

Additive Relationship Matrices

David Butler

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In a genetic analysis there are observations on a set of individuals that are genetically linked via a pedigree. The genetic effects are therefore correlated, and assuming normal modes of inheritance the correlation expected from additive genetic effects can be derived from the pedigree, provided all the genetic links are present. The additive genetic relationship matrix can be calculated from the pedigree, however, it is actually the **inverse** relationship matrix that is required by **asreml**.

For example, the following call calculates the inverse relationship matrix for the pedigree data frame `harvey.ped`.

```
> data(harvey)
> harvey.ainv <- asreml.Ainverse(harvey.ped)$ginv
```

```
Pedigree insert: Individual "Sire_1" inserted at record 1
Pedigree insert: Individual "Sire_2" inserted at record 2
Pedigree insert: Individual "Sire_3" inserted at record 3
Pedigree insert: Individual "Sire_4" inserted at record 4
Pedigree insert: Individual "Sire_5" inserted at record 5
Pedigree insert: Individual "Sire_6" inserted at record 6
Pedigree insert: Individual "Sire_7" inserted at record 7
Pedigree insert: Individual "Sire_8" inserted at record 8
Pedigree insert: Individual "Sire_9" inserted at record 9
```

```
> harvey.ainv[1:10, ]
```

	Row	Column	Ainverse
1	1	1	3.6666667
2	2	2	3.6666667
3	3	3	2.6666667
4	4	4	3.6666667
5	5	5	3.3333333
6	6	6	3.0000000
7	7	7	3.6666667
8	8	8	3.3333333
9	9	9	3.6666667
10	10	1	-0.6666667

The data frame `harvey.ainv` is a sparse representation of the inverse relationship matrix where the non zero values are indexed by their row and column coordinates.

The genetic relationships are included in an `asreml` analysis by linking this inverse matrix to the relevant term in the model through the `ginverse` argument, and the `ped` special model function.

```
> adg.asr <- asreml(y3 ~ Line, random = ~ped(Calf), ginverse = list(Calf = harvey.ainv),  
+ data = harvey)
```

The variance components and BLUP estimates are given by:

```
> summary(adg.asr)$varcomp
```

	gamma	component	std.error	z.ratio	constraint
ped(Calf)!ped	1.828629	499.5207	500.5071	0.9980292	Positive
R!variance	1.000000	273.1669	410.0170	0.6662330	Positive

```
> summary(adg.asr, all = TRUE)$coef.random[1:12, ]
```

	solution	std error	z ratio
ped(Calf)_Sire_1	11.0252269	17.44614	0.63195779
ped(Calf)_Sire_2	-17.6384263	17.44614	-1.01102146
ped(Calf)_Sire_3	6.6131994	18.02684	0.36685305
ped(Calf)_Sire_4	-8.0184818	18.76558	-0.42729721
ped(Calf)_Sire_5	8.0184818	18.76558	0.42729721
ped(Calf)_Sire_6	8.4824077	17.13024	0.49517161
ped(Calf)_Sire_7	0.4445005	16.60102	0.02677549
ped(Calf)_Sire_8	-26.9639154	16.83815	-1.60135896
ped(Calf)_Sire_9	18.0370073	16.60102	1.08649996
ped(Calf)_101	-7.3119157	14.75469	-0.49556549
ped(Calf)_102	16.3992349	14.75469	1.11145905
ped(Calf)_103	2.5195370	14.75469	0.17076176