

Additional file 1: Supplementary output files

The four GREML output files (Files 1-4) below are GREML estimates by GREML_CE and GREML_QM for the two test data sets. Files 1 and 2 use the dataset with 3000 SNP markers and 1000 individuals, and Files 3 and 4 use the dataset with 1000 SNP markers and 3000 individuals. In addition to showing GREML estimates from GVCBLUP, these four files are numerical examples in support the following conclusions:

- 1) GREML_CE and GREML_QM have identical results (same results at every iteration and the same number of iterations), as shown by the comparison between File 1 and File 2, and between File 3 and File 4;
- 2) GREML_CE and GREML_QM have complementary computing advantages, as shown by the comparison between File 1 and File 3, and between File 2 and File 4.

File 5 is an example of the output file of the GCORRMX program.

File 1: Estimates of variance components and heritabilities by GREML_CE for 3000 SNP markers and 1000 individuals (file name: output_greml_ce)

Output of GREML results from GREML_CE.

Number of markers: 3000

Number of chromosomes: 3

Number of phenotypic observations: 1000

Number of individuals with phenotypic observations: 1000

Number of individuals without phenotypic observations: 0

Iteration	VA	Tolerance_VA	VD	Tolerance_VD	VE	Tolerance_VE
1	4.706959e-001	5.293041e-001	6.244678e-001	1.375532e+000	1.629727e+000	5.370273e+000
2	6.567722e-001	1.860762e-001	6.919474e-001	6.747955e-002	1.426925e+000	2.028014e-001
3	9.783415e-001	3.215693e-001	1.133466e+000	4.415185e-001	8.480809e-001	5.788443e-001
4	1.103954e+000	1.256125e-001	1.101448e+000	3.201764e-002	9.287548e-001	8.067394e-002
5	1.128407e+000	2.445282e-002	1.093826e+000	7.622571e-003	9.343307e-001	5.575851e-003
6	1.131210e+000	2.803324e-003	1.093079e+000	7.465113e-004	9.341486e-001	1.820620e-004
7	1.131519e+000	3.087446e-004	1.092976e+000	1.028650e-004	9.341331e-001	1.550429e-005
8	1.131554e+000	3.463923e-005	1.092965e+000	1.134782e-005	9.341312e-001	1.924986e-006
9	1.131557e+000	3.878090e-006	1.092964e+000	1.277036e-006	9.341310e-001	2.124590e-007
10	1.131558e+000	4.343798e-007	1.092964e+000	1.429360e-007	9.341310e-001	2.387022e-008

11	1.131558e+000	4.865057e-008	1.092964e+000	1.601138e-008	9.341310e-001	2.672083e-009
12	1.131558e+000	5.448952e-009	1.092964e+000	1.793256e-009	9.341310e-001	2.993082e-010
SE	2.070319e-001		1.492317e-001		9.426440e-002	

Inverse of AI matrix:

4.286222e-002	-6.019587e-003	-2.955132e-003
-6.019587e-003	2.227011e-002	-7.730389e-003
-2.955132e-003	-7.730389e-003	8.885777e-003

Additive heritability, SE : 3.582407e-001, 4.883500e-002
 Dominance heritability, SE : 3.460221e-001, 4.613524e-002
 Heritability in the broad sense, SE : 7.042628e-001, 3.678706e-002

Total running time: 0 days 0 hours 0 minutes 5 seconds.

File 2: Estimates of variance components and heritabilities by GREML_QM for 3000 SNP markers and 1000 individuals (file name: output_greml_qm)

Output of GREML results from GREML_QM.

Number of markers: 3000
 Number of chromosomes: 3

Number of phenotypic observations: 1000
 Number of individuals with phenotypic observations: 1000
 Number of individuals without phenotypic observations: 0

Iteration	VA	Tolerance_VA	VD	Tolerance_VD	VE	Tolerance_VE
1	4.706959e-001	5.293041e-001	6.244678e-001	1.375532e+000	1.629727e+000	5.370273e+000
2	6.567722e-001	1.860762e-001	6.919474e-001	6.747955e-002	1.426925e+000	2.028014e-001
3	9.783415e-001	3.215693e-001	1.133466e+000	4.415185e-001	8.480809e-001	5.788443e-001
4	1.103954e+000	1.256125e-001	1.101448e+000	3.201764e-002	9.287548e-001	8.067394e-002
5	1.128407e+000	2.445282e-002	1.093826e+000	7.622571e-003	9.343307e-001	5.575851e-003
6	1.131210e+000	2.803324e-003	1.093079e+000	7.465113e-004	9.341486e-001	1.820620e-004
7	1.131519e+000	3.087446e-004	1.092976e+000	1.028650e-004	9.341331e-001	1.550429e-005
8	1.131554e+000	3.463923e-005	1.092965e+000	1.134782e-005	9.341312e-001	1.924986e-006
9	1.131557e+000	3.878090e-006	1.092964e+000	1.277036e-006	9.341310e-001	2.124590e-007
10	1.131558e+000	4.343798e-007	1.092964e+000	1.429360e-007	9.341310e-001	2.387022e-008

11	1.131558e+000	4.865058e-008	1.092964e+000	1.601137e-008	9.341310e-001	2.672094e-009
12	1.131558e+000	5.448938e-009	1.092964e+000	1.793271e-009	9.341310e-001	2.992959e-010
SE	2.070319e-001		1.492317e-001		9.426440e-002	

Inverse of AI matrix:

4.286222e-002	-6.019587e-003	-2.955132e-003
-6.019587e-003	2.227011e-002	-7.730389e-003
-2.955132e-003	-7.730389e-003	8.885777e-003

Additive heritability, SE : 3.582407e-001, 4.883500e-002
Dominance heritability, SE : 3.460221e-001, 4.613524e-002
Heritability in the broad sense, SE : 7.042628e-001, 3.678706e-002

Total running time: 0 days 0 hours 1 minutes 19 seconds.

File 3: Estimates of variance components and heritabilities by GREML_CE for 1000 SNP markers and 3000 individuals (file name: output_greml_ce)

Output of GREML results from GREML_CE.

Number of markers: 1000
Number of chromosomes: 3

Number of phenotypic observations: 3000
Number of individuals with phenotypic observations: 3000
Number of individuals without phenotypic observations: 0

Iteration	VA	Tolerance_VA	VD	Tolerance_VD	VE	Tolerance_VE
1	6.138855e-001	3.861145e-001	7.062130e-001	1.293787e+000	1.272038e+000	5.727962e+000
2	8.448634e-001	2.309779e-001	8.718213e-001	1.656083e-001	1.090407e+000	1.816303e-001
3	1.052127e+000	2.072634e-001	1.053719e+000	1.818977e-001	9.855451e-001	1.048622e-001
4	1.095827e+000	4.369979e-002	1.074924e+000	2.120526e-002	9.902820e-001	4.736905e-003
5	1.097768e+000	1.941963e-003	1.075502e+000	5.776256e-004	9.902018e-001	8.017934e-005
6	1.097788e+000	1.923879e-005	1.075513e+000	1.091585e-005	9.901979e-001	3.903467e-006
7	1.097788e+000	3.272541e-007	1.075513e+000	1.004536e-007	9.901978e-001	5.073248e-008
8	1.097788e+000	3.679218e-009	1.075513e+000	1.921815e-009	9.901978e-001	7.512063e-010
SE	1.402329e-001		8.048602e-002		3.230763e-002	

Inverse of AI matrix:

```
1.966526e-002 -3.194976e-004 -6.312981e-004
-3.194976e-004 6.477999e-003 -4.945340e-004
-6.312981e-004 -4.945340e-004 1.043783e-003
```

Additive heritability, SE : 3.470171e-001, 3.097606e-002
Dominance heritability, SE : 3.399758e-001, 2.330417e-002
Heritability in the broad sense, SE : 6.869928e-001, 1.863563e-002

Total running time: 0 days 0 hours 0 minutes 32 seconds.

File 4: Estimates of variance components and heritabilities by GREML_QM for 1000 SNP markers and 3000 individuals (file name: output_greml_qm)

Output of GREML results from GREML_QM.

Number of markers: 1000
Number of chromosomes: 3

Number of phenotypic observations: 3000
Number of individuals with phenotypic observations: 3000
Number of individuals without phenotypic observations: 0

Iteration	VA	Tolerance_VA	VD	Tolerance_VD	VE	Tolerance_VE
1	6.138855e-001	3.861145e-001	7.062130e-001	1.293787e+000	1.272038e+000	5.727962e+000
2	8.448634e-001	2.309779e-001	8.718213e-001	1.656083e-001	1.090407e+000	1.816303e-001
3	1.052127e+000	2.072634e-001	1.053719e+000	1.818977e-001	9.855451e-001	1.048622e-001
4	1.095827e+000	4.369979e-002	1.074924e+000	2.120526e-002	9.902820e-001	4.736905e-003
5	1.097768e+000	1.941963e-003	1.075502e+000	5.776256e-004	9.902018e-001	8.017934e-005
6	1.097788e+000	1.923879e-005	1.075513e+000	1.091585e-005	9.901979e-001	3.903467e-006
7	1.097788e+000	3.272541e-007	1.075513e+000	1.004536e-007	9.901978e-001	5.073248e-008
8	1.097788e+000	3.679212e-009	1.075513e+000	1.921814e-009	9.901978e-001	7.512053e-010
SE	1.402329e-001		8.048602e-002		3.230763e-002	

Inverse of AI matrix:

```
1.966526e-002 -3.194976e-004 -6.312981e-004
-3.194976e-004 6.477999e-003 -4.945340e-004
-6.312981e-004 -4.945340e-004 1.043783e-003
```

Additive heritability, SE : 3.470171e-001, 3.097606e-002

Dominance heritability, SE : 3.399758e-001, 2.330417e-002

Heritability in the broad sense, SE : 6.869928e-001, 1.863563e-002

Total running time: 0 days 0 hours 0 minutes 6 seconds.

File 5: Example of the output file of GCORRMX for calculating genomic relationships (file name: output_greml_qm)

GCORRMX: Definition I for additive and dominance relationships

Ind_1	Ind_2	Additive	Dominance
2121	2122	5.8511e-001	2.4373e-001
2121	2123	5.1428e-001	3.1196e-001
2121	2124	4.7795e-001	3.5445e-001
2121	2125	2.6133e-001	-2.2135e-002
2121	2126	7.1610e-001	5.2187e-001
2121	2127	2.6133e-001	-2.2135e-002
2121	2128	5.3774e-001	3.5330e-001
2121	2129	8.4005e-001	7.5453e-001
2122	2123	6.3007e-001	2.5615e-001
2122	2124	5.9785e-001	1.8100e-001
2122	2125	6.6044e-001	3.1495e-001
2122	2126	8.4215e-001	7.2798e-001
2122	2127	6.6044e-001	3.1495e-001
2122	2128	3.7226e-001	1.0287e-002
2122	2129	7.2590e-001	4.8420e-001
2123	2124	9.4378e-001	8.9339e-001
2123	2125	7.5385e-001	5.0227e-001
2123	2126	7.6106e-001	5.3429e-001
2123	2127	7.5385e-001	5.0227e-001
2123	2128	2.8295e-001	7.2152e-002
2123	2129	6.4480e-001	5.0274e-001
2124	2125	7.9554e-001	5.7780e-001
2124	2126	7.2884e-001	4.5913e-001
2124	2127	7.9554e-001	5.7780e-001

2124	2128	3.7186e-001	1.7851e-001
2124	2129	6.1258e-001	4.2758e-001
2125	2126	5.0195e-001	3.4453e-004
2125	2127	1.0511e+000	1.0822e+000
2125	2128	2.7637e-001	2.3282e-001
2125	2129	3.8570e-001	-3.1209e-002
2126	2127	5.0195e-001	3.4453e-004
2126	2128	4.9915e-001	7.1613e-002
2126	2129	8.5689e-001	7.6234e-001
2127	2128	2.7637e-001	2.3282e-001
2127	2129	3.8570e-001	-3.1209e-002
2128	2129	6.2309e-001	3.0428e-001