1. Consider a pair of affected siblings genotyped for a marker with 2 alleles, with frequencies $p_1 = 0.6$ and $p_2 = 0.4$. The two siblings and their mother were genotyped and all three had genotype 1/2.

   a) List all possible inheritance vectors for this pedigree. For convenience, it may be useful to apply the founder symmetry of Kruglyak and colleagues to reduce the number of inheritance vectors.

   b) Calculate the probability of observed genotypes for each of the inheritance vectors and calculate the posterior probability of each inheritance vector conditional on the observed genotypes.

   c) Calculate information content for this family.

   d) Calculate the Z-score for a non-parametric linkage statistic based on the $S_{pairs}$ scoring function. The $S_{pairs}$ scoring function sums IBD sharing among all pairs affected individuals for each inheritance vector.

   e) Calculate the parametric LOD score for this family, assuming a disease model where the disease allele frequency is $p_D = 0.001$ and the disease allele frequencies are $f_{DD} = 0.20$, $f_{Dd} = 0.10$ and $f_{dd} = 0.0$. 
2. Consider the pedigree and the inheritance graph below:

Calculate the probability of the observed genotypes conditional on the inheritance graph. In your calculations, denote the allele frequency of alleles 1, 2, 3 and 4 as $p_1$, $p_2$, $p_3$ and $p_4$ respectively. You can assume there is no genotyping error.