GGEbiplot version 5

In addition to being the most complete, most powerful, and most user-friendly software package for biplot analysis, GGEbiplot also has powerful components for on-the-fly data manipulation, powerful components for conventional statistical analysis (ANOVA, Correlation, Regression, Multiple Comparison), and special components to meet plant breeders' needs (Stability index, superiority index, independent culling, and multi-trait selection index). ALL functions are operated through button-clicking.

GGEbiplot Version 5 MENU LIST			Description/Comment *(if not self-evident)*
File			
	Open New Data File		To finish the current project and start a new project.
	Open a text data file		To finish the current project and start a new project, with the data in a "*.csv" file.
	Save image		To save the current biplot or plot image to a bitmap or jpeg file/
	Copy Image		To copy the current image for pasting to any Microsoft Office file.
	Print Image		To print to any printer connected to your computer. Note: It can also be printed to a file such as a PDF file if your computer is installed with appropriate software such as ADOBE Writer. This will give the best quality of the image.
	Close		To close the biplot window.
	Exit		To exit GGEbiplot.
View			
	Remove background Noise		

	Remove Projection Lines		
	Display Original Names		
	Add/Remove symbols		Anything can be added as a prefix to the labels on the biplot.
	Indexing Labels…		The entries and testers can be displayed by their indices (1, 2, 3,...).
		Tester	In GGEbiplot, “Testers” are used equivalently to “columns”, “environments”, “traits”, “variables”, etc.
		Entry	“Entries” are used equivalently to “rows”, “genotypes”, etc.
	Free Labeling...		The entries and testers can be labeled by anything the user specifies.
		Tester	
		Entry	
	Label with last N letters…		N is any number you specify.
		Tester	
		Entry	
	Label with first N letters		
		Tester	
		Entry	
	Label without first N letters...		
		Tester	
		Entry	
	Label without last N letters...		
		Tester	
		Entry	

	Show Both		"Biplot".
	Show Testers Only		To generate a "plot" of testers.
	Show Entries Only		To generate a "plot" of entries.
	Show/Hide Image Title		
	Show/Hide Guidelines		
	Show/Hide Data Source		
	Show/Hide Model Description		
ANOVA			This is a new addition of GGEbiplot. It allows reading any type of data with factors and traits in parallel columns. No particular order is required for the columns. For most plant breeders and agricultural scientists, this group of functions should be sufficient for needs for conventional statistical analysis. This ANOVA functions here are superior to some of the GLM functions in the SAS software, in addition to its user-friendliness: all operations are through button-clicking.
	Univariate Biplot		To generate all possible biplots (genotype vs. environment, genotype vs. location, genotype vs. year, etc.) regarding any of the traits.
	Multivariate Biplot		To generate a genotype by trait biplot
	Main Effects ANOVA		To conduct analysis of variance regarding any of the traits, to calculate mean values and LSD (least-significant difference) scaled mean values for the selected factor, which allows easy comparison among different levels of any the factor (year, location, variety, etc.)
	4-Way ANOVA		To conduct ANOVA for variety test data from a single environment, from multi-environments in a single year, and from multi-environments in multiple years for ALL or SELECTED traits.

4-Way Data			This group of functions allows genotype-environment-trait 3-way data and year-location-genotype-trait 4-way data to be explored from all possible perspectives.
	Geno by Yr biplot for any Trait...		
	Geno by Loc biplot for any Trait...		
	Geno by Env biplot for any Trait...		Each Environment is a Year-Site combination.
	Geno by Trait biplots		To study the relationships among traits and the trait profiles of the genotypes.
		In one Env...	
		Across selected Env	
		Across all Env	
		In selected Years	
	Trait-Association by Env biplot		To study the relationships among traits (and/or genetic markers) as influenced by the environment.
		Associations among all Traits	To study the relationships among ALL traits (and/or genetic markers) as influenced by the environment.
		Associations with a Trait	To study the associations of explanatory traits/markers with a target trait as influenced by the environment. This biplot can be used to identify traits that can explain the observed genotype-by-environment interaction regarding the target trait.
		Associations with a Trait - 'V-V biplot'	Similar to the above except that the associations are calculated using mean values of the traits across environments, as opposed to using genetic values in individual environments.
	Yr by Trait biplot		
	Loc by Trait biplot		
	Env by Trait biplots		To study if the expression of some traits is particularly favored in specific environments.

		For any Geno	For better understanding a particular genotype.
		Across selected Geno	
		Across all Geno	
	Phenotype by Trait biplot		Each phenotype is a genotype-environment combination.
	Geno by Env-Trait biplot		Measurements of a trait in different environments are treated as different variables.
	Yr by Loc biplot for any Trait...		
Biplot Tools			This is the core of GGEbiplot.
	Rank on any Entry		The testers are ranked based on any chosen entry by rotating the biplot
	Rank on any Tester		The entries are ranked based on any chosen tester by rotating the biplot
	Relation among Testers		This function is one of the most useful functions. It is used to visualize the relationships among testers and the degree to which each tester is represented in the biplot.
	Relation among Entries		To visualize the similarities among entries.
	Show/Hide Concentric circles		This helps to see the vector lengths of the testers or of entries.
	Combine two Testers		To see the ranks of the entries based on two testers.
	Compare two entries		To compare two entries for their relative performances regarding each of the testers.
	Entry-tester relationship		To show how each of the entries interacts with each of the testers.
	Which Won Where		Produces a “polygon view of the biplot” with perpendicular lines to its sides dividing the biplot into sectors. This is one of the most important functions of “GGE Biplot Analysis,” which identifies entries that have the highest values regarding one or more testers.

	Mean vs. Stability		This is another very important function of "GGE Biplot Analysis", that shows simultaneously the mean performance and the stability of the entries.
	Average Tester Coordination		This adds the "Average Tester Coordination" (ATC view of the biplot), which is the basis for genotype (entry) evaluation based on mean and stability, and for test environment (tester) evaluation based on its discrimination of the genotypes and representativeness of the other test environments.
	Rank Entries/Testers		This group of functions produces concentric circles using an entry or a tester as the concentric center. This graphically ranks the entries or testers with a selected reference.
		with ref. to an Entry	Any selected entry as the concentric center.
		with ref. to a Tester	Any selected tester as the concentric center.
		with ref. to the "Ideal" Tester	The "Ideal" tester is the concentric center, which is defined to be the most discriminating of the entries and the most representative of other testers. This is a very useful tool for *test environment evaluation.*
		with ref. to the "Ideal" Entry	The "Ideal" entry is the concentric center, which is defined as to having the highest mean performance and being absolutely stable. This function is very important *for selecting high yielding and stable genotypes*.
	Flip Biplot		Biplot flip will not change its interpretation, because *it is the relative positions of the entries and the testers rather than their PC values that is important.*
		Vertical flip	
		Horizontal flip	
		Switch Axes	
	Connect...		
		Entries	
		Testers	
	Linear Map of...		To mimic the genetic maps to the association among traits or markers to see the relationships among them.
		Testers	
		Entries	

Association			This group of functions is to visually study the associations among traits and/or genetic markers by means of correlation and multiple-regression as assisted by biplots.
	Find associated variables...		To find variables that are significantly associated with a target (dependent) variable at a specified significance level, and the associations are presented in a biplot to better understand the nature of the associations.
	More Stringent Criterion		To delete Less closely associated variables.
	Multiple Linear Regression		
		Conduct Regression	To conduct multiple-regression to show how much of the variation of the target (dependent) variable is explained by the variables that associated with it at the specified level. A biplot is used to help understand the relationships. The use will be prompted if he/she wishes to use some variables as covariates before multiple regression is conducted.
		Remove Linked Markers	Some variables selected based on linear associations may not be directed associated with the target (dependent) variable. This function can help identify and remove such variables from the equation.
		Delete Variables on Log Ratio	This method is often used to remove indirectly lined markers in the literature, but it has some pitfalls. For example, two tightly linked markers that have large effects on a trait may be mistakenly deleted and thereby a major QTL is missed.
		Delete Variables on Log Ratio--refine	
	Include Interaction (epitasis) Terms		This function adds two-marker interactions to the multiple-regression, which can be used to identify significant epistatic effects in the determination of the expression of a trait.
		Between all markers	
		Between selected markers	
	Include Quadratic Terms		Adds significant quadratic terms to the equation.

V-V biplot			V-V Biplots stands for variable-by-variable biplots, which depicts the relationships between two types of variables: response variables and explanatory variables. This function can be used to identify traits/markers that can explain the observed genotype-by-environment interaction for a target trait. If the explanatory variables are genetic markers and the response variables are a trait measured in different environment, this function can be used to identify QTL based on multi-environment data that explains the G and/or GE of the trait.
	Generate biplot		After the variables into response variables and explanatory variables are specified by the user, this function calculates the Pearson correlations between each of the response variables and each of the explanatory variables, and generate a biplot based on this matrix of correlations. Meanwhile, the user is prompted to provide a probability level that is used to remove explanatory variables that are less associated with the response variables based on a simple correlation as well a simulated group-wise type I error control..
	Eliminate short-vector variables/markers		This allows elimination of explanatory variables with short vectors at a user-specified level, because these variables tend to be less closely associated with the response variables.
	Geno by variable/marker biplot		This generates a GGE biplot to show the G+GE pattern of the target trait. This pattern can be compared with the V-V biplot pattern to see how the former is explained by the latter.
	Congruence coefficient		This is a measure of how well the V-V biplot explains the GGE pattern for the target trait.
	Goodness of fit		
Format			This group of functions is to modify the appearance of the biplot: color, type, and size of the various components of the image.
	Plot Title		To give the biplot or plot a desired title.
	Plot Size		The plot size can be scaled up or down.
	Get label Format		Allows picking up a color and a font type, size, and format.
	Apply format to...		The user-specified format can be applied to any selected entries or testers.

		Selected entries	
		Selected testers	
	Reverse last change		To reverse the last change.
	Back to default format		To restore the default format.
	Color Scheme		
		Black-White	This function is useful before some journals require black and white pictures for publication.
		Color1	The default format.
		Color2	A pre-set color scheme.
	Change Color		
		Background	
		Lines	
		Tester labels	
		Entry labels	
		Plot title	
	Change Case		The labels can be set to lower case, upper case, or title case.
		Testers	
		Entries	
	Change Font		Font type, size, bold, italic, bold italic can be changed.
		Larger	
		Smaller	
		Specified Size	
		Tester Labels	

		Entry Labels	
		Plot Title	
		Legend	
		Linear Map	
Models			For any entry-by-tester two-way data, GGEbiplot provides **4** options of data transformation, **4** option of data centering, **4** options of data scaling, and **3** types of singular value partition, resulting in **192** biplots of different shapes. Each biplot has different interpretations and can be useful depending on research purposes.
	Data Transformation		
		0. No transformation	
		1. Natural log	
		2. Log10	
		3. Square root	
	Scaled (divided) By		Each value in the to-way table is divided by some properties of the testers so that the data is somehow "standardized.".
		0. No scaling	
		1. Tester Std Deviation	All tested as treated equally important in evaluating the entries.
		2. Tester Std Error	Any heterogeneity among testers is removed by this scaling. This is the desired option if replicated data are available.
		3. Tester LSD5%	Similar to above but the tabulated data is more meaningful.
	Centered By		The means (main effects) of the entries and/or testers are removed from the biplot.
		0. No centering	
		1. Global-centered (E+G+GE)	

		2. Tester-centered (G+GE)	This results in the recommended GGE biplots for mega-environment analysis, genotype evaluation, and test environment evaluation.
		3. Double-centered (GE)	This results in the GE biplot, which contains only genotype by environment interaction.
	Singular Value Partition		Different options are equally valid in visualizing the entry-tester interactions, but they lead to different shapes of the biplot, which have different interpretations.
		1. Entry-metric (f=1)	This biplot is most appropriate for entry evaluation.
		2. Tester-metric (f=0)	This biplot is most appropriate for tester evaluation.
		3. Symmetrical (f=0.5)	This option has been the most used but it is least useful. It is not ideal for either entry evaluation or tester evaluation.
Data			This group of functions saves a lot of time and makes GGEbiplot many times more efficient. *Everyone who values time should select this module.*
	Entry/Tester Switch Roles		This is a very useful function. It means many additional models for the same set of data. It is particularly useful when the dataset has too many columns but relatively fewer rows (e.g., genetic mapping data usually have many markers while Microsoft spreadsheets have only 255 columns. Such data will have to be prepared in Excel with genotypes as few columns and genetic markers as rows. This function becomes essential in such cases as markers are "testers" and genotypes are "entries."
	Fill Missing Cells By...		
		Weighed from Similar Entries	This function chooses five rows that are most similar to the row that has missing values. Weights are then assigned to these rows according to their similarities, and the missing cells are estimated and filled.
		Entry Means	To fill the missing cell with the entry mean.
		Tester Means	To fill the missing cell with the tester mean.
		Entry and Tester Means	To fill the missing cell with the average of the entry mean and the tester mean.
	Derived variable		A new variable can be derived and added from existing variables

	Run BALANCED Subset by...		This allows the generation of a balanced subset out of the data that is read. This function save the researcher a lot of time and hassle.
		Deleting Testers	
		Deleting Entries	
	Run Partially Balanced Subset by...		Similar to above but it allows the user to specify a degree of tolerance on the unbalancedness of the data so that more entries and/or testers are included in the biplot.
		Deleting Testers	
		Deleting Entries	
	Run ANY subset by...		To generate a biplot based on ANY possible subset of the original data. It is therefore extremely handy for researchers.
		Deleting Testers	
		Deleting Entries	
	Entry Stratification		This group of functions allows subset of the entries to be selected based on their biplot position.
		Vertex Entries only	Only the entries that are on the "vertices" of the "vertex hulls" are selected.
		Entries outside a sector	Entries within a specified sector are excluded from the biplot
		Entries within a sector	Entries within a specified sector are included in the biplot
		High mean entries	Entries with higher mean values across testers are selected based on a criterion specified by the user. This allows a better appreciation of the entry by tester (genotype by environment) interactions and the identification of specifically adapted genotypes. Note: some genotypes may be universally inferior with regard to a particular trait. Meaningful patterns can be discovered after such genotypes are removed from the biplot.
		Low mean entries	Entries with lower mean values across testers are selected based on a user-specified criterion.
		Possible winners only	Only entries that are a winner for one or more of the testers are selected.
		Long Vector Entries	Only entries that have vectors longer than a specified value are included. These entries (genotypes) are more responsive to the testers (environments).

		Short Vector Entries	Only entries that have vectors shorter than a specified value are included. These entries (genotypes) are less responsive to the testers (environments).
	Tester Stratification		
		Testers outside a sector	Testers within a specified sector are excluded from the biplot
		Testers within a sector	Testers within a specified sector are included in the biplot.
		Long vector testers	Testers that have vectors longer than a specified value are included. These entries (genotypes) may be more discriminating of the entries
		Short vector testers	Testers that have vectors shorter than a specified value are included. These testers are either less well represented in the original biplot or have little associations with those that have longer vectors in the original biplot
	Back to Previous Subset		This generates a biplot based on a previous subset of the original data
	Back to Original Data		This generates a biplot based on the full dataset as it was first read from the data file or generated by GGEbiplot from a 3-way or 4-way or multi-way dataset
	Reverse the Sign of...		
		One Tester	Sometimes a trait is so measured that a smaller value means more desirable. In such case, this function will be useful to visualize the desirable genotypes.
		All Testers	Sometimes smaller values mean more desirable. In such case, this function will be useful to visualize the desirable genotypes.
	For Diallel Data Analysis...		This group of functions are useful for Diallel Cross data only.
		Complete the Two-way Table	Dataset from diallel crosses without reciprocals contains data only half of the 2-way table. This function can automatically fill the other half so that biplot analysis can be completed.
		Remove Reciprocal Effect	Dataset from diallel crosses with reciprocals contains data consisting of two unsymmetrical triangles. This function can automatically averages the corresponding reciprocals and makes the two-way table symmetrical, whereby the reciprocal effects are removed.
		Exclude Parents Per se	Values of the parents per se are removed and treated as missing values.

Biplots			While the biplot of PC1 vs. PC2 is the default biplot, biplots of other PCs might be useful.
	PC1 vs. PC2 (Default)		
	PC3 vs. PC4		
	PC5 vs. PC6		
	PC1 vs. PC3		
	PC2 vs. PC3		
	AMMI1 biplot		This is the "biplot" most commonly used in AMMI analysis. AMMI stands for Additive Main Effect and Multiplicative Interaction effects. AMMI analysis was a popular method for yield trial data analysis before the GGE Biplot Analysis system has been developed since 2000. Note But: Since the AMMI1 biplot is not a real biplot, it does not have most of the interpretations a real biplot has.
	3-D biplot		This produces a rotating 3-D biplot that displays the first three principal components. This is a very touchy feature of GGEbiplot. It is particularly useful for datasets that are large and contain complex patterns.
Accessories			Although not biplot analysis per se, accessories in GGEbiplot they are very useful for researchers to understand their data. Many of the functions under this title are unique to other statistical software packages.
	Data Plotting		This data plotting tool is unique and very useful. Even the graphics of Microsoft Excel does not have such functionality.
		Two Testers	Comparing two testers for each of the individual entries
		Two Entries	Comparing two entries for each of the individual testers
		Equality Line	
	Numerical Output		
		Original Data in a 2-way table	Prints the original data, organized into a two-way table if it was not read so, to a log file, which records the numerical events during the biplot analysis.
		Current (Subset) Data	Prints the current subset that is displayed in the biplot to the log file.
		Predicted Values	Prints predicted values based on the biplot to the log file.

		Eigenvectors	Prints the eigenvector values to the log file.
		Biplot Axes	Prints the values that are used to generate the current biplot to the log file in case the user desires to generate their own biplot using other programs such as Microsoft Excel.
		Correlation matrix among testers	Calculates the Pearson correlation between each pair of the testers and printed the correlation matrix into the log file. Threshold values for 5% and 1% significance are also provided.
		Distance matrix among testers	Calculates the biplot distance (dissimilarity) between each pair of the entries and prints the distance matrix into the log file.
		Tester Vector Length	Calculates and prints the vector length of the testers. Under certain models, vector length is a measure of the power of the tester for discriminating the entries.
	Breeder's Kit		
		Mean vs. Stability Deviation	To generate a plot of the entries, with X as the means across testers and Y as the square root of Shukla’s interaction variance, which is a measure of the entry’s stability.
		YREM (Superiority Index)	This is a measure of the superiority of the entries (genotypes) across testers (environments). It is defined between 0 and 1.
		Independent Culling	This evokes a function that allows the user to visually discard entries based on their performance with regard to each selected tester.
		Multi-Trait Selection Index	When this functions is evoked, the data are first standardized based on each trait/variable. A weight between -1 to +1 is assigned for each trait by the user. A Selection Index is then calculated for each genotype and the genotypes are ranked based on this selection index and printed to the log file.
		Plot Randomization	This evokes a plot randomization procedure. Compete or incomplete block designs can be generated instantly.
		R-t-P converter	This is a correlation (r), student t (t), and probability (p) calculator. Give any one of them, given the number of observations, the other two will be automatically calculated.
Help			
	Help File		Opens the Windows based, searchable GGEbiplot.hlp file.
	GGEbiplot Online		Opens the www.ggebiplot.com.
	Open Log File		Opens the log file in a Microsoft Excel environment.