

Additional file 1 - G matrix computation based on similarities

Similarity (S) can be measured as the number of shared alleles between individuals j and k for each genotype at locus i , such as [1]

$$S_{jk,i} = \frac{I_{j1k1} + I_{j1k2} + I_{j2k1} + I_{j2k2}}{4}$$

For a single locus, $S_{jk} =$

ind_j/ind_k	AA	AB	BB
AA	1	0.5	0
AB	0.5	0.5	0.5
BB	0	0.5	1

We shall now show that this is similar to computing relationships using the following equations as outlined by Yang et al [2], with allele frequency p_i fixed at 0.5 for all variants.

$$G_{jk} = \frac{1}{N} \sum_i G_{ijk} = \begin{cases} \frac{1}{N} \sum_i \frac{(x_{ij} - 2p_i)(x_{ik} - 2p_i)}{2p_i(1 - p_i)}, & j \neq k \\ 1 + \frac{1}{N} \sum_i \frac{x_{ij}^2 - (1 + 2p_i)x_{ij} + 2p_i^2}{2p_i(1 - p_i)}, & j = k \end{cases} \quad (1)$$

$$(1) \quad \frac{(x_{ij} - 2p_i)(x_{ik} - 2p_i)}{2p_i(1 - p_i)} = \frac{(x_{ij} - 1)(x_{ik} - 1)}{0.5}$$

$$(2) \quad 1 + \frac{x_{ij}^2 - (1 + 2p_i)x_{ij} + 2p_i^2}{2p_i(1 - p_i)} = 1 + \frac{x_{ij}^2 - 2x_{ij} + 0.5}{0.5}$$

$$= \frac{x_{ij}^2 - 2x_{ij} + 1}{0.5} = \frac{(x_{ij} - 1)(x_{ij} - 1)}{0.5}$$

If $x_{ij} = x_{ik}$ then (1) = (2) and only one equation is needed to calculate both diagonal and off-diagonal elements.

In this case, $G_{jk} =$

ind_j/ ind_k	AA [2]	AB [1]	BB [0]
AA [2]	2	0	-2
AB [1]	0	0	0
BB [0]	-2	0	2

S and G are linked by the following transformation: $4 * (S_{jk} - \bar{S}_{jk}) = G_{jk}$, with $\bar{S}_{jk} = 0.5$.

In the case of multiple loci,

$$G_{jk} = \frac{1}{N} \sum_i G_{ijk} = \frac{1}{N} \sum_i \frac{(x_{ij} - 1)(x_{ik} - 1)}{0.5}$$

Which is equivalent, in matrix notation, to $\mathbf{G} = \frac{(\mathbf{M}-1)(\mathbf{M}-1)'}{(N/2)}$, where \mathbf{M} is the genotype matrix containing values of 0, 1 and 2.

1. Eding H, Crooijmans R, Groenen MAM, Meuwissen THE: **Assessing the contribution of breeds to genetic diversity in conservation schemes.** *Genet Sel Evol* 2002, **34**(5):613-633.
2. Yang JA, Benyamin B, McEvoy BP, Gordon S, Henders AK, Nyholt DR, Madden PA, Heath AC, Martin NG, Montgomery GW, Goddard ME, Visscher PM: **Common SNPs explain a large proportion of the heritability for human height.** *Nat Genet* 2010, **42**(7):565-569.