

An Acad Bras Cienc (2022) 94(1): e20200001 DOI 10.1590/0001-3765202220200001 Anais da Academia Brasileira de Ciências | Annals of the Brazilian Academy of Sciences Printed ISSN 0001-3765 I Online ISSN 1678-2690 www.scielo.br/aabc | www.fb.com/aabcjournal

CELLULAR AND MOLECULAR BIOLOGY

A SAS code to estimate phenotypicgenotypic covariance and correlation matrices based on expected value of statistical designs to use in plant breeding

MEHDI RAHIMI & MATEO V. HERNANDEZ

Abstract: Phenotypic-genotypic covariance and correlation have been useful in crop and animal breeding programs. In the study of diversity of natural populations and different cultivars of plants that are examined based on statistical design, estimation of genotypic-phenotypic covariance through expected value of statistical designs mean square is hard and time-consuming when the number of studied traits is high. Moreover, the lack of a program in this field and manual calculations make the estimation more complicated. Therefore, in this study, one program was developed in SAS that can be used to calculate the genotypic-phenotypic covariance matrix through the first part of the program based on the expected value of applied statistical designs mean square. Then, based on the covariance matrix computed from the previous design model, their correlation matrix was calculated using the second part of the program based on the interactive matrix language (IML) of SAS. The phenotypic-genotypic covariance matrices of the 12 studied traits of rice are calculated based on this code. This program could compute phenotypic-genotypic covariance and correlation matrices based on the expected value of any statistical designs.

Key words: Computer program, covariance matrix, estimation, genetic correlation, plant breeding, statistical design.

INTRODUCTION

Diversity in plant species is extremely important in plant breeding because it provides the basis for effective selection of cultivars. The overall diversity within a population (phenotypic diversity) is due to the effects of genotype and environment (Govindaraj et al. 2015). Phenotypic changes are the visible variation in a trait within a population. This variation consists of two elements of environmental and genotypic variation and therefore its value differs in different environmental conditions. On the other hand, genotypic variation is related to genotypic difference between individuals within a population and is a major objective in plant breeding (Hermisson & Wagner 2004, Lewontin 2008).

Phenotypic variance (Vp) or observed variance is composed partly of genetic or heritable (Vg) and partly of non-heritable (Ve) variation. The ratio of the total genotypic variation to total phenotypic or observed variation is termed as coefficient of heritability in broad sense (Hill et al. 1998, Mather & Jinks 1977).

Phenotypic correlations between two traits can be influenced by inheritance, environment, or both. When the correlation is mainly genetic, genetic advancement is of more significance in breeding programs. Genetic correlations indicate to the amount of covariance of two similar genes or strong linkage in two different traits and the correlation of the environment is due to this fact that an environment can cause different

et al. 1998). One of the most important aims in plant breeding is to increase the yield per unit area. Finding suitable indices considering relationship between yield and important agricultural traits can play a significant role in selection plans for improving yield (Sölkner et al. 2008). In plant breeding, correlation between traits is also important because it measures amount and type of genetic and non-genetic relationship between two or more traits. Genotypic and phenotypic correlations between different traits may help the breeder in indirect selection for important traits through less complex traits that can be easily measured (Crossa et al. 2014. Stinchcombe et al. 2012).

variances in the both traits (Sultan 2000, Wolf

In study of chilli (*Capsicum* spp.) based on morphological traits were used genetic and phenotypic correlations and by using these correlations, traits affecting chilli yield were identified through path analysis (Deepo et al. 2020). Also, in a study on seventy seven rice genotypes, phenotypic and genotypic correlations, genetic parameters and coefficients of genotypic and phenotypic variation were estimated by expected value of mean square of sources of variation for the traits and used to identify important traits (Parimala et al. 2020). In other study on wheat, genetic and phenotypic correlations were used to identify traits affecting yield, and through these correlations an effective step was taken to improve wheat yield (Kumari et al. 2020).

Perhaps the most important activity in all plant breeding programs is selection. Selection plans such as mass selection, progeny selection and recurrent selection are considered according to crop pollination method, gene action type and breeding purpose. The selecting action takes place in both pure and segregated populations (Acquaah 2009, Moreno-Gonzalez & Cubero 1993). Selection efficiency depends largely on the genetic diversity of the population and inheritance of the studied trait. The variation can be obtained from estimated variance components of a sample from total variance (Hallauer 2007). To achieve this purpose, one of the methods is to use evaluation of different traits of individuals or different genotypes based on repeated statistical designs and estimation of phenotypic, genotypic and environmental variance-covariance matrices through expected value of desired statistical designs. The phenotypic, genotypic and environmental correlation matrices are estimated through the above matrices (Roff 1997, Zeng et al. 1999). Many studies have shown that plant breeders have used phenotypic-genotypic variancecovariance and correlation for direct and indirect improvement of traits in different plants (Akhtar et al. 2011, Malik et al. 2005, Munir et al. 2007, Seyoum et al. 2012, Tripathi et al. 2011).

So far, no simple program has been available to estimate these matrices through the expected value of design. Therefore, the aim of this research was to develop a SAS program for estimating phenotypic, genotypic and environmental variance-covariance and correlation matrices through expected value of desired statistical designs.

MATERIALS AND METHODS

Formulas for combined analysis based on randomized complete block design (RCBD)

There are different designs to estimate phenotypic and genotypic covariance based on expected value of statistical designs such as completely randomized designs (CRD), randomized complete block design (RCBD), and split-plot designs in one or several environments. Here, estimation of phenotypic and genotypic covariance is explained based on combined analysis for randomized complete block design and its formulas. However, based on the expected value of other designs, this covariance can also be calculated. In order to estimate phenotypic and genotypic variance of one trait, expected value of combined analysis was used according to Table I and the following relationships.

$$\sigma_{ge}^{2}(X) = \frac{MSge - MSe}{r} \tag{1}$$

$$\sigma_g^2(X) = \frac{MSg - MSge}{re}$$
(2)

$$\sigma_p^2(X) = \sigma_g^2(X) + \sigma_{ge}^2(X) + \sigma_e^2 \tag{3}$$

W where σ_p^2 is the phenotypic variance (Vp), σ_g^2 , genotypic variance (Vg), σ_{ge}^2 , genotype × environment interaction variance (Vge) and σ_e^2 , environmental variance (Ve).

Moreover, phenotypic and genotypic covariance of two traits was calculated according to Table II and the following relationships based on the expected value of combined covariance analysis.

$$\sigma(xy)_{ge} = \frac{MPge - MPe}{r} \tag{4}$$

 Table I. The combined variance analysis table and

 expected values of sources of variation for the trait x.

S.O.V.	DF.	SS _x	MS _x	E(MS _x)
Env	e-1	SSEnv.	MSEnv.	
Rep(Env)	e(r-1)	SSr	MSr	
Trt	t-1	SSg	MSg	
Trt×Env	(t-1)×(e-1)	SSge	MSge	
Error	e×(t-1)×(r-1)	SSe	MSe	

S.O.V.= sources of variation, DF.= degrees of freedom, SS_x=sum of squares of trait x, MS_x= mean squares of trait x, E(MS_x)= Expected value of MS, Env= environment, Rep=replication, Trt= treatment, e= number of environment, r= number of replication, t= number of treatment.

$$\sigma(xy)_g = \frac{MPg - MPge}{re} \tag{5}$$

$$\sigma(xy)_p = \sigma(xy)_g + \sigma(xy)_{ge} + \sigma(xy)_e \quad (6)$$

where $\sigma(xy)_p$ is the phenotypic covariance (COVp), $\sigma(xy)_g$, genotypic covariance (COVg), $\sigma(xy)_{ge}$, genotype × environment interaction covariance (COVge) and $\sigma(xy)_e$, environmental covariance (COVe). Combined variance analysis was performed for all the traits. If the effects of the treatment and treatment×environment interaction for all of them are significant, the traits are used to estimate phenotypic, genotypic and environmental variance-covariance matrices through expected value of the proposed design.

Development of a SAS code for phenotypicgenotypic covariance and correlations matrices

Here, we reported the development of a new SAS macro which computes phenotypic and genetic covariance as well as correlation matrices for several traits based on combined analysis (Supplementary Material-Table SI). Although this program is written for combined analysis of variance, it can be used for any statistical designs with some changes in the program. As

Table II. The combined covariance analysis table andexpected value of sources of variation for the trait xand y.

S.O.V.	DF.	SP _{xy}	MP _{xy}	E(MP _{xy})
Env	e-1	SPEnv	MPEnv	
Rep(Env)	e(r-1)	SPr	MPr	
Trt	t-1	SPg	MPg	
Trt×Env	(t-1)×(e-1)	SPge	MPge	
Error	e×(t-1)×(r-1)	SPe	MPe	

S.O.V.= sources of variation, DF.= degrees of freedom, SP^{xy}= sum of the products for the trait x and y, $M_{Px}y$ = mean of the products for the trait x and y, $E(MP_{xy})$ =Expected value of MP, Env= environment, Rep=replication, Trt= treatment, e= number of environment, r= number of replication, t= number of treatment. an example, this macro has been done based on a randomized complete block design (Table SII) and is presented with combined analysis of variance SAS macro. Thus, researchers, by comparing the program), could be able to modify this SAS macro based on their desired statistical designs (Table SI and SII).

General features of the program: an example

In this study, the data of 12 measured traits of 30 rice lines were used which were performed in a randomized complete block design with three replications in two separate experiments, i.e., normal and drought stress conditions (Table SIII). Users can bring data in CVS Excel format like sample data (Figure 1, Table SIII). General linear models were used for analyzing experimental design. In the INFILE section, path and name of data must be specified and changed based on user data (Figure 1). In the INPUT statement of the program, the variables namely ENV, REP, TRT and X1-Xn were internal to the program and showed the environment, replication, treatment, and number of traits (from one to n), respectively (Figure 1). Data input can be changed based on desired statistical designs and number of traits. In the phenotypic covariance and correlation matrices section, it should be specified that the number of traits for Var and Format statement such as Var x1-x12. Moreover, the 'Proc export'

must specify the path for saving phenotypic covariance matrix and phenotypic correlations matrix (Figure 2).

The genotypic covariance and correlation matrices section is used to estimate the genotypic covariance and correlation matrices, whose class and model statement must be specified based on the desired statistical designs for proc GLM (Figure 3). In the Data DoF, the degrees of freedom are determined for the sources of variation based on type of statistical designs (Figure 3). In this section, some sources of variation should be added or decrease based on type of statistical designs used (Figure 3).

In the macro calculation section, the drop column should be changed based on the number of traits (Figure 4). In the next section, the true variance of the sources of variation is calculated based on the statistical designs used. In next part of this section, these variances need to be modified according to the desired statistical designs (Figure 4). After that in the IML section, the Read all var {} part must be changed according to the number of traits. Moreover, the TraitNames and Format parts should be changed according to number of traits. Finally, a path should be specified in the proc export to save the genetic covariance matrix and genetic correlations matrix.



Figure 1. The prepared and saved data for use in the program.

SAS - [SAS Code for Phenotypic & Genetic Covariance & Correlations Matrices(Combined-RCBD design).SAS]
🖹 File Edit View Tools Run Solutions Window Help
 D 🖨 🖬 🖨 Q % 🖻 🛍 v 🐌 Q * X O 🛷
*** Phenotypic Covariance & Correlation Matrices *** ·
Title2 'Phenotypic Covariance & Correlation Matrices';
Proc Corr Data = Raw nosimple cov noprob outp=CovCorrMatr noprint ;
<pre>Var x1 - x12 ;* You need to change here according to the number of traits ; Run;</pre>
Data Covar: Set CovCorrMatr : if Type = "COV": Drop Type :
Data Correl; Set CovCorrMatr; if Type = "CORR"; Drop Type;
Title2 'Phenotypic Covariance Matrix';
Proc print data = Covar noobs;
Format X1-X12 8.3; * You need to change here according to the number of traits ; Run;
Title2 'Phenotypic Correlation Matrix';
<pre>Proc print data = Correl noobs; Format X1-X12 8.3; * You need to change here according to the number of traits;</pre>
Kun;
Writing Results at a EXCEL File, you need to change the route and name *
* of the file according to your own specific Data ;
Bproc export data=Covar
outfile='D:\paper\paper-2019\A SAS program to estimated phenotypic\sas-macro\New folder\Phenotypic Covariance Matrix.csv' dbms=csv replace;
Bpros export data=Correl
outfile="0:\paper\paper-2019\A SAS program to estimated phenotypic\sas-macro\New folder\Phenotypic Correlations Matrix.csv' dbms=osy replace:
Run;
4
🖾 Output - (Untitled) 🖹 Log - (Untitled) 🕅 SAS Code for Phenoty
Automic complete





Figure 3. The model section of used statistical design.

```
SAS - [SAS Code for Phenotypic & Genetic Covariance & Correlations Matrices(Combined-RCBD design).SAS]
🖹 File Edit View Tools Run Solutions Window Help
                         - 🗋 🖻 🔚 🎒 🐧 👗 🖻 🛍 က 🎁 🔍 🛪 X 🛈 🥔
 - %Macro calculate:
   data x4;
      set x3 (drop=col13-col36);***dropb colum should be changed based on the number of traits ***;
   Data X4:
      Merge X3 DF;
   Declare here the global macro variables:
       nt : number of traits ,
       nrep : number of replications ,
       envxrep : product of multiplying environments by replications
   %let nt = 12;***number of traits ***;
   %let nrep = 3;***number of replication ***;
   %let envxrep = 6;***multiplication of replication*environment***;
   %do j = 1 %to &nt;
      %let k = %eval(&j+(3*&nt));
         %let m = %eval(&j+(4*&nt));
          mse&j = col&j / &DFE ;
          msg&j = col&k / &DFG ;
          msge&j = col&m / &DFGE ;
          ge&j = (msge&j -mse&j) / &nrep ;
          g&j = (msg&j-msge&j) / &envxrep ;
          p&j = g&j+ge&j+mse&j ;
    %end;
```

Figure 4. The macro calculated section for genotypic covariance and correlation matrices.

RESULTS

The SAS macro is shown for estimating variance-covariance matrix for 12 traits based on combined analysis. This recommendation can be changed for any number of traits as well as for any experimental design. This program stores the phenotypic and genotypic covariance and correlations matrices based on desired statistical designs and store it in a CVS Excel format for any number of traits measured in the path given to the program. The results are also shown in the result viewer or output section of the SAS program (Figure 5 and Table SIV to SVII). Researchers can use the information stored in Excel format for their breeding program. This program as well as data and output files are included in the supplemental data.

In first section of Figure 5, the phenotypic covariance matrices of the 12 studied traits are shown, and the same information is shown in Table SIV. In the next section of Figure 5, the correlation matrix of the 12 studied traits is shown and in Table SV, the phenotypic correlation matrix of 12 traits is stored in Excel format. Also, in the following sections of Figure 5, the genotypic covariance matrix and then the genotypic correlation matrix of the traits are shown. The genotypic covariance matrix and genotypic correlation matrix traits are stored in Table SVI and SVII in Excel format, respectively.

DISCUSSION

The phenotypic and genotypic correlation matrices are shown in Table SV and SVII,

						F	heno	typic	Covar	iance M	latrix										
	NA	ME	X	1 X	2	X3	X4	X5	X6	X7	X8	X	X	10	X11	X12					
	- X1	-	54.59	8 18.88	0 -4.6	26 -1.2	91 -	7.367	0.105	-2.162	-7.977	-36.290	-28.9	97 -	13.590	-0.894					
	X2		18.88	0 27.65	9 1.7	50 -1.8	89 2	2.879	0.040	-0.729	11.091	26.866	3.4	97	8.642	4.543					
	Х3		-4.62	6 1.75	0 34.6	54 -3.0	69 3	0.680	-0.013	-3.078	46.661	52.036	21.5	18 -	15.020	2.080					
	X4		-1.29	1 -1.88	9 -3.0	69 2.3	168 -	8.278	-0.047	-1.844	-8.267	-2.149	6.4	14	-2.201	-1.799					
	X6		-7.30	5 0.04	9 30.0	13 .0 0	43	0.142	0.020	-9.511	0.221	-0.417	-1.2	10 1	42.214	0.019					
	X7		-2.16	2 -0.72	9 -3.0	78 -1.8	44 -	9.511	0.002	23.077	17.777	-21,192	-11.8	70	11.692	5.000					
10 10 <th< td=""><td>X8</td><td></td><td>-7.97</td><td>7 11.09</td><td>1 46.6</td><td>61 -8.2</td><td>67 16</td><td>2.006</td><td>0.221</td><td>17.777</td><td>141.712</td><td>211.824</td><td>49.9</td><td>50</td><td>19.135</td><td>11.520</td><td></td><td></td><td></td><td></td><td></td></th<>	X8		-7.97	7 11.09	1 46.6	61 -8.2	67 16	2.006	0.221	17.777	141.712	211.824	49.9	50	19.135	11.520					
No 2009 3.47 21.00 1.41.00 1.80 49.00 21.00 1.45.0 40.00 40.00 <	X9		-36.29	0 26.86	6 52.0	36 -2.1	49 53	0.691	-0.417	-21.192	211.824	951.621	429.4	31 1	58.545	18.345					
N11 1500 6.62 1500 2.20 4.214 0.412 11.802 1913 6.65 13.641 19.56 N22 0.884 4.43 2.00 1.709 11.420 0.010 5.000 11.500 18.345 6.65 13.511 15.65 NUME X1 X2 X1 X1 X1 X1 X1 X1 X1 X1 NUME X1 X2 X1 X1 X2 X1	X10		-28.99	7 3.49	7 21.5	18 6.4	14 9	5.643	-1.280	-11.870	49.950	429.481	342.8	96	14.534	6.856					
11 10 14.32 2001 11.20 11.20 11.20 12.31 6.35 12.361 17.43 1000 0.466 0.106 0.156 0.057 0.222 0.211 1.222 0.222 0.112 0.227 0.237 1.232 0.135 0.103 0.207 0.227 0.211 0.227 0.211 0.227 0.211 0.227 0.221 0.211 0.011 0.111 0.001 0.277 0.051 0.027 0.027 0.022 0.221 <td>X11</td> <td></td> <td>-13.59</td> <td>0 8.64</td> <td>2 -15.0</td> <td>20 -2.2</td> <td>01 4</td> <td>2.214</td> <td>0.142</td> <td>11.692</td> <td>19.135</td> <td>58.545</td> <td>14.5</td> <td>34 2</td> <td>68.311</td> <td>13.561</td> <td></td> <td></td> <td></td> <td></td> <td></td>	X11		-13.59	0 8.64	2 -15.0	20 -2.2	01 4	2.214	0.142	11.692	19.135	58.545	14.5	34 2	68.311	13.561					
	X12		-0.89	4 4.54	3 2.0	80 -1.7	99 1	1.422	0.019	5.000	11.520	18.345	6.8	. 90	13.561	17.388					
NUME N X							Pheno	otypic	: Corre	lation	Matrix										
xi 100 0.46 100 0.16 0.22 0.02 0.22 0.11 0.06 0.22 0.11 0.06 0.22 0.11 0.06 0.22 0.11 0.01 0.01 0.02 0.01 <th< td=""><td></td><td></td><td>AME.</td><td>X1</td><td>X2</td><td>X3</td><td>X4</td><td>X</td><td>5 X</td><td>6 X7</td><td>X8</td><td>X9</td><td>X10</td><td>X1</td><td>1 X</td><td>12</td><td></td><td></td><td></td><td></td><td></td></th<>			AME.	X1	X2	X3	X4	X	5 X	6 X7	X8	X9	X10	X1	1 X	12					
12 0.46 100 0.07 0.23 0.20 0.07 0.02 0.07 0.00 0.07 14 0.16 0.07 100 0.33 0.20 0.22 0.22 0.10 0.05 0.20 0.21 0.10 0.20 0.21 0.20 0.21 0.22 0.21 0.22 0.21 0.20 0.21 0.22 0.21 0.22 0.21 0.22 0.21 0.22 0		X1	-	1.000	0.486	-0.106	-0.114	-0.04	8 0.13	6 -0.061	-0.091	-0.159	-0.212	-0.11	2 -0.0	29					
X3 -0.00 0.00 -0.00 0.00		X2	2	0.486	1.000	0.057	-0.233	0.20	6 0.07	3 -0.029	0.177	0.166	0.036	0.10	0 0.2	07					
Image: space		X3	3	-0.106	0.057	1.000	-0.339	0.25	0 -0.02	2 -0.109	0.666	0.287	0.197	-0.15	6 0.0	85					
1 0 0.80 0.20 <th0.20< th=""> 0.20 0.20<</th0.20<>		X4		-0.114	-0.233	-0.339	1.000	-0.25	8 -0.29	1 -0.250	-0.451	-0.045	0.225	-0.08	7 -0.2	80					
N 0		XE		-0.048	0.208	0.250	-0.258	1.00	0 0.37	9 -0.095	0.652	0.824	0.247	0.12	3 0.1	31					
10 0.00 0.17 0.66 0.45 0.62 0.77 0.07 0.77 0.07 <		X7	, ,	-0.061	-0.029	-0.109	-0.251	-0.09	5 0.00	4 1.000	0.170	-0.123	-0.133	0.00	9 0.2	50					
N N		XE	3	-0.091	0.177	0.666	-0.451	0.65	2 0.17	8 0.311	1.000	0.577	0.227	0.09	8 0.2	32					
N 0 0.272 0.080<		XS)	-0.159	0.166	0.287	-0.045	0.82	4 -0.12	9 -0.143	0.577	1.000	0.752	0.11	6 0.1	43					
X11 0.112 0.103 0.166 0.007 0.123 0.034 0.089 0.180 0.081 0.080 0.180 0.010 0.010 0.000																					
X12 0.029 0.207 0.086 0.200 0.11 0.044 0.220 0.13 0.086 0.220 0.13 0.086 0.220 0.13 0.086 0.220 0.13 0.086 0.220 0.13 0.086 0.220 0.13 0.086 0.220 0.13 0.08 0.220 0.13 0.08 0.220 0.13 0.08 0.220 0.13 0.08 0.220 0.13 0.08 0.220 0.13 0.08 0.220 0.13 0.08 0.11 11		X1	0	-0.212	0.036	0.197	0.225	0.24	7 -0.66	2 -0.133	0.227	0.752	1.000	0.04	8 0.0	89			-	- Test	
Constitu 1 <th></th> <th>X1 X1</th> <th>10</th> <th>-0.212 -0.112</th> <th>0.036</th> <th>0.197</th> <th>0.225</th> <th>0.24</th> <th>7 -0.66 3 0.08</th> <th>2 -0.133 3 0.149</th> <th>0.227</th> <th>0.752</th> <th>1.000</th> <th>0.04</th> <th>8 0.0 0 0.1</th> <th>89</th> <th>0.</th> <th>• • (</th> <th>ompute</th> <th>r 🕨 Local Disk (D:)</th> <th>▶ pape</th>		X1 X1	10	-0.212 -0.112	0.036	0.197	0.225	0.24	7 -0.66 3 0.08	2 -0.133 3 0.149	0.227	0.752	1.000	0.04	8 0.0 0 0.1	89	0.	• • (ompute	r 🕨 Local Disk (D:)	▶ pape
1 12 13 14 15 16 17 18 19 10 11 171 12 13 14 15 16 17 18 19 10 11 171 <th></th> <th>X1 X1 X1</th> <th>10 11 12</th> <th>-0.212 -0.112 -0.029</th> <th>0.036 0.100 0.207</th> <th>0.197 -0.156 0.085</th> <th>0.225 -0.087 -0.280</th> <th>0.24 0.12 0.13</th> <th>7 -0.66 3 0.08</th> <th>2 -0.133 3 0.149 4 0.250</th> <th>0.227</th> <th>0.752 0.116 0.143</th> <th>1.000 0.048 0.089</th> <th>0.04 1.00 0.19</th> <th>8 0.0 0 0.1 9 1.0</th> <th>89 99 00</th> <th>Organize •</th> <th>• •</th> <th>ompute</th> <th>r 🕨 Local Disk (D:) Print Burn</th> <th> pape No </th>		X1 X1 X1	10 11 12	-0.212 -0.112 -0.029	0.036 0.100 0.207	0.197 -0.156 0.085	0.225 -0.087 -0.280	0.24 0.12 0.13	7 -0.66 3 0.08	2 -0.133 3 0.149 4 0.250	0.227	0.752 0.116 0.143	1.000 0.048 0.089	0.04 1.00 0.19	8 0.0 0 0.1 9 1.0	89 99 00	Organize •	• •	ompute	r 🕨 Local Disk (D:) Print Burn	 pape No
9 9.4.37 10.888 -3.944 -1.482 -5.455 -3.403 -2.920 -1.555 -1.103 7 7 6.455 -3.403 -2.920 -1.555 -1.103 7		X1 X1	10 11 12	-0.212 -0.112 -0.029	0.036 0.100 0.207	0.197 -0.156 0.085 Gen	0.225 -0.087 -0.280 etic C	0.24 0.12 0.13 ovari	7 -0.66 3 0.08 1 0.04 ance M	2 -0.133 3 0.149 4 0.250 Matrix	0.227	0.752 0.116 0.143	1.000 0.048 0.089	0.04	8 0.0 0 0.1 9 1.0	89 99 00	Organize +	b • (ompute	r Local Disk (D:) Print Burn Name	► pape Ne
18.86 22.505 2.207 0.208 5.41 0.208 2.441 0.304 0.217 0.218 0.417 0.248 0.241 0.208 0.217 0.208 0.218 0.241 0.208 0.221 0.208 0.218 0.218 0.218 0.218 0.221 0.223 0.223 0.218 0.218 0.218 0.211 0.211 0.221 0.223 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.218 0.221 0.268 0.218 0.218 0.218 0.221 0.268 0.218 0.218 0.221 0.268 0.218 0.218 0.221 0.268 0.221 0.268 0.221 0.268 0.221 0.268 0.221 0.268 0.221 0.268 0.224 0.208 0.221 0.268 0.224 0.223 0.268 0.224 0.221 <t< td=""><td>8</td><td>X1 X1 X1</td><td>10 11 12 T2</td><td>-0.212 -0.112 -0.029</td><td>0.036 0.100 0.207</td><td>0.197 -0.156 0.085 Gen</td><td>0.225 -0.087 -0.280 etic C</td><td>0.24 0.12 0.13 ovaria T6</td><td>7 -0.66 3 0.08 1 0.04 ance M</td><td>2 -0.133 3 0.149 4 0.250 Matrix T8</td><td>0.227 0.098 0.232</td><td>0.752 0.116 0.143 9 T1</td><td>1.000 0.048 0.089</td><td>0.04 1.00 0.19</td><td>8 0.0 0 0.1 9 1.0 T12</td><td>89 99 00</td><td>Organize • * Favorite Deskt</td><td>es op</td><td>ompute</td><td>r > Local Disk (D:) Print Burn Name (A) DataCombine (A) Genetic Corre</td><td> pape Ne rd-RCBD lations I </td></t<>	8	X1 X1 X1	10 11 12 T2	-0.212 -0.112 -0.029	0.036 0.100 0.207	0.197 -0.156 0.085 Gen	0.225 -0.087 -0.280 etic C	0.24 0.12 0.13 ovaria T6	7 -0.66 3 0.08 1 0.04 ance M	2 -0.133 3 0.149 4 0.250 Matrix T8	0.227 0.098 0.232	0.752 0.116 0.143 9 T1	1.000 0.048 0.089	0.04 1.00 0.19	8 0.0 0 0.1 9 1.0 T12	89 99 00	Organize • * Favorite Deskt	es op	ompute	r > Local Disk (D:) Print Burn Name (A) DataCombine (A) Genetic Corre	 pape Ne rd-RCBD lations I
3.93 4.287 2.877 2.872 2.871 2.871 7.89 2.99 1.435 2.671 7.755 2.76 7.89 2.971 7.575 2.76 7.89 2.987 7.89 7.89 2.971 7.575 7.55 2.67 7.752 0.56 0.673 4.991 2.971 1.265 7.572 0.56 2.595 2.591 4.98 2.224 6.583 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 2.591 5.57 2.680 5.57 2.680 5.57 2.680 5.251 5.51 5.66 5.57 5.67 5.782<	a I 54	X1 X1 X1 X1 X1	10 11 12 T2 18.886	-0.212 -0.112 -0.029 2 1 3.90	0.036 0.100 0.207 3 - 4 -1.4	0.197 -0.156 0.085 Gen 14 52 -5	0.225 -0.087 -0.280 etic C T5 243 (0.24 0.12 0.13 ovaria T6	7 -0.66 3 0.08 11 0.04 ance M T7 -1.886	2 -0.133 3 0.149 4 0.250 Matrix T8 -5.455	0.227 0.098 0.232 T -34.93	0.752 0.116 0.143 9 T1 3 -29.92	1.000 0.048 0.089 0 1 0 -13.6	0.04 1.00 0.19	8 0.0 0 0.1 9 1.0 T12 -1.103	89 99 00 00	Organize	es op nt Place	ompute	r > Local Disk (D:) Print Burn Name PataCombine Genetic Corre Genetic Cova	 pape Ne nd-RCBE Ideirons I Intrance Iv
1 1	s 1 54 2 18	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 18.886 25.205	-0.212 -0.112 -0.029 2 1 3 3.90 3.90 3.90	0.036 0.100 0.207 3	0.197 -0.156 0.085 Gen 14 52 -5. 58 5.	0.225 -0.087 -0.280 etic C 75 243 (0 551 -0	0.24 0.12 0.13 ovaria T6 1.118	7 -0.66 3 0.08 1 0.04 ance M 77 -1.886 -2.889	2 -0.133 3 0.149 4 0.250 Matrix T8 -5.455 -2.441	0.227 0.098 0.232 T -34.93 10.59	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80	1.000 0.048 0.089 0 1 0 -13.6 1 4.7	0.04 1.00 0.19	8 0.0 0 0.1 9 1.0 T12 -1.103 1.604	89	Organize • A Favorite Deskt Down Recer Librarie	i + (i op iloads nt Place	'ompute Open	r Local Disk (D:) Print Burn Name DataCombine Genetic Corre Genetic Corre Menotypic C Phenotypic C Phenotypic C	pape No d+RCBD d+RCBD dations I riance N orrelatic ovarian
1 1 0 0 1 0	5 18 3 -3	X1 X1 X1 X1 4.307 8.886 3.904	10 11 12 18.886 25.205 -2.821	-0.212 -0.112 -0.029 2002000 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 2000 2000 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20000 20000 20000 20000 2000 2000 2000 2000 2000 20000 20000 20000 20000 200	0.036 0.100 0.207 3	0.197 -0.156 0.085 Gen [4 52 -5. 58 5. 13 -2.	0.225 -0.087 -0.280 etic C 155 1-0 551 -0 196 -0	0.24 0.12 0.13 ovaria T6 1.118 1.017 1.119	7 -0.66 3 0.08 1 0.04 ance M -1.886 -2.889 -7.268 0 293	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2 099	0.227 0.098 0.232 0.232 T -34.93 10.59 21.43	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31	1.000 0.048 0.089 0 1 0 -13.6 1 4.7 0 -22.5 7 0 7	0.04 1.00 0.19 11 51 51 51 531	8 0.0 0 0.1 9 1.0 T12 -1.103 1.604 -2.729 0 216	89 99 00	Organize V Arporite Deskt Down Construction Construct	il > 0	ompute	r > Local Disk (D:) Print Burn Name Construction Construction Print Burn Print Burn Print Burn Print Burn Print Conv Construction Print Burn Print Conv Construction Print Burn Print Conv Conv Print Burn Print Burn Print Conv Print Conv Print Conv Print Conv Print Burn Print Conv Print Conv P	pape Ne d-RCBD dations P riance M orrelatio ovarianc Phenoty
1 1.86 2.89 7.26 0.73 2.5 16 0.04 21.84 6.066 5.22 1.126 6.78 2.88 2.5 16 0.04 21.844 6.066 5.154 12.267 7.742 0.876 2.88 2.5 16 0.04 6.75 0.066 6.75 0.752 2.876 2.816 2.5 16 1.5 16 2.5 16 2.5 16 3.5 22 4.5 14 2.5 16 5.5 16 4.5 16 2.5 16 5.5 16 4.5 16 2.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 5.5 16 <td>i 54 2 18 3 -3 4 -1 5 -5</td> <td>X1 X1 X1 X1 4.307 8.886 3.904 1.462 5.243</td> <td>11 12 12 18.886 25.205 -2.821 0.068 5.551</td> <td>-0.212 -0.112 -0.029 2 3 3 4 3 5 3 9 5 2 6.282 2 6.282 2 6.282 2 6.282 2 6.241 2 6.241 2 6.242 2 6.242 2 6.242 2 6.242 2 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7</td> <td>0.036 0.100 0.207 3</td> <td>0.197 -0.156 0.085 Gen 14 52 -5. 58 5. 13 -2. 34 4. 59 322.</td> <td>0.225 -0.087 -0.280 etic C 243 (0 551 -0 196 -0 869 -0 546 (0</td> <td>0.24 0.12 0.13 0varia T6 1.118 1.017 1.119 1.007</td> <td>7 -0.66 3 0.08 1 0.04 ance M -1.886 -2.889 -7.268 -0.293 -25.016</td> <td>2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633</td> <td>0.227 0.098 0.232 0.232 T -34.93 10.59 21.43 10.49 426.09</td> <td>0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22</td> <td>1.000 0.048 0.089 0 -13.6 1 4.1 0 -22.6 7 0.7 1 14.6</td> <td>0.04 1.00 0.19 711 551 747 531 755 569</td> <td>8 0.0 0 0.1 9 1.0 T12 -1.103 1.604 -2.729 0.216 -7.219</td> <td>89 99 00</td> <td>Organize V Favorite Deskt Down Recer Librarie Docu J Music Docu</td> <td>s ments res</td> <td>Compute</td> <td>r > Local Disk (D:) Print Burn Name DataCombins Genetic Corre Genetic Corre Marchenotypic C Marchenotypic C SAS Code for</td> <td>pape Ne drRCBD dations P riance M orrelatio ovarianc Phenoty</td>	i 54 2 18 3 -3 4 -1 5 -5	X1 X1 X1 X1 4.307 8.886 3.904 1.462 5.243	11 12 12 18.886 25.205 -2.821 0.068 5.551	-0.212 -0.112 -0.029 2 3 3 4 3 5 3 9 5 2 6.282 2 6.282 2 6.282 2 6.282 2 6.241 2 6.241 2 6.242 2 6.242 2 6.242 2 6.242 2 7 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	0.036 0.100 0.207 3	0.197 -0.156 0.085 Gen 14 52 -5. 58 5. 13 -2. 34 4. 59 322.	0.225 -0.087 -0.280 etic C 243 (0 551 -0 196 -0 869 -0 546 (0	0.24 0.12 0.13 0varia T6 1.118 1.017 1.119 1.007	7 -0.66 3 0.08 1 0.04 ance M -1.886 -2.889 -7.268 -0.293 -25.016	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633	0.227 0.098 0.232 0.232 T -34.93 10.59 21.43 10.49 426.09	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22	1.000 0.048 0.089 0 -13.6 1 4.1 0 -22.6 7 0.7 1 14.6	0.04 1.00 0.19 711 551 747 531 755 569	8 0.0 0 0.1 9 1.0 T12 -1.103 1.604 -2.729 0.216 -7.219	89 99 00	Organize V Favorite Deskt Down Recer Librarie Docu J Music Docu	s ments res	Compute	r > Local Disk (D:) Print Burn Name DataCombins Genetic Corre Genetic Corre Marchenotypic C Marchenotypic C SAS Code for	pape Ne drRCBD dations P riance M orrelatio ovarianc Phenoty
4.6.2 4.41 9.98 6.99 6.93 6.99 6.93 6.99 6.93 6.99 6.93 6.9 6.9	i 54 2 18 3 -3 1 -1 5 -5 5 0	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	T2 18.886 25.205 -2.821 0.068 5.551 -0.017	-0.212 -0.112 -0.029 2002000 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 2000 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 2000 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20020 20000 20000 20000 2000 2000 2000 2000 2000 2000 20000 20000 20000 20000 20000 20000 20000 20000 200000 200000 2000000	0.036 0.100 0.207 3	0.197 -0.156 0.085 Gen 14 52 -5. 58 5. 13 -2. 34 4. 59 322. 07 0.	0.225 -0.087 -0.280 etic C 155 196 -0 869 -0 546 0 470 0	0.24 0.12 0.13 0 varia 0 varia 1.118 0.017 1.119 0.007 0.007 0.010	7 -0.66 3 0.08 1 0.04 arce N T7 -1.886 -2.889 -7.268 -0.293 -25.016 -0.044	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633 -0.091	0.227 0.098 0.232 T -34.93 10.69 21.43 10.49 426.09 -0.79	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29	1.000 0.048 0.089 0 -13.6 1 4.7 0 -22.6 7 0.7 1 14.6 1 0.0	0.04 1.00 0.19 551 551 551 531 755 5669 068	8 0.0 0 0.1 9 1.0 T12 -1.103 1.604 -2.729 0.216 -7.219 -0.037	89 99 00	Organize Favorite Favorite Favorite Deskt Down Recer Librarie Docu Music Fictur Video	s ments res s res s	ompute	r > Local Disk (Dr) Print Burn Name StataCombine Senetic Corre Senetic Corre Phenotypic C Phenotypic C SAS Code for	pape Ne Ad-RCBD detions P riance M orrelatio ovarianc Phenoty
4.933 0.0530 2.4.13 10.039 2.4.13 10.039 2.4.13 10.039 2.4.13 10.039 2.4.13 10.039 2.4.13 10.039 2.4.13 10.239 2.4.13 10.239 2.4.13 10.239 2.4.13 10.239 2.4.21 1.22.1 1.22.61 6.2.28 5.2.21 6.5.48 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 1.6.24 8.2.24 9.2.14 1.4.14 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.24 9.411 1.4.75 1.6.24 8.2.41 9.411 1.4.75 1.6.24 8.2.41 9.411 1.4.75 1.6.24	i 54 : 18 i -1 i -5 i 0 : -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	T2 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.889	-0.212 -0.112 -0.029 2 -0.029 2 -3.90 5 -3.90 5 -2.82 2 6.22 2 6.22 2 6.22 2 6.22 1 0.41 2 -0.11 2 -0.11 2 -2.82 2 -0.11 2 -2.82 2 -0.11 2 -2.82 2 -0.11 2 -2.82 2 -0.11 2 -2.82 2 -0.11 2 -2.82 2 -2.82 2 -2.92 -2.92 -2.92 -2.92 2 -2.92 2 -2.92 2 -2.92 2 -2.92 2 -2.92 -	0.036 0.100 0.207 3 -1.4 1 0.0 9 0.4 3 0.9 6 4.8 9 -0.0 8 -0.2	0.197 -0.156 0.085 (Gen (4) 52 -5. 58 5. 13 -2 34 4. 59 322 07 0. 33 -25	0.225 -0.087 -0.280 etic C 243 (551 -0 196 -0 869 -0 546 (470 (016 -0	0.24 0.12 0.13 OVARIA 1.118 1.017 1.119 0.007 1.470 0.007	7 -0.66 3 0.08 1 0.04 arce N -1.886 -2.889 -7.268 -0.293 -25.016 -0.044 21.884	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633 -0.091 6.086	0.227 0.098 0.232 1.34 10.59 21.43 10.49 426.09 -0.79 -36.29	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29 8 -11.26	1.000 0.048 0.089 0 -13.6 1 4.7 0 -22.6 7 0.7 1 14.6 1 0.0 5 8.6	0.04 1.00 0.19 (11 (47 (55) (55) (56) (56) (56) (57) (5	8 0.0 0 0.1 9 1.0 -1.103 1.604 -2.729 0.216 -7.219 -0.037 2.888	89	Organize	s ments s s tter	ompute C Open	r > Local Disk (Dr.) Print Burn Name StataCombins Senetic Corre Genetic Corre Phenotypic C SAS Code for SAS Code for	 pape Ne d-RCBD lations h riance M orrelatio ovarianc Phenoty
1 300 4 400 2 300 1 400 1 1200 9 142 4 2400 1 200 1 201 1 200 9 142 4 2400 1 201 1 201 1 201 1 201 1 201 1 201 1 201 1 201 1 201 1 201 0 201 1 200 0 201 2 800 2 201 0 201 1 201 0 201 2 800 2 201 0 201 2 800 2 201 0 201 1 800 2 201 0 201 2 800 2 201 0 201 2 800 2 201 0 201 0 201 2 800 2 201 0 201 0 201 2 800 2 201 0 201 0 201 2 800 2 201 0 201 2 800 2 201 2 800 2 801	; 54 ; 18 ; -3 ; -1 ; -5	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	T2 11 12 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.869 -2.441	-0.212 -0.112 -0.029 -0.029 -0.029 -3.90 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.82 -2.95 -2.95 -2.82 -2.95 -2	0.036 0.100 0.207 3	0.197 -0.156 0.085 Gen 14 52 -5. 58 5. 13 -2. 34 4. 59 322. 37 0. 33 -25. 34 4. 39 322. 37 0. 39 66.	0.225 -0.087 -0.280 etic C T5 243 0 551 -0 555 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0	0.24 0.12 0.13 0.13 0.14 0.13 0.12 0.13 0.12 0.13 0.11 0.11 0.017 1.119 0.007 1.119 0.007 0.010 0.044 0.091	7 -0.66 3 0.08 1 0.04 ance M -7.268 -0.293 -25.016 -0.044 21.884 6.086	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633 -0.091 6.086 61.549	0.227 0.098 0.232 T -34.93 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67	0.752 0.116 0.113 9 71 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29 8 -11.26 1 5.7.44	1.000 0.048 0.089 0 -13.6 1 4.1 0 -22.6 7 0.7 1 14.6 1 0.0 5 8.6 2 -0.6	0.04 1.00 0.19 711 551 747 555 569 168 578 196	8 0.0 0 0.1 9 1.0 -1.103 1.604 -2.729 0.216 -7.219 -0.037 2.888 -2.519	89	Organize V A Favorite Deskt	s ments res res res res res res	Copen Copen S	r • Local Disk (D2) Print Burn Name DataCombini Ganetic Corre Genetic Corre Prenotypic C SAS Code for	pape Ne d-RCBD dations I iniance M orrelatio ovarianc ovarianc
1 1	i 54 18 i -3 i -1 i -5 i 0 · -1 i -5 i -34	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.889 -2.441 10.593 4.800	-0.212 -0.112 -0.029 -0.0	0.036 0.100 0.207 3 4 -1.41 1 0.09 9 0.4 3 0.99 6 4.8 9 0.09 8 -0.22 8 2.00 1 10.41 0.207 0	0.197 -0.156 0.085 Cen 14 22 -5. 58 5 -5. 58 5 -5. 58 5 -3 -2. 34 4 4. 4. 59 322. 7 0. 33 -2. 59 -5. 59 -5. 59 -5. 59 -5. 59 -5. 59 -5. 59 -5. 59 -5. 59 -5. 50 -5. -5. 50	0.225 -0.087 -0.280 etic C T5 551 -0 555 -0 556 -0 556 -0 556 -0 -0 -0.280	0.24 0.12 0.13 0.13 0.13 0.13 0.12 0.13 0.17 1.118 0.017 1.119 0.007 0.010 0.044 0.091 1.791 0.24	7 -0.66 3 0.08 3 0.08 3 0.08 5 -0.28 -0.293 -7.268 -0.293 -7.268 -0.293 -7.268 -0.293 -0.293 -0.044 21.884 6.086 6.086 -36.298	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633 -0.091 6.086 61.549 122.671	0.227 0.098 0.232 10.232 10.59 21.43 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67 865.03	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29 8 -11.26 1 57.94 6 449.26 8 449.26	1.000 0.048 0.089 0 -13.6 1 4.1 1 4.1 1 0.0 5 8.5 2 -0.0 8 32.9 6 16 6	0.04 1.00 0.19 551 47 555 569 968 578 896 124 49	8 0.0 0 0.1 9 1.0 -1.103 1.604 -2.729 0.216 -7.219 0.037 2.688 -2.519 0.903	89 99 00 00	Grganize V Favorite Deskt Down Deskt Down Compu Music Video Video Compu Com	s ments res res res res res res res res res re	iompute <u>K</u> Open s s :)	Load Disk (D) Print Burn Name Data Combine Genetic Coar Genetic Coar Genetic Coar Phonosysic C SAS Code for	pape Ne A
Obs T4 T2 T3 T4 T5 T6 T7 T6 T9 T0 T1 T1 T12 1 1000 650 1013 100 000 1000 000 1010 1010 1010 1010 1010 1010 1010 1010 1010 1010 0000 1010 0000 1010 0000 1010 0000 0000 1010 0000	54 54 18 53 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	T2 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.889 -2.441 10.593 4.801 4.747	-0.212 -0.112 -0.029 2 -0.029 -0.029 -0.029 -0.029 -0.282 -0.282 -0.41 -0.282 -0.41 -0.215 -0.41 -0.282 -0.41 -0.29 -0.29 -0.292 -0.212 -0.029	0.036 0.100 0.207 3 4 4 1.14 0.00 9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 1.0 0.2 1.0 0.2 0.2 0.2 0.2 0.2 0.2 0.2 0	0.197 -0.156 0.085 Gen 14 5 5 5 5 5 5 5 5	0.225 -0.087 -0.280 etic C T5 243 0 551 -0 -0 -0 -0 -0 -0 -0 -0 -0 -0	0.24 0.12 0.13 0varia 1.118 0.017 1.119 0.007 1.010 0.044 0.091 0.091 0.091 0.091 0.091	7 -0.66 3 0.08 1 0.04 -1.886 -2.889 -0.293 -2.5.016 -0.044 21.884 6.086 -36.298 11.265 8.578	2 -0.133 3 0.145 4 0.250 Matrix T8 -5.455 -2.441 19.918 2.099 66.633 -0.091 6.086 61.549 122.671 57.942 -0.896	0.227 0.098 0.232 7 -34.93 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67 865.03 449.26	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29 8 -11.26 1 57.94 6 449.26 8 352.21 4 16.54	1.000 0.048 0.089 0 -13.5 7 013.5 7 022.5 7 022.5 7 1 14.6 1 0.0 5 8.5 2 -0.6 8 32.5 6 16.5 6 16.5	0.04 1.00 0.19 711 551 747 531 755 569 968 578 896 124 148 142	8 0.0 0 0.1 9 1.0 -1.103 1.604 -2.729 0.216 -7.219 -0.037 2.888 -2.519 0.903 8.240 9.411	89 99 000	Corganize V Favorite Deskt Down Recer Librarie Pictur Nusic Pictur Video Compu Local Local	s res res res res res res res re	Compute C Open S S S	r + Local Disk (D). Print Burn Morne DataCombine Genetic Coar Genetic Coar Genet	pape Ne Ne o
Obs TI TZ TA TA TS TG TF TB TH TH TH TH 1 1000 0.101 0.103 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.001 0.005 0.001 0.005 0.001 0.005 0.001	54 18 -3 -5 -5 -34 -29 -13 -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 12 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.889 -2.441 10.593 4.801 4.747 1.604	-0.212 -0.112 -0.029	0.036 0.100 0.207 3 4 -1.4 4 -1.4 1 0.0 9 0.4 3 0.9 4 8 0.0 8 0.2 8 2.0 1 1.0.4 1 0.0 4 8 2.0 1 0 0.0 1 0 1 0 1 0 1 0 1 1 0 1 1 0 1 1 1 1 1	0.197 -0.156 0.085 F F F F F F F F	0.225 -0.087 -0.280 etic C 551 -0 551 -0 5546 -0 633 -0 633 -0 633 -0 221 -1 669 -0 219 -0	0.24 0.12 0.13	7 4.666 3 0.08 1 0.04 EVEN 1 0.04 EVEN 1 0.04 1 0.05 1	2 0.133 3 0.145 4 0.256 Matrix T8 5.455 -2.441 19.918 -0.091 -6.633 -0.091 -6.686 61.549 122.671 -7.942 -0.886 -7.942 -2.519	0.227 0.098 0.032 T -34.93 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67 865.03 32.92 0.90	0.752 0.116 0.143 9 T1 3 -29 92 3 4.80 1 24 31 3 5.74 4 106 22 1 -1.22 8 -11.26 4 302 22 4 4 32 22 4 4 16 54 3 8.24	1.000 0.048 0.089 0.13.6. 1 4.1. 1 4.1. 1 4.1. 1 0.0 5 8.5 2 -0.8 8 32.5 6 16.5.8 8 22.5 6 16.5.8 8 22.5 7 0.7	0.04 1.00 0.19 711 755 769 755 769 768 768 768 778 896 896 896 896 896 896 896 89	8 0.0 0 0.1 9 1.0 7.103 1.604 -2.729 0.216 -2.519 0.903 8.240 9.411 14.790	89 99 000	Corganize Favorite Favorite Deskt Down Recer Congu Occu Occu Pictur Video Compu Local Local	is op loads s ments s res rs ter Disk (f Disk (f	() Open s s ;;) ;;)	r > Local Disk (D); Print Burn More Data Combin Genetic Coor Genetic Coor Geneti	pape Ne A
1 1000 0.510 0.4103 0.410 0.410 0.401 0.403 0.423 0.323 0.423 0.423 0.423 0.413 0.410 0.401 0.401 0.403 0.423 0.433 0.423 0.423 0.424 0.423 0.433 0.423 0.423 0.424 0.423 0.431 0.401 0.401 0.403 0.423 0.433 0.441 0.445 0.445 0.441 0.403 0.433 0.431 0.431 0.431 0.431 0.431 0.441 0.463 0.441 0.463 0.441 0.463 0.441 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.461 0.46	5 1 54 2 18 3 -3 4 -1 5 -5 5 0 -1 5 -5 9 -34 0 -29 1 -13 2 -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 18.886 25.205 2.621 0.068 5.551 0.0017 -2.889 -2.841 10.593 4.801 4.747 1.604	-0.212 -0.112 -0.029 -0.029 -0.029 -0.029 -0.112 -2.62 -0.114 -2.62 -0.114 -2.62 -0.114 -2.62 -0.112 -0.029 -0	0.036 0.100 0.207 4 -1.41 1 0.00 9 0.4 3 0.9 6 4.8 9 -0.0 8 2.00 1 10.47 1 0.77 9 0.2	0.197 -0.156 0.085 Cen 14 2 5 5 5 5 5 5 5 5	0.225 -0.087 -0.280 etic C 243 0 551 -6 555 -6 546 0 546 0 016 -6 633 -7 6094 -6 221 -1 669 0 221 -1 669 0 219 -6 219 -6	0.24 0.12 0.13 0.13 0.13 0.017 1.118 0.017 1.119 0.007 1.470 0.007 1.007 1.007 1.007 0.00700000000	7 4.66 3 0.08 3 0.08 5 0.08 5 0.09 5 0.04 1 88 5 0.04 1	2 0.133 3 0.145 4 0.250 Matrix T8 4 0.250 5 .455 -2.441 19.918 2.099 66.633 -0.091 6.086 61.549 122.671 57.942 -0.896 -2.519 WORNER MARK	T -34.93 10.59 21.43 10.49 -0.79 -36.29 122.67 865.03 32.92 0.90	0.752 0.116 0.116 0.143 9 T11 3 -29.92 3 34.80 1 24.31 3 5.74 4 106.22 1 -1.26 6 449.26 6 52.21 4 16.52 3 8.24	1.000 0.048 0.089 0.089 0.13.5 1.4.1 022.5 7.0.7 1.14.6 1.0.0 5.8.5 20.0.8 8.32.5 6.16.5 8.268.3 9.4 1.4.1	0.04 1.00 0.19 711 551 747 555 569 568 578 596 524 548 542 541 542 541 542 544 544 544 544 544 544 544	8 0.0 0 0.1 9 1.0 1.0 1.0 1.0 1.0 0.2 1.0 0.2 16 16 16 16 16 16 16 16 16 16 16 16 16	89 99 00 0	Corganice V Corganice V Corga	s res res res res res res res re	iompute S S S	Local Disk (D): Print Sum Name Grants Combine Grants Could Grants Could Grants Could Grants Could Phenotypic C SAS Code for	pape Ne Ne del-RCBD delations 1 orrelatio ovariance Phenoty
2 0.510 1000 1010 0.061 0.023 0.031 0.021 0.031 0.021 0.031 0.021 0.031 0.021 0.031 0.021 0.031 0.021 0.031 0.021 0.031 0.021	54 54 18 54 55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	T2 18.886 25.205 -2.821 0.068 5.551 0.017 -2.889 -2.441 10.593 4.801 4.747 1.604	-0.212 -0.112 -0.029 -0.029 -3.90 -2.82 -2.62 -2.62 -2.15 -2.15 -2.15 -2.15 -2.15 -2.15 -2.12	0.036 0.100 0.207 4 -1.4 1 0.0 9 0.4 3 0.9 6 4.8 9 -0.0 8 -0.2 8 2.0 1 10.4 0 5.7 1 0.7 9 0.2 T2	0.197 -0.156 0.085 Cen 4 22 -6. 58 5. 53 3 -2. 44 4. 99 322 77 0. 33 -25 99 66 33 426 66 34 426 16 5 14. 16 6 -7.	0.225 -0.087 -0.280 etic C T5 243 0 551 - 556 - 556 0 556 0 470 0 063 - 633 - 669 0 221 - 669 0 219 - C E E E E E E E E E E E E E	0.24 0.12 0.13 0.13 0.13 0.13 0.13 0.13 0.13 0.13	7 -0.66 3 0.08 0.08 1 0.04 77 -1.886 -2.889 -7.268 -0.293 25.016 -0.044 21.884 6.086 -36.298 11.265 8.578 2.888 -2.8888 -2.8888 -2.888 -2.888 -2.	2 0.133 3 0.145 4 0.250 T8 -5.455 -2.441 19.918 -6.633 -0.091 -6.086 61.549 122.671 -2.519 T2.579 -2.519 T7 T7	T -34.93 10.29 -34.93 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67 865.03 21.43 10.49 449.26 32.92 0.90 449.26 32.92 0.90 449.26 32.92 0.90 122.77 122.67 123.67 123.78 124.78 123.78 125	0.752 0.116 0.143 9 T11 3 -29.92 3 4.80 1 24.31 3 5.74 4 106.22 1 -1.29 4 106.22 1 -1.29 4 106.22 1 -1.29 4 31 5.74 4 66.49 26.49 4 16.57 4 3 3 8.24 T9	1.000 0.048 0.089 0 -13.5 7 0.7 7 0.7 7 0.7 7 0.7 7 1.14.6 1 1.0.0.5 5 5.5.5 2 -0.0.6 8 32.5 6 16.5 8 32.5 6 16.5 8 2.5 8 32.5 7 0.7 7 0.7 7 10 0.7 7 10 0.7 8 10 00	0.04 1.00 0.19 551 551 555 569 968 578 596 968 578 596 968 578 100 100 100 100 100 100 100 10	8 0.0 0 0.1 9 1.0 1.103 1.604 -2.729 0.216 -7.219 0.903 8.240 9.411 14.790	89 99 90 90 90 90 90 90 90 90 90 90 90 90	Cryanice * Cryanice * Construction of the second secon	ss op eloads tt Place s ments res rs tter Disk (I Disk (I Disk (I	iompute S Open S S S S	Local Dak (D) Print Burn Manne Das Combine Da	pape Nee A A A
a 0.110 0.001 0.0	i 54 i 54 i -34 i -1 i -5 i 0 i -5 i -1 i -5 i -1 i -5 i -13 i -13 i -13	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.889 -2.441 10.593 4.801 4.747 1.604 Obs 1 -	-0.212 -0.112 -0.029	0.036 0.100 0.207 4 -1.41 1 0.00 9 0.4 3 0.9 6 4.8 9 0.0 8 0.2 8 2.0 1 10.41 0 5.77 1 0.77 9 0.2 TZ	0.197 -0.156 0.085 Cen 14 2 5 5 3 4 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5	0.225 -0.087 -0.280 etic C T5 243 0 551 - 556 - 566 0 016 - 6633 - 0094 - 2219 - 0219 - C C T4 0.199	0.24 0.12 0.13 0.13 0.13 0.13 0.13 0.13 0.13 0.13	7 40.66 0.08 0.08 0.08 0.08 0.09 0.288 0.293 0.293 0.25016 0.044 2.884 0.029 0.293 0.25016 0.044 2.884 0.086 0.36298 0.086 0.288 0.293 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.05788 0.05788 0.05788 0.05788 0.05788 0.05788 0.05788 0.05788 0.0578	2 0.133 3 0.145 4 0.250 Natrix 19.918 2.099 2.099 122.671 57.942 -0.896 61.549 122.671 57.942 -0.896 122.671 4.055	T -34.93 10.59 21.43 10.49 426.09 -0.79 -36.29 122.67 32.92 0.90 449.26 32.92 0.90 449.26 -3.0.90 -3.292 0.90 -3.292	0.752 0.116 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 4 106.22 1 5.74 6 435.22 1 5.74 4 106.52 1 5.74 4 106.22 1 5.74 4 105.24 1 5.74 3 8.24	1.000 0.048 0.048 0.089 0 -13.6 0 -13.6 1 14.2 1 14.2 2 -0.6 8 32.9 6 16.6 8 268.3 0 9.4	0.04 1.00 0.19 (11 (551 (47 (555 (555 (555 (569) (56) (569)	8 0.0 0 0.1 9 1.0 7 112 -1.103 1.604 -2.729 0.216 -7.219 0.216 -2.519 0.903 8.240 9.411 14.790 T112 -0.035	899 999 900 900 900 900 900 900 900 900	Cryanice * Cryanice * Dest D	ss op iloads tt Place s res is tter Disk ((Disk (E	iompute S Open S S S S	I Local Dak (D): Print Burn Remote Card Combine Genetic Core Genetic Core Principie: C Principie: C SAS Code for	pape Nee A
5 0.00 0.02 0.	; 54 ; 18 ; -3 ; -1 ; -5 ; 0 ; -1 ; -5 ; -34 ; -29 ; -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 12 18.886 25.205 -2.821 0.068 5.551 -0.017 -2.869 -2.441 1.0593 4.801 4.747 1.604 Obs 1 -2.84 -2.441 1.0593 -2.441 -2.695 -2.695 -2.6	-0.212 -0.112 -0.029 2 -0.282 -0.282 -0.282 -0.212 -0.282 -0.212 -0.282 -0.212 -0.212 -0.282 -0.212 -0.292 -0.212 -0.292 -0.	0.036 0.100 0.207 3 4 4 1 0.00 9 0.4 3 0.9 0.4 8 0.02 9 0.4 8 0.02 1 0.5 7 1 0.7 9 0.2 7 1 0.4 1 0.0 1	0.197 -0.156 0.085 Cen 14 2 5 5 5 5 5 5 5 5	0.225 -0.087 -0.280 T5 243 0.551 -0.548 0.554 -0.548 -0.633 -0.04 -0.199 -0.044 -	0.24 0.12 0.13 0.13 0.13 0.13 0.13 0.13 0.017 1.119 0.007 0.001 0.004 0.001 0.068 0.037 0.068 0.037 0.068 0.037	7 40.66 0.008 0.008 0.008 0.008 0.004 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.044 0.084 0.086 0.086 0.086 0.086 0.086 0.088	2 0.133 3 0.145 4 0.250 Natrix 19.918 6 6.633 -0.091 6 0.66 6 1.549 122.671 57.942 -0.896 6 1.549 122.671 -0.896 6 1.549 122.671 -0.896 6 1.549 122.671 -0.55 -2.519 12.519 -0.55 -2.519 -0.55 -0.225 -0.255 -0.225 -0.25	T -34.93 10.59 21.43 10.59 21.43 10.49 426.09 -0.79 -3.629 122.67 865.03 449.26 32.92 0.90 Hatrix T8 -0.064 -0.064	0.752 0.116 0.143 9 T-1 3 -29 92 3 4.80 1 24.31 1 24.31 1 24.31 1 24.31 4 106 22 1 5.74 4 106 22 1 5.74 5.	1.000 0.048 0.089 0.13.6 1.1.4.1 1.0.0.2.2 7.0.1 1.1.4.8 3.2.2 2.0.6 8.52 2.0.2 8.52 2.0.2 8.52 2.0.2 9.4 1.1.4 1.2.15 0.0 0.9.4 1.1.4	0.04 1.00 0.19 (11 (55 (55 (56) (56	8 0.0 0 0.1 9 1.0 7.2 9 1.0 9		Crganice * Crganice * Deskt	ss op iloads tt Place s res is ter Disk ((Disk (F	Compute C Open s s (:) (:) (:) (:)	Local Disk (D) Print Burn Name @ DataContent Corn @ Grants Count @ Grants Count @ Grants Count @ Panextypic C @ Panextypic C @ SAS Code For	pape Ne A c
6 0.161 0.003 0.223 0.069 0.283 1.000 0.096 0.117 4.270 0.591 0.141 0.697 7 0.055 0.123 0.089 0.283 0.009 0.001 0.117 0.161 0.201 0.117 0.161 0.203 0.201	54 54 33 4 -1 34 55 30 -1 34 -5 34 -5 34 -5 34 -29 -13 32 -13 -13	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 12 18 886 25 20 5 5 5 5 5 5 5 5 5 5 5 5 5	-0.212 -0.112 -0.029 2 -0.262 -0.215 -0.29 -0.112 -0.29 -0.11 -2.25 -0.11 -7.28 -0.11 -7.28 -0.11 -7.28 -0.12 -0.212 -0.27 -0.112 -0.29 -0.212	0.036 0.100 0.207 3 4 -1.41 1 0.0 9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 1 0.0 0 0.2 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0.197 -0.156 0.085 F4 42 -5.58 5.58 5.53 33 -2. 44 4. 4. 4. 4. 4. 4. 4. 4. 4	0.225 -0.087 -0.280 T5 243 (551 -0.546 -0.546 -0.546 -0.633 -0.094 -0.199 -0.014 -0.081	0.24 0.12 0.13 T6 1.118 0.017 1.119 0.007 1.470 0.010 0.044 0.091 1.791 0.007 0.040 0.068 0.037 EEEC C T5 0.040 0.062	7 40.66 0.008 0.008 0.008 0.008 0.008 0.004 0.004 0.004 0.004 0.004 0.004 0.004 0.004 0.004 0.008	2 0.133 3 0.145 4 0.250 Matrix TB 8 -5.455 5 -5.455 -0.091 6 0.63 -0.091 122.671 57.942 -0.896 -2.519 122.671 57.942 -0.896 -2.519 122.671 57.942 -0.896 -2.519 122.671 -0.896 -2.519	0.227 0.098 0.232 -34.93 10.59 21.43 10.49 426.09 -0.79 32.92 0.90 449.26 32.92 0.90 -2.42 0.90 -2.62 0.90 -2.142 0.90 -2.094 -0.094 -0.052 0.496	0.752 0.116 0.143 9 T11 3 -29.92 4 20 1 -2.93 4 80 1 -2.93 4 80 4 105 2 4 31 3 5.74 4 105 2 4 31 5.74 4 105 2 4 31 5.74 5.	1.000 0.048 0.048 0.089 0 -13.6 1 -4.1 0 -22.5 7 0.0.1 1 1.4.1 0 -22.5 2 -0.6 8 263.2 0 9.4 V -0.051 0 -2.4 0.051 0 0.263 0.026	0.04 1.00 0.19 (11 551 555 569 068 578 569 068 578 569 068 578 569 068 578 578 569 068 578 578 578 578 578 578 578 57	8 0.0 0 0.1 9 1.0 1.00 2.729 0.216 -7.219 0.216 -7.219 0.216 -7.219 0.216 9.411 14.790 14.790 14.790		Crganice * Crganice * Deskt	ss op aloads rt Place s res rs tter Disk (I Disk (I Disk (I	Compute (C) Open (S) (S) (S) (S) (S) (S) (S) (S)	Local Disk (D): Print Burn Bara Data combine Genetic Com Genetic Com G	pape Ne Ne d-RCBD dations h orrelatio orrelatio variane Phenoty
7 0.055 0.123 0.303 0.063 0.284 0.095 1.000 0.166 0.264 0.284 0.121 0.161 8 0.064 0.026 0.426	i 54 : 18 i -1 i -5 i -5 i -34 i -29 -13 : -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	0 11 12 18.866 25.2021 2.521 0.066 5.551 0.017 -2.869 -2.821 10.593 4.801 4.747 1.604 0 0 0 1 1 2 4.80 1 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.821 -0.017 -2.89 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.821 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -0.017 -2.89 -2.81 -2.8	-0.212 -0.112 -0.029 -0.029 -0.029 -0.029 -0.029 -0.25 -0.112 -0.25 -0.112 -0.26 -2.12 -0.112 -2.62 -0.112 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12	0.036 0.100 0.207 3 4 -1.41 1 0.0 9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 3 0.9 0.4 1 0.0 0 0.4 1 0.0 0 0.4 1 0.0 0 0 0 0 0 0 0 0 0 0 0 0 0	0.197 -0.156 0.085 F4 42 -5. 58 5. 53 -2. 44 4. 4. 4. 4. 4. 4. 4. 4. 4	0.225 -0.087 -0.280 T5 243 (551 -0.551 -0.546 -0.546 -0.546 -0.633 -0.044 -0.199 -0.044 -1.000 -0.272	0.24 0.12 0.13 0.13 0.11 1.119 0.007 1.119 0.007 0.010 0.044 0.091 0.044 0.091 0.044 0.091 0.044 0.091 0.068 0.037 EECC T5 0.040 0.062 0.024	7 40.66 0.008 0.008 0.008 0.008 0.008 0.008 0.004 0.004 0.004 0.004 0.004 0.008	2 0.133 3 0.145 4 0.250 Matrix TB 8 -5.455 5 -455 -2.441 19.918 -2.099 66.633 -0.091 6.085 6.1549 122.671 57.942 -0.896 6.1549 122.671 57.942 -0.896 -2.519 TT -0.055 -0.055 -0.023 -0.023 -0.023 -0.025	T 0.227 0.098 0.232 T T 34.93 10.59 21.43 10.49 426.09 -0.79 -0.79 -0.79 -0.79 -0.22 0.90 449.26 32.92 0.90 449.26 -0.90 449.26 -0.90 -0.90 -0.90 -0.79 -0.90 -0.90 -0.79 -0.90 -0.90 -0.79 -0.90	0.752 0.116 0.143 3 -29.92 4 80 1 24.31 3 5.74 4 106.22 1 -1.25 6 449.26 8 -11.26 8 -11.26 4 105.22 1 -1.25 6 449.26 8 -11.25 6 449.26 8 -11.25 8 -11.25 9 -1	1.000 0.048 0.089 0.13.8.3 1.4.1 1.4.1 1.0.0 7.7 0.7 2.0.7 1.4.6 1.4.6 1.4.1 1.4.1 1.4.1 1.4.1 1.4.1 1.4.1 1.4.1 1.4.1 1.4.2 1.4	0.04 1.00 0.19 551 551 555 569 568 569 568 568 568 568 568 568 568 568	8 0.0 0 0.1 9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0		Crganice * Crganice * Crgan	as op aloads tt Place s ments s tter Disk ((Disk (E	() () () () () () () () () () () () () (I Local Dak (D): Print Burn Name Gradest. Con Gradest. Con Gradest. Con Gradest. Con Print@ Gradest. Con Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ Print@ P	pape No A A A A
8 0.094 4.062 0.48 0.473 0.117 0.166 1.000 0.532 0.344 0.007 0.063 9 0.161 0.072 0.442 0.358 0.807 0.270 0.464 0.532 1.000 0.814 0.668 0.008 10 0.215 0.051 0.233 0.307 0.376 6.954 0.532 0.004 0.814 0.668 0.008 10 0.215 0.051 0.233 0.307 0.376 6.954 0.532 0.004 0.814 0.068 0.144	i 54 18 i -1 i -5 i -5 i -34 i -29 -13 i -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	0 11 11 12 18.866 25.205 25.205 2.821 0.068 5.551 -0.017 -2.839 -2.824 10.593 -4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 4.801 5.41 4.801 6.6 6.80	-0.212 -0.112 -0.029 -0.029 -0.029 -0.029 -0.029 -0.25 -0.112 -0.25 -0.112 -0.26 -2.12 -0.11 -2.62 -0.11 -2.62 -0.11 -2.62 -0.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12 -2.62 -2.12	0.036 0.100 0.207 3 4 4 1.00 9 0.4 4 1.00 9 0.4 8 9 0.09 8 8 2.07 1 0.57 1 0.77 9 0.2 1 0.07 1 0.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.09 0.4 8 2.07 1 0.07 7 7 0.07 7 1 0.77 7 0.02 1 0.07 1 0.07 7 1 0.00 1 0 0 0 0 0 0 0 0 0 0 0 0 0	0.197 -0.156 0.085 Cen 14 2 -5.58 -5. -5.58 -5. -5. -5. -5. -5. -5. -5. -5.	0.225 -0.087 -0.280 etic C 75 243 (551 - 551 - 556 - 568 (470 (568 - 546 (470 (016 - 546 (196 - 196 (196 - 546 (196 (196 - 546 (196 (19	0.24 0.12 0.13 0.13 0.13 0.07 0.11 0.07 0.010 0.044 0.001 0.044 0.091 0.044 0.091 0.044 0.091 0.044 0.091 0.068 0.037 0.068 0.037 0.068 0.037 0.068 0.037 0.068 0.037 0.068 0.024 0.022 0.024 0.022 0.024 0.022 0.024 0.025 0.024 0.025 0.024 0.025 0.	7 40.66 0.008 0.008 0.008 0.008 0.008 0.008 0.004 0.004 0.004 0.004 0.004 0.004 0.004 0.004 0.008 0.008 0.008 0.0161 0.033 0.0283 1.000 0.283 1.000 0.283 0.086	2 0.133 3 0.145 4 0.250 Attack 5.455 -2.441 19.918 5.945 -2.441 19.918 6.633 -0.091 6.086 61.549 122.671 -0.856 -0.957 -0.955	T 0.227 0.098 0.232 T -3.4.93 10.59 21.43 10.49 426.09 -0.79 -3.629 20.90 449.26 32.92 0.90 449.26 0.26 0.2	0.752 0.116 0.133 9 T4 3 -29 92 1 22 93 3 4 80 1 24 31 3 5.74 4 106 22 8 -11.26 8 -322 8 -322 1 6 54 3 8 -24 9 T4 9 T4 10	1.000 0.048 0.089 0.13.8.3 1.4.1 1.4.1 1.0.0 7.7 0.7 2.0.7 1.4.6 1.4.2 1.4.1 1.4.1 1.4.1 1.4.1 1.4.1 1.4.2 1.4	0.04 1.00 0.19 711 551 747 531 755 569 669 668 778 669 668 778 747 747 747 747 747 747 74	8 0.0 9 1.0 9 1.0 1.0 9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0		Crganice Crganice Cr	ss opp iloads st Place s res is ter Disk (I Disk (F	() () () () () () () () () () () () () (Local Disk (D) Print Burn Name BataConstruction Genetic Coar Genetic Coar Genetic Coar Genetic Coar Genetic Coar Genetic Coar SAS Code for	 pape No <li< td=""></li<>
9 .0.161 0.072 0.142 0.356 0.807 -0.270 0.286 0.532 1.000 0.814 0.068 0.006 10 .0.216 0.051 0.233 0.307 0.356 0.697 0.128 0.334 0.814 1.000 0.656 0.144	54 188 33 4 -1 5 5 7 -1 5 -5 7 -1 -5 -34 -29 -13 -1	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	00 11 12 12 18 25 25 25 25 25 25 25 25 25 25	-0.212 -0.112 -0.029 -0.039	0.036 0.100 0.207 3 4 -1.41 1 0.0 9 0.4 8 9 0.0 9 0.4 8 8 2.0 1 1 0.57 1 0.77 9 0.2 1 0.07 - 1 0.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.4 8 2.07 - 1 0.0 9 0.0 - 2.07 - - - - - - - - - - - - -	0.197 -0.156 0.085 Cen 14 2 -5.58 -5. -5.58 -5. -5. -5. -5. -5. -5. -5. -5.	0.225 -0.087 -0.280 etic C T5 243 (551 - 554 (554 - 556 - 556 (470 (006 - 0016 - 546 (006 - 0016 - 00014 - 00014 - 00014 - 00014 - 00014 - 00014 - 00014 - 00014 - 00014 - 000014 - 00014 - 0014 - 000	0.24 0.12 0.13 0.13 0.14 0.11 1.118 0.017 1.119 0.000 0.041 0.044 0.092 0.044 0.092 0.044 0.092 0.044 0.092 0.044 0.000 0.044 0.000 0.044 0.000 0.044 0.000 0.044 0.000 0.044 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.0000 0.00000 0.000000	7 40.66 0.009 1 0.04 1 0.04 1 0.04 1 0.04 1 0.04 1 0.04 0.023 0.024 0.044 1 2.65 8.578 0.298 0.023 0.044 1.265 8.578 0.088 0.0161 0.033 0.033 0.023 0.023 0.023 0.024 0.025 0.024 0.024 0.024 0.025 0.024 0.024 0.025 0.024 0.025 0.024 0.025 0.024 0.025 0.024 0.025	2 0.133 3 0.145 4 0.250 Attack 5 455 -2.441 19.918 5 -3455 -2.441 19.918 5 -3455 -2.441 19.918 6 6.633 -0.091 6 0.665 6 1.549 122.671 5 7.942 -0.896 6 0.255 -0.251 -0.896 -0.251 -0.896 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.123 -0.905 -0.295 -0.123 -0.905 -0.905 -0.123 -0.905 -0.9	0.227 0.088 0.232 -34.93 10.59 21.43 10.59 21.43 10.69 -34.93 10.59 21.43 10.69 -36.29 122.67 865.03 32.92 0.90 Latrix T8 0.094 0.062 0.496 0.473 0.473 0.417 0.166	0.752 0.116 0.143 9 T1 3 -29.92 3 4.80 1 24.31 1 -1.25 6 -11.25 6 -11.25 8 -352 -21 4 106 -22 1 -1.25 8 -11.25 8 -352 -21 1 -7.94 4 49.26 8 -352 -21 1 -7.94 6 -49.26 8 -352 -21 1 -7.94 6 -49.26 8 -352 -21 1 -7.94 6 -49.25 8 -352 -21 1 -7.94 1 -7	1.000 0.048 0.089 0.089 0 -13.6 0 -13.6 0 -22.6 7 0.13.6 1 1.4.7 1 0.22.6 2 -0.0 6 16.6 8 22.6 0 9.4 1.216 -0 0.51 0 .253 -0 .307 0 .315 0 .128 0	0.04 1.00 0.19 11 551 551 555 569 569 569 5669 578 578 596 578 596 578 596 1224 48 442 511 512 514 514 515 515 516 516 517 517 517 517 517 517 517 517	8 0.0 0 0.1 9 1.0 1.0 1.0 1.0 1.0 1.0 1.0 1.0		Corganice • Corganice • Co	ss opp iloads st Place s res s res res res res ter Disk (I Disk (I	2) () () () () () () () () () () () () ()	I Local Disk (Dr) Print Burn Name Gabascanter	 pape No notations norrelatic ovariante phenoty
10 -0.216 0.051 0.253 0.307 0.315 -0.691 -0.128 0.394 0.814 1.000 0.054 0.114	i 54 i 54 i 18 i -3 i -1 i -5 i 0 i -5 i -34 i -13 i -13 i -13	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	10 11 12 12 12 15 15 10 10 10 10 10 10 10 10 10 10	-0.212 -0.112 -0.029 -0.029 -0.029 -0.029 -0.029 -0.029 -0.26 -2.62 -2.62 -2.62 -2.12 -0.112 -2.62 -1.12 -0.112 -2.62 -1.12 -2.15 -0.112 -2.62 -2.72	0.036 0.100 0.207 0.207 0.207 0.007 0.04 0.04 0.04 0.04 0.04 0.07	0.197 -0.156 0.085 Centre 2.5. 3.3 2.2. 5.3 3.4 4.4. 4.4	0.225 -0.087 -0.280 etic C 75 243 0 551 -0. 556 -0. 556 -0. -0. -0. -0. -0. -0. -0. -0.	0.24 0.12 0.13 0.13 0.14 0.118 0.017 1.118 0.017 0.010 0.041 0.091 1.291 0.044 0.091 1.291 0.044 0.092 0.044 0.022 0.044 0.022 0.044 0.022 0.044 0.022 0.044 0.022 0.044 0.0220 0.02200000000	7 0.66 0.08 0.08 0.08 0.08 0.08 0.08 0.08 0.28 0.28 0.293 0.25 0.04 0.28 0.293 0.293 0.293 0.293 0.293 0.293 0.044 2.888 0.293 0.044 2.888 0.293 0.044 2.888 0.293 0.044 0.045 0.044 0.044 0.044 0.045 0.044 0.044 0.044 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045 0.044 0.045	2 0.133 3 0.145 4 0.250 Matrix T8 5.455 -2.441 19.918 -5.455 -2.441 19.918 -0.091 -0.091 -0.095 -0.091 -0.095 -1.22.671 -2.519 T7 -0.055 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.123 -0.125 -0.125 -2.441 -5.455 -2.441 -5.455 -2.441 -5.455 -2.441 -5.455 -2.441 -5.455 -2.441 -5.455 -2.499 -0.991 -2.519 -2.529 -	0.227 0.088 0.232 -34.93 10.59 21.43 10.59 21.43 10.49 -36.29 122.67 865.03 22.87 0.90 -32.26 0.90 -32.22.67 865.03 0.90 -32.92 0.90 -0.094 -0.052 0.4735 0.4735 0.4735 0.4735 0.4735 0.4735 0.4735 0.4735 0.4735 0.4735 0.117 0.166 1.000	0.752 0.116 0.143 9 T1 3 -29.92 3 4.60 1 2431 1 -29.92 3 4.60 1 2431 4 10622 1 -1.29 6 -11.26 4 3 574 4 10622 1 -1.29 6 -11.26 4 3 574 4 10622 1 -2.98 6 -1.12 6 -1.29 6 -1.12 6 -1.29 6 -1.12 6 -1.29 6 -1.29 7 -	1.000 0.048 0.089 0.089 0 -13.6 0 -25.7 7 0.13.6 1 1.4.7 1 0.22.6 6 16.5 8 22.6 6 16.6 0 9.4 2.16 0.0 0.51 0 2.53 0 0.51 0 1.253 0.0 1.128 0.0	0.044 1.00 0.19 (11 (55 (47 (55 (569) (569) (568) (568) (568) (568) (568) (568) (578) (568) (578) (568) (578) (568) (578) (568) (578)	8 0.0 0 0.1 9 1.0 1.103 1.604 -2.729 0.216 -7.219 0.216 -7.219 0.216 -0.037 8.240 9.411 14.790 14.790 14.790 0.082 -0.035 0.082 -0.105 -0.037 0.056 -0.105 -0.097 0.161 -0.082 -0.097 0.161 -0.082 -0.097 0.161 -0.082 -0.097 0.161 -0.082 -0.097 0.161 -0.082 -0.097 0.161 -0.082 -0.097 0.056 -0.097 -0		Corpanie -	s res res res res reter Disk (I Disk (I	2) () () () () () () () () () () () () ()	Local Dark (D): Print Burn Name Data combine Societaria Societaria Societaria Societaria	paper Ne Account of the second
14 0 440 0 0FD 0 0FD 0 040 0 050 0 044 0 440 0 007 0 055 0 055 0 055	5 1 54 2 18 3 -3 4 -1 5 -5 5 0 -4 -5 5 -5 -5 -5 -5 -5 -5 -5 -5 -5 -5	X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X1 X	0 11 11 2 18 86 25 25 -2 82 0 06 5 55 10 54 10 54 4 747 1 64 1 2 1 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 5 4 6 4 7 4 8 4 9 4	-0.212 -0.112 -0.029 -0.029 -0.225 -0.2622 -0.2622 -0.2622 -0.2622 -0.112 -0.112 -0.12 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.112 -0.125 -0.112 -0.125 -0.115 -0.125 -0.125 -0.115 -0.125 -0.115 -0.155 -0.055 -0.	0.036 0.100 0.207 0.207 0.207 0.007 0.04 0.04 0.04 0.04 0.04 0.07	0.197 -0.156 0.085 CU 14 25 5. 5. 5. 5. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4	0.225 -0.087 -0.280 etic C 75 243 0 551 -0. 556 -0. 556 -0. -0. 556 -0. -0. -0. -0. -0. -0. -0. -0.	0.24 0.12 0.13 0.01 0.01 0.01 0.01 0.01 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.007 0.008 0.007 0.008 0.007 0.002 0.002 0.002 0.0220 0.022 0.0220 0.0220 0.0220 0.0220 0.0220 0.0220 0.0200000000	7 0.66 3 0.08 1 0.04 -1.88 -2.889 -7.268 -2.889 -7.268 -2.889 -7.268 -0.293 -0.044 2.884 6.086 -0.588 8.578 8.578 8.578 8.578 0.161 -0.033 -0.233 -0.233 1.000 -0.955 -0.958	2 0.133 3 0.145 4 0.250 Natrix TR 5.455 -2.441 19.918 -5.455 -2.441 19.918 -6.633 -0.091 -6.085 -6.1549 -6.085 -6.1549 -6.085 -6.1549 -7.942 -0.896 -2.519 TT -0.055 -0.123 -0.031 -0.053 -0.228 -0.303 -0.051 -0.298 -0.305 -0.	0.227 0.088 0.232 -34.93 10.59 21.43 10.59 21.43 10.59 21.43 10.59 21.43 10.59 21.43 10.59 32.52 0.79 -36.29 0.865.03 449.26 32.92 0.90 449.26 32.92 0.90 449.26 32.92 0.90 449.26 32.92 0.90 449.26 32.92 0.90 449.26 32.92 0.90 449.26 9.090 0.90 0.904 0.435 0.435 0.435 0.1176 0.435 1.000	0.752 0.116 0.143 9 T11 3 -29 92 4 105 22 1 -122 4 105 22 1 -122 4 105 22 4 165 22 1 -122 0.072 0.072 0.072 0.072 0.072 0.072 0.072 0.072 0.075	1.000 0.048 0.048 0.089 0 -13.8 1 4.1 0 -22.8 7 0.0.2 7 0.4.8 0 -22.8 2 -0.6 8 32.2 2 -0.6 8 32.6 1.64.1 -0.0 0.051 0 .253 -0 .307 0 .307 0 .315 0 .324 -0.8 .324 -0.8	0.04 1.00 0.19 (11 (55 (47 (55 (56)	8 0.0 0 0.1 9 1.0 1.0 1.0 0.2 1.0 0.0 0.2 1.0 0.0 0.2 1.0 0.0 0.2 1.0 0.0 0.2 1.0 0.0 0.2 1.0 0.0 0.2 1.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0		Computer -	s sop eloads tt Place s res s tter Disk (I Disk (I	::) ;;) ;;)	I Local Duk (D): Print Burn Name Data Combine Genetic Coox Gonetic Coox Printige Contention Genetic Coox Printige Contention Solution Solution Solution Solution	papereiron Ne C

Figure 5. The output results.

ed) 🕅 SAS Code for Phenotyp...

respectively. These correlations can be used in correlational studies as well as path analysis (Anilkumar et al. 2019, Jhanavi et al. 2019, Mishra & Nandi 2018, Nirmal Raj & Gokulakrishnan 2018, Shivakumar et al. 2018) to identify important traits and used them in breeding programs. Also, the phenotypic and genotypic covariance matrices are shown in Table SIV and SVI, respectively that the variances are located in the diameter and covariance are placed outside the diameter. These variances can be used selection index (Almeida et al. 2019, Ghosh et al. 2018, Kour et al. 2018) studies as well as heritability of traits (Banik et al. 2018, Kumar et al. 2019, Raval et al. 2018).

9 • A SAS program to estimated

In plant breeding programs, selection of traits based on genetic correlations is more beneficial because genotypic variance is passed on to the next generation. Heritability was also calculated based on the genotypic / phenotypic variance ratio. Traits that have higher heritability are easier to select. Evaluation of variability components and inheritance of traits help plant breeders to improve crop. Breeders can use the knowledge of genetic variability available among and between crops as a guide to improving crop. Genetic and phenotypic correlations for plant breeding have been used in many researches in recent years. The SAS program for calculating genetic or phenotypic variance-covariance and genetic or phenotypic correlation can be a useful aid to plant and animal breeders and it will prevent mistakes in manual calculation.

CONCLUSION

The SAS program reported here was easy to use and the outputs were easy to understand and user-friendly. This program could compute phenotypic-genotypic covariance and correlation matrices based on the expected value of any statistical designs. The goodness and attraction of this program is that it doesn't need to know the language of the SAS program and the users can easily analyze data with this program. The program is not computationally intensive and should therefore run-on slower computers. Users are advised against making any changes to the program code based on your need and your statistical design.

Acknowledgments

The authors gratefully thank Dr. José Crossa for his comments and suggestions on this paper.

REFERENCES

ACQUAAH G. 2009. Principles of plant genetics and breeding. USA: J Wiley & Sons, 756 p.

AKHTAR N, NAZIR M, RABNAWAZ A, MAHMOOD T, SAFDAR M, ASIF M & REHMAN A. 2011. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). J Anim Plant Sci 21: 660-664.

ALMEIDA GQD, SILVA JDO, RESENDE MDVD, MENEGUCI JLP & MATOS GR. 2019. Selection index via REML/BLUP for identifying superior banana genotypes in the central region of Goiás state, Brazil. Rev Ceres 66: 26-33.

ANILKUMAR G, UMESHA K, SHIVAPRIYA M, HALESH G, MARUTHIPRASAD B & DARSHAN G. 2019. Character association and path analysis for yield traits in coriander (*Coriandrum sativum* L.). Elec J Plant Breed 10: 224-229.

BANIK M, DEORE G, MANDAL AK & MHASE L. 2018. Genetic Variability and Heritability Studies in Chickpea (*Cicer arietinum* L.). Curr J Appl SciTech: 1-6.

CROSSA J, PEREZ P, HICKEY J, BURGUEÑO J, ORNELLA L, CERÓN-ROJAS J, ZHANG X, DREISIGACKER S, BABU R & LI Y. 2014. Genomic prediction in CIMMYT maize and wheat breeding programs. Heredity 112: 48-60.

DEEPO DM, SARKER A, AKTER S, ISLAM MM, HASAN M & ZEBA N. 2020. Diversity and path analysis of chilli (*Capsicum* spp.) based on morphological traits in northern region of Bangladesh. Turkish J Agric Food SciTech 8: 179-185.

GHOSH T, ISLAM S, SHAHANAZ S, BISWAS S & TAREQ M. 2018. Genetic variability and selection index evaluation of some selected tomato lines for their yield and yield components. Bangladesh J Environ Sci 34: 73-78.

GOVINDARAJ M, VETRIVENTHAN M & SRINIVASAN M. 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. Genet Res Int 2015: Article ID 431487, 14 p.

HALLAUER AR. 2007. History, contribution, and future of quantitative genetics in plant breeding: lessons from maize. Crop Sci 47: 4-19.

HERMISSON J & WAGNER GP. 2004. The population genetic theory of hidden variation and genetic robustness. Genet 168: 2271-2284.

HILL J, BECKER HC & TIGERSTEDT PM. 1998. Quantitative and ecological aspects of plant breeding. Netherlands: Springer Science & Business Media, 275 p.

JHANAVI D, PATIL H, RANJITHA B & JUSTIN P. 2019. Correlation and path analysis studies for growth, yield and quality traits in French bean (*Phaseolus vulgaris* L.). Environ Ecol 37: 22-26.

KOUR S, PRADHAN U, PATEL J & VAISHNAV P. 2018. Comparative study of selection indices based on different weights in forage sorghum [Sorghum bicolor (L.) Moench]. J Crop Weed 14: 17-23.

KUMAR N, PANDEY S, MISHRA S, MISHRA D & PANDEY V. 2019. Studies on heritability and genetic advance for the quantitative characters in Pea (*Pisum sativum* L.) in sodic condition. J Pharmacogn Phytochem 8: 310-312.

KUMARI P, DE N & KUMARI AKA. 2020. Genetic variability, correlation and path coefficient analysis for yield and quality traits in wheat (*Triticum aestivum* L.). Int J Curr Microbiol App Sci 9: 826-832.

LEWONTIN R. 2008. The genotype/phenotype distinction. Stanford Encyclopedia of Philosophy.

MEHDI RAHIMI & MATEO V. HERNANDEZ

MATHER K & JINKS JL. 1977. Introduction to biometrical genetics. Boston, USA: Springer Science & Business Media, 231 p.

MISHRA A & NANDI A. 2018. Correlation and path coefficient analysis for quality traits in tomato (*Solanum lycopersicon* L.). J Pharmacogn Phytochem 7: 1733-1738.

MORENO-GONZALEZ J & CUBERO J. 1993. Selection strategies and choice of breeding methods. In: Hayward MD, Bosemark NO, Romagosa I & Cerezo C (Eds), Plant Breeding: Principles and prospects. Netherlands: Springer Science+Business Media Dordrecht, p. 281-313.

MUNIR M, CHOWDHRY M & MALIK T. 2007. Correlation studies among yield and its components in bread wheat under drought conditions. Int J Agr Biol 9: 287-290.

NIRMAL RAJ R & GOKULAKRISHNAN J. 2018. Indirect selection for various yield attributing characters of maize hybrids across environments using correlation and path analysis. J Pharmacogn Phytochem 7: 1810-1812.

PARIMALA K, RAJU CS, PRASAD AH, KUMAR SS & REDDY SN. 2020. Studies on genetic parameters, correlation and path analysis in rice (*Oryza sativa* L.). J Pharmacogn Phytochem 9: 414-417.

RAVAL V, PATEL A, RATHOD S, SUMITA Z, JM V & CHAUDHARI B. 2018. Genetic variability, heritability and genetic advance studies in okra (*Abelmoschus esculentus* (L.) Moench). Int J Chem Stud 6: 3319-3321.

ROFF DA. 1997. Evolutionary quantitative genetics. USA: Springer Science & Business Media, 494 p.

SEYOUM M, ALAMEREW S & BANTTE K. 2012. Genetic variability, heritability, correlation coefficient and path analysis for yield and yield related traits in upland rice (*Oryza sativa* L.). J Plant Sci 7: 13-22.

SHIVAKUMAR M, RADHIKA K, SARLA N & VENKANNA V. 2018. Character association and path analysis for yield and its component characters in rice. Environ Ecol 36: 876-880.

SÖLKNER J, GRAUSGRUBER H, OKEYO AM, RUCKENBAUER P & WURZINGER M. 2008. Breeding objectives and the relative importance of traits in plant and animal breeding: a comparative review. Euphytica 161: 273-282.

STINCHCOMBE JR, KIRKPATRICK M & GROUP F-VTW. 2012. Genetics and evolution of function-valued traits: understanding environmentally responsive phenotypes. Trends Ecol Evol 27: 637-647.

SULTAN SE. 2000. Phenotypic plasticity for plant development, function and life history. Trends Plant Sci 5: 537-542.

TRIPATHI S, MARKER S, PANDEY P, JAISWAL K & TIWARI D. 2011. Relationship between some morphological and physiological traits with grain yield in bread wheat (*Triticum aestivum* L. em. Thell.). Trends Appl Sci Res 6: 1037-1045.

WOLF JB, BRODIE III ED, CHEVERUD JM, MOORE AJ & WADE MJ. 1998. Evolutionary consequences of indirect genetic effects. Trends Ecol Evol 13: 64-69.

ZENG Z-B, KAO C-H & BASTEN CJ. 1999. Estimating the genetic architecture of quantitative traits. Genet Res 74: 279-289.

SUPPLEMENTARY MATERIAL

Tables SI - SVII

How to cite

RAHIMI M & HERNANDEZ MV. 2022. A SAS code to estimate phenotypicgenotypic covariance and correlation matrices based on expected value of statistical designs to use in plant breeding. An Acad Bras Cienc 94: e20200001. DOI 10.1590/0001-3765202220200001.

Manuscript received on January 01, 2020; accepted for publication on March 20, 2020

MEHDI RAHIMI¹

https://orcid.org/0000-0001-5625-3275

MATEO V. HERNANDEZ²

https://orcid.org/0000-0002-0735-3242

¹Graduate University of Advanced Technology, Institute of Science and High Technology and Environmental Sciences, Department of Biotechnology, Kerman Province, End of Haft Bagh-e-Alavi Highway Knowledge Paradise, Kerman, Iran

²Universidad Autónoma Chapingo, Department of Suelos, Carr. Federal México-Texcoco, Km 38.5, 56230 Texcoco, México

Correspondence to: **Mehdi Rahimi** *E-mail: mehdi83ra@yahoo.com*

Author contributions

Rahimi M has designed and written the program and wrote the article. Hernandez MV developed and edited the program and also read and revised the manuscript. All authors have read and approved the manuscript.

