Forensic Medicine

There are several problems in forensic medicine for which a statistical approach is particularly apt. These include, in particular, estimation of the post-mortem interval, or time since death, the estimation of the age at death, determination of sex from skeletal remains and, amongst the living, the estimation of the quantity of alcohol consumed, as well as issues of paternity. Simple summary statistics are used often; for example, in recording variations in relative frequencies amongst genetic marker systems in different populations. This issue is extended to a general discussion of problems of forensic identification, with particular reference to DNA profiling, by Dawid & Mortera [2]. Many standard statistical techniques, such as regression, are used. Only recently have other techniques, e.g. kernel density estimation and Bayesian methods been suggested.

Post-Mortem Interval

Accurate estimation of the post-mortem interval (PMI) is of obvious importance in the resolution of an investigation involving a corpse. The most common approach is to study factors, such as the temperature of various parts of the body, which vary with PMI, and to determine a suitable relationship between these factors and temperature. In 1962 Marshall & Hoare [9] published the following formula modeling rectal body temperature:

$$\frac{T_r - T_a}{T_0 - T_a} = A \exp(Bt) + (1 - A) \exp \left( \frac{AB}{A - 1} \times t \right).$$

where $T_r$ denotes rectal temperature at any time, $T_a$ denotes ambient temperature, $T_0$ denotes rectal temperature at death ($t = 0$), $A$ is a constant that expresses the relative duration of a post-mortem temperature plateau phase, $B$ is a constant that describes the cooling rate for as long as there is a difference between the ambient temperature and that of the body, and $t$ is the time of death. Note, however, that it is a mathematical formula. While no attempt appears to have been made to model the errors implicit in the estimation of the parameters, there have been many empirical studies to determine the magnitude of the errors. Correction factors have been introduced to allow for different environmental factors, for example. Sometimes nomograms are used that relate rectal temperature, ambient temperature and body weight to time since death. The Marshal–Hoare formula measures time since death in the early post-mortem period (i.e. in hours). For longer periods of time, measurement of post-mortem enzyme activity may be used [5].

Age at Death

Gustafson [6] determined age at death on the basis of a regression of adult human age on morphological changes of six characteristics in the structure of teeth. This was based on applying normal linear regression techniques to ordinal and categorical data. Gustafson claimed an error of about three to four years, though later estimates of about seven years or even 16 years have been determined. Various Bayesian approaches that account for the data structure and provide results with mean absolute deviations of four to six years are advocated by Lucy et al. [7] and kernel density methods are described by Aykroyd et al. [1].

Sex Determination

Linear discriminant analysis is used to aid the determination of the sex of skeletal remains. The high accuracies of discrimination obtained have their basis in the unique form of sexual dimorphism exhibited by the adult human pelvis. One recent study [8] derived a score function, using discriminant analysis, from 122 adults of known sex and applied this to 230 other adults of known sex with 100% correct classification.

Blood Alcohol Measurements

The amount ($A$) of alcohol consumed based on the blood alcohol concentration ($C_t$) is calculated using Widmark’s [12] formula:

$$A = r \times p \times [C_t + (\beta \times t)],$$

where $r$ is the ratio of the total body ethanol concentration to the blood ethanol concentration, $p$ is the body weight, and $\beta$ is the ethanol elimination rate constant. Note that $r$ varies between males and females. Various empirical studies have investigated
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the relationship between predicted and actual concentrations. The formula is also used for breath alcohol concentration by the substitution of its value for \( C_t \) in (2). This introduces another source of error, generally leading to a reduction in the estimated amount of alcohol consumed [4].

Inverse Prediction

Notice that (1) gives an equation for determining rectal temperature from time since death and that (2) gives an equation for determining the amount of alcohol consumed from a blood alcohol concentration. In both cases, the inverse prediction is required. This has been discussed briefly by Aykroyd et al. [1], where age at death is regressed on a score determined from six dental indicators of Gustafson [6].

Paternity

In a paternity case, a male is alleged by the mother of a child to be the father of the child. The truth of the allegation can be partially tested by calculating a so-called “probability of nonpaternity” or “probability of exclusion” \( Q \) in a specific genetic system. The genotypes of the mother and child provide information about the true father in that males with certain genes are excluded from fatherhood of the child.

Consider a co-dominant system where all genotypes are detectable (in contrast to a dominant/recessive system in which only phenotypes are detectable). Let

\[
p_1, p_2, \ldots, p_k, \quad \left( \sum_{i=1}^{k} p_i = 1.0 \right)
\]

represent the gene frequencies associated with a co-dominant system with \( k \) alleles, then

\[
Q = \sum_{i=1}^{k} \left[ p_i (1 - p_i) \right]^2 + \sum_{j=1}^{k-1} \sum_{i=i+1}^{k} p_i p_j \left[ (1 - p_i)^3 + (1 - p_j)^3 + (p_i + p_j)(1 - (p_i + p_j))^2 \right],
\]

where the assumption is made that all individuals involved in the paternity case come from a large random mating population at equilibrium [10].

Consider now several loci and let \( Q_l \) be the probability of exclusion at locus \( l \). The overall probability of exclusion (i.e. the probability the system will exclude a falsely accused male in a paternity action), \( Q \), follows from being able to exclude the alleged father from at least one locus. Thus, if the loci are independent [11],

\[
Q = 1 - \prod_{l} (1 - Q_l).
\]

A related approach expresses the probability that the alleged father is the true father \( (F) \), given the evidence \( (E_1, E_2, \ldots, E_n) \) of \( n \) phenotypic systems, as follows:

\[
Pr(F|E_1, E_2, \ldots, E_n) = \left\{ 1 + \frac{Pr(F)}{Pr(F)} \prod_{i=1}^{n} Pr(E_i|F) \right\}^{-1},
\]

where \( F \) is the event that the alleged father is not the true father. A particular example of this approach with \( Pr(F) = Pr(F) \) is described by Essen-Möller [3].

References


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