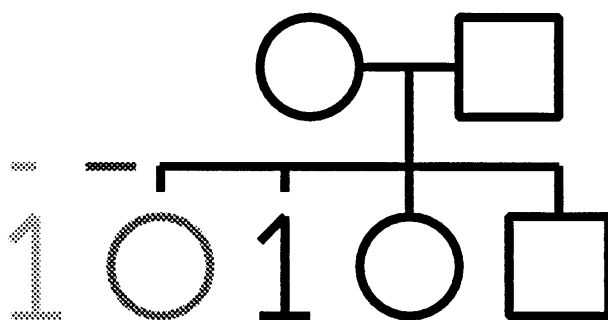


# The Genometric Analysis Simulation Program

(G.A.S.P.)



Software version 3.30 (10/21/97)

Documentation Draft 10/24/97

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## Overview

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Development of computer software for statistical genetic analysis can be facilitated by the availability of software tools that can be used to (1) verify the algorithms underlying a particular method of analysis (i.e. statistical test), (2) determine empirical type I error rates for a statistical test, (3) determine the power of a test, and (4) determine the robustness of a test with respect to failures of underlying assumptions. The Genometric Analysis Simulation Program (G.A.S.P.) is a software tool that can generate samples of family data based on user specified genetic models. Data generated can be as simple as a single sample of random individuals with a single normally distributed trait or as complex as thousands of samples of extended families with multiple traits based on a linear combination of major locus, polygenic, common sibship environment and covariate components. Traits can be generated based on a number of user specified components, and components can be unique to a single trait or shared by multiple traits. The user first specifies a list of all desired components and then creates each trait by specifying the desired component weighted by its contribution to the phenotypic variance.

G.A.S.P. can be used in two ways. First, data can be generated in a standalone fashion. The resulting family data can be saved and then used as sample data for demonstrating applications and methods of genetic analysis or for testing and verifying newly developed algorithms in statistical genetics. A simple driver ("dataonly") is provided for this application. Second, data can be generated and analyzed immediately using an existing statistical package. A driver can be designed to call subroutine versions of widely available genetic analysis programs.

What can G.A.S.P. be used for?

- Verify analysis algorithms with respect to the underlying theory
- Test the statistical validity of newly developed methods of genetic segregation and linkage analysis and investigate the statistical properties of the test statistics
- Determine the power and robustness of these methods
- Apply insights gained from these simulation experiments to ongoing collaborative genetic analyses

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See also:

Methods

Current options

Usage

Supported platforms

Studies: A list of published simulation studies that have used G.A.S.P

Citation

Disclaimer

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Registration

Availability

Copyright

Authors/Contacts

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## Methods

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The simulation model is defined on the basis of a set of components specified by the user. Pseudo-random number generation, either from the provided module (PRNG) or from IMSL, if it is available, is used to model single-locus and polygenic inheritance, to generate other components, and (optionally) to determine sibship sizes. The genetic and other components are then combined into traits according to weights (proportions of total phenotypic variance) specified by the user. Models can be further customized by modifying traits in the driver.

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See also:

[Components](#)

[Traits](#)

[Parameter descriptions](#)

[References](#)

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## Summary of Current Options

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- Maximum number of repetitions: none
  - Maximum number of individuals per sample: 5000
  - Maximum number of components (including loci): 32
  - Maximum number of traits: 5
  - Maximum number of user-specified loci: 20
  - Maximum number of alleles at a given locus: 12
  - Maximum number of trait specific environmental components: 3
  - Maximum number of polygenic components: 3
  - Maximum number of common sibship environmental components: 3
  - Maximum number of random covariates: 3
  - Type of family
    - unrelated individuals
    - sibships
    - nuclear family
    - CEPH-type family
    - simple pedigree
  - Type of sibship size
    - fixed
    - random
  - Genotypes of founders
    - random
  - Type of trait
    - quantitative
    - qualitative
  - Type of marker
    - quantitative
    - qualitative
-

## Using G.A.S.P.

---

The Genometric Analysis Simulation Program (G.A.S.P.) generates samples of family data based on user specified models. Both trait and marker data can be generated. The user first specifies a list of components, including genetic markers. Each trait is then created by specifying the desired components weighted by their respective contributions to the phenotypic variance for that trait. Components can be unique to a single trait or shared by multiple traits to create pleiotropic effects. The user sets parameters, specifying information about the simulation (e.g. title, number of samples, family size and structure, as well as generating models, in the G.A.S.P. parameter file.

Version 3.30 of G.A.S.P. is written in ANSI standard FORTRAN-77. Simulation and random number generation modules are provided, as well as source code for a skeleton driver and an example including a "dataonly" driver. The user may also customize the driver to modify generated traits, to build more complex models, and to write out data which can be saved for external analysis or immediately analyzed by directly invoked procedures.

---

See also:

Components: A description of the types of components that can be used to create traits

Traits: A description of the kinds of traits that can be simulated

Parameter descriptions: A description of the parameters of the simulation

Parameter file: A description of the format of the G.A.S.P. parameter file that defines the model to be simulated

Examples: Several examples of G.A.S.P. input parameter files and the resulting simulated data files

Variable and array descriptions: A table of the variables and arrays used in G.A.S.P. and available to the driver, with a brief description of each.

Citation

Disclaimer

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Copyright

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## **Supported Platforms**

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G.A.S.P. is currently available for the following processor/operating system platforms:

DEC Alpha / Digital Unix 4.0B

Silicon Graphics Challenge / IRIX 6.2

Sun Sparestation / SunOS 5.5

Please contact the authors about the need for additional versions.

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## **Selected Studies that Have Used the Genometric Analysis Simulation Program**

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- Amos CI, Elston RC, Wilson AF, Bailey-Wilson JE. A more powerful robust sib-pair test of linkage for quantitative traits. *Genet Epidemiol* 1989; 6:435-449.
  - Wilson AF, Elston RC. Statistical validity of the Haseman-Elston sib-pair test in small samples. *Genet Epidemiol* 1993; 10:593-598.
  - Nick TG, George VT, Elston RC, Wilson AF. Statistical validity for testing associations between genetic markers and quantitative traits in family data. *Genet Epidemiol* 1995; 12:145-161.
  - Lindpaintner KL, Lee M, Larson MG, Rao VS, Pfeffer MA, Ordovas JM, Schaefer EJ, Wilson AF, Wilson PWF, Ramachandran VS, Myers RH, Levy D. Lack of association or genetic linkage between the ACE gene and left ventricular mass. *N Engl J Med* 1996; 334:1023-1028.
  - Guo X, Wickremasinghe AR, Wilson AF, Elston RC. Goodness-of-fit tests for the major gene model. *Proceedings of the American Statistical Association* 1996; in press.
-

## Citation

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Wilson AF, Bailey-Wilson JE, Pugh EW, Sorant AJM. The Genometric Analysis Simulation Program (G.A.S.P.): a software tool for testing and investigating methods in statistical genetics. *Am J Hum Genet* 1996; 59:A193.

---

## **Disclaimer**

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No warranty, either expressed or implied, is made with respect to the functioning and accuracy of this program. No responsibility is assumed by the authors. Please report any problems or bugs to the authors.

---

## **License Agreement**

---

Use of the Genometric Analysis Simulation Program (G.A.S.P.) signifies that the user agrees to the following conditions:

### **Installation**

The author will be notified of the installation of G.A.S.P. on each processor using the accompanying form. G.A.S.P. will be used only on the specified processor(s), and only by the person or persons designated on the form.

### **Distribution**

G.A.S.P. will not be distributed in any form to any other user or to any other site. Users shall take appropriate measures to prevent the distribution of G.A.S.P. from their site and to ensure that source, object and executable files are held in confidence. If the user leaves a designated site, the user agrees to destroy all existing copies (including backups) of G.A.S.P. at that site.

### **Modification**

Except for the modules specifically designated to be modified by the user (i.e. the driver module), G.A.S.P. shall not be modified in anyway.

### **Acknowledgment**

G.A.S.P. shall be acknowledged using the appropriate citation in any publication that uses the software.

### **Disclaimer**

The user accepts full responsibility for the use of G.A.S.P. and for the interpretation of results generated using this software. The user acknowledges that no warranty, either expressed or implied, is made with respect to the functioning and accuracy of the software.

---

Please register as a G.A.S.P. user.

---

## Registration

---

Please send the following information to the G.A.S.P. contacts:

Site:

Department:

Institution:

Designated Contact:

Contact's address:

Contact's telephone:

Contact's fax:

Contact's e-mail address:

Users:

Processor manufacturer:

Processor model:

Processor operating system:

---

## Availability

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G.A.S.P. is available by anonymous ftp:

- 1) "ftp" to nhgri.nih.gov
- 2) Log in as "anonymous", and give your E-mail address as the password
- 3) "cd" to pub/outgoing/gasp
- 4) "get" (in binary mode) the appropriate files, which are:

README	General information
htmldoc.tar	Archived directory of HTML documentation (but the newest version will be at <a href="http://www.nhgri.nih.gov/DIR/IDRB/GASP/">http://www.nhgri.nih.gov/DIR/IDRB/GASP/</a> )
doc.ps	Essentially, a postscript version of the HTML files all together, in case you want to print it out
gasp_v33.platform.tar	Archive containing everything else you need for platform <i>platform</i> (fill in alpha, sun, or sgi)

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## Copyright

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(c) 1997 Alexander F. Wilson

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## Authors/Contacts

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Please direct comments, questions, requests to:

Alexander F. Wilson, Ph.D.  
NIH/NHGRI  
333 Cassell Drive, Suite 2000  
Baltimore, MD 21224

Tel: (410) 550-7510  
Fax: (410) 550-7513  
E-mail: [afw@nhgri.nih.gov](mailto:afw@nhgri.nih.gov)

or to:

Alexa J. M. Sorant, A.M.  
NIH/NHGRI  
333 Cassell Drive, Suite 2000  
Baltimore, MD 21224

Tel: (410) 550-7512  
Fax: (410) 550-7513  
E-mail: [ajms@nhgri.nih.gov](mailto:ajms@nhgri.nih.gov)

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## Components

---

### Individual Components

- Single locus component
  - Polygenic component
  - Common sibship environment component
  - Covariate component (random effect)
  - Trait specific environment component
- 

### Component Descriptions

- Single locus component. Each single locus can be used either as a marker locus or as a locus that contributes to a trait. Each locus is parameterized in terms of the following: locus name, number of alleles, recombination fraction between that locus and the previous locus, allele name and frequency (one for each allele), genotype name (one for each genotype corresponding to allele 11, 12, 13, ..., 1n, 22, 23, ..., nn), genotypic value (one for each genotype), and a genotype specific "variance" (the same for each genotype). The genotype specific variance indicates whether the locus is qualitative or quantitative. A genotype specific variance of 0 indicates a locus with a "qualitative" effect, typically used as a marker locus. A genotypic variance of 1 indicates a locus with a "quantitative" effect.
  - Polygenic component. The polygenic component for parents is generated using a random deviate from a normal distribution  $N(0,1)$ . The polygenic component for children is based on the parents' breeding value (mid-parental value) and a random deviate from a normal distribution  $N(0,1)$ .
  - Common sibship environment component. The common sibship environment component assigns a single random deviate drawn from a normal distribution  $N(0,1)$  to all members of a common full sibship.
  - Covariate component (random effect). The covariate component is based on a single random deviate drawn from a normal distribution  $N(0,1)$ .
  - Trait specific environment component. A random environment component must be included with any single locus component in the specification of a trait, although different components can be paired with different single locus components. The random environment component is based on a single deviate from a normal distribution  $N(0,1)$ , and is used to specify the proportion of variation not due to the other specified components.
-

## Traits

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- A quantitative trait is produced as a normally distributed variate with mean 0 and variance 1. The user may choose to adjust the location and/or scale in the driver.
  - A qualitative trait can be generated directly as a "marker" locus or indirectly (in the driver), using a quantitative trait as an underlying genetic liability.
- 

- A trait is determined by a list of its components, with the corresponding proportion of the total phenotypic variance attributed to each.
  - Traits can share components, enabling models with pleiotropy and other complex situations.
-

## References

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IMSL Math/Library, IMSL Stat/Library 1994; Houston, Texas.

Wichura MJ. Algorithm AS241: The percentage points of the normal distribution. *Appl Statist* 1988; 37(3):477-484.

---

## Parameter Descriptions

---

<i>title</i>	Any text up to 55 characters; may be used to identify the run
<i>#_of_reps</i>	Number of separate samples to be generated
<b>unrelated</b>	Unrelated individuals generated
<b>sibship</b>	Sibships generated
<b>nuclear</b>	Nuclear families generated
<b>ceph</b>	CEPH families generated (sibship plus parents and grandparents)
<b>simple</b>	Simple pedigrees generated
<i>#_of_families</i>	Number of families in each sample (1-5000)
<i>fam_size</i>	Maximum family size, including parents ( $\geq 1$ )
<b>fixed</b>	Fixed sibship size
<b>random</b>	Randomly generated sibship size
<i>sib_size</i>	Size of sibship ( $\geq 0$ ), if fixed (if <b>family type</b> is <b>unrelated</b> , must be 0; if <b>family type</b> is <b>nuclear</b> or <b>sibship</b> , must be $fam\_size - 2$ ; if <b>family type</b> is <b>ceph</b> , must be $fam\_size - 6$ )
<i>nb_par1</i>	Negative binomial parameter 1 (1-15), if sibship size is random
<i>nb_par2</i>	Negative binomial parameter 2 ( $>0$ , $<1$ ), if sibship size is random
<i>int_seed</i>	Seed for random number generator (9-digit integer)
<i>locus_name</i>	Name for a single-locus component
<i>n_alleles</i>	Number of alleles for a particular single-locus component
<i>recomb_frac</i>	Recombination fraction between a particular single locus and the previously specified one
<i>al_i_name</i>	Name of i'th allele of a particular single locus component (1 character)
<i>al_i_freq</i>	Relative frequency of i'th allele of a particular single locus component (these must sum to 1 for a particular single locus component)

<i>gt_ij_val</i>	Genotypic value for a genotype formed by i'th and j'th alleles, for a particular single locus component
<i>gt_ij_var</i>	"Genotypic variance" for a genotype formed by i'th and j'th alleles, for a particular single locus component (0 for a locus with a "qualitative" effect, such as a marker locus, or 1 for a locus with a "quantitative" effect)
<i>env_name</i>	Name of a trait-specific environment component
<i>polygn_name</i>	Name of a polygenic component
<i>covar_name</i>	Name of a covariate component
<i>com_env_name</i>	Name of a common sibship environment component
<i>trt_name</i>	Name of a trait
<i>n_trt_cmpts</i>	Number of components involved in a particular trait
<i>trt_cmpti</i>	Name of i'th component of a particular trait (one of the component names already defined)
<i>trt_cmpti_%var</i>	Proportion of the phenotypic variance of a particular trait due to its i'th component

---

## Parameter File

---

Parameter values are specified in the G.A.S.P. parameter file. A parameter file is made up of a series of statements, each of which defines generating parameters for the simulation model. The general syntax for each statement in the parameter file is

*keyword/variable=expression;*

with:

*keyword*

a 10 character alphanumeric field (left justified)

/

a delimiter in column 11

*variable*

a 10 character alphanumeric field (left justified)

=

a delimiter in column 22

*expression*

a 10 character alphanumeric field (text strings are left justified; numerics are right justified)

Additional fields and delimiters

all subsequent fields are 10 characters in length with delimiters in columns 33, 44, 55.

;

sentence terminator

---

See also:

Parameter descriptions

Keywords and statements

Examples

---

## Keywords and Statements

---

Conventions:

**Bold** text denotes a valid keyword or delimiter.

A permissible value must be substituted for *italicized* text.

*Text* must be left justified, and *numeric values* must be right justified.

---

Columns

1 - 10    11    12 - 21    22    23 - 77

---

1) **sample** / **title** = *title*

---

Columns

1 - 10    11    12 - 21    22    23 - 32    33    34 - 43    44    45 - 54    55

---

2) **sample** / **repetition** = *#\_of\_reps;*

3) One of:

```

family / type = unrelated ;
family / type = sibship   ;
family / type = nuclear   ;
family / type = ceph     ;
family / type = simple    ;

```

4) **family** / **number** = *#\_families;*

5) **family** / **size** = *fam\_size;*

6) One of:

```

family / offspring = fixed   = sib_size;
family / offspring = random  = nb_par_1, nb_par_2;

```

7) **seed** / **autoseed** = *int\_seed;*

For each single locus component (0 - 20):

8a) **component** / **locus** = *locus\_name ;*

---

Columns

17 - 21    22    23 - 32    33

---

8b) *n\_alleles*    *recomb\_frac;*

---

Columns

21    22    23 - 32    33

---

8c)

```

al_1_name    al_1_freq;
al_2_name    al_2_freq;
al_3_name    al_3_freq;
.            .
.            .
.            .
al_n_name    al_n_freq;

```

---

Columns	1 - 10	11	12 - 21	22	23 - 32	33	34 - 43	44
---------	--------	----	---------	----	---------	----	---------	----

---

```

8d)
      gt_11_val      gt_11_var;
      gt_12_val      gt_12_var;
      .              .
      .              .
      gt_1n_val      gt_1n_var;
      gt_22_val      gt_22_var;
      gt_23_val      gt_23_var;
      .              .
      .              .
      gt_nn_val      gt_nn_var;

```

For each trait-specific environment component (0 - 3):

```

9)  component /   environmen =   env_name   ;

```

For each polygenic component (0 - 3):

```

10) component /   polygene   =   polygn_name;

```

For each covariate component (0 - 3):

```

11) component /   covariate  =   covar_name ;

```

For each common sibship environment component (0 - 3):

```

12) component /   common_env =   com_env_nam;

```

For each trait (0 - 5):

```

13a) trait      /   trt_name  =   n_trt_cmpts;

```

For each component of the trait, indicate the component with the proportion of the trait phenotypic variance due to that specific component:

```

13b)
      trt_cmpt1 * trt_cmpt1_%var+
      trt_cmpt2 * trt_cmpt2_%var+
      .         .
      .         .
      trt_cmptn * trt_cmptn_%var;

```

```

14) genotypes /   random    ;

```

```

15) end       ;

```

---

See also:

Parameter descriptions

---

## Examples

---

You can use the following sample parameter files as templates for creating new genetic models. Note that the simulated data output file format is determined by the driver.

---

### Example 1

In this example we generate a single quantitative trait due to one two-allele locus tightly linked (recombination fraction 0.05) to a two-allele marker locus. One sample of 100 nuclear families is generated. Each family has two parents and three offspring. Seventy percent of the variation in the trait is due to a single major locus, with 30% of the variation due to random effects.

See:    Example 1 input parameter file            Example 1 data output

---

### Example 2

In this example we generate a single quantitative trait due to one two-allele locus not linked to a second two-allele locus. This example is nearly identical to Example 1 except that the recombination fraction between the first and second loci is 0.50.

See:    Example 2 input parameter file            Example 2 data output

---

### Example 3

In this example we generate a single quantitative trait due to one two-allele locus tightly linked to a six-allele marker locus. One sample of 100 nuclear families is generated. Each family has two parents and three offspring. Thirty percent of the variation in the trait is due to a single major locus, with 70% of the variation due to random effects.

See:    Example 3 input parameter file            Example 3 data output

---

### Example 4

In this example we generate a quantitative trait due to a polygenic component and two two-allele loci. Each trait locus is linked to a different two-allele marker locus. One sample of 100 nuclear families is generated. Each family has two parents and three offspring. Four two-allele loci are generated in two linkage groups. Locus1 and marker1 are in the first linkage group; locus2 and marker2 are in the second. The distances between loci are: pterm - locus1 0.5; locus1 - marker1 0.05; marker1 - locus2 0.50; locus2 - marker2 0.05. Thirty percent of the variation of the trait is due to locus1, 30% to locus2 and 30% to a trait-specific random effect. The remaining 10% of the variation of the trait is due to a polygenic component.

See:    Example 4 input parameter file            Example 4 data output

---

### **Example 5**

In this example we generate two quantitative traits, each due to a different major locus, but with a common polygenic component, and different trait-specific random effects. Otherwise the model is similar to Example 4.

See:    Example 5 input parameter file            Example 5 data output

---

### **Example 6**

In this example we generate a single quantitative trait due to a random ("covariate") effect. We generate one sample of 20 simple pedigrees, each having random sibship size but a total of 30 family members.

See:    Example 6 input parameter file            Example 6 data output

---

### **Example 7**

In this example we generate three tightly linked marker loci, one of which could be used as a qualitative trait. One sample of 20 "CEPH" type pedigrees with fixed offspring size of 3 is generated.

See:    Example 7 input parameter file            Example 7 data output

---

### **Example 8**

In this example we generate a single quantitative trait due to two unlinked major loci, a polygenic component, a common sibship environment, and a trait-specific random effect. One sample of 100 random size sibships is generated.

See:    Example 8 input parameter file            Example 8 data output

---

### **Example 9**

In this example we generate a derived qualitative trait that has an underlying genetic liability that is identical to the quantitative trait generated in Example 1. The derived trait is considered to be "affected" if the normally distributed genetic liability is greater than 1.64, so that approximately 5% of the population is affected.

See:    Example 9 input parameter file            Example 9 data output

---

## Example 10

In this example we generate a single qualitative trait due to a two-allele locus which is linked to markers 4, 5, and 6. Markers 1, 2, and 3 are part of a different linkage group, as are markers 7, 8, 9, and 10. This example imitates a small "genome screen" situation.

See:    Example 10 input parameter file            Example 10 data output

---

## Example 1 Input Parameter File

---

```
sample /title =Example 01 parameter file;
sample /repetition= 1;
family /type =nuclear ;
family /number = 100;
family /size = 5;
family /offspring =fixed = 3;
seed /autoseed = 653541991;
component /locus =locus1 ;
                2 0.500;
                1 0.500;
                2 0.500;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /locus =marker1 ;
                2 0.050;
                1 0.500;
                2 0.500;
                1.0 0.000;
                2.0 0.000;
                3.0 0.000;
component /environmen=environ1 ;
trait /trait1 = 2;
                locus1 * 0.70 +
                environ1 * 0.30 ;
genotypes /random ;
end ;
```

## Example 1 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
      IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$           AID(K),AFATHR(K),
$           AMOTHR(K),SEX(K),TRAIT(1,K),
$           (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,2(2X,A2))
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Trait1	Loc 1	Mrk 1
HGAR0001	.0001				M	0.9109	12	22
HGAR0001	.0002				F	0.7074	12	12
HGAR0001	.0003	0001	0002		M	-0.0294	12	12
HGAR0001	.0004	0001	0002		F	0.6419	22	12
HGAR0001	.0005	0001	0002		F	-0.3908	12	12
HGAR0002	.0001				M	0.5491	22	22
HGAR0002	.0002				F	0.1806	12	12
HGAR0002	.0003	0001	0002		M	0.7712	22	22
HGAR0002	.0004	0001	0002		M	1.1020	22	22
HGAR0002	.0005	0001	0002		F	2.3403	22	22
HGAR0003	.0001				M	1.9709	22	12
HGAR0003	.0002				F	0.8311	12	11
HGAR0003	.0003	0001	0002		F	1.3048	22	11
HGAR0003	.0004	0001	0002		M	0.5363	12	12
HGAR0003	.0005	0001	0002		M	0.8880	12	11
.	.	.	.	.	.	.	.	.
HGAR0100	.0001				F	-0.3998	12	22
HGAR0100	.0002				M	-0.1357	12	22
HGAR0100	.0003	0002	0001		M	0.2602	12	22
HGAR0100	.0004	0002	0001		M	-1.6299	11	22
HGAR0100	.0005	0002	0001		F	-1.8823	11	22

---

## Example 2 Input Parameter File

---

```
sample /title =Example 02 parameter file;
sample /repetition= 1;
family /type =nuclear ;
family /number = 100;
family /size = 5;
family /offspring =fixed = 3;
seed /autoseed = 653541991;
component /locus =locus1 ;
                2 0.500;
                1 0.500;
                2 0.500;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /locus =marker1 ;
                2 0.500;
                1 0.500;
                2 0.500;
                1.0 0.000;
                2.0 0.000;
                3.0 0.000;
component /environmen=environ1 ;
trait /trait1 = 2;
                locus1 * 0.70 +
                environ1 * 0.30 ;
genotypes /random ;
end ;
```

## Example 2 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
      IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$          AID(K),AFATHR(K),
$          AMOTHR(K),SEX(K),TRAIT(1,K),
$          (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,2(2X,A2))
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Trait1	Loc 1	Mrk 1
HGAR0001.0001					M	0.9109	12	22
HGAR0001.0002					F	0.7074	12	12
HGAR0001.0003	0001	0002			M	-0.0294	12	12
HGAR0001.0004	0001	0002			F	0.6419	22	22
HGAR0001.0005	0001	0002			F	-0.3908	12	12
HGAR0002.0001					M	0.5491	22	22
HGAR0002.0002					F	0.1806	12	12
HGAR0002.0003	0001	0002			M	0.7712	22	12
HGAR0002.0004	0001	0002			M	1.1020	22	12
HGAR0002.0005	0001	0002			F	2.3403	22	12
HGAR0003.0001					M	1.9709	22	12
HGAR0003.0002					F	0.8311	12	11
HGAR0003.0003	0001	0002			F	1.3048	22	11
HGAR0003.0004	0001	0002			M	0.5363	12	12
HGAR0003.0005	0001	0002			M	0.8880	12	12
.								
.								
.								
HGAR0100.0001					F	-0.3998	12	22
HGAR0100.0002					M	-0.1357	12	22
HGAR0100.0003	0002	0001			M	0.2602	12	22
HGAR0100.0004	0002	0001			M	-1.6299	11	22
HGAR0100.0005	0002	0001			F	-1.8823	11	22

---

### Example 3 Input Parameter File

---

```
sample /title =Example 03 parameter file;
sample /repetition= 1;
family /type =nuclear ;
family /number = 100;
family /size = 5;
family /offspring =fixed = 3;
seed /autoseed = 854954349;
component /locus =locus1 ;
      2 0.500;
      1 0.500;
      2 0.500;
      -1.0 1.000;
      0.0 1.000;
      1.0 1.000;
component /locus =marker1 ;
      6 0.050;
      1 0.166;
      2 0.167;
      3 0.167;
      4 0.167;
      5 0.167;
      6 0.166;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
      4.0 0.000;
      5.0 0.000;
      6.0 0.000;
      7.0 0.000;
      8.0 0.000;
      9.0 0.000;
      10.0 0.000;
      11.0 0.000;
      12.0 0.000;
      13.0 0.000;
      14.0 0.000;
      15.0 0.000;
      16.0 0.000;
      17.0 0.000;
      18.0 0.000;
      19.0 0.000;
      20.0 0.000;
      21.0 0.000;
component /environmen=environ1 ;
trait /trait1 = 2;
      locus1 * 0.30 +
      environ1 * 0.70 ;
genotypes /random ;
end ;
```

### Example 3 Data Output

---

#### Relevant portion of the driver used to format the output:

```
C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
      IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$          AID(K),AFATHR(K),
$          AMOTHR(K),SEX(K),TRAIT(1,K),
$          (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,2(2X,A2))
2000 CONTINUE
C
```

---

#### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Trait1	Loc	Mrk
							1	1
HGAR0001.0001					M	-1.3131	12	34
HGAR0001.0002					F	-1.0166	11	11
HGAR0001.0003	0001	0002			F	-0.6166	11	14
HGAR0001.0004	0001	0002			F	0.7023	11	14
HGAR0001.0005	0001	0002			M	-0.1132	12	14
HGAR0002.0001					M	-0.2859	12	35
HGAR0002.0002					F	-0.5964	22	46
HGAR0002.0003	0001	0002			M	0.1079	22	34
HGAR0002.0004	0001	0002			F	-0.0209	22	34
HGAR0002.0005	0001	0002			F	-0.1779	12	45
HGAR0003.0001					F	-1.2613	11	14
HGAR0003.0002					M	0.3870	22	23
HGAR0003.0003	0002	0001			F	0.5464	12	13
HGAR0003.0004	0002	0001			M	0.6852	12	13
HGAR0003.0005	0002	0001			M	0.9881	12	24
.								
.								
.								
HGAR0100.0001					F	-2.0164	11	15
HGAR0100.0002					M	0.7886	22	13
HGAR0100.0003	0002	0001			F	0.5026	12	13
HGAR0100.0004	0002	0001			M	0.2145	12	35
HGAR0100.0005	0002	0001			F	1.5944	12	11

---

## Example 4 Input Parameter File

---

```
sample /title =Example 04 parameter file;
sample /repetition= 1;
family /type =nuclear ;
family /number = 100;
family /size = 5;
family /offspring =fixed = 3;
seed /autoseed = 983494343;
component /locus =locus1 ;
                2 0.500;
                1 0.500;
                2 0.500;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /locus =marker1 ;
                2 0.050;
                a 0.500;
                b 0.500;
                1.0 0.000;
                2.0 0.000;
                3.0 0.000;
component /locus =locus2 ;
                2 0.500;
                1 0.400;
                2 0.600;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /locus =marker2 ;
                2 0.050;
                1 0.200;
                2 0.800;
                1.0 0.000;
                2.0 0.000;
                3.0 0.000;
component /environmen=environ1 ;
component /polygene =polygene1 ;
trait /trait1 = 4;
                locus1 * 0.30 +
                locus2 * 0.30 +
                environ1 * 0.30 +
                polygene1 * 0.10 ;
genotypes /random ;
end ;
```

## Example 4 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
      IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$           AID(K),AFATHR(K),
$           AMOTHR(K),SEX(K),TRAIT(1,K),
$           (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,4(2X,A2))
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Trait1	Loc 1	Mrk 1	Loc 2	Mrk 2
HGAR0001	.0001				M	-1.2911	11	bb	12	22
HGAR0001	.0002				F	-2.2117	11	ab	12	22
HGAR0001	.0003	0001	0002		M	-0.2870	11	ab	12	22
HGAR0001	.0004	0001	0002		M	-0.6103	11	bb	12	22
HGAR0001	.0005	0001	0002		M	-1.1386	11	bb	12	22
HGAR0002	.0001				M	-0.4451	12	bb	12	22
HGAR0002	.0002				F	0.8140	22	ab	12	22
HGAR0002	.0003	0001	0002		F	-0.6141	12	bb	12	22
HGAR0002	.0004	0001	0002		F	0.1989	22	bb	12	22
HGAR0002	.0005	0001	0002		M	-0.0604	22	bb	12	22
HGAR0003	.0001				F	-0.8877	12	bb	12	22
HGAR0003	.0002				M	-1.1635	12	bb	12	11
HGAR0003	.0003	0002	0001		M	1.1905	22	bb	22	12
HGAR0003	.0004	0002	0001		F	-1.5703	12	bb	11	12
HGAR0003	.0005	0002	0001		F	1.0065	22	bb	22	12
.	.	.	.	.	.	.	.	.	.	.
HGAR0100	.0001				M	0.6577	12	ab	12	12
HGAR0100	.0002				F	-0.3348	11	ab	12	12
HGAR0100	.0003	0001	0002		F	-1.3494	12	aa	12	12
HGAR0100	.0004	0001	0002		F	-1.1099	11	ab	22	22
HGAR0100	.0005	0001	0002		M	-0.4406	11	ab	12	11

---

## Example 5 Input Parameter File

---

```

sample /title      =Example 05 parameter file;
sample /repetition=      1;
family /type       =nuclear ;
family /number     =      100;
family /size       =      5;
family /offspring  =fixed      =      3;
seed   /autoseed   = 339099325;
component /locus   =locus1    ;
                2      0.500;
                1      0.500;
                2      0.500;
                -1.0   1.000;
                0.0   1.000;
                1.0   1.000;
component /locus   =marker1   ;
                2      0.050;
                a      0.500;
                b      0.500;
                1.0   0.000;
                2.0   0.000;
                3.0   0.000;
component /locus   =locus2    ;
                2      0.500;
                1      0.400;
                2      0.600;
                -1.0   1.000;
                0.0   1.000;
                1.0   1.000;
component /locus   =marker2   ;
                2      0.050;
                1      0.200;
                2      0.800;
                1.0   0.000;
                2.0   0.000;
                3.0   0.000;
component /environmen=environ1 ;
component /environmen=environ2 ;
component /polygene  =polygene1 ;
trait   /trait1     =      3;
                locus1   *      0.60 +
                environ1 *      0.30 +
                polygene1 *      0.10 ;
trait   /trait2     =      3;
                locus2   *      0.60 +
                environ2 *      0.30 +
                polygene1 *      0.10 ;
genotypes /random   ;
end       ;

```

## Example 5 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C  WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
        IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
          $              AID(K),AFATHR(K),
          $              AMOTHR(K),SEX(K),TRAIT(1,K),TRAIT(2,K),
          $              (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2(2X,F8.4),4(2X,A2))
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Trait1	Trait2	Loc 1	Mrk 1	Loc 2	Mrk 2
HGAR0001.0001					M	-1.9089	-0.5230	11	aa	12	22
HGAR0001.0002					F	2.0260	0.7520	22	ab	22	22
HGAR0001.0003	0001	0002	0001	0002	M	0.0665	0.2720	12	aa	22	22
HGAR0001.0004	0001	0002	0001	0002	M	-0.3429	0.6231	12	ab	22	22
HGAR0001.0005	0001	0002	0001	0002	M	-0.7198	1.1154	12	ab	22	22
HGAR0002.0001					F	0.0828	-0.2218	12	ab	12	22
HGAR0002.0002					M	0.8040	-1.3143	12	aa	11	22
HGAR0002.0003	0002	0001	0002	0001	M	-1.2853	-1.4392	11	aa	11	22
HGAR0002.0004	0002	0001	0002	0001	F	-0.5099	-0.2010	11	aa	12	22
HGAR0002.0005	0002	0001	0002	0001	M	-1.3242	-1.1832	11	aa	11	22
HGAR0003.0001					F	1.5775	-0.3355	22	aa	12	22
HGAR0003.0002					M	0.7117	-0.2974	22	bb	12	22
HGAR0003.0003	0002	0001	0002	0001	M	0.9406	-0.0072	22	ab	12	22
HGAR0003.0004	0002	0001	0002	0001	M	0.5145	-0.3021	22	ab	12	22
HGAR0003.0005	0002	0001	0002	0001	F	0.1743	-1.7199	22	ab	11	22
.											
.											
.											
HGAR0100.0001					M	-0.6415	-0.0935	11	ab	12	22
HGAR0100.0002					F	-1.3604	0.3362	11	aa	12	22
HGAR0100.0003	0001	0002	0001	0002	F	-0.8261	1.2460	11	ab	22	22
HGAR0100.0004	0001	0002	0001	0002	M	-0.2311	0.3982	11	ab	12	22
HGAR0100.0005	0001	0002	0001	0002	F	-1.8120	-1.6442	11	aa	11	22

---

## Example 6 Input Parameter File

---

```
sample /title =Example 06 parameter file;
sample /repetition= 1;
family /type =simple ;
family /number = 20;
family /size = 30;
family /offspring =random = 6; 0.5;
seed /autoseed = 126454643;
component /covariate =covar1 ;
trait /trait1 = 1;
covar1 * 1.00 ;
genotypes /random ;
end ;
```

## Example 6 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
      IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$      AID(K),AFATHR(K),
$      AMOTHR(K),SEX(K),TRAIT(1,K)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4)
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy	Fam	Ind	Fath	Moth	Sex	Trait1
ID	ID	ID	ID	ID		
HGAR0001.0001					M	0.6764
HGAR0001.0002					F	0.2862
HGAR0001.0003	0001	0002			M	-0.1761
HGAR0001.0004	0001	0002			F	1.1633
HGAR0001.0005	0001	0002			F	-0.1741
HGAR0001.0006	0001	0002			F	-0.3805
HGAR0001.0007	0001	0002			M	-0.3604
HGAR0001.0008	0001	0002			M	-0.9739
HGAR0001.0009					F	-2.0438
HGAR0001.0010	0003	0009			F	-0.3717
HGAR0001.0011	0003	0009			M	0.2541
HGAR0001.0012	0003	0009			M	1.8231
HGAR0001.0013	0003	0009			F	-0.9221
HGAR0001.0014	0003	0009			F	0.6878
HGAR0001.0015					M	-0.6825
HGAR0001.0016	0015	0004			F	1.8793
HGAR0001.0017	0015	0004			M	-1.1088
HGAR0001.0018	0015	0004			F	-0.9839
HGAR0001.0019	0015	0004			F	0.3980
HGAR0001.0020	0015	0004			F	0.0782
HGAR0001.0021					M	0.0435
HGAR0001.0022	0021	0005			M	-1.1269
HGAR0001.0023	0021	0005			M	1.9858
HGAR0001.0024	0021	0005			F	0.1266
HGAR0001.0025					M	1.0161
HGAR0001.0026	0025	0006			M	0.2495
HGAR0001.0027	0025	0006			M	-1.2983
HGAR0001.0028	0025	0006			M	0.8855
HGAR0001.0029	0025	0006			M	-0.8371
HGAR0001.0030					F	0.0011
HGAR0002.0001					M	0.5253
HGAR0002.0002					F	-0.2972
HGAR0002.0003	0001	0002			F	0.9118

HGAR0002.0004			M	-2.0559
HGAR0002.0005	0004	0003	M	-0.2873
HGAR0002.0006	0004	0003	F	-0.4886
HGAR0002.0007	0004	0003	M	-0.1338
HGAR0002.0008	0004	0003	F	-0.4962
HGAR0002.0009	0004	0003	F	1.8437
HGAR0002.0010	0004	0003	M	1.3356
HGAR0002.0011	0004	0003	M	-0.9500
HGAR0002.0012	0004	0003	M	2.0017
HGAR0002.0013			F	-0.9092
HGAR0002.0014	0005	0013	F	0.3466
HGAR0002.0015	0005	0013	F	0.4088
HGAR0002.0016	0005	0013	F	-0.9141
HGAR0002.0017	0005	0013	M	0.3534
HGAR0002.0018			M	1.2632
HGAR0002.0019	0018	0006	F	0.4063
HGAR0002.0020	0018	0006	F	-0.1848
HGAR0002.0021	0018	0006	F	-1.0575
HGAR0002.0022	0018	0006	M	-0.7292
HGAR0002.0023	0018	0006	F	-2.1031
HGAR0002.0024	0018	0006	F	2.1409
HGAR0002.0025	0018	0006	F	0.6179
HGAR0002.0026			F	-0.1149
HGAR0002.0027	0007	0026	M	2.0792
HGAR0002.0028	0007	0026	M	-2.6850
HGAR0002.0029	0007	0026	F	1.5919
HGAR0002.0030	0007	0026	M	0.8669

.  
.  
.

HGAR0020.0001			F	0.0993
HGAR0020.0002			M	1.6003
HGAR0020.0003	0002	0001	M	0.2881
HGAR0020.0004	0002	0001	M	0.8480
HGAR0020.0005			F	-0.4101
HGAR0020.0006	0003	0005	M	0.3416
HGAR0020.0007	0003	0005	F	1.2067
HGAR0020.0008	0003	0005	M	0.5074
HGAR0020.0009			F	-0.2477
HGAR0020.0010	0004	0009	F	0.1264
HGAR0020.0011	0004	0009	M	0.3005
HGAR0020.0012	0004	0009	F	-0.6355
HGAR0020.0013			F	0.5716
HGAR0020.0014	0006	0013	M	-0.7612
HGAR0020.0015	0006	0013	F	-0.0125
HGAR0020.0016	0006	0013	F	-2.2039
HGAR0020.0017	0006	0013	M	-0.2877
HGAR0020.0018	0006	0013	F	-0.0784
HGAR0020.0019	0006	0013	F	-0.7776
HGAR0020.0020	0006	0013	M	0.7789
HGAR0020.0021	0006	0013	M	0.1566
HGAR0020.0022			M	1.5712
HGAR0020.0023	0022	0007	M	-1.5038
HGAR0020.0024	0022	0007	F	0.2803
HGAR0020.0025			F	0.0095
HGAR0020.0026	0008	0025	M	-1.2986

HGAR0020.0027	0008	0025	M	1.9520
HGAR0020.0028	0008	0025	F	1.6251
HGAR0020.0029	0008	0025	F	1.3291
HGAR0020.0030	0008	0025	F	-0.9394

---

## Example 7 Input Parameter File

---

```
sample /title =Example 07 parameter file;
sample /repetition= 1;
family /type =ceph ;
family /number = 20;
family /size = 9;
family /offspring =fixed = 3;
seed /autoseed = 675748543;
component /locus =marker1 ;
      2 0.500;
      1 0.500;
      2 0.500;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
component /locus =qualtrait ;
      2 0.050;
      A 0.500;
      a 0.500;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
component /locus =marker2 ;
      2 0.050;
      1 0.200;
      2 0.800;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
genotypes /random ;
end ;
```

## Example 7 Data Output

---

### Relevant portion of the driver used to format the output:

```

C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
          IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$              AID(K),AFATHR(K),
$              AMOTHR(K),SEX(K),
$              (GENTYP(I,K),I=1,NUMLOC)
9010          FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,3(3X,A2))
2000 CONTINUE
C

```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Mrk 1	Qual trt	Mrk 2
HGAR0001.0001					M	22	aa	12
HGAR0001.0002					F	22	Aa	12
HGAR0001.0003	0001	0002			F	22	aa	12
HGAR0001.0004					F	22	aa	22
HGAR0001.0005					M	22	aa	22
HGAR0001.0006	0005	0004			M	22	aa	22
HGAR0001.0007	0006	0003			M	22	aa	12
HGAR0001.0008	0006	0003			F	22	aa	12
HGAR0001.0009	0006	0003			M	22	aa	22
HGAR0002.0001					F	11	AA	22
HGAR0002.0002					M	12	aa	22
HGAR0002.0003	0002	0001			M	11	Aa	22
HGAR0002.0004					F	12	Aa	22
HGAR0002.0005					M	12	aa	22
HGAR0002.0006	0005	0004			F	22	Aa	22
HGAR0002.0007	0003	0006			F	12	Aa	22
HGAR0002.0008	0003	0006			M	12	AA	22
HGAR0002.0009	0003	0006			M	12	Aa	22
HGAR0003.0001					M	12	Aa	22
HGAR0003.0002					F	12	Aa	22
HGAR0003.0003	0001	0002			M	12	AA	22
HGAR0003.0004					F	22	AA	22
HGAR0003.0005					M	12	Aa	22
HGAR0003.0006	0005	0004			F	12	Aa	22
HGAR0003.0007	0003	0006			F	11	Aa	22
HGAR0003.0008	0003	0006			M	12	Aa	22
HGAR0003.0009	0003	0006			M	22	AA	22
.								
.								
.								
HGAR0020.0001					F	11	Aa	12

HGAR0020.0002			M	11	aa	22
HGAR0020.0003	0002	0001	M	11	aa	22
HGAR0020.0004			F	12	Aa	22
HGAR0020.0005			M	12	Aa	12
HGAR0020.0006	0005	0004	F	12	Aa	12
HGAR0020.0007	0003	0006	F	11	Aa	22
HGAR0020.0008	0003	0006	F	11	Aa	22
HGAR0020.0009	0003	0006	F	11	Aa	22

---

## Example 8 Input Parameter File

---

```
sample /title =Example 08 parameter file;
sample /repetition= 1;
family /type =sibship ;
family /number = 100;
family /offspring =random = 5; 0.3;
seed /autoseed = 398934359;
component /locus =locus1 ;
                2 0.500;
                1 0.500;
                2 0.500;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /locus =locus2 ;
                2 0.500;
                1 0.400;
                2 0.600;
                -1.0 1.000;
                0.0 1.000;
                1.0 1.000;
component /environmen=environ1 ;
component /polygene =polygene1 ;
trait /trait1 = 4;
                locus1 * 0.30 +
                locus2 * 0.30 +
                environ1 * 0.30 +
                polygene1 * 0.10 ;
genotypes /random ;
end ;
```

## Example 8 Data Output

---

### Relevant portion of the driver used to format the output:

```
C
C  WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
        IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
          $           AID(K),AFATHR(K),
          $           AMOTHR(K),SEX(K),TRAIT(1,K),
          $           (GENTYP(I,K),I=1,NUMLOC)
9010      FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,2(2X,A2))
2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy	Fam	Ind	Fath	Moth	Sex	Trait1	Loc	Loc
ID	ID	ID	ID	ID			1	2
HGAR0001	.0003	0002	0001	F	-0.3452	11	22	
HGAR0001	.0004	0002	0001	F	-1.0439	12	12	
HGAR0001	.0005	0002	0001	M	-1.7702	11	12	
HGAR0001	.0006	0002	0001	F	0.2152	11	12	
HGAR0001	.0007	0002	0001	M	-1.8323	12	11	
HGAR0002	.0003	0002	0001	M	1.3952	22	22	
HGAR0002	.0004	0002	0001	F	1.0232	22	22	
HGAR0003	.0003	0002	0001	F	2.1337	22	22	
HGAR0004	.0003	0002	0001	M	0.7013	22	12	
HGAR0005	.0003	0001	0002	M	-3.1718	11	11	
HGAR0006	.0003	0001	0002	M	1.3672	22	12	
HGAR0006	.0004	0001	0002	M	-0.5096	12	12	
HGAR0006	.0005	0001	0002	M	-0.1851	22	12	
HGAR0007	.0003	0001	0002	M	0.5323	12	12	
HGAR0007	.0004	0001	0002	F	-0.2258	12	12	
.	.	.	.	.	.	.	.	.
HGAR0099	.0003	0001	0002	F	-0.0481	11	12	
HGAR0099	.0004	0001	0002	F	-2.1032	11	11	
HGAR0099	.0005	0001	0002	F	-1.9879	11	11	
HGAR0100	.0003	0002	0001	M	0.6616	11	22	
HGAR0100	.0004	0002	0001	F	-0.1041	12	12	

---

## Example 9 Input Parameter File

---

```
sample /title =Example 09 parameter file;
sample /repetition= 1;
family /type =nuclear ;
family /number = 100;
family /size = 5;
family /offspring =fixed = 3;
seed /autoseed = 653541991;
component /locus =locus1 ;
          2 0.500;
          1 0.500;
          2 0.500;
          -1.0 1.000;
          0.0 1.000;
          1.0 1.000;
component /locus =marker1 ;
          2 0.050;
          1 0.500;
          2 0.500;
          1.0 0.000;
          2.0 0.000;
          3.0 0.000;
component /environmen=environ1 ;
trait /liability = 2;
          locus1 * 0.70 +
          environ1 * 0.30 ;
genotypes /random ;
end ;
```

## Example 9 Data Output

---

### Relevant portion of the driver used to format the output:

```
C LOCAL DECLARATIONS
C
C     CHARACTER*3      AFFSTAT
C
C
C
C
C WRITE THE SAMPLE INTO A FILE
C
C     DO 2000, K = 1, P
C
C         IF (TRAIT(1,K) .GE. 1.64) THEN
C             AFFSTAT = 'AFF'
C         ELSE
C             AFFSTAT = 'NOR'
C         ENDIF
C
C         IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
C             $             AID(K),AFATHR(K),
C             $             AMOTHR(K),SEX(K),TRAIT(1,K),AFFSTAT,
C             $             (GENTYP(I,K),I=1,NUMLOC)
C 9010     FORMAT (A4,A4,'.',A4,2(1X,A4),1X,A1,2X,F8.4,2X,A3,2(2X,A2))
C 2000 CONTINUE
C
```

---

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Liablty	Qual trt	Loc 1	Mrk 1
HGAR0001	.0001				M	0.9109	NOR	12	22
HGAR0001	.0002				F	0.7074	NOR	12	12
HGAR0001	.0003	0001	0002		M	-0.0294	NOR	12	12
HGAR0001	.0004	0001	0002		F	0.6419	NOR	22	12
HGAR0001	.0005	0001	0002		F	-0.3908	NOR	12	12
HGAR0002	.0001				M	0.5491	NOR	22	22
HGAR0002	.0002				F	0.1806	NOR	12	12
HGAR0002	.0003	0001	0002		M	0.7712	NOR	22	22
HGAR0002	.0004	0001	0002		M	1.1020	NOR	22	22
HGAR0002	.0005	0001	0002		F	2.3403	AFF	22	22
HGAR0003	.0001				M	1.9709	AFF	22	12
HGAR0003	.0002				F	0.8311	NOR	12	11
HGAR0003	.0003	0001	0002		F	1.3048	NOR	22	11
HGAR0003	.0004	0001	0002		M	0.5363	NOR	12	12
HGAR0003	.0005	0001	0002		M	0.8880	NOR	12	11
.	.	.	.	.	.	.	.	.	.

HGAR0100.0001			F	-0.3998	NOR	12	22
HGAR0100.0002			M	-0.1357	NOR	12	22
HGAR0100.0003	0002	0001	M	0.2602	NOR	12	22
HGAR0100.0004	0002	0001	M	-1.6299	NOR	11	22
HGAR0100.0005	0002	0001	F	-1.8823	NOR	11	22

---

## Example 10 Input Parameter File

---

```
sample /title =Example 10 parameter file;
sample /repetition= 1;
family /type =simple ;
family /number = 20;
family /size = 30;
family /offspring =random = 7; 0.4;
seed /autoseed = 324776834;
component /locus =marker1 ;
      4 0.500;
      1 0.250;
      2 0.250;
      3 0.250;
      4 0.250;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
      4.0 0.000;
      5.0 0.000;
      6.0 0.000;
      7.0 0.000;
      8.0 0.000;
      9.0 0.000;
      10.0 0.000;
component /locus =marker2 ;
      4 0.100;
      1 0.250;
      2 0.250;
      3 0.250;
      4 0.250;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
      4.0 0.000;
      5.0 0.000;
      6.0 0.000;
      7.0 0.000;
      8.0 0.000;
      9.0 0.000;
      10.0 0.000;
component /locus =marker3 ;
      4 0.050;
      1 0.250;
      2 0.250;
      3 0.250;
      4 0.250;
      1.0 0.000;
      2.0 0.000;
      3.0 0.000;
      4.0 0.000;
      5.0 0.000;
      6.0 0.000;
      7.0 0.000;
      8.0 0.000;
```

```

          9.0      0.000;
          10.0     0.000;
component /locus   =marker4   ;
          4      0.500;
          1      0.250;
          2      0.250;
          3      0.250;
          4      0.250;
          1.0    0.000;
          2.0    0.000;
          3.0    0.000;
          4.0    0.000;
          5.0    0.000;
          6.0    0.000;
          7.0    0.000;
          8.0    0.000;
          9.0    0.000;
          10.0   0.000;
component /locus   =marker5   ;
          4      0.100;
          1      0.250;
          2      0.250;
          3      0.250;
          4      0.250;
          1.0    0.000;
          2.0    0.000;
          3.0    0.000;
          4.0    0.000;
          5.0    0.000;
          6.0    0.000;
          7.0    0.000;
          8.0    0.000;
          9.0    0.000;
          10.0   0.000;
component /locus   =qualtrait ;
          2      0.010;
          A      0.500;
          a      0.500;
          1.0    0.000;
          2.0    0.000;
          3.0    0.000;
component /locus   =marker6   ;
          4      0.050;
          1      0.250;
          2      0.250;
          3      0.250;
          4      0.250;
          1.0    0.000;
          2.0    0.000;
          3.0    0.000;
          4.0    0.000;
          5.0    0.000;
          6.0    0.000;
          7.0    0.000;
          8.0    0.000;
          9.0    0.000;
          10.0   0.000;

```

```

component /locus      =marker7      ;
    4      0.500;
    1      0.250;
    2      0.250;
    3      0.250;
    4      0.250;
    1.0    0.000;
    2.0    0.000;
    3.0    0.000;
    4.0    0.000;
    5.0    0.000;
    6.0    0.000;
    7.0    0.000;
    8.0    0.000;
    9.0    0.000;
    10.0   0.000;
component /locus      =marker8      ;
    4      0.050;
    1      0.250;
    2      0.250;
    3      0.250;
    4      0.250;
    1.0    0.000;
    2.0    0.000;
    3.0    0.000;
    4.0    0.000;
    5.0    0.000;
    6.0    0.000;
    7.0    0.000;
    8.0    0.000;
    9.0    0.000;
    10.0   0.000;
component /locus      =marker9      ;
    4      0.100;
    1      0.250;
    2      0.250;
    3      0.250;
    4      0.250;
    1.0    0.000;
    2.0    0.000;
    3.0    0.000;
    4.0    0.000;
    5.0    0.000;
    6.0    0.000;
    7.0    0.000;
    8.0    0.000;
    9.0    0.000;
    10.0   0.000;
component /locus      =marker10     ;
    4      0.100;
    1      0.250;
    2      0.250;
    3      0.250;
    4      0.250;
    1.0    0.000;
    2.0    0.000;
    3.0    0.000;

```

```
4.0      0.000;  
5.0      0.000;  
6.0      0.000;  
7.0      0.000;  
8.0      0.000;  
9.0      0.000;  
10.0     0.000;  
genotypes /random ;  
end      ;
```

## Example 10 Data Output

### Relevant portion of the driver used to format the output:

```

C
C WRITE THE SAMPLE INTO A FILE
C
      DO 2000, K = 1, P
          IF (INCLUD(K)) WRITE (OUTPT2,9010) STDCDE(K),AFNUM(K),
$              AID(K),AFATHR(K),
$              AMOTHR(K),SEX(K),
$              (GENTYP(I,K),I=1,NUMLOC)
9010  FORMAT (A4,A4,'.',A4,2(1X,A4),2X,A1,1X,6(2X,A2),1X,5(2X,A2))
2000  CONTINUE
C

```

### Simulated data (annotated):

Stdy ID	Fam ID	Ind ID	Fath ID	Moth ID	Sex	Mrk 1	Mrk 2	Mrk 3	Mrk 4	Mrk 5	Qual trt	Mrk 6	Mrk 7	Mrk 8	Mrk 9	Mrk 10
HGAR0001.0001					F	44	12	22	24	34	AA	33	12	23	12	24
HGAR0001.0002					M	12	22	34	34	24	Aa	13	23	33	23	12
HGAR0001.0003	0002	0001			M	14	22	23	34	44	AA	13	22	33	23	12
HGAR0001.0004	0002	0001			M	14	12	23	23	34	AA	13	22	33	23	12
HGAR0001.0005	0002	0001			F	24	22	23	34	44	AA	13	22	33	23	12
HGAR0001.0006	0002	0001			F	14	22	23	24	23	Aa	33	13	23	22	24
HGAR0001.0007	0002	0001			F	24	12	24	24	44	AA	13	13	23	12	24
HGAR0001.0008	0002	0001			F	24	22	24	34	44	AA	13	23	33	22	22
HGAR0001.0009	0002	0001			F	14	12	23	34	34	AA	13	23	33	22	22
HGAR0001.0010					F	34	12	34	24	13	aa	22	14	23	23	44
HGAR0001.0011	0003	0010			F	13	22	34	23	34	Aa	23	24	23	33	14
HGAR0001.0012	0003	0010			M	14	12	23	34	14	Aa	23	24	23	23	14
HGAR0001.0013	0003	0010			M	34	12	24	23	34	Aa	12	12	23	23	14
HGAR0001.0014	0003	0010			F	44	12	23	34	14	Aa	12	12	33	33	14
HGAR0001.0015					F	34	33	14	33	14	Aa	12	23	11	22	13
HGAR0001.0016	0004	0015			M	13	13	13	23	13	AA	23	22	13	23	11
HGAR0001.0017	0004	0015			M	34	13	12	23	13	AA	23	22	13	23	11
HGAR0001.0018	0004	0015			F	14	23	34	33	44	Aa	11	22	13	22	12
HGAR0001.0019	0004	0015			M	13	23	13	33	14	AA	12	22	13	23	11
HGAR0001.0020	0004	0015			F	34	13	12	33	14	AA	12	22	13	22	12
HGAR0001.0021					M	22	33	34	34	33	AA	22	12	13	22	44
HGAR0001.0022	0021	0005			M	22	23	24	33	34	AA	12	22	33	22	24
HGAR0001.0023					M	12	44	14	14	44	aa	24	14	14	24	44
HGAR0001.0024	0023	0006			M	12	24	12	12	34	Aa	34	11	24	22	44
HGAR0001.0025					M	34	22	23	23	13	Aa	13	11	11	14	13
HGAR0001.0026	0025	0007			F	34	12	22	22	14	Aa	33	11	12	12	23
HGAR0001.0027	0025	0007			M	24	22	34	24	34	AA	13	11	12	11	34
HGAR0001.0028	0025	0007			M	23	22	24	24	14	Aa	13	13	13	12	23
HGAR0001.0029	0025	0007			M	24	22	34	34	14	Aa	13	13	13	24	12
HGAR0001.0030					M	13	33	44	34	22	Aa	24	13	44	14	24
HGAR0002.0001					M	12	33	14	33	13	aa	14	23	24	44	34
HGAR0002.0002					F	12	13	34	23	13	Aa	23	23	12	33	33
HGAR0002.0003	0001	0002			M	12	13	44	23	13	Aa	34	23	24	34	34
HGAR0002.0004	0001	0002			M	12	33	13	33	33	Aa	13	33	12	34	33
HGAR0002.0005	0001	0002			M	11	33	34	23	13	aa	12	33	12	34	33

HGAR0002.0006	0001	0002	F	11	33	13	23	11	aa	24	23	14	34	34
HGAR0002.0007	0001	0002	F	12	33	13	33	13	Aa	34	33	12	34	33
HGAR0002.0008			F	24	24	14	11	13	Aa	14	22	24	23	14
HGAR0002.0009	0003	0008	M	24	14	14	12	13	AA	34	23	24	24	44
HGAR0002.0010	0003	0008	F	24	14	14	13	13	aa	13	22	22	23	34
HGAR0002.0011	0003	0008	M	14	14	14	13	11	Aa	14	22	22	23	13
HGAR0002.0012			F	13	11	34	11	24	AA	22	33	12	12	14
HGAR0002.0013	0004	0012	M	11	13	33	13	34	Aa	12	33	22	14	13
HGAR0002.0014	0004	0012	F	13	13	14	13	34	Aa	12	33	12	13	34
HGAR0002.0015	0004	0012	F	12	13	13	13	23	AA	23	33	22	24	13
HGAR0002.0016	0004	0012	F	13	13	34	13	23	Aa	12	33	12	24	34
HGAR0002.0017	0004	0012	M	23	13	14	13	34	AA	12	33	12	24	34
HGAR0002.0018	0004	0012	F	11	13	34	13	34	AA	23	33	22	14	13
HGAR0002.0019	0004	0012	F	11	13	33	13	34	AA	23	33	12	24	34
HGAR0002.0020			F	12	11	22	34	34	aa	23	12	24	14	14
HGAR0002.0021	0005	0020	M	11	13	24	33	14	aa	22	13	24	14	13
HGAR0002.0022	0005	0020	F	11	13	24	24	13	aa	23	13	14	34	34
HGAR0002.0023	0005	0020	M	11	13	23	33	33	aa	13	23	12	13	13
HGAR0002.0024	0005	0020	M	11	13	23	33	34	aa	12	13	14	34	13
HGAR0002.0025	0005	0020	M	11	13	23	34	13	aa	22	13	24	44	34
HGAR0002.0026			M	13	22	33	23	22	AA	22	24	23	14	12
HGAR0002.0027	0026	0006	M	13	23	13	33	12	Aa	24	22	24	44	24
HGAR0002.0028	0026	0006	M	13	23	13	22	12	Aa	22	23	12	34	24
HGAR0002.0029	0026	0006	M	13	23	13	23	12	Aa	24	24	34	13	13
HGAR0002.0030	0026	0006	M	13	23	13	23	12	Aa	22	23	12	44	24

.

.

.

HGAR0020.0001			M	22	13	22	13	24	Aa	33	34	33	14	13
HGAR0020.0002			F	11	13	34	24	14	Aa	13	23	24	23	24
HGAR0020.0003	0001	0002	M	12	13	24	12	24	Aa	13	23	23	24	23
HGAR0020.0004	0001	0002	M	12	11	24	12	44	AA	13	33	23	34	14
HGAR0020.0005	0001	0002	F	12	33	23	23	24	Aa	13	23	23	24	12
HGAR0020.0006	0001	0002	M	12	33	23	12	44	AA	13	24	23	24	12
HGAR0020.0007	0001	0002	F	12	33	23	12	44	AA	33	33	34	34	14
HGAR0020.0008	0001	0002	M	12	33	23	12	44	AA	13	23	23	24	12
HGAR0020.0009			F	14	14	24	34	24	Aa	23	11	12	22	34
HGAR0020.0010	0003	0009	F	11	13	44	23	44	Aa	13	12	12	24	24
HGAR0020.0011	0003	0009	F	24	14	22	13	24	aa	33	13	13	24	33
HGAR0020.0012			F	13	14	44	11	34	Aa	44	22	22	44	23
HGAR0020.0013	0004	0012	F	11	11	44	12	44	AA	14	23	23	44	12
HGAR0020.0014	0004	0012	M	23	14	24	12	44	AA	14	23	22	34	24
HGAR0020.0015	0004	0012	M	11	11	44	11	34	Aa	34	23	22	34	13
HGAR0020.0016	0004	0012	M	23	14	24	11	34	Aa	34	23	23	44	24
HGAR0020.0017	0004	0012	M	13	14	44	11	34	Aa	34	23	23	34	24
HGAR0020.0018			M	44	11	11	13	14	Aa	22	13	33	24	12
HGAR0020.0019	0018	0005	M	14	13	13	23	44	AA	12	33	33	44	11
HGAR0020.0020	0018	0005	F	14	13	12	12	14	Aa	12	12	23	22	22
HGAR0020.0021			F	23	14	13	24	23	aa	34	12	12	34	12
HGAR0020.0022	0006	0021	M	23	34	23	12	24	Aa	34	24	22	23	12
HGAR0020.0023			M	33	34	23	34	44	Aa	23	12	13	24	44
HGAR0020.0024	0023	0007	M	13	34	33	24	44	Aa	33	13	14	24	14
HGAR0020.0025			F	12	14	12	44	34	aa	24	24	12	13	34
HGAR0020.0026	0008	0025	M	12	13	12	24	34	Aa	14	34	23	34	13
HGAR0020.0027	0008	0025	M	12	34	23	14	34	Aa	34	22	12	12	23
HGAR0020.0028	0008	0025	M	12	13	23	24	34	Aa	14	24	22	23	13
HGAR0020.0029			M	33	24	44	24	14	aa	22	12	33	13	34
HGAR0020.0030	0029	0010	M	13	23	44	34	44	aa	23	12	23	14	24

## Variable and Array Descriptions

### PARAMETERS

Type	Parameter Value	Description
INTEGER	MXPMSN = 5000	Maximum # of persons (individuals) per sample
INTEGER	MAXLOC = 20	Maximum # of single loci
INTEGER	MAXALL = 12	Maximum # of alleles at a given locus
INTEGER	MAXGEN = 78	Maximum # of genotypes at a locus
INTEGER	MAXCPN = 32	Maximum # of components
INTEGER	MAXPGT = 3	Maximum # of polygenotype components
INTEGER	MAXGSE = 3	Maximum # of trait specific environment components
INTEGER	MAXCSE = 3	Maximum # of common sibship environment components
INTEGER	MAXCOV = 3	Maximum # of covariates
INTEGER	MAXTRT = 5	Maximum # of traits
CHARACTER*5	VRSION = 3.30	Version number

### EXTERNAL MODULES (use IMSL or PRNG)

RNOPT	Set random number generator option
RNISD	Skip 100,000 random numbers to reset generator seed
RNSET	Set random number generator seed
RNGET	Get random number generator seed
DRNUN	Uniform random number generator
RNNBN	Negative binomial random number generator
DRNNOR	Normal random number generator
UMACH	Set I/O unit

### GLOBAL VARIABLES AND ARRAYS

Type	Variable/Array	Description
INTEGER	INPUT	Logical unit for input
INTEGER	OUTPT1	Logical unit for G.A.S.P. summary output
INTEGER	NALLEL(1:MAXLOC)	Number of alleles for each locus (input)
INTEGER	NGTYPE(1:MAXLOC)	Number of genotypes for each locus
DOUBLE PRECISION	THETA(1:MAXLOC)	Recombination fractions (input)
DOUBLE PRECISION	AFREQ(1:MAXALL,1:MAXLOC)	Allele frequencies (input)
DOUBLE PRECISION	GFREQ(1:MAXGEN,1:MAXLOC)	Genotypic frequencies (derived)
DOUBLE PRECISION	GMEAN(1:MAXGEN,1:MAXLOC)	Genotypic means (input)
DOUBLE PRECISION	GVAR(1:MAXGEN,1:MAXLOC)	Genotypic variances (input)
DOUBLE PRECISION	CUMGFQ(1:MAXGEN,1:MAXLOC)	Cumulative genotypic frequencies (derived)
DOUBLE PRECISION	CPNPOV(1:MAXCPN,1:MAXTRT)	Proportion of variance for each component (input)
DOUBLE PRECISION	KI(1:MAXLOC,1:MAXTRT)	Weight for each single locus
DOUBLE PRECISION	MEAN(1:MAXTRT)	Overall means for single locus components
DOUBLE PRECISION	KE(1:MAXTRT)	Overall weights for single locus components
CHARACTER*10	LOCNAM(1:MAXLOC)	Locus names (input)
CHARACTER*1	ALLELE(1:MAXALL,1:MAXLOC)	Allele names (input)
CHARACTER*2	GTYPE(1:MAXGEN,1:MAXLOC)	Genotype "names" (derived from alleles)
CHARACTER*10	CPNLST(1:MAXCPN)	Component names
CHARACTER*10	PGTNAM(1:MAXPGT)	Polygenotype names (input)
CHARACTER*10	GSENAM(1:MAXGSE)	Trait specific environment names (input)
CHARACTER*10	CSENAM(1:MAXCSE)	Common sibship environment component names (input)
CHARACTER*10	COVNAM(1:MAXCOV)	Covariate names (input)
CHARACTER*10	TRTNAM(1:MAXTRT)	Trait names (input)
CHARACTER*10	CPNNAM(1:MAXCPN,1:MAXTRT)	Component names for each trait

DOUBLE PRECISION	LOCPOV(1:MAXLOC,1:MAXTRT)	Proportions of variance - single locus
DOUBLE PRECISION	PGTPOV(1:MAXPGT,1:MAXTRT)	Proportions of variance - polygene
DOUBLE PRECISION	GSEPOV(1:MAXGSE,1:MAXTRT)	Proportions of variance - trait specific environment
DOUBLE PRECISION	CSEPOV(1:MAXCSE,1:MAXTRT)	Proportions of variance - common sibship environment
DOUBLE PRECISION	COVPOV(1:MAXCOV,1:MAXTRT)	Proportions of variance - covariate
DOUBLE PRECISION	QVAL(1:MAXLOC,1:MXPRSN)	Quantitative phenotype for each individual's genotype
DOUBLE PRECISION	QNTTYP(1:MAXLOC,1:MXPRSN)	Polygenotype values
DOUBLE PRECISION	PGTTYP(1:MAXPGT,1:MXPRSN)	Common sibship environment values
DOUBLE PRECISION	CSETYP(1:MAXCSE,1:MXPRSN)	Covariate values
DOUBLE PRECISION	COVTYP(1:MAXCOV,1:MXPRSN)	Cumulative quantitative phenotypes
DOUBLE PRECISION	CUMQNT(1:MAXTRT,1:MXPRSN)	Cumulative polygenotype values
DOUBLE PRECISION	CUMPGT(1:MAXTRT,1:MXPRSN)	Cumulative common sibship environment values
DOUBLE PRECISION	CUMCSE(1:MAXTRT,1:MXPRSN)	Cumulative covariate values
DOUBLE PRECISION	CUMCOV(1:MAXTRT,1:MXPRSN)	Trait values
DOUBLE PRECISION	TRAIT(1:MAXTRT,1:MXPRSN)	Trait specific random deviates
DOUBLE PRECISION	RNDEV(1:MAXTRT,1:MXPRSN)	
INTEGER	FNUM(1:MXPRSN)	Family numbers
INTEGER	ID(1:MXPRSN)	Individual IDs
INTEGER	FATHR(1:MXPRSN)	Father IDs
INTEGER	MOTHR(1:MXPRSN)	Mother IDs
INTEGER	PREL(1:MXPRSN)	Rel numbers
INTEGER	PMATE(1:MXPRSN)	Mate pointers
INTEGER	PMR(1:MXPRSN)	Multiple record pointers
INTEGER	POFF(1:MXPRSN)	Offspring pointers
INTEGER	PSIB(1:MXPRSN)	Sib pointers
INTEGER	PFATH(1:MXPRSN)	Father pointers
INTEGER	PMOTH(1:MXPRSN)	Mother pointers
INTEGER	AGE(1:MXPRSN)	Reserved for future use
LOGICAL	INCLUD(1:MXPRSN)	Inclusion status
CHARACTER*4	STDCDE(1:MXPRSN)	Study codes
CHARACTER*4	AFNUM(1:MXPRSN)	Family numbers (character version)
CHARACTER*4	AID(1:MXPRSN)	Individual IDs (character version)
CHARACTER*4	AFATHR(1:MXPRSN)	Father IDs (character version)
CHARACTER*4	AMOTHR(1:MXPRSN)	Mother IDs (character version)
CHARACTER*1	SEX(1:MXPRSN)	Sex (male = M, female = F)
CHARACTER*2	LOCUS(1:MAXLOC,1:MXPRSN)	Genetic components - locus line
CHARACTER*2	GENTYP(1:MAXLOC,1:MXPRSN)	Switched qualitative phenotypes for the locus line
INTEGER	IOPT	Option for random number generator
INTEGER	AGSEED	Reserved for future use
INTEGER	SXSEED	Sex seed
INTEGER	OFSEED	Offspring size seed
INTEGER	GTSEED(0:MAXLOC)	Genotype seeds
INTEGER	GSEED	Trait specific environment seed
INTEGER	CHSEED	Chromatid seed
INTEGER	XOSEED	Crossover seed
INTEGER	PHSEED	Phenotype seed
INTEGER	PGSEED	Polygenotype seeds
INTEGER	CSEED	Common sibship environment seed
INTEGER	COVSD	Covariate seed
CHARACTER*6	ERRSUB	Subroutine where error occurs
CHARACTER*10	ERRLEV	Error level
CHARACTER*100	ERRMSG	Error message
INTEGER	P	Index for number of persons in sample
INTEGER	CPNTOT	Number of components in component list
INTEGER	NUMLOC	Number of loci
INTEGER	NUMPGT	Total # of polygenotypes
INTEGER	NUMGSE	Total # of trait specific environments
INTEGER	NUMCSE	Total # of common sibship environments
INTEGER	NUMCOV	Total # of covariates
INTEGER	NUMTRT	Total # of traits
INTEGER	NUMCPN(1:MAXTRT)	Total # of components in each trait
INTEGER	TRTLOC(1:MAXTRT)	# of single locus components in each trait
INTEGER	TRTPGT(1:MAXTRT)	# of polygenotype components in each trait
INTEGER	TRTGSE(1:MAXTRT)	# of trait specific environment components in each trait

INTEGER	TRTCSE(1:MAXTRT)	# of common sibship environment components in each trait
INTEGER	TRTCOV(1:MAXTRT)	# of covariate components in each trait
INTEGER	LSTLOC(1:MAXLOC,1:MAXTRT)	Locus names for each trait
INTEGER	LSTPGT(1:MAXPGT,1:MAXTRT)	Polygenotype names for each trait
INTEGER	LSTGSE(1:MAXTRT)	Trait specific environment names for each trait
INTEGER	LSTCSE(1:MAXCSE,1:MAXTRT)	Common sibship environment names for each trait
INTEGER	LSTCOV(1:MAXCOV,1:MAXTRT)	Covariate names for each trait
INTEGER	SAMPLE	Number of samples
INTEGER	NFAM	Number of families
INTEGER	FAMSIZ	Size of family
LOGICAL	LSTNUM	Reserved for internal use
DOUBLE PRECISION	NBP1	Negative binomial parameter 1
DOUBLE PRECISION	NBP2	Negative binomial parameter 2
INTEGER	HSIB	Reserved for internal use
INTEGER	POINTR	Reserved for internal use
INTEGER	FAMILY	Reserved for internal use
INTEGER	IDPTR	Reserved for internal use
INTEGER	FXTYPE	Reserved for internal use
INTEGER	PSTACK(1:MXPRSN)	Reserved for internal use
INTEGER	MATE1	Reserved for internal use
INTEGER	MATE2	Reserved for internal use
INTEGER	M	Reserved for internal use
INTEGER	N	Reserved for internal use
INTEGER	PERSON	Reserved for internal use
INTEGER	NOFFSP	Reserved for internal use
INTEGER	PLUSHS	Reserved for internal use
CHARACTER*4	STUDY	Study code
CHARACTER*2	FXLOC(1:MAXLOC,1:2)	Reserved for internal use
CHARACTER*10	FAMTYP	Family type
CHARACTER*10	OFFTYP	Offspring type

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