

Multi-Site (GxE) Analysis

BMS 12.0 Tutorials

Summary

This tutorial describes a genotype by environment (GxE) analysis for a four location maize field trial. This tutorial builds upon the adjusted means (BLUEs) and summary statistics calculated for the individual locations in the previous tutorial, <u>Single</u> <u>Site Analysis: 4 Location Batch</u>.

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Select Data from Database
Generate BV Input Files from BMS
Load Project & Data
Run Analysis
Analysis Report & Graphs
     Descriptive Statistics
          Trait Summary Statistics
           Best Variance-Covariance Model for Each Trait
     Genotype By Environment (GxE) Interactions
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           Static Stability Measures Coefficients
          Wrick's Ecovalence Stability Coefficients
          Finlay and Wilkinson Modified Joint Regression Analysis
           AMMI Model
          GGE Model
          Variance-Covariance Model & Correlation Matrix
          Correlation Heat Map
          Scatter Plot Matrix
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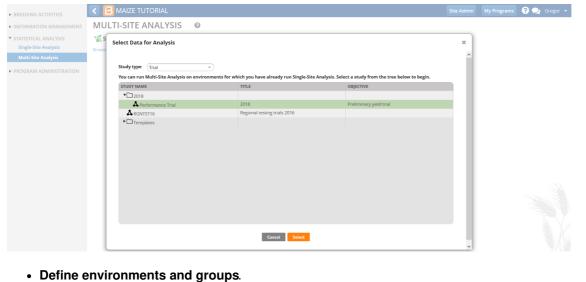
References

Select Data from Database

• Open Multi-Site Analysis from the Statistical Analysis menu of the Workbench. SelectBrowse.



• Select Performance Trial 2018 to use the BLUEs and summary statistics uploaded to the BMS after the single site analysis.



- Environments: TRIAL_INSTANCE
- Genotype: DESIGNATION
- Environment Grouping Factor: None

BREEDING ACTIVITIES	< 🔁 MAIZE TUTORIAL		Site Admin	My Programs	? 👤 Grege	or 🔻
► INFORMATION MANAGEMENT	MULTI-SITE ANALYSIS 🛛 🛛 🛛 🛛 🛛 🖗					^
STATISTICAL ANALYSIS Single-Site Analysis Multi-Site Analysis	Select Data for Analysis Browse for a study to work with. Performance Trial ×					
 PROGRAM ADMINISTRATION 	DEFINE ENVIRONMENTS AND GROUPS Which factor defines the environment? TRIAL_INSTANCE Which factor defines the genospe? DESIGNATION Specify a grouping factor if you wish to split your environme Specify a factor to define environment groups <u>None</u> REVIEW THE FACTORS AND VARIATES IN T	• •				
	GID	w for your review. DESCRIPTION Sermplasm identifier - assigned (DBID) Sermplasm identifier - assigned (DBCV)				
		se mpaann uen une - aosegneu (1901) Germplasm entry - enumerated (number)				

Traits with means available from all trial locations are selected by default. Traits that are not observed or could not be fitted with a mixed model in more than one environment in the single site analysis are not selected for Multi-Site analysis.

• Review the factors and variables in the dataset. Leave the default selections and selectNext.

EDING ACTIVITIES	< 🔁 MAIZE T	UTORIAL	Site Admin My Programs ? 🔍 Greg
ORMATION MANAGEMENT	GID	Germplasm identifier - assigned (DBID)	
	DESIGNATION	Germplasm identifier - assigned (DBCV)	
TISTICAL ANALYSIS	ENTRY_NO	Germplasm entry - enumerated (number)	
ingle-Site Analysis			
Iulti-Site Analysis			
GRAM ADMINISTRATION			
	TRAITS		
	The traits in the data	set you have selected are shown below, together with the number of environments in which they were tested.	
	V NAME	DESCRIPTION	TESTED IN
	Ant_DT_day	Anthesis time BY Days to anthesis - Computation IN Day	3 of 4
	EH_M_cm	Ear height BY EH - Measurement IN Cm	4 of 4
	GMoi_NIRS_pc	Grain moisture BY NIRS Moi - Measurement IN %	3 of 4
	GY_DW_gPlot	Grain yield BY DW GY - Measurement IN G/plot	4 of 4
		Grain yield BY FW GY - Measurement IN Kg/plot	4 of 4
	PH_M_cm	Plant height BY PH - Measurement IN cm	4 of 4
	(a) righten	Thank height of the measurement of the	
	Select All		

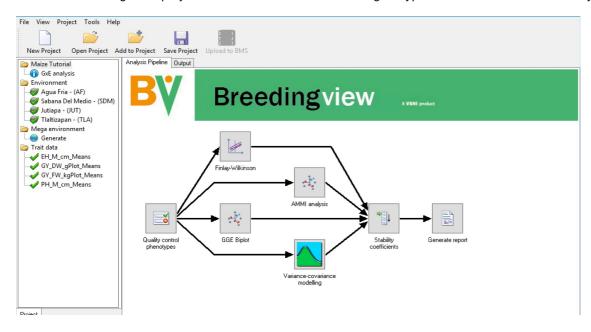
Generate BV Input Files from BMS

• Review the four environments and four traits to be included in the multi-site analysis. SelectDownload Input Files.

		AIZE TUTORIAL						Site Admin	My Programs	0.0	Gregor 👻
BREEDING ACTIVITIES		S OF SELECTED DA	TASET								
INFORMATION MANAGEMENT											
STATISTICAL ANALYSIS	Dataset:	Performance Trial-M	EANS Environme	nt is Defined By:	TRIAL_INSTANC	E					
Single-Site Analysis	Data Sour	rce: Performance Trial	Environme	nt Grouping Factor	None None						
Multi-Site Analysis											
	👗 ADJ	USTED MEANS DA	TASETS								
PROGRAM ADMINISTRATION	For each t	rait, the table below shows	s the number of tim	es the trait was obs	erved, followed by	the heritability value (in parenthese	es). Select the environments you would like	to submit for ana	ilysis.		
		TRIAL_INSTANCE		EH_M_CM		GY_DW_GPLOT	GY_FW_KGPLOT		PH_M_CM		
		1		32 (0.61673	840972635)	32 (0.846670609012086)	32 (0.853270834143048)		32 (0.758279152	297128)	
		2		32 (1.23066	74634921e-07)	32 (0.200786332582026)	32 (0.154153411338736)		32 (4.945836933	133439e-07)	
		3		32 (0.44258	3579303254)	32 (0.664884258040636)	32 (0.650653068184929)		32 (0.514961828	(061983)	
		4		32 (0.68105	6556868914)	32 (0.901775874800624)	32 (0.901353850007153)		32 (0.693519067	(622379)	
	Select	all environments									
	Select the	trait(s) you would like to s	end for analysis:								
	EH_M_CM	GY_DW_GPLOT	GY_FW_KGPLOT	PH_M_CM							
		2									
	Select	all traits									
								Back R	eset Downloa	d Input Files	

Load Project & Data

• The BV Input Files are located within a compressed folder automatically titled Performance Trial. The Breeding View .xml file is located within the Performance Trial folder. Open BV application and select Open Project and browse to the .xml Breeding View project file. The .xml file will load the genotypic and environmental summary statistics.

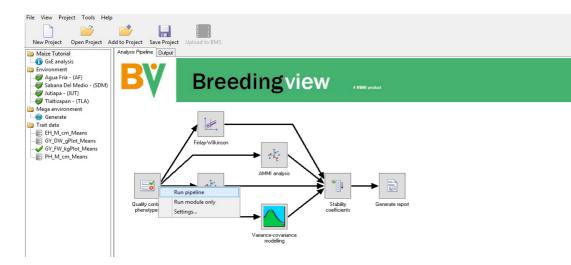


Run Analysis

When a project has been created or opened, a visual representation of the analytical pipeline is displayed in the Analysis Pipeline tab. The analysis pipeline includes a set of connected nodes, which can be used to run and configure pipelines.

Node Descriptions:

- Quality Control Phenotypes: Summary statistics within and between environments for the trait(s)
- · Finlay-Wilkinson: Performs a Finlay-Wilkinson joint regression (Finlay and Wilkinson, 1963)
- AMMI Analysis: Fits an AMMI model and generates summaries and a biplot (Gauch, 1988)
- GGE Biplot: Fits a GGE model and generates a biplot (Yan et al., 2000).
- Variance-Covariance Modeling: Fits different variance-covariance models to the GxE data and selects the best one for the data
- Stability Coefficients: Estimates different stability coefficient parameters to assess genotype performance
- · Generate report: Generates an HTML report of the results
- Exclude all traits except grain yield t/ha (GY_FW_kgPlot_Means) from the analysis.
- Run the analysis using the default settings by right clicking the Quality Control Phenotype node and choosing Run Pipeline.



When the analysis is complete a popup notifies the user.

• Select OK.

File View Project Tools Help	id to Project Save Project Upl	ead to BMS								
Maize Tutorial GxE analysis Environment Gya Bria - (AF) Sabana Del Medio - (SDM) Jutiapa - (JUT)	Analysis Pipeline Dutput Graphs	-								
Vitatizapan - (TLA) Mega environment Generate Trait data	Project: Maize Tutoria	1								
EH_M_cm_Means	Date: 2017-05-18T21-12-18		Breeding View	v ×						
GY_FW_kgPlot_Means	File containing means: <u>GxE</u> File containing AMMI estima		Pipeline comp	lete.						
	Summary statistic			ок						
	Trait: GY_FW_kgPlot_	Means								
		No. of observations	No. of missing values	Mean	Median	Min	Max	Lower quartile	Upper quartile	Variance
	Tlaltizapan - (TLA)	32.00	0	11.140	11.757	5.136	13.664	9.989	12.535	4.419
Project	Agua Fria - (AF)	32.00	0	6.618	6.735	3.990	8.652	6.214	7.099	1.032

Analysis Report & Graphs

The analysis output can be viewed from Breeding View interface under the results and graphs tabs. Analysis results can also be reviewed as individual files are automatically saved in the location specified by your browser settings, generally the Downloads folder.

Descriptive Statistics

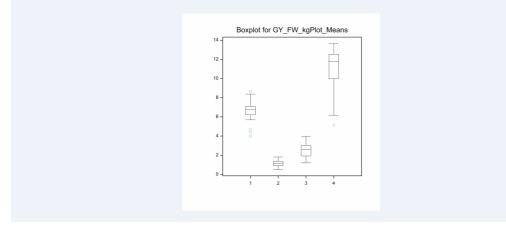
Breeding View provides descriptive statistics that describe the variance and covariance of the entire dataset.

Trait Summary Statistics

The trait summary statistics describe each trait based on the means calculated for each environment in the single site analysis.

New Project Open Project A	dd to Project Save Project Upl	ead to BMS								
Maize Tutorial	Analysis Pipeline Output Graphs	Report								
🚯 GxE analysis										
Environment										
🦪 Agua Fria - (AF)	Trait: GY_FW_kgPlot_	Means								
- 🥩 Agua Fria - (AF) - 🥪 Sabana Del Medio - (SDM)	Trait: GY_FW_kgPlot_	Means								
- 🏈 Agua Fria - (AF) - 🥪 Sabana Del Medio - (SDM) - 🥪 Jutiapa - (JUT)	Trait: GY_FW_kgPlot_	Means								
- 🥪 Agua Fria - (AF) - 🥪 Sabana Del Medio - (SDM) - 🥪 Jutiapa - (JUT) - 🎯 Tlaltizapan - (TLA)	Trait: GY_FW_kgPlot_		No. of missing values	Mean	Median	Min	Max	Lower	Upper	Variance
 Agua Fria - (AF) Sabana Del Medio - (SDM) Jutiapa - (JUT) Tlaltizapan - (TLA) Mega environment 		No. of observations	No. of missing values		Median	Min	Мах	quartile	quartile	Variance
 Agua Fria - (AF) Sabana Del Medio - (SDM) Jutiapa - (JUT) Tlaltizapan - (TLA) Mega environment 	Trait: GY_FW_kgPlot_	No. of observations	No. of missing values 0	Mean 11.140	Median 11.757	Min 5.136	Max 13.664			Variance 4.419
🥔 Agua Fria - (AF) 🥪 Sabana Del Medio - (SDM) 🥪 Jutiapa - (JUT) 🕪 Tlaltizapan - (TLA)		No. of observations 32.00	0					quartile	quartile	
 Agua Fria - (AF) Sabana Del Medio - (SDM) Jutiapa - (JUT) Tlaltizapan - (TLA) Mega environment Generate 	Tlaltizapan - (TLA)	No. of observations 32.00 32.00	0	11.140	11.757	5.136	13.664	quartile 9.989	quartile 12.535	4.419

The box plot of means provides a visual representation of the summary statistics.



Boxplot of Grain Yield Means: Tlalzipan has the highest grain yield and the highest variance. Sabana Del Medio has the lowest grain yield and the lowest variance.

Best Variance-Covariance Model for Each Trait

The GxE analysis pipeline formally models the variance-covariance structure in the means data and selects the best model for each trait. The main purpose is to establish a model for later testing of fixed effects, like determining marker effects in a quantitative trait loci by environment (QTLxE) analysis using BLUPs calculated in the single site analysis.

i Maize Tutorial	Analysis Pipeline Output Graphs Report	
GxE analysis		
🗁 Environment		
🛛 🥪 Agua Fria - (AF)	Best variance-covariance model	
- 🥩 Agua Fria - (AF) - 🥪 Sabana Del Medio - (SDM)		
🗆 🥪 Tlaltizapan - (TLA)		
🗁 Mega environment	Trait Variance-covariance model	
- Generate	GY_FW_kgPlot_Means Unstructured	
🗁 Trait data		
Trait data Ant_DT_day_Means		

Covariance Model: In this example, grain yield means are best described by an unstructured model, where each variance and covariance is estimated uniquely from the data?

Genotype By Environment (GxE) Interactions

Stability, or lack of phenotypic plasticity, is calculated for each genotype considering all traits using the following analyses:

- Cultivar-Superiority Measure
- Static Stability Measures Coefficients
- Wricke's Ecovalence Stability Coefficients

GxE interactions are also examined for each individual trait using the following analyses:

- Finlay and Wilkinson Modified Joint Regression
- AMMI Model
- GGE Model
- Best Variance-Covariance Model
- Correlation Matrix
- Scatter Plot Matrix

Stability Superiority Measure

Stability Superiority Measure (Lin & Binns, 1988) is the sum of the squares of the difference between genotypic mean in each environment and the mean of the best genotype, divided by twice the number of environments. Genotypes with the smallest values of the superiority tend to be more stable, and closer to the best genotype in each environment.

New Project Open Project Ad	d to Project Save Project Upload to BMS	
Maize Tutorial	Analysis Pipeline Output Graphs Report	
GxE analysis Environment	Stability superiority measure coefficients	
 Agua Fria - (AF) Sabana Del Medio - (SDM) Jutiapa - (JUT) Tlaltizapan - (TLA) Mega environment 	Genotypes with smaller values are more stable	
Generate	Genotype	
Trait data EH_M_cm_Means	AF12A-423-2/14	0.3350
GY_DW_gPlot_Means	AF12A-423-6/21	0.4751
GY_FW_kgPlot_Means	AF12A-423-6/22	0.4941
PH_M_cm_Means	AF12A-423-4/21	0.5315
Buildinguidens	AF12A-423-4/22	0.6395
	AF12A-210-2/6	0.7153
	AF12A-210-2/7	0.7450
	AF12A-210-15/23	0.7543
	AF12A-210-2/12	0.8175
	AF12A-210-2/9	0.8245
	AF12A-423-5/22	0.8866
	AF12A-423-2/21	1.0259
	Commercial Check 1	1.0582
	Commercial Check 2	1.0649
	AF12A-423-2/16	1.1475
	AF12A-210-2/8	1.1640
	AF12A-209-2/8	1.2075
	AF12A-423-6/16	1.2515
	AF12A-209-3/8	1.3652
	AF12A-423-4/16	1.3668

Static Stability Measures Coefficients

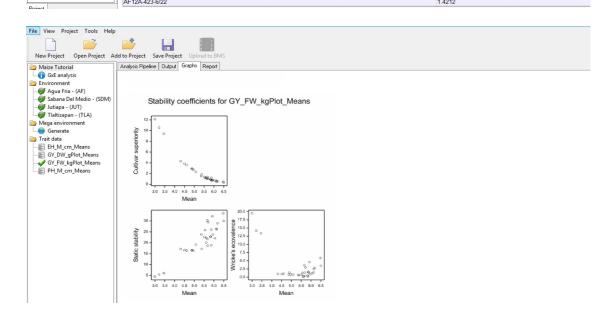
The Static Stability Coefficient is defined as the variance around the germplasm's phenotypic mean across all environments. This provides a measure of the consistency of the genotype, without accounting for performance.

📂 🔲 🔳	
Analysis Pipeline Output Graphs Report	
Static stability measure coefficients	
Genotypes with smaller values are more stable	
Geneture	
	4.45
	5.48
	6.11
	16.35
	16.55
	16.48
	16.61
	16.68
	17.13
	17.15
	18.69
	18.84
	19.17
	20.07
	20.07
	22.06
	22.19
	22.19
	22.63
AF 12A-209-3/8 AF 12A-423-5/22	22.64
	Genotype Freedback Ar12A-423-5/20 AF12A-423-5/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/20 AF12A-423-6/16 AF12A-423-6/16 AF12A-423-6/16 AF12A-423-6/16 AF12A-423-6/16 AF12A-423-6/16 AF12A-423-7/8 AF12A-423-6/16 AF12A-423-7/8 AF12A-423-6/16 AF12A-423-7/8 AF12A-423-6/16 AF12A-423-7/8 AF12A-423-7/8 AF12A-423-7/8 AF12A-423-7/8

Wrick's Ecovalence Stability Coefficients

Wricke's Ecovalence Stability Coefficient (Wricke, 1962) is the contribution of each genotype to the genotype-byenvironment sum of squares, in an un-weighted analysis of the genotype-by-environment means. A low value indicates that the genotype responds in a consistent manner to changes in environment; i.e. stable from a dynamic point of view. Like static stability, the Wricke's Ecovalence does not account for genotype performance.

File View Project Tools Help	d to Project Save Project Upload to BMS	
Diaize Tutorial	Analysis Pipeline Output Graphs Report	
GxE analysis	Wricke's ecovalence stability coefficients	
	Genotypes with smaller values are more stable	
	Genotype	
🧁 Trait data	AF12A-423-6/16	0.1289
	AF12A-423-2/16	0.1512
	AF12A-210-2/9	0.2429
	Commercial Check 2	0.3393
PH_M_cm_Means	AF12A-423-5/22	0.4964
	AF12A-423-5/16	0.6237
	AF12A-210-14/17	0.6578
	AF12A-209-3/8	0.6711
	AF12A-210-2/10	0.7396
	AF12A-210-1/4	0.8050
	Local Check 1	0.8132
	AF12A-210-2/7	0.9167
	AF12A-423-5/20	0.9466
	AF12A-423-4/20	1.0233
	AF12A-423-6/20	1.0642
	AF12A-210-2/6	1.1304
	AF12A-210-2/8	1.3085
	AF12A-423-4/16	:1.3494
	AF12A-210-1/5	1.3759
	AF12A-423-6/22	1.4212

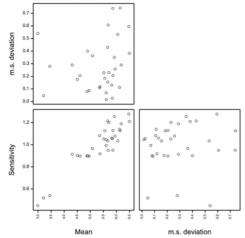


Finlay and Wilkinson Modified Joint Regression Analysis

The Finlay and Wilkinson Modified Joint Regression Analysis ranks germplasm based on phenotypic stability for each individual trait.

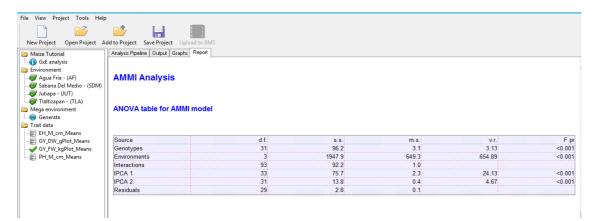
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New Project Open Project Ad	d to Project Save Proj	ect Upload to BMS					
Maize Tutorial	Analysis Pipeline Output	t Graphs Report					
GxE analysis	Sorted sensitivi	the estimates					
Environment	Sorted sensitivi	ity estimates					
	20 least sensitive (m	nost stable) genotypes					
🥪 Jutiapa - (JUT)							
Mega environment		Genotype	Sensitivity	s.e.	Mean	S.e.	Mean squa
							deviati
EH_M_cm_Means							
GY_DW_gPlot_Means	1)	AF12A-423-4/23	0.4489	0.06894	2.992	0.2689	0.53
GY_DW_gPlot_Means	2)	AF12A-423-5/23	0.5184	0.06894	3.211	0.2689	0.04
- PH_M_cm_Means	3)	AF12A-423-2/23	0.5401	0.06894	3.452	0.2689	0.27
- Cincentineans	4)	AF12A-210-1/4	0.8961	0.06894	4.960	0.2689	0.08
	5)	AF12A-423-6/20	0.8969	0.06894	4.607	0.2689	0.20
	6)	AF12A-210-1/5	0.8994	0.06894	4.895	0.2689	0.40
	7)	AF12A-210-2/10	0.8999	0.06894	4.871	0.2689	0.07
	8)	AF12A-423-5/20	0.9017	0.06894	4.504	0.2689	0.17
	9)	AF12A-423-4/20	0.9137	0.06894	4.309	0.2689	0.28
	10)	AF12A-423-5/16	0.9171	0.06894	5.369	0.2689	0.11
	11)	AF12A-423-4/16	0.9494	0.06894	5.681	0.2689	0.60
	12)	AF12A-209-2/8	0.9508	0.06894	5.861	0.2689	0.73
	13)	Local Check 1	0.9659	0.06894	5.083	0.2689	0.36
	14)	AF12A-423-6/16	0.9934	0.06894	5.606	0.2689	0.06
	15)	AF12A-210-2/6	1.0342	0.06894	6.050	0.2689	0.53
	16)	Commercial Check 2	1.0343	0.06894	5.668	0.2689	0.15
	17)	AF12A-423-2/16	1.0455	0.06894	5.610	0.2689	0.01
	18)	AF12A-209-3/8	1.0528	0.06894	5,519	0.2689	0.22
	19)	AF12A-210-2/9	1.0556	0.06894	5.843	0.2689	0.02

Finlay & Wilkinson analysis for GY_FW_kgPlot_Means

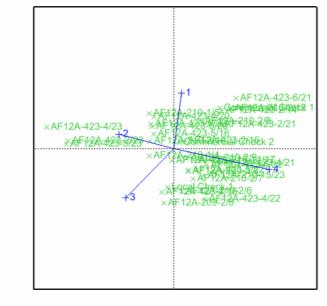


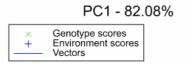
AMMI Model

In the Additive Main Effects and Multiplicative Interaction (AMMI) model, a two-way ANOVA additive model is performed (additive main effects), followed by a principal component analysis on the residuals (multiplicative interaction). As a result, the interaction is characterized by Interaction Principal Components (IPCA), where genotypes and environments can be simultaneously plotted in biplots.



GY_FW_kgPlot_Means: AMMI biplot (symmetric scaling)

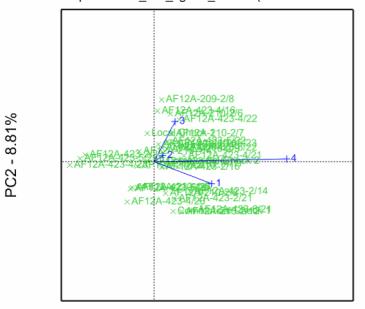




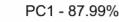
PC2 - 14.93%

GGE Model

In the Genotype Main Effects and Genotype × Environment Interaction Effects (GGE) model (Yan et al. 2000 & 2003) a 1way ANOVA, including environment as a main effect, is run followed by a principal component analysis on the residuals. Like AMMI, principal component scores can be used to construct biplots. Unlike the AMMI Model, in GGE the genotypic main effects are also represented in the plot. The GGE model is superior to AMMI analysis at differentiating megaenvironments (Yan et al. 2007)

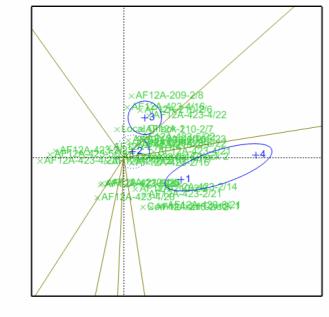


GGE biplot for GY_FW_kgPlot_Means (environment scaling)



 × Genotype scores + Environment scores Vectors 	s
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GGE biplot for GY_FW_kgPlot_Means (environment scaling)



PC1 - 87.99% × Genotype scores + Environment scores Sectors of convex hull Mega-Environments

PC2 - 8.81%

Environments 1 & 4 cluster, indicating that these two locations have similar environmental effects on phenotype and small GxE interactions.

Variance-Covariance Model & Correlation Matrix

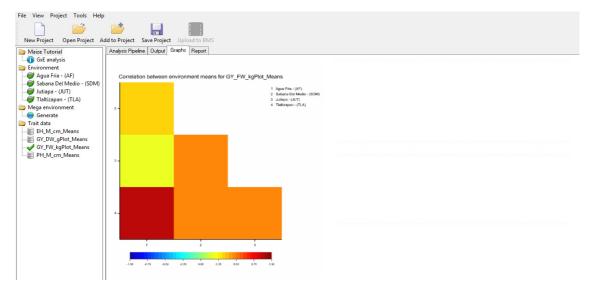
Details on the variance-covariance model, including the pairwise correlation matrix from the covariance model is presented in a table in the Report tab. In the correlation matrix values close to 1 indicate higher correlation between environments. A value of 1 indicates a perfect correlation, such as when an environment is compared to itself.

New Project Open Project A	Add to Project Save Project Upload to BMS							
🍃 Maize Tutorial	Analysis Pipeline Output Graphs Report							
GxE analysis								
Environment	Residual variance model							
😻 Sabana Del Medio - (SDM)	Term Fact	tor	Model(order)	Parar	neter	Estim	nate	S.E
	DESIGNATION.LOCATION NAME							
				Sigm	a2	1	000	fixe
Mega environment	DES	SIGNATION	Identity	oigin				
		CATION_NAME	Unstructured	v_11		4	032	0.26
Trait data	Log		Charactered	v 21			305	0.136
EH_M_cm_Means				v_21			436	0.138
				v_22 v 31			436 010	0.055
	[]			v_32			036	0.042
				v_33		0.08		0.0211
				v_41			843	0.50
				v_42			002	0.305
				v_43			898	0.120
				v 44		4.	419	1.12
Maize Tutorial) Gx£ analysis) Environment Ø Agua Fria - (AF) Ø Sabana Del Medio - (SDM) Ø Jutiapa - (JUT)	dd to Project Save Project Upload to BMS Analysis Pipeline Output Graphs Report Estimated covariance model Residual term: Genetures Environments							
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y Maize Tutorial () GKz analysis) Environment () Sabana Del Medio - (SDM) () Jutipa - (UT) () Taltizapan - (TLA)) Mega environment () Generate) Ford data () EH_M_cm_Means () GY_UW_gPiot_Means () GY_UW_gPiot_Means	Analysis Pipeline Output Graphs Report Estimated covariance model Residual term: Genotypes . Environments Factor: Genotypes Model: Identity Factor: Environments							
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Correlation Matrix for Grain Yield (GY_FW_kgPlot): Environment 1 is most positively correlated to the Environment 4 (0.8631), suggesting that the two locations have similar environmental effects on phenotype.

Correlation Heat Map

The correlation heat matrix visualizes correlations with color; warm colors (red) indicating high positive correlation between environments, and cool colors (blue) indicating high negative correlation between environments.

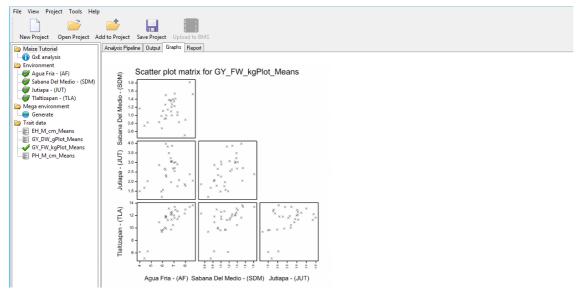


Correlation Heat Map of Grain Yield (GY_FW_kgPlot): Environment 1 is most positively correlated (red) to Environment 4

environment, suggesting that these two locations have similar environmental effects on phenotype and small GxE interactions.

Scatter Plot Matrix

The scatter plot matrix illustrates the association of genotypic performance between each pair of environments.



Scatter Plot Matrix for Grain Yield (GY_FW_kgPlot): A positive correlation is observed between genotypic performance at Environments 1 & 4 indicating similar environmental effects on phenotype for these environments and small GxE interactions. However, little correlation is observed between genotypic performance at Environment 1 and 3, indicating large GxE interactions between these two environments.

References

Gauch, H. G. (1988). Model selection and validation for yield trials with interaction. Biometrics, 44, 705–715.

Gauch, H.G. (1992). Statistical Analysis of Regional Yield Trials – AMMI analysis of factorial designs. Elsevier, Amsterdam.

Finlay, K.W. & Wilkinson, G.N. (1963). The analysis of adaptation in a plant-breeding programme. Australian Journal of Agricultural Research, 14, 742-754.

Murray, D. Payne, R, & Zhang, Z. (2014) <u>Breeding View, a Visual Tool for Running Analytical Pipelines: User Guide. VSN</u> International Ltd. (.pdf) (Sample data .zip).

Lin, C.S. & Binns. M.R. (1988). A superiority performance measure of cultivar performance for cultivar x location data. Canadian Journal of Plant Science, 68, 193-198.

Lin, C. S., Binns, M. R., & Lefkovitch, L. P. (1986). Stability analysis: Where do we stand? Crop Science, 26, 894–900.

Oakey, H., Verbyla, A. P., Pitchford, W., Cullis, B., & Kuchel, H. (2006). Joint modeling of additive and non-additive genetic line effects in single field trials. Theoretical and Applied Genetics, 113, 809–819.

Wricke, G. (1962). Uber eine method zur erfassung der okogischen streubreite in feldversuchen. Zeitschriff Fur Pflanzenzuchtung, 47, 92-96.

Yan, W., Hunt, L. A., Sheng, Q., & Szlavnics, Z. (2000). Cultivar Evaluation and Mega-Environment Investigation Based on the GGE Biplot. Crop Science, 40, 597–605.

Yan, W. & Kang, M.S. (2003). GGE Biplot Analysis: a Graphical Tool for Breeders, Geneticists and Agronomists. CRC Press, Boca Raton.

Yan, W., Kang, M.S. Ma, B., Woods, S., Cornelius, P.L. (2007) GGE Biplot vs. AMMI Analysis of Genotype-by-Environment Data. Crop Science. 47, 643–653.

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