



Letter to the Editor

Likelihood ratios in kinship analysis: Contrasting kinship classes, not genealogies

The standard universally accepted framework for evaluating the probability of a disputed kinship is the likelihood ratio formalism: the probability of the genetic observations assuming the kinship is contrasted with the probability of the same observations under the alternative hypothesis of a different degree of relationship (usually its absence) [1]. The common forensic genetics practice assumes that distinguishing between relationships is, given enough genetic information, always feasible in the double meaning that (a) convincing figures are reachable and (b) two alternative relationships correspond to different likelihood values. The first question is of great importance but depends upon technical and material issues that are outside the scope of this note (for a discussion on this topic see [2–4]); on the second we fear that some misunderstandings may occur among practitioners.

In fact, it has been shown that identical genetic probabilities correspond to distinct genealogies and so the aim of distinguishing any pair of alternative relatedness hypotheses (using solely unlinked autosomal markers) is essentially unattainable [4,5] (identity, paternity/maternity and full-brotherhood excepted). However, the common forensic geneticist—as well as the “consumers” of genetic expertise in court—may be misguided to the opposite inference when using the “avuncular index” [1] or employing kinship analysis software to calculate likelihoods of «alternative pedigrees» [6].

It is essential to bear in mind that, quoting [4], “identity-by-descent is crucial to measuring relatedness; however, it is an unobservable quantity”. Moreover, still quoting [4], “it is reasonably straightforward to find the probability of the genotypes of individuals when their relationship is known, but that it can be difficult to do the reverse and infer the probability of a relationship given the genotypes—as is required for most practical applications”. Relatedness between two individuals can be measured through the *coancestry coefficient* (θ), the probability that two randomly chosen alleles, one from each individual, at a given locus are identical-by-descent (IBD). Considering non-inbred individuals, this coefficient can further be decomposed in a more detailed description, into the probabilities of sharing: (a) both alleles— k_2 ; (b) just one— k_1 ; and (c) none— k_0 [4]. The values of these probabilities for some common kinships are shown in Table 1 (note that: $\theta = k_1/4 + k_2/2$). Two distinct genealogical relationships with coancestry coefficient θ belong to the same n -th kinship class, $KC(\theta, n)$, if they possess the same allele sharing probabilities k_0, k_1 and k_2 . It should be noted that all members of the same kinship class share the same coancestry coefficient, the reciprocal not being true (i.e., various genealogical relationships with identical coancestry coefficient do not belong to the same kinship class). This fact has profound implications for forensics, as it is shown in the following examples.

Table 1

Coancestry coefficient (θ), allele sharing probabilities through identity-by-descent (both alleles— k_2 ; one— k_1 ; none— k_0) and kinship class (see text for definition) for various common genealogical relationships between pairs of non-inbred individuals.

genealogical relationship	allele sharing partitions			θ	kinship class $KC(\theta, n)$
	k_2	k_1	k_0		
Parent–Child	0	1	0	1/4	$KC_{(1/4, 1)}$
Full-siblings	1/4	1/2	1/4	1/4	$KC_{(1/4, 2)}$
Half-siblings	0	1/2	1/2	1/8	$KC_{(1/8, 1)}$
Avuncular					
Grandparent–Grandchild					
Double first cousins	1/16	3/8	9/16	1/8	$KC_{(1/8, 2)}$
First Cousins	0	1/4	3/4	1/16	$KC_{(1/16, 1)}$
Parent's half-sib/ Half-sib's child					
Great-grandparent/ Great-grandchild					
Double half-cousins	1/64	7/32	49/64	1/16	$KC_{(1/16, 2)}$

Table 2

Probabilities of genotypes observed in a pair of individuals (A, B) with the same coancestry coefficient ($\theta = 1/8$), and belonging to the same kinship class ($KC_{1/8}$) such as half-siblings, avuncular or grandparent–grandchild, given the allele frequencies (f_i, f_j, f_k, f_l) at an autosomal locus.

A	B	Probability
$A_i A_i$	$A_i A_i$	$0.5 f_i^3 (f_i + 1)$
$A_i A_i$	$A_j A_j$	$0.5 (f_i f_j)^2$
$A_i A_i$	$A_i A_j$	$0.5 f_i^2 f_j (2f_i + 1)$
$A_i A_i$	$A_j A_k$	$f_i^2 f_j f_k$
$A_i A_j$	$A_i A_j$	$f f_j (2f_j + 0.5f_i + 0.5f_j)$
$A_i A_j$	$A_i A_k$	$f f_j f_k (2f_i + 0.5)$
$A_i A_j$	$A_k A_l$	$2f f_j f_k f_l$

The probability of genotype pairs conditional on the conjecture of two individuals being half-siblings is shown in Table 2. The formulas are exactly the same under the hypotheses of A being the uncle or the grandparent of B (or vice-versa). This means that the

Table 3

Probabilities of genotypes observed in a pair of individuals (A, B) with the same coancestry coefficient ($\theta = 1/4$), but belonging to different kinship classes ($KC_{1/4}$ and $KC_{1/4}$), such as parent–child and full-siblings, given the allele frequencies (f_i, f_j, f_k, f_l) at an autosomal locus.

A	B	Probability	
		parent–child	full-siblings
$A_i A_i$	$A_i A_i$	f_i^3	$0.25 f_i^2 (f_i + 1)^2$
$A_i A_i$	$A_j A_j$	0	$0.25 (f_i f_j)^2$
$A_i A_i$	$A_i A_j$	$f_i^2 f_j$	$0.5 f_i^2 f_j (f_i + 1)$
$A_i A_i$	$A_j A_k$	0	$0.5 f_i^2 f_j f_k$
$A_i A_j$	$A_i A_j$	$f f_j (f_i + f_j)$	$f f_j (f f_j + 0.5f_i + 0.5f_j + 0.5)$
$A_i A_j$	$A_i A_k$	$f f_j f_k$	$0.5 f f_j f_k (2f_i + 1)$
$A_i A_j$	$A_k A_l$	0	$f f f_j f_l$

probability we calculate in the likelihood ratio's numerator is the same for various distinct genealogical relationships. Inversely, two distinct genealogical relationships sharing the same coancestry coefficient, but belonging to distinct kinship classes do not share the same likelihood ratio (Table 3).

We conclude therefore that when calculating likelihood ratios in a specific kinship, (a) experts must be aware that the probability value in the odds-ratio numerator is the same for various kinship configurations, and (b) they should clearly convey this information to the court, (c) enabling a decision that takes into account the possibility of occurrence of alternative genealogical relationships.

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