



Figure S4 An example of a genealogy underlying sequence data from three diploid individuals (*a*, *b*, and *c*). Homozygous sites (filled circles) or single heterozygous sites in an individual (white square on the branch leading to *b*1) present no phasing problem. Random phasing of unique heterozygous sites (green and red squares) does not affect the inferred topology of an *a*, *b*, *c* triplet alignment which is uniquely determined by shared derived mutations which may be homozygous (black circles) or complex heterozygous sites (yellow square). Similarly, random phasing of unique heterozygous sites does not introduce biases if the branches of the underlying genealogy have the same length (green squares).