**Supplementary Material S2 – Derivation of imputation accuracy when imputation is based on allele frequencies**

An alternative derivation to demonstrate that the imputation accuracy is zero when imputation is solely based on the allele frequencies, considering genotypes instead of alleles, is as follows. Consider the 3×3 possibilities of true () and predicted genotypes () and using 2, 1 and 0 for the genotypes:

|  |  |  |  |
| --- | --- | --- | --- |
|  | Imputed genotype | | |
| Observed genotype | 2 | 1 | 0 |
| 2 |  |  |  |
| 1 |  |  |  |
| 0 |  |  |  |

The covariance between the observed and predicted genotype is then