

Example of evaluation /variance component estimation using phenotypic, pedigree and genomic information in a single-step evaluation

IM, 8/6/2011 – 9/13/2011

Files simulated by Huiyu Wang using program QMSim by Mehdi Sargolzaei.

```
[ignacy@dodo6 gen_examp]$ cat renum.par
DATAFILE
phenotypes.txt
TRAITS
3
FIELDS_PASSED TO OUTPUT

WEIGHT(S)

RESIDUAL_VARIANCE
0.9038
EFFECT
1 cross alpha #fixed effect
EFFECT
2 cross alpha #animal
RANDOM
animal
FILE
pedigree
SNP_FILE
marker.geno.clean
(CO)VARIANCES
0.9951E-01
```

Parameter file for renumbering
program RENUMF90

Phenotypes.txt – phenotype file
Single trait in position 3
Fixed effect in position 1 read as alphanumeric
Random animal effect in position 3
Pedigree file pedigrees
SNP file marker.geno.clean

```
[ignacy@dodo6 gen_examp]$ head phenotypes.txt
1 1 4.16 0
1 2 3.47 0
1 3 4.5 0
1 4 4.97 0
1 5 5.98 0
1 6 6.63 0
1 7 3.32 0
1 8 5.85 0
1 9 4.77 0
1 10 4.22 0
```

Phenotype file

```
[ignacy@dodo6 gen_examp]$ head pedigree
1 0 0 0
2 0 0 0
3 0 0 0
4 0 0 0
5 0 0 0
6 0 0 0
7 0 0 0
8 0 0 0
9 0 0 0
10 0 0 0
```

Pedigree file

```
[ignacy@dodo6 gen_examp]$ cut -c1-50 marker.geno.clean|head -10
8002 21101011002012011011010110111111211111210100
8014 2111010111110112022111011111112101112210100
8016 21100101202202021120210121102111202212111101
8018 21110111112201120210200020101022212211111100
8024 21110102201201111220210111102122201221111111
8038 11110000102100120201211121201022112111121111
8041 22210001201201121110210121202111102102121001
8063 20110101202202020212211101101120222012120021
8065 21110101111112111221110101010220212001110012
8083 10111011110010111111110112100111121011010121
```

SNP file for the first 50 SNP

```
[ignacy@dodo6 gen_examp]$ $a/renumf90
RENUMF90 version 1.86
name of parameter file?renum.par
renum.par
datafile:phenotypes.txt
traits: 3
fields passed: 4
R
0.9038
```

Run of RENUMF90

```
Processing effect 1 of type cross
item_kind=alpha
```

```
Processing effect 2 of type cross
item_kind=alpha
```

```
pedigree file name "pedigree"
positions of animal, sire, dam, alternate dam and yob 1 2
3 0 0
```

```
SNP file name "marker.geno.clean"
all pedigrees to be included
Reading (CO)VARIANCES: 1 x 1
```

```
Maximum size of character fields: 20
```

```
Maximum size of record (max_string_readline): 800
```

```
Maximum number of fields innput file (max_field_readline): 100
```

```
hash tables for effects set up
table expanded from 10000 to 20000 records
table expanded from 20000 to 40000 records
read 15800 records
table with 1 elements sorted
added count
Effect group 1 of column 1 with 1 levels
table expanded from 10000 to 10000 records
added count
Effect group 2 of column 1 with 15800 levels
wrote statistics in file "renf90.tables"
```

```
Basic statistics for input data (missing value code is 0)
Pos Min Max Mean SD N
3 0.73000 8.8300 4.9793 1.0069 15800
```

```
random effect with SNPs 2
type: animal
file: marker.geno.clean
read SNPs 1500 records
Effect group 2 of column 1 with 15800 levels
```

```
random effect 2
type:animal
opened output pedigree file "renadd02.ped"
read 15800 pedigree records
```

```
Pedigree checks
```

```
Number of animals with records: 15800
```

1500 genotypes

```

Number of animals with genotypes:      1500
Number of animals with records or genotypes: 15800
Number of animals with genotypes and no records: 0
Number of parents without records or genotypes: 0
Total number of animals:      15800

```

Wrote cross reference IDs for SNP file "marker.geno.clean_XrefID"

Wrote parameter file "renf90.par"
Wrote renumbered data "renf90.dat"

Parameter file for application programs with renumbered fields

```

[ignacy@dodo6 gen_examp]$ cat renf90.par
# BLUPF90 parameter file created by RENF90
DATAFILE
  renf90.dat
NUMBER_OF_TRAITS
  1
NUMBER_OF_EFFECTS
  2
OBSERVATION(S)
  1
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF
  2          1 cross
  3          15800 cross
RANDOM_RESIDUAL_VALUES
  0.9038
RANDOM_GROUP
  2
RANDOM_TYPE
  add_animal
FILE
renadd02.ped
(CO)VARIANCES
  0.9951E-01
OPTION SNP_file marker.geno.clean

```

renf90.par – phenotype file
Single trait in position 1
Two effects in model
Fixed effect in position 1 cross-classified with 1 level (μ)
Animal effect in position 3
Second effect (Random Group 2) is additive-animal with pedigree file renadd02.ped
SNP file marker.geno.clean

```

[ignacy@dodo6 gen_examp]$ head renadd02.ped
1 5742 14705 1 0 2 1 0 0 14670
2 2302 1384 1 0 2 1 0 0 12367
3 4248 15309 1 0 12 1 0 2 9123
4 4241 3492 1 0 2 1 0 0 7455
5 14459 14202 1 0 2 1 0 0 5736
6 1029 1292 1 0 2 1 0 3 5877
7 10876 7596 1 0 2 1 0 0 9638
8 13589 12642 1 0 2 1 0 0 14136
9 7070 11562 1 0 2 1 0 0 6010
10 6449 2448 1 0 2 1 0 0 15498

```

Renumbered pedigree file

```

[ignacy@dodo6 gen_examp]$ head renf90.dat
4.16 1 5903 0
3.47 1 3628 0
4.5 1 1329 0
4.97 1 14808 0
5.98 1 12481 0
6.63 1 10205 0
3.32 1 7935 0
5.85 1 5639 0
4.77 1 3348 0
4.22 1 1951 0

```

Renumbered phenotype file

```

[ignacy@dodo6 gen_examp]$ $a/blupf90
name of parameter file?renf90.par

```

Run of BLUPF90

* SNP file: marker.geno.clean
 * SNP Xref file: marker.geno.clean_XrefID
 * Frequency to Center Z=M-p to create G=ZZ'/k (default whichfreq = 2):
 2
 BLUPF90 1.42

Parameter file: renf90.par
 Data file: renf90.dat
 Number of Traits 1
 Number of Effects 2
 Position of Observations 1
 Position of Weight (1) 0
 Value of Missing Trait/Observation 0

EFFECTS

#	type	position (2)	levels	[positions for nested]	
1	cross-classified	2			1
2	cross-classified	3			15800

Residual (co)variance Matrix
 0.90380

Random Effect(s) 2
 Type of Random Effect: additive animal
 Pedigree File: renadd02.ped
 trait effect (CO)VARIANCES
 1 2 0.9951E-01

REMARKS
 (1) Weight position 0 means no weights utilized
 (2) Effect positions of 0 for some effects and traits means that such effects are missing for specified traits

Data record length = 3
 # equations = 15801
 G
 0.99510E-01
 read 15800 records in 3.5994001E-02 s, 31601 nonzeros
 read 15800 additive pedigrees

```

*-----*
*           Setup Genomic: Version 1.76           *
*-----*
* Modified relationship matrix (H) created for effect: 2 *
*-----*
  
```

Read 15800 animals from pedigree file
 Pedigree was in not chronological order (parent first format), reordering will be performed!!!

Current OPTIONS

Genomic Matrix

Make/Read	Which	Save	Test	File	StorageType
Make	1	F	F	G	densem

Rel. Matrix A22

Make/Read	Which	Save	Test	File	StorageType
Make	4	F	F	A22	densem

Inv. Genomic Matrix

Make/Read	Which	Save	Test	File	StorageType
Make	9	F	F	Gi	densem

Inv. Rel. Matrix A22

Make/Read	Which	Save	Test	File	StorageType
Make	9	F	F	A22i	densem

Genomic - A22 Matrix

Make/Read	Which	Save	Test	File	StorageType
None	9	F	F	GmA22	densem

```

Inv. Genomic- A22 Matrix
  Make/Read  Which  Save  Test File  StorageType
      Make      0      F      F      GimA22i  densem

```

Other options

```

Allele Frequency file:  freqdata
Center Allele Frequency:  2
Scale Allele Frequency:  2
Scale Method:           1
Regression G on A:      F
Tuned G Method:        2

```

Creation of GimA22i

```

tau inv(alpha G + beta A22 + gamma I + delta) - omega inv(A22)
  alpha,beta      0.950  0.050
  gamma,delta     0.000  0.000
  tau,omega       1.000  1.000

```

Number of Genotyped Animals 1500

Creating A22

```

Extracting subset of: 3432 pedigrees from: 15800 elapsed time: 0.0000
Calculating Inbreeding by M&L function.. elapsed time 1.0000020E-03
Calculating A22 Matrix by Colleau ...elapsed time 0.3299500

```

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	1.000	1.250	0.000
Off-diagonal	2248500	0.003	0.000	0.750	0.001

Statistics for A22

Reading SNP file

```

Column position in file for the first marker: 7
Format to read SNP file: (6x,400000i1)
Number of SNPs : 3000
Number of Genotyped animals: 1500
Reading SNP file elapsed time 0.4639290

```

Statistics for SNP file

Statistics of alleles frequencies in the current population

```

N: 3000
Mean: 0.501
Min: 0.132
Max: 0.890
Var: 0.014

```

Quality Control - Check call rate for animals

Quality Control - Check Parent-Progeny Mendelian conflicts

```

Total animals: 15800 - Genotyped animals: 1500
Number of Individual - Sire pairs: 470
Number of Individual - Dams pairs: 256
Number of Individual - Sire - Dam trios: 152

```

Several quality checks performed; no error messages as all files for this example have been simulated

Checking SNPs for Mendelian conflicts

```

Total number of parent-progeny evaluations: 726
Number of SNPs with Mendelian conflicts: 0

```

Checking Animals for Mendelian conflicts

Statistics of alleles frequencies in the current population after

Quality Control (MAF, monomorphic, call rate)

```

N: 3000
Mean: 0.501
Min: 0.132
Max: 0.890
Var: 0.014

```

Locus	Freq	0-2p	1-2p	2-2p

```

1 0.751333 -1.502667 -0.502667 0.497333
2 0.382333 -0.764667 0.235333 1.235333
3 0.568667 -1.137333 -0.137333 0.862667
4 0.680000 -1.360000 -0.360000 0.640000
5 0.184333 -0.368667 0.631333 1.631333
6 0.298333 -0.596667 0.403333 1.403333
7 0.392000 -0.784000 0.216000 1.216000
8 0.379667 -0.759333 0.240667 1.240667
9 0.596667 -1.193333 -0.193333 0.806667
10 0.352333 -0.704667 0.295333 1.295333
Genotypes missings (%): 0.000000E+00

```

```

Average denom. (scale): 1415.90178466665
Center Matrix elapsed: 8.3986998E-02

```

Creating G Matrix

```

Calculating G Matrix
Wall time: 08-05-2011 16h 57m 34s 213
MMP - OPTML
Elapsed time 18.47419
Wall time: 08-05-2011 16h 58m 09s 371

```

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	0.999	0.889	1.463	0.002
Off-diagonal	2248500	-0.001	-0.147	0.830	0.002

Statistics of G calculated assuming current allele frequencies

```

Correlation of Genomic Inbreeding and Pedigree Inbreeding
Correlation: 0.3220

```

```

All elements - Diagonal / Off-Diagonal
Estimating Regression Coefficients G = b0 11' + b1 A + e
Regression coefficients b0 b1 = -0.004 0.997

Correlation all elements G & A 0.644

```

```

Off-Diagonal
Using 70386 elements from A22 >= 0.02000

```

```

Estimating Regression Coefficients G = b0 11' + b1 A + e
Regression coefficients b0 b1 = -0.006 1.000

Correlation Off-Diagonal elements G & A 0.660

```

Correlations of off-diagonal elements of G and A22 is 0.660; low numbers indicated genotyped mistakes or poor pedigrees

```

Blend G as alpha*G + beta*A22: (alpha,beta) 0.950 0.050

```

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	0.999	0.894	1.446	0.002
Off-diagonal	2248500	0.000	-0.139	0.820	0.002

Frequency - Diagonal of G

```

N: 1500
Mean: 0.999
Min: 0.894
Max: 1.446
Range: 0.028
Class: 20

```

#Class	Class	Count
1	0.8942	9
2	0.9218	86
3	0.9494	343
4	0.9770	480
5	1.005	361
6	1.032	139
7	1.060	51
8	1.087	16

Diagonal elements of G should be 1± 0.2. Too large or too small elements indicate:

- Genotyping mistakes
- Mixed lines

See Simeone et al. (2011)

9	1.115	6
10	1.142	2
11	1.170	1
12	1.198	1
13	1.225	1
14	1.253	1
15	1.280	0
16	1.308	0
17	1.336	0
18	1.363	2
19	1.391	0
20	1.418	1
21	1.446	0

Scale G matrix according to A22 - Method: 2

Diagonal A:	1.001	Offdiagonal A:	0.003	All A:	0.004	Difference:	0.998
Diagonal G:	0.999	Offdiagonal G:	0.000	All G:	0.000	Difference:	0.999
Diff G Diag - G OffDiag:	0.999	(da-oa) / (dg-og):	0.998				
Diff A OffDiag - G OffDiag:	0.004						
Diff A all - G all:	0.004						
New Alpha:	0.948	New Beta:	0.050	:New Delta	0.004		

Final Pedrigree-Based Matrix

Statistic of Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	1.000	1.250	0.000
Off-diagonal	2248500	0.003	0.000	0.750	0.001

Statistics of G after scaling as in Chen et al (2011) or Vitezica et al. (2011)

Final Genomic Matrix

Statistic of Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	1.001	0.896	1.447	0.002
Off-diagonal	2248500	0.003	-0.134	0.822	0.002

Statistics should be same as for A22.

Correlation of Genomic Inbreeding and Pedigree Inbreeding
Correlation: 0.3363

All elements - Diagonal / Off-Diagonal

Estimating Regression Coefficients G = b0 11' + b1 A + e
Regression coefficients b0 b1 = 0.000 0.995

Correlation all elements G & A 0.663

Off-Diagonal

Using 70386 elements from A22 >= 0.02000

Estimating Regression Coefficients G = b0 11' + b1 A + e
Regression coefficients b0 b1 = -0.001 0.998

Correlation Off-Diagonal elements G & A 0.679

Creating A22-inverse

Wall time: 08-05-2011 16h 58m 10s 866

Inverse using ginv2

elapsed time 3.544461000000000

Wall time: 08-05-2011 16h 58m 17s 691

Statistic of Inv. Rel. Matrix A22

	N	Mean	Min	Max	Var
Diagonal	1500	1.607	1.056	9.221	0.575
Off-diagonal	2248500	-0.001	-1.067	0.533	0.001

Statistics of A₂₂⁻¹

Creating G-inverse

Wall time: 08-05-2011 16h 58m 17s 987
Inverse using ginv2
elapsed time 4.24635400000000
Wall time: 08-05-2011 16h 58m 26s 044

Statistic of Inv. Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	8.007	3.597	64.893	21.055
Off-diagonal	2248500	-0.005	-12.697	6.632	0.056

Creating GimA22i in file: "GimA22i"
Calculating GmA22/GimA22i Matrix Densem storage
Calculating GmA22/GimA22i Matrix...elapsed time 0.1269817
Setup Genomic Done.

wGimA22i 1.0000000000000000
hash matrix increased from 100000 to 150000 % filled: 0.9000
hash matrix increased from 150000 to 225000 % filled: 0.9000
hash matrix increased from 225000 to 337500 % filled: 0.9000
hash matrix increased from 337500 to 506250 % filled: 0.9000
hash matrix increased from 506250 to 759375 % filled: 0.9000
hash matrix increased from 759375 to 1139062 % filled: 0.9000
hash matrix increased from 1139062 to 1708593 % filled: 0.9000
finished peds in 30.68333 s, 1193064 nonzeros
round 1 convergence= 3.234776127905992E-004
round 2 convergence= 1.615955145159698E-005
round 3 convergence= 9.675137058360991E-006
round 4 convergence= 6.533482675941447E-006
round 5 convergence= 2.711751165983321E-006
round 6 convergence= 2.332461269941776E-006
round 7 convergence= 2.456943894174467E-006
round 8 convergence= 1.871032262736868E-006
round 9 convergence= 1.284186412756008E-006
round 10 convergence= 1.329888669790924E-006
round 11 convergence= 1.013837286072782E-006
round 12 convergence= 5.114506114473881E-007
round 13 convergence= 3.753500188088944E-007
round 14 convergence= 3.820984393489448E-007
round 15 convergence= 2.095981856753111E-007
round 16 convergence= 2.169734927778480E-007
round 17 convergence= 1.510655955054585E-007
round 18 convergence= 1.223093271086398E-007
round 19 convergence= 1.144208797870038E-007
round 20 convergence= 8.131400946583559E-008
round 21 convergence= 5.970377107478620E-008
round 22 convergence= 4.958048582709506E-008
round 23 convergence= 4.511531620309364E-008
round 24 convergence= 4.048457052994330E-008
round 25 convergence= 2.937262745711369E-008
round 26 convergence= 2.648645348704001E-008
round 27 convergence= 2.150250889347419E-008
round 28 convergence= 1.746122045422689E-008
round 29 convergence= 1.618313870088509E-008
round 30 convergence= 1.165694097818618E-008
round 31 convergence= 1.031631309612105E-008
round 32 convergence= 9.788567182973487E-009
round 33 convergence= 8.063648929061496E-009
round 34 convergence= 7.153780294469294E-009
round 35 convergence= 5.260743186938735E-009
round 36 convergence= 3.944149400934007E-009
round 37 convergence= 3.253701927083573E-009
round 38 convergence= 2.678116204640105E-009
round 39 convergence= 2.074353186297683E-009
round 40 convergence= 1.653655058622966E-009
round 41 convergence= 1.401145065904429E-009
round 42 convergence= 9.373315892660401E-010
round 43 convergence= 8.724286299791461E-010
round 44 convergence= 6.553627830375191E-010
round 45 convergence= 4.716428667053116E-010

Iteration starts


```

round      46      convergence= 3.649381502432734E-010
round      47      convergence= 2.625651139847919E-010
round      48      convergence= 2.325031252144926E-010
round      49      convergence= 1.771064062729349E-010
round      50      convergence= 1.325427181900545E-010
round      51      convergence= 1.111050096588042E-010
round      52      convergence= 7.436448040171382E-011
round      53      convergence= 5.441259669264766E-011
round      54      convergence= 4.768035322194510E-011
round      55      convergence= 3.580400573533355E-011
round      56      convergence= 2.523714298051495E-011
round      57      convergence= 2.004049279348854E-011
round      58      convergence= 1.403093079468600E-011
round      59      convergence= 1.103086717074418E-011
round      60      convergence= 9.775746799707215E-012
round      61      convergence= 6.370679446364921E-012
round      62      convergence= 4.929036857250291E-012
round      63      convergence= 3.714643905760963E-012
round      64      convergence= 2.721030958617683E-012
round      65      convergence= 1.931029578758311E-012
round      66      convergence= 1.610472992188148E-012
round      67      convergence= 1.259204136643006E-012
round      68      convergence= 9.025592862452768E-013
      68 iterations, convergence criterion= 9.025592862452768E-013
solutions stored in file: "solutions"
[ignacy@dodo6 gen_examp]$

```

```

[ignacy@dodo6 gen_examp]$ head solutions
trait/effect level solution
1 1 1 4.97591211
1 2 1 0.10194865
1 2 2 0.33749439
1 2 3 0.04475742
1 2 4 -0.31055520
1 2 5 0.22368631
1 2 6 -0.09454804
1 2 7 -0.03186435
1 2 8 0.18033163
[ignacy@dodo6 gen_examp]$

```

Solution file

```

[ignacy@dodo6 gen_examp]$ $a/airemlf90
name of parameter file?renf90.par

```

```

* SNP file: marker.geno.clean
* SNP Xref file: marker.geno.clean_XrefID
* Frequency to Center Z=M-p to create G=ZZ'/k (default whichfreq = 2):
  2
  AI-REMLF90 ver. 1.96

```

```

Parameter file:      renf90.par
Data file:          renf90.dat
Number of Traits    1
Number of Effects   2
Position of Observations 1
Position of Weight (1) 0
Value of Missing Trait/Observation 0

```

```

.....:
.....:

```

Statistic of Inv. Genomic Matrix

	N	Mean	Min	Max	Var
Diagonal	1500	8.007	3.597	64.893	21.055
Off-diagonal	2248500	-0.005	-12.697	6.632	0.056

Variance component estimation by
AIREMLF90

```

Creating GimA22i in file: "GimA22i"
Calculating GmA22/GimA22i Matrix Densem storage
Calculating GmA22/GimA22i Matrix...elapsed time 0.1089821
Setup Genomic Done.
wGimA22i 1.0000000000000000
hash matrix increased from 85428 to 128142 % filled: 0.9000
hash matrix increased from 128142 to 192213 % filled: 0.9000
hash matrix increased from 192213 to 288319 % filled: 0.9000
hash matrix increased from 288319 to 432478 % filled: 0.9000
hash matrix increased from 432478 to 648717 % filled: 0.9000
hash matrix increased from 648717 to 973075 % filled: 0.9000
hash matrix increased from 973075 to 1459612 % filled: 0.9000
hash matrix increased from 85428 to 128142 % filled: 0.9000
hash matrix increased from 128142 to 192213 % filled: 0.9000
hash matrix increased from 192213 to 288319 % filled: 0.9000
hash matrix increased from 288319 to 432478 % filled: 0.9000
hash matrix increased from 432478 to 648717 % filled: 0.9000
hash matrix increased from 648717 to 973075 % filled: 0.9000
hash matrix increased from 973075 to 1459612 % filled: 0.9000
finished peds in 32.01313 s, 1193064 nonzeros
rank= 15801

```

```

*****
**** FSPAK ***
*****
MPE / IM / MAE
Jun 1994

```

SPARSE STATISTICS

```

DIMENSION OF MATRIX = 15801
RANK = 15801
STORAGE AVAILABLE = 7061497
MAXIMUM NEEDED = 7061497
NZE IN UPPER TRIANGULAR = 1208865
NZE IN FACTOR = 1521840
NO. OF CALLS NUM FACT = 1
NO. OF CALLS SOLVE = 1
NO. OF CALLS SPARS SOLV = 0
NO. OF CALLS DET / LDET = 1
NO. OF CALLS SPARS INV = 1
TOTAL CPU TIME IN FSPAK = 9.465561
TIME FOR FINDING ORDER = 2.568611
TIME FOR SYMBOLIC FAC = 0.676899
TIME FOR NUMERICAL FAC = 2.017693
TIME FOR SOLVE = 0.008995
TIME FOR SPARSE SOLVE = 0.000000
TIME FOR SPARSE INVERSE = 4.147369
-2logL = 43515.7413644011 : AIC = 43519.7413644011
In round 1 convergence= 0.423851780381002
delta convergence= 0.252173522062583
new R
0.58510
new G
0.28516
-2logL = 53013.2734486053 : AIC = 53017.2734486053
In round 2 convergence= 0.141351613622645
delta convergence= 0.117430758820623
new R
0.52205
new G
0.45696
-2logL = 52800.6601605267 : AIC = 52804.6601605267
In round 3 convergence= 1.725330565925358E-002
delta convergence= 4.769938966058494E-002
new R
0.49575
new G
0.52606
-2logL = 52785.2479463395 : AIC = 52789.2479463395
In round 4 convergence= 1.101891763451498E-004
delta convergence= 3.662497104484009E-003
new R

```

```
0.49400
new G
0.53164
-2logL = 52785.1635385807 : AIC = 52789.1635385807
In round 5 convergence= 2.804695847240073E-009
delta convergence= 1.777604045032979E-005
new R
0.49400
new G
0.53167
```

Final Estimates

```
Genetic variance(s) for effect 2
0.53167
Residual variance(s)
0.49400
inverse of AI matrix (Sampling Variance)
0.40448E-03 -0.17367E-03
-0.17367E-03 0.14702E-03
Correlations from inverse of AI matrix
1.0000 -0.71219
-0.71219 1.0000
SE for R
0.12125E-01
SE for G
0.20112E-01
solutions stored in file: "solutions"
[ignacy@dodo6 gen_examp]$
```

Estimates of variance components