

Multi-Site (GxE) Analysis

BMS 11.0 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>.

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 Stability Superiority Measure 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

References Related Materials

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	😯 喿 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	• •				
	FACTORS The factors of the dataset you have selected are shown belo NAME GID DESIGNATION	w for your review. DESCRIPTION Germplasm identifier - assigned (DBD) Germplasm identifier - assigned (DBD)				
	ENTRY_NO	Germplasm noentine - examples (sourt) 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.

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INFORMATION MANAGEMENT	GID		Ge	ermplasm identifier - assigned (DBID)			
	DESIGNA	ATION	Ge	ermplasm identifier - assigned (DBCV)			
STATISTICAL ANALYSIS	ENTRY_N	10	Ge	ermplasm entry - enumerated (number)			
Single-Site Analysis							
Multi-Site Analysis							
 PROGRAM ADMINISTRATION 		ITS					
	The traits	in the datase	et you have selected are shown below, to	ogether with the number of environments in which they were tested.			
	🖌 NAI	ME	DESCRIPTION			TESTED IN	
	Ant	_DT_day	Anthesis time BY Days to anthesis - Cor	mputation IN Day		3 of 4	
	EH_	_M_cm	Ear height BY EH - Measurement IN Cm	n		4 of 4	
	GM	loi_NIRS_pct	Grain moisture BY NIRS Moi - Measurer	ment IN %		3 of 4	
	GY_	_DW_gPlot	Grain yield BY DW GY - Measurement II	N G/plot		4 of 4	
	GY_	_FW_kgPlot	Grain yield BY FW GY - Measurement IN	N Kg/plot		4 of 4	
	PH_	_M_cm	Plant height BY PH - Measurement IN c	cm		4 of 4	
	Select	All					
						Rese	t Next

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 TUTORIAI						Site Admin	My Programs	0.0	Gregor 🔻
BREEDING ACTIVITIES	DETAIL	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	Analysis Pipeline Output Graphs	Report									
GxE analysis Finite Content GxE analysis Finite Content Gymean Agua Fria - (AF) Gymean Agua Fria - (AF) Gymean Agua Fria - (AF) Gymean Agua Friance (UTD)	Report from GxE a	Report from GxE analysis									
Hitiga - (01) Hitiga	Project: Maize Tutoria	1									
EH_M_cm_Means 	Date: 2017-05-18T21-12-18		Breeding View	v ×							
GY_FW_kgPlot_Means	File containing means: GxE	<u>Means.xlsx</u>	Pipeline comp	lete.							
	File containing AMMI estima	tes: <u>GxE_AMMI.xlsx</u>									
	Summary statistic	s		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.

File View Project Tools Help										
New Project Open Project Add	d to Project Save Project Up	and to BMS								
🗁 Maize Tutorial	Analysis Pipeline Output Graphs	Report								
GxE analysis										
Environment										
	Trait: GY_FW_kgPlot_	Means								
		No. of obconvations	No. of missing values	Moon	Modian	Min	Max	Lower	Upper	Varianco
🗁 Mega environment			No. or missing values	wicun	wiculan		WIGA	quartile	quartile	vanance
	Tlaltizapan - (TLA)	32.00	0	11.140	11.757	5.136	13.664	9.989	12.535	4.419
🗁 Trait data	Agua Fria - (AF)	32.00	0	6.618	6.735	3.990	8.652	6.214	7.099	1.032
EH_M_cm_Means	Jutiapa - (JUT)	32.00	0	2.523	2.597	1.211	3.983	1.922	3.034	0.544
GY_DW_gPlot_Means	Sabana Del Medio - (SDM)	32.00	0	1.138	1.128	0.509	1.819	0.921	1.364	0.083
	L			******						
- PH M cm Means										

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	
🗆 🥪 Tlaltizapan - (TLA)		
🗁 Mega environment	Trait Variance-covariance model	
	GY_FW_kgPlot_Means Unstructured	
🗁 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.

File View Project Tools Help	dd to Project Save Project Upload to BMS						
Maize Tutorial Content Content Content Agua Fria - (AF)	Analysis Pipeline Dutput Grapher Report						
Sabana Del Medio - (SDM) Jutiapa - (JUT) Tlaltizapan - (TLA) Mega environment	Genotypes with smaller values are more stable						
Generate	Genotype						
Irait data	AF12A-423-2/14	0.3350					
GV DW aPlot Mapro	AF12A-423-6/21	0.4751					
GV EW kgPlot Means	AF12A-423-6/22	0.4941					
PH M cm Means	AF12A-423-4/21	0.5315					
	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.

File View Project Tools Help		
New Project Open Project A	dd to Project Save Project Upload to BMS	
Maize Tutorial	Analysis Pipeline Output Graphs Report	
GxE analysis		
Environment	Static stability measure coefficients	
🛛 🦪 Agua Fria - (AF)	,	
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Mega environment		
Generate	Creatives	
Trait data	Genotype	4.45
EH_M_cm_Means	AF12A-423-4/23	4.40 E 40
GY_DW_gPlot_Weans	AF 12A-423-5/23	0.40 C 11
PH M cm Means	AF 12A-423-2723	10.11
- In ongenetineans	AF12A 423 6/20	10.30
	AF12A 210 2/10	16.48
	AF12A-423-5/20	16.40
	ΔΕ12Δ-210-1/5	16.68
	ΔΕ12Δ_423_4/20	17.13
	ΔF12Δ_423_5/16	17.15
	AF12A-423-4/16	18.69
	AF12A-209-2/8	18.84
	l ocal Check 1	19 17
	AF12A-423-6/16	20.07
	Commercial Check 2	21.81
	AF12A-210-2/6	22.06
	AF12A-423-2/16	22.19
	AF12A-210-2/9	22.63
	AF12A-209-3/8	22.64
During	AF12A-423-5/22	22.86
I I IOIECA		***************************************

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		
New Project Open Project A	id to Project Save Project Upload to BMS	
Maize Tutorial	Analysis Pipeline Output Graphs Report	
GxE analysis	Wricke's ecovalence stability coefficients	
- 🥪 Agua Fria - (AF)		
Jutiapa - (JUT)	Genotypes with smaller values are more stable	
Ilaltizapan - (ILA)		
Generate		
Trait data	Genotype	
EH M cm Means	AF12A-423-6/16	0.1289
GY DW gPlot Means	AF12A-423-2/16	0.1512
GY FW kgPlot Means	AF12A-210-2/9	0.2429
	Commercial Check 2	0.3393
	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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Maize Tutorial	Analusis Pineline Dutout	Graphs Report					
GrE analysis	Andysis Tipeline Output						
Environment	Sorted sensitivi	ty estimates					
Agua Fria - (AF)							
Sabana Del Medio - (SDM)	20 loget consitive (m	unst stable) genetypes					
- 🥑 Jutiapa - (JUT)	20 least sensitive (in	lost stable) genotypes					
🗁 Mega environment		Genotype	Sensitivity	S.e.	Mean	s.e.	Mean square
							deviation
i Trait data							
EH_M_cm_Means	1)	AF12A-423-4/23	0.4489	0.06894	2,992	0.2689	0.5395
GY_DW_gPlot_Means	2)	AF12A-423-5/23	0.5184	0.06894	3.211	0.2689	0.0462
GY_FW_kgPlot_Means	3)	AF12A-423-2/23	0.5401	0.06894	3.452	0.2689	0.2794
PH_M_cm_Means	4)	AF12A-210-1/4	0.8961	0.06894	4.960	0.2689	0.0869
	5)	AF12A-423-6/20	0.8969	0.06894	4.607	0.2689	0.2063
	6)	AF12A-210-1/5	0.8994	0.06894	4.895	0.2689	0.4001
	7)	AF12A-210-2/10	0.8999	0.06894	4.871	0.2689	0.0790
	8)	AF12A-423-5/20	0.9017	0.06894	4.504	0.2689	0.1754
	9)	AF12A-423-4/20	0.9137	0.06894	4.309	0.2689	0.2894
	10)	AF12A-423-5/16	0.9171	0.06894	5.369	0.2689	0.1180
	11)	AF12A-423-4/16	0.9494	0.06894	5.681	0.2689	0.6067
	12)	AF12A-209-2/8	0.9508	0.06894	5.861	0.2689	0.7385
	13)	Local Check 1	0.9659	0.06894	5.083	0.2689	0.3626
	14)	AF12A-423-6/16	0.9934	0.06894	5.606	0.2689	0.0698
	15)	AF12A-210-2/6	1.0342	0.06894	6.050	0.2689	0.5322
	16)	Commercial Check 2	1.0343	0.06894	5.668	0.2689	0.1548
	17)	AF12A-423-2/16	1.0455	0.06894	5.610	0.2689	0.0152
	18)	AF12A-209-3/8	1.0528	0.06894	5.519	0.2689	0.2281
	19)	AF12A-210-2/9	1.0556	0.06894	5.843	0.2689	0.0255
	20)	AF12A-423-5/22	1.0594	0.06894	5.819	0.2689	0.1302

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
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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.

File View Project Tools Help											
New Project Open Project A	dd to Project Save Project Upload to BMS										
🗁 Maize Tutorial	Analysis Pipeline Output Graphs Report										
GxE analysis											
Environment	Residual variance model										
Agua Fria - (AF)											
Jutiapa - (JUT)	Term Factor	Model(order)	Parameter	Estima	ate s.e.						
🛛 🦪 Tlaltizapan - (TLA)	DESIGNATION.LOCATION_NAME		Cirme?	10	00 5						
🗁 Mega environment	DESIGNATION	Identity	Sigmaz	1.0	uu iixed						
Generate	LOCATION NAME	Unstructured	v 11	10	32 0.262						
Trait data		on or a deal of a	v 21	0,13	05 0.1365						
GV DW aBlot Means			v 22	0.54	36 0.1381						
GY FW koPlot Means			v_31	0.10	10 0.0557						
PH_M_cm_Means			v_32	0.10	36 0.0425						
			v_33	0.083	33 0.02117						
			v_41	1.8	43 0.507						
			v_42	0.70	02 0.3055						
			v_43	0.28	98 0.1208						
			v_44	4.4	19 1.122						
Agua Fria - (AF) Sabana Del Medio - (SDM) Jutipa - (UT) Taltizapan - (TLA) Generate Generate (Y, DW, gPlot, Means (Y, DW, gPlot, Means (Y, TW, KgPlot, Means (Y, TW, KgPlot, Means	Estimated covariance model Residual term: Genotypes . Environments Factor: Genotypes Model: Identity Factor: Environments Model: Unstructured										
	Covariance matrix:										
	America (AD)	4 0000									
	Agua Fria - (AF) Sabara Dal Media (SDM)	0.1305	0.5436								
	Jutiana - (IIIT)	0.1005	0.1036	0.0833							
	Tlatizanan - (TLA)	1 8431	0.7002	0.2898	4 4191						
	Hundeput (123)	Agua Fria - (AF)	Sabana Del Medio - (SDM)	Jutiapa - (JUT)	Tlaltizapan - (TLA)						
	Correlation between environments according to model:	<u> </u>									
	Agua Fria - (AF)	1.0000									
	Sabana Del Medio - (SDM)	0.1742	1.0000								
	Jutiapa - (JUT)	0.3443	0.4870	1.0000							
	Tlaltizapan - (TLA)	0.8631	0.4517	0.4776	1.0000						
		Agua Fria - (AF)	Sabana Del Medio - (SDM)	Jutiapa - (JUT)	Tlaltizapan - (TLA)						

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.

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Related Materials

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