

Manual of GSCA 1.0

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GSCA is a Windows software for computing general combining abilities (GCA) and specific combining abilities (SCA) in a diallel mating design. The algorithm is based on restricted linear models and can be deal with missing data. In addition to providing GCA and SCA estimates, GSCA gives hypothesis testing for model, various factors and differences between GCAs or SCAs.

GSCA focuses on treating the following linear model of diallel mating design with fixed effects:

$$y_{ijklkm} = \mu + E_k + B_{l(k)} + G_i + G_j + S_{ij} + R_{ij} + GE_{ik} + GE_{jk} + SE_{ijk} + RE_{ijk} + e_{ijklkm}$$

where y_{ijklkm} is the m th observation of the l th block within k th environment for the ij th cross; μ is the overall mean; E_k is the k th environment effect; $B_{l(k)}$ is the l th block effect in the k th environment; G_i and G_j are the GCA effects of the i th female and the j th male respectively; S_{ij} is the SCA effect of the i th and j th parents; R_{ij} is the reciprocal effect due to the cross between the i th female and the j th male; GE_{ik} and GE_{jk} are the k th environment with the i th and the j th GCA interactions respectively; SE_{ijk} is the k th environment with the ij th SCA interaction; RE_{ijk} is the interaction of the k th environment with the reciprocal effect of R_{ij} ; and e_{ijklkm} is the within plot error term.

The model can be reduced to some simpler forms that include Griffing's four kinds of diallel cross. For a half-diallel mating design in a single site, the model will be altered to

$$y_{ijlm} = \mu + B_l + G_i + G_j + S_{ij} + e_{ijlm}$$

1 Data Format

The raw data should be put into a text file as shown in Table 1. The first line lists the names of factors and traits that must be "Pi", "Pj", "Blk", "Env", "Trt1", "Trt2", etc., and must be in such order, where "Pi" stands for female parent, "Pj" for male parent, "Blk" for block, "Env" for environment, "Trt1" for trait 1, "Trt2" for trait 2, and so on. From the second line on,

each line is the data for an individual that corresponds to factors and traits of the first line. Since GSCA can deal with the flexible model, either block or environment factor or both can be missed in the raw data file.

Table 1 Data format of GSCA. Either block or environment factor or both can be missed.

Pi	Pj	Blk	Env	Trt1	Trt2
1	2	1	1	213	175
1	2	1	1	211	158
1	2	2	1	186	169
1	2	2	2	220	227
1	2	2	1	172	192
2	3	1	2	203	179
2	3	1	1	151	260
2	3	1	1	184	187
2	3	1	2	220	203
2	3	2	1	178	183
.....					

2 Data Analysis

After running GSCA, you can open the data file by clicking the menu “File” and then the option “Open”. If the data format is correct, then the data will be successfully opened and shown as fig. 1. The pine data (Wu et al. 2003) can be used as an example for diallel analysis. You can find the data file, “pinedata.txt”, in the folder where GSCA has been installed.

To analyze the data, please click the menu “Analysis” and then the option “Run”. A dialog window as fig. 2 will pop out and then you can choose factors to fit an appropriate model for your diallel mating design. When you accept the chosen model, GSCA will begin to compute. After a while, results of fixed effect estimates, such as GCAs and SCAs, and hypothesis testings for various factors and differences between GCAs or SCAs are shown on screen as fig. 3. You can save the results as a text file.

3 References

Wu HX and AC MATHESON, 2001 Analysis of Half-diallel Mating Design with Missing Crosses: Theory and SAS Program for Testing and Estimating GCA and SCA Fixed Effects. *Silvae Genetica*, 49(3):130-137

Pi	Pj	Blk	Env	Trtl
1	2	1	1	213.0000
1	2	1	1	185.0000
1	2	1	1	197.0000
1	2	1	1	211.0000
1	2	2	1	186.0000
1	2	2	2	220.0000
1	2	2	1	175.0000
1	2	2	2	207.0000
1	2	2	1	172.0000
1	2	2	2	235.0000
1	2	2	1	173.0000
1	2	2	2	237.0000
1	2	3	1	186.0000
1	2	3	2	218.0000
1	2	3	1	187.0000
1	2	3	2	215.0000
1	2	3	1	167.0000
1	2	3	1	188.0000

Figure 1: The window of an opened data file

Dialog

Parameter Selection

<input checked="" type="checkbox"/> GCA	<input checked="" type="checkbox"/> ENV
<input checked="" type="checkbox"/> SCA	<input type="checkbox"/> GCA*ENV
<input checked="" type="checkbox"/> RCA	<input type="checkbox"/> SCA*ENV
<input checked="" type="checkbox"/> BLK	<input type="checkbox"/> RCA*ENV

OK Cancel

Figure 2: Dialog window for choosing factors

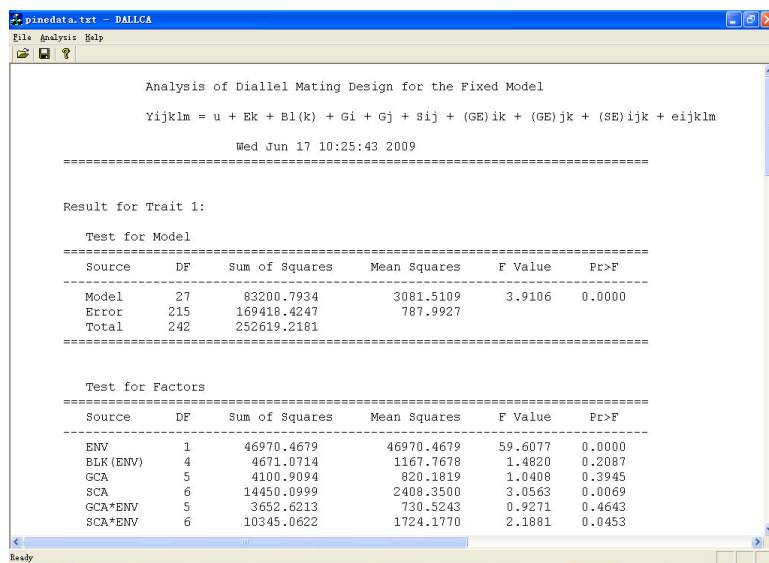


Figure 3: Results of parameter estimates and hypothesis testing