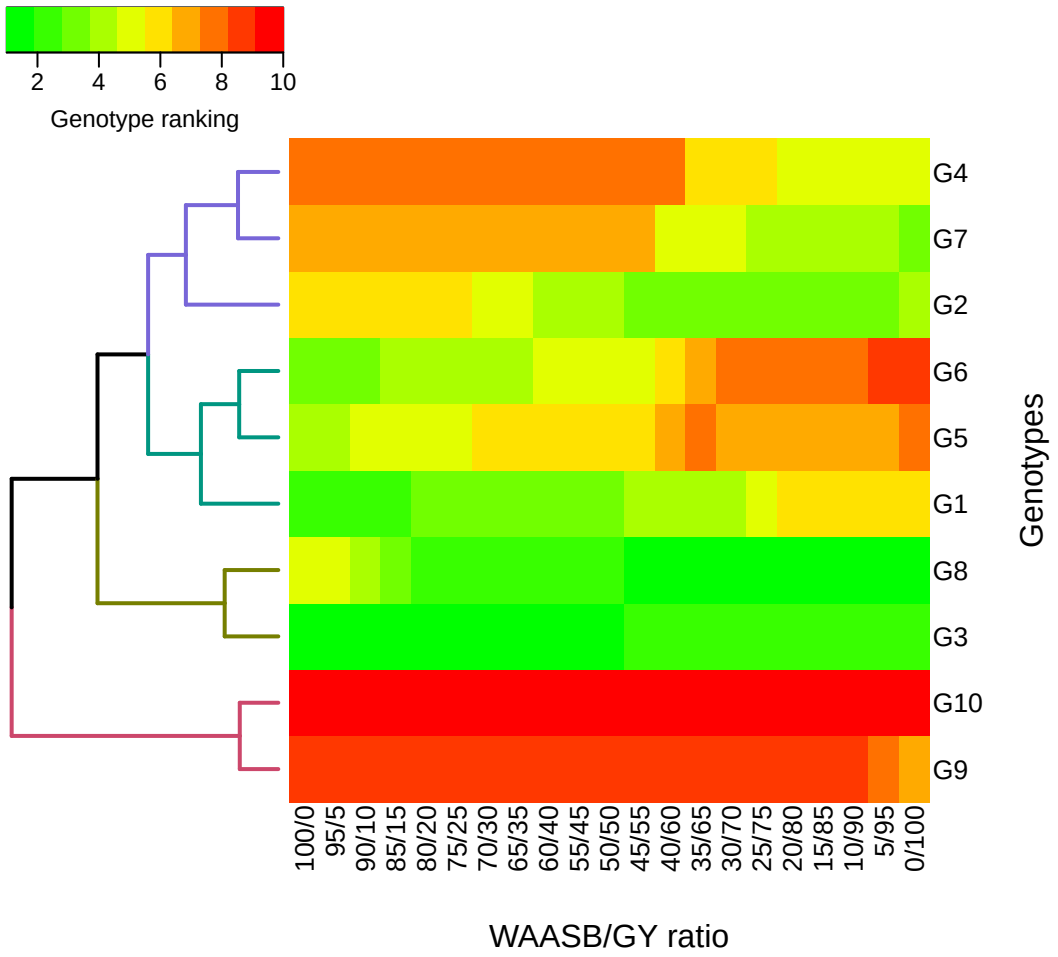
3.6.2 Ranks of genotypes depending on the number of IPCA

```
plot(scenarios, type = 1)
```



3.6.2.1 Ranks of genotypes depending on the WAASB/GY ratio

```
plot(scenarios, type = 2)
```



3.7 Others BLUP-based stability indexes

Colombari Filho et al. (2013) have shown the use of three BLUP-based indexes for selecting genotypes with performance and stability. The first is the harmonic mean of genotypic values -or BLUPS- (HMGV) a stability index that considers the genotype with the highest harmonic mean across environments as the most stable, as follows:

$$HMGV_i = \frac{1}{e}\sum_{j=1}^{e}\frac{1}{BLUP_{ij}}$$

The second is the relative performance of genotypic values (RPGV), an adaptability index estimated as follows:

$$RPGV_i = \frac{1}{e}\sum_{j=1}^{e} BLUP_{ij}/\mu_j$$

The third and last is the harmonic mean of relative performance of genotypic values (HMRPGV), a simultaneous selection index for stability, adaptability and mean performance, estimated as follows:

$$HMRPGV_i = \frac{1}{e}\sum_{j=1}^{e}\frac{1}{BLUP_{ij}/\mu_j}$$

```
res_inde <- Resende_indexes(WAASB)
print_table(res_inde$GY)
```

GEN	Y	HMGV	HMGV_R	RPGV	RPGV_Y	RPGV_R	HMRPGV	HMRPGV_Y	HMRPGV_R
G1	2.624	2.359	6	0.971	2.612	6	0.968	2.606	6
G10	2.506	2.177	10	0.923	2.483	10	0.907	2.440	10
G2	2.703	2.460	4	1.006	2.707	4	0.999	2.687	5
G3	2.941	2.695	2	1.093	2.941	2	1.091	2.937	2
G4	2.697	2.450	5	1.002	2.697	5	0.999	2.688	4
G5	2.566	2.349	7	0.958	2.578	7	0.956	2.573	7
G6	2.549	2.342	8	0.954	2.567	8	0.952	2.562	8
G7	2.710	2.502	3	1.017	2.737	3	1.009	2.714	3
G8	3.039	2.793	1	1.130	3.041	1	1.127	3.032	1
G9	2.574	2.260	9	0.945	2.544	9	0.936	2.518	9

4 References

Colombari Filho, J. M., M. D. V. Resende, O. P. Morais, A. P. Castro, É. P. Guimarães, J. A. Pereira, M. M. Utumi, and F. Breseghello. 2013. "Upland rice breeding in Brazil: a simultaneous genotypic evaluation of stability, adaptability and grain yield." *Euphytica* 192 (1): 117–29. https://doi.org/10.1007/s10681-013-0922-2.

Farshadfar, E. 2008. "Incorporation of AMMI stability value and grain yield in a single non-parametric index (GSI) in bread wheat." *Pakistan Journal of Biological Sciences* 11 (14): 1791–6. https://doi.org/10.3923/pjbs.2008.1791.1796.

Gauch, H. G. 1988. "Model selection and validation for yield trials with interaction." *Biometrics* 44 (3): 705–15. https://doi.org/10.2307/2531585.

Gollob, H. F. 1968. "A statistical model which combines features of factor analytic and analysis of variance techniques." *Psychometrika* 33 (1): 73–115. https://doi.org/10.1007/BF02289676.

Oliveira, A. C., F. I.F. Carvalho, L. C. Maia, J. A.G. Silva, M. C. Hawerroth, R. Nornberg, D. A.M. Schmidt, I. Hartwig, and G. Benin. 2012. "FAEM Chiarasul: new white oat cultivar with high yield and grain-processing quality." *Crop Breeding and Applied Biotechnology* 12 (4): 289–92. https://doi.org/10.1590/S1984-70332012000400010.

Oliveira, A. C., M. Crestani, F. I.F. Carvalho, J. A.G. Silva, I. P. Valério, I. Hartwig, G. Benin, D. A.M. Schmidt, and I. Bertan. 2011. "Brisasul: a new high-yielding white oat cultivar with reduced lodging." *Crop Breeding and Applied Biotechnology* 11 (4): 370–74. https://doi.org/10.1590/S1984-70332011000400012.

Oliveira, A. C.O., F. I.F Carvalho, L. C. Maia, J. A.G. Silva, M. Crestani, R. Nornberg, I. Hartwig, and G. Benin. 2012. "FAEM Carlasul: new white oat cultivar with high grain

yield." *Crop Breeding and Applied Biotechnology* 12 (2): 156–59. https://doi.org/10.1590/S1984-70332012000200010.

Piepho, H.-P. 1994. "Best Linear Unbiased Prediction (BLUP) for regional yield trials: a comparison to additive main effects and multiplicative interaction (AMMI) analysis." *Theoretical and Applied Genetics* 89 (5): 647–54. https://doi.org/10.1007/BF00222462.

Purchase, J. L., H. Hatting, and C. S. van Deventer. 2000. "Genotype × environment interaction of winter wheat (Triticum aestivum L.) in South Africa: II. Stability analysis of yield performance." *South African Journal of Plant and Soil* 17 (3): 101–7. https://doi.org/10.1080/02571862.2000.10634878.

Sneller, C. H., L. Kilgore-Norquest, and D. Dombek. 1997. "Repeatability of yield stability statistics in soybean." *Crop Science* 37 (2): 383–90. https://doi.org/10.2135/cropsci1997.0011183X003700020013x.

Zali, H., E. Farshadfar, S. H. Sabaghpour, and R. Karimizadeh. 2012. "Evaluation of genotype × environment interaction in chickpea using measures of stability from AMMI model." *Annals of Biological Research* 3 (7): 3126–36. http://eprints.icrisat.ac.in/7173/.