

## **Supplementary Material**

# **Impact of missing pedigrees in single-step genomic evaluation**

*Karin Meyer*

Animal Genetics and Breeding Unit, University of New England, Armidale, NSW 2351, Australia.  
Email: [kmeyer@une.edu.au](mailto:kmeyer@une.edu.au)

## Impact of missing pedigrees in single-step genomic evaluation – Electronic supplement

Table S1: Example pedigree and alternative assignment to unknown parent groups together with resulting matrices of group proportions ( $\mathbf{Q}$ )

Animal	Sire	Dam	Gen. <sup>a</sup>	Genotyped	UPG standard <sup>b</sup>		UPG extended <sup>c</sup>	
					Sire	Dam	Sire	Dam
A	?	?	0	No	G1	G1	G1	G1
B	?	?	0	No	G1	G1	G1	G1
C	?	?	0	No	G1	G1	G1	G1
D	A	B	1	No	-	-	-	-
E	A	C	1	Yes	-	-	-	-
F	A	?	1	No	-	G2	-	G2
G	A	?	1	Yes	-	G2	-	GX
H	D	?	2	No	-	G3	-	G3
I	D	?	2	Yes	-	G3	-	GX
J	?	?	2	Yes	G3	G3	GX	GX
K	I	H	3	Yes	-	-	-	-
L	I	?	3	No	-	G4	-	G4
M	I	?	3	Yes	-	G4	-	GX

<sup>a</sup>Generation number

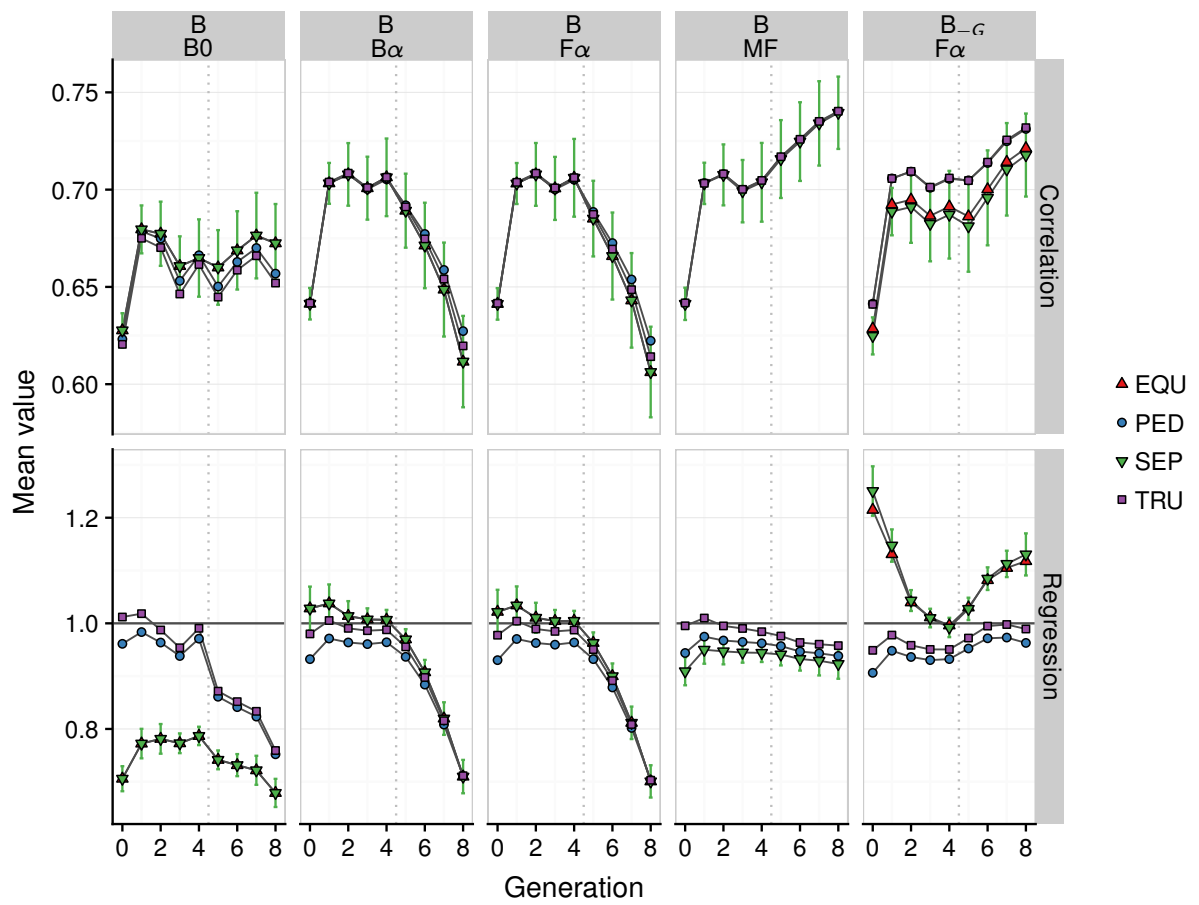
<sup>b</sup>Unknown parent groups for all animals assigned according to generation number

<sup>c</sup>Unknown parent groups for non-genotyped animals assigned according to generation number and assigned to an extra group (GX) for genotyped animals, regardless of generation number

$$\mathbf{Q}_B = \begin{matrix} & \begin{matrix} G1 & G2 & G3 & G4 \end{matrix} \\ \begin{matrix} A \\ B \\ C \\ D \\ E \\ F \\ G \\ H \\ I \\ J \\ K \\ L \\ M \end{matrix} & \begin{pmatrix} 1.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 \\ 0.50 & 0.50 & 0.00 & 0.00 \\ 0.50 & 0.50 & 0.00 & 0.00 \\ 0.50 & 0.00 & 0.50 & 0.00 \\ 0.50 & 0.00 & 0.50 & 0.00 \\ 0.00 & 0.00 & 1.00 & 0.00 \\ 0.50 & 0.00 & 0.50 & 0.00 \\ 0.25 & 0.00 & 0.25 & 0.50 \\ 0.25 & 0.00 & 0.25 & 0.50 \end{pmatrix} \end{matrix}$$

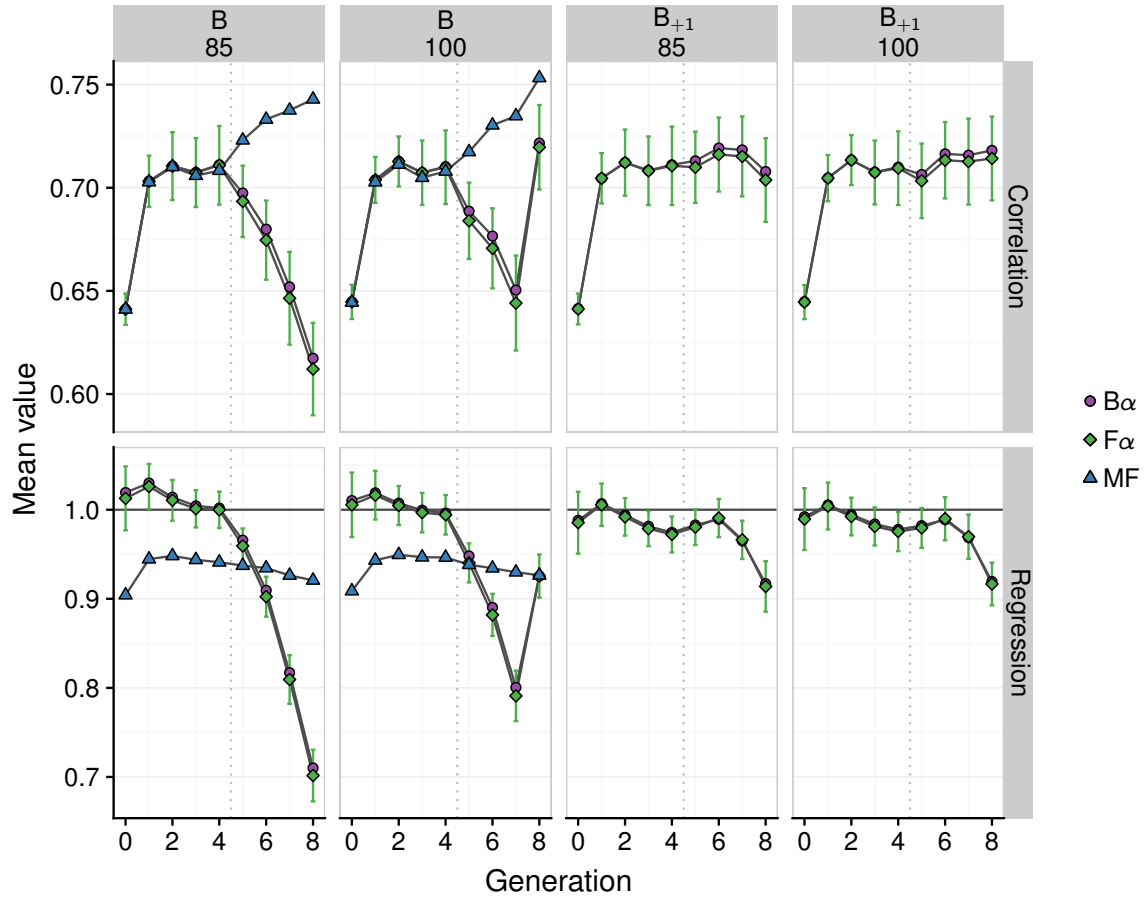
$$\mathbf{Q}_{B+1} = \begin{matrix} & \begin{matrix} G1 & G2 & G3 & G4 & GX \end{matrix} \\ \begin{matrix} A \\ B \\ C \\ D \\ E \\ F \\ G \\ H \\ I \\ J \\ K \\ L \\ M \end{matrix} & \begin{pmatrix} 1.00 & 0.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 & 0.00 \\ 1.00 & 0.00 & 0.00 & 0.00 & 0.00 \\ 0.50 & 0.50 & 0.00 & 0.00 & 0.00 \\ 0.50 & 0.00 & 0.00 & 0.00 & 0.50 \\ 0.50 & 0.00 & 0.50 & 0.00 & 0.00 \\ 0.50 & 0.00 & 0.00 & 0.00 & 0.50 \\ 0.00 & 0.00 & 0.00 & 0.00 & 1.00 \\ 0.50 & 0.00 & 0.25 & 0.00 & 0.25 \\ 0.25 & 0.00 & 0.00 & 0.50 & 0.25 \\ 0.25 & 0.00 & 0.00 & 0.00 & 0.75 \end{pmatrix} \end{matrix}$$

Fig. S1: Means and standard deviations across replicates for within generation correlations between and regressions of true on predicted breeding values for different variance components<sup>a</sup>



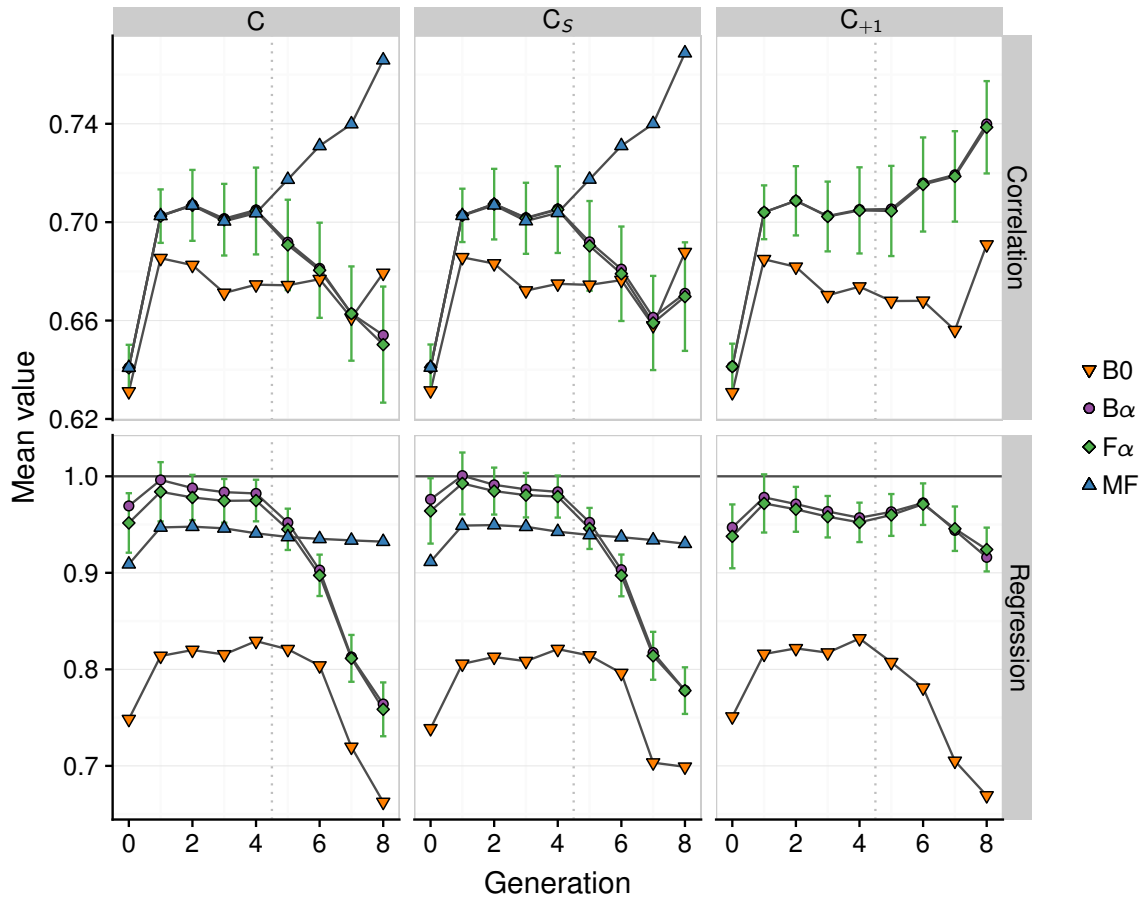
<sup>a</sup>SEP: Separate estimates for  $\sigma_A^2$  and  $\sigma_Q^2$ ; PED: as SEP, but considering pedigree relationships only; EQU: Forcing  $\sigma_Q^2$  to be equal to estimate for  $\sigma_A^2$ ; TRU: Population values; B0: Base frequencies,  $\alpha = 0$ ; B $\alpha$ : Base frequencies, estimate  $\alpha$ ; F $\alpha$ : Observed frequencies, estimate  $\alpha$ ; MF: Fitting metafounders; P: Using pedigree relationships only

Fig. S2: Means and standard deviations across replicates for within generation correlations between and regressions of true on predicted breeding values for analyses B with 85% or 100% known parents for non-genotyped animals in generation 8 ( B: assigning genotyped and non-genotyped animals to the same group per generation  $B_{+1}$ : as B for non-genotyped animals but assigning all genotyped animals to one additional group) <sup>a</sup>



<sup>a</sup> $B\alpha$ : Base frequencies, estimate  $\alpha$ ;  $F\alpha$ : Observed frequencies, estimate  $\alpha$ ; MF: Fitting metafounders;

Fig. S3: Means and standard deviations across replicates for within generation correlations between and regressions of true on predicted breeding values for analyses including an additional, large group of genotyped individuals without pedigree information in generation 8 (C: standard grouping according to generation number,  $C_S$ : as C but assigning additional individuals to separate UPG,  $C_{+1}$ : assign all genotyped individuals with unknown parents to an additional, separate UPG)<sup>a</sup>



<sup>a</sup>B0: Base frequencies,  $\alpha = 0$ ; B $\alpha$ : Base frequencies, estimate  $\alpha$ ; F $\alpha$ : Observed frequencies, estimate  $\alpha$ ; MF: Fitting metafounders;