# Statistical Evaluation of the Evidential Value of Human Hairs Possibly Coming from Multiple Sources 

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#### Abstract

A concept of the mathematical evaluation of human hair evidence is derived. This concept can be realized in a special computer program, the output of which is an incrimination probability. The problems of not knowing the true number of sources and the correct partition of hairs corresponding to their sources are solved from the point of view of avoiding an unjustified incrimination.


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KEYWORDS: forensic science, hair, probability, human identification

The first attempts to interpret human hair comparisons in forensic casework by probabilities were by Gaudette and Keeping [ 1 ] and by Gaudette [2-4]. In Ref 1 , the discrimination probability of two randomly taken hairs is estimated on the basis of more than 360000 comparisons. But this statistical approach has since been criticized by several authors [5-7], whose concern is with improper statistical treatment of the data as well as with experimental bias. The estimated probability has no actual significance for criminalistics, since already one hair in the comparison process is not randomly chosen. Moreover, the calculated number for the considered probability heavily depends on the ability of the hair examiner, so that each examiner needs his own number.

A standardized method of evaluating hair evidence is necessary to overcome this weakness. Therefore, the creation of a united database proposed by Aitken and Robertson [8] is welcomed. It seems that the hair examination form given in Ref 9 can facilitate the setup of such a database.

The present paper deals with the statistical interpretation of human hairs found at the scene of crime or on the suspect's clothing, using a large database. A Bayesian approach is chosen which, in contrast to the method of Aitken and Robertson [7], also admits the existence of multiple sources for the examined hairs. The application of this approach in forensic science casework requires special software. The mathematical foundations for such software are represented in the paper. The one-hair case and the one-source case are initially described separately to avoid confusion.

## The One-Hair Case

In principle, the scientist has to choose between two possibilities:

[^0]$C$ the hair in question did, in fact, come from the suspected source, or
$\bar{C}$ the hair in question did not come from the suspected source.
In order for the scientist to make a more informed and valid choice, several macroscopic features such as the color, the shaft profile, the root end, and the tip end and several microscopic features such as pigment density, pigment distribution, granule shape of the pigments, and medulla type must be examined. According to the hair examination form of Aitken and Robertson [9], most of the features are discrete and can be described using a few categories.

For the sake of simplicity, we consider now only one abstract feature $X$ with the categories $x_{1}, \ldots, x_{k}$. The occurrence probabilities of the categories in the population can be estimated by the corresponding relative frequencies $\bar{p}_{1}, \ldots, \bar{p}_{k}$, by means of an existing database. If we assume that the questioned hair falls into the category $x_{i}$, then the database yields the estimated probability of this event $E=\left\{X=x_{i}\right\}$ under the hypothesis $\bar{C}$, written as

$$
P\left\{\frac{E}{\bar{C}}\right\}=\bar{p}_{i}
$$

Here, as is usual in mathematics, $P\{E / \bar{C}\}$ is the conditional probability of $E$, supposing that $\bar{C}$ is true. The smaller the value $\bar{p}_{i}$ is, the rarer is the category $x_{i}$ in the population. However, the significance of this value is only recognizable in connection with the corresponding probability

$$
P\left\{\frac{E}{C}\right\}=p_{i}
$$

The value $p_{i}$ must be estimated by the relative frequency of category $x_{i}$ within the suspected source. For this, a representative and large sample of hairs from the suspected source has been drawn. Now, the so-called likelihood ratio

$$
Q=\frac{P\left\{\frac{E}{C}\right\}}{P\left\{\frac{E}{\bar{C}}\right\}}=\frac{p_{i}}{\bar{p}_{i}}
$$

gives us the desired information to what extent the scientist's evidence $E$ favors the hypothesis $C$. Therefore, the likelihood ratio turns out to be an incrimination measure. However, it is not a probability. In order for scientists to obtain a probability relevant in criminalistics. prior knowledge about the hypotheses $C$ and $\bar{C}$ in form of prior probabilities $P(C)$ and $P(\bar{C})$ is necessary. Then, where Bayes' Theorem is applied, the incrimination probability is

$$
\begin{equation*}
P\left\{\frac{C}{E}\right\}=\left[1+\left(\frac{P(C)}{P(\bar{C})} Q\right)^{-1}\right]^{-1} \tag{1}
\end{equation*}
$$

This equation yields the probability that the hypothesis $C$ is true under the condition that the questioned hair belongs to category $x_{i}$. Obviously, two information sourcesthe prior information and the information contained in the evidence-enter into the resulting incrimination probability $P\{C / E\}$. The incrimination probability is, in fact, the unique probability summarizing and adequately reflecting both the experiences of the
examiners and the observed or measured attributes of the trace. It seems to be the probability many scientists such as Stoney [10] seek.

## Multiple-Hair Cases

## The case of n Hairs Coming From One Source

Sometimes case-relevant information is available which implies that all recovered hairs have come from one source. The two initial hypotheses can then be formulated as
$C$ the $n$ hairs in question did, in fact. come from the suspected source, or the $n$ hairs in question came from one source different from the suspected.

First, it should be noted that hairs coming from the same source can differ in the attribute considered. Now, assume that there are $n_{i}$ hairs of the recovered sample belonging to category $x_{i}(i=1, \ldots, k)$. Obviously, $n=n_{1}+\ldots+n_{k}$ must hold, where often some of the numbers $n_{i}$ are zero. Then, under hypothesis $C$, the probability of this evidence $E$ characterized by the observed categories is given by the multinomial distribution

$$
\begin{equation*}
P\left\{\frac{E}{C}\right\}=\frac{n!}{n_{1}!^{*} \ldots .^{*} n_{k}!} p_{1}^{n_{1} *} \ldots .^{*} p_{k}^{n_{k}} \tag{2}
\end{equation*}
$$

In order to calculate the likelihood ratio, we need the corresponding probability $P\{E /$ C\} of the evidence, supposing the hairs have come from one source different from the suspected. At first glance, the relative frequencies $\bar{p}_{i}$ of the database seem to be informative and the probability being of interest should be estimated by

$$
P\left\{\frac{E}{\bar{C}}\right\}=\frac{n!}{n_{1}!{ }^{*} \ldots{ }^{*} n_{k}!} \bar{p}_{1}^{n_{1} *} \ldots{ }^{*} \bar{p}_{k}^{n k}
$$

But, this calculation formula is only applicable if all hairs came from different sources. The values $\bar{p}_{i}$ reflect the variability of the feature $X$ within the population approximated by the database, whereas an intraindividual variability is required. Consequently, another way of estimating the probability $P\{E / \bar{C}\}$ must be found. For this purpose, a certain structure of the database, or more exactly of the file, is necessary. Each record must correspond to one source and must contain the relative frequencies of the categories $x_{i}$ ( $i=1, \ldots, k$ ) within this source. Denote the relative frequency of $x_{i}$ within the $t$ th source by $p_{i}(t)$; then the desired probability can be estimated by

$$
\begin{equation*}
P\left\{\frac{E}{\bar{C}}\right\}=\frac{1}{N} \frac{n!}{n_{1}!^{*} \ldots .^{*} n_{k}!} \sum_{i=1}^{N} p_{i}(t)^{n!} * \ldots .^{*} p_{k}(t)^{n k} \tag{3}
\end{equation*}
$$

where $N$ is the number of records. Equation 3 can be interpreted as a simulation of the unknown source which is carried out in the database. The likelihood ratio becomes

$$
\begin{equation*}
Q=\left[\frac{1}{N} \sum_{t=1}^{N}\left(\frac{p_{1}(t)}{p_{1}}\right)^{n 2} * \ldots *\left(\frac{p_{k}(t)}{p_{k}}\right)^{n k}\right]^{-1} \tag{4}
\end{equation*}
$$

Here $p_{i}>0$ is required if $n_{i}>0$, since in the other case the suspect is discharged de facto. Again, Eq 1 holds for the incrimination probability. It is easy to see that in the one-hair case ( $n=n_{i}=1, n_{j}=0$ for $j \neq i$ ), the likelihood ratio $Q$ is reduced to the more familiar form of the previous section.

## The Case of n Hairs Coming from Multiple Sources

We begin with the artificial assumption that there exist $r$ sources and that the assignment of the hairs to the sources is known. Then the hypothesis $C$ must be split into $r$ subhypotheses

$$
C_{i}=\text { the } i \text { th source is the suspected, } i=1, \ldots, r
$$

whereas the remaining alternative is

$$
\bar{C}=\text { all } r \text { sources are different from the suspected one }
$$

Also, the prior probability of $C$ must be split up into specified prior probabilities $P\left(C_{i}\right)$ of $C_{i}$, taking into account the relation

$$
P\left(C_{1}\right)+\ldots+P\left(C_{r}\right)=P(C)
$$

Simultaneously, the whole evidence $E$ is divided into partial evidences, $E_{i}$ only referring to the hairs of the $i$ th source.

It can be shown (see Appendix) that Eq 1 for the incrimination probability remains valid, where $Q$ is substituted by the weighted mean of source-dependent likelihood ratios, that is,

$$
\begin{equation*}
Q=\sum_{i=1}^{r} \frac{P\left(C_{i}\right)}{P(C)} * \frac{P\left\{\frac{E_{i}}{C_{i}}\right\}}{P\left\{\frac{E_{i}}{\bar{C}}\right\}} \tag{5}
\end{equation*}
$$

The conditional probabilities $P\left\{E_{i} / C_{i}\right\}$ and $P\left\{E_{i} / \bar{C}\right\}$ can be estimated according to Eqs 2 and 3, where the frequencies $n_{j}$ of the categories $x_{j}$ refer only to the hairs of the $i$ th source.

Thus, the exact incrimination probability can be calculated, if both the number of sources and the assignment of the hairs to the sources are known. However, these two assumptions are seldom realistic in practice. It is clear that the lack of knowledge about the true clusters of hairs must not affect the decision against the interests of the suspect. Consequently, the smallest incrimination probability or, equivalently, the smallest value $Q$ defined in Eq 5 is searched, where the minimum is taken over a set $S$ of possible partitions of the $n$ hairs. This can be done by software. Today, microcomputers allow relatively easy calculation and comparison of many incrimination probabilities. In order for the running time of the software to be reduced and the knowledge of the scientific expert to be taken in account, it should be possible to restrict the admissible partitions by an appropriate dialogue directed by the computer program.

## Discussion

The probabilistic interpretation of human hair evidence demands a well-structured, large database and a special computer program. The algorithm for the computer program should be based upon the Bayes formula. The problem of multiple sources has to be handled within the software by simulation of different partitions of the recovered hairs and determination of those clusters which minimize the incrimination probability. In this way, an unjustified incrimination of the suspect which results from not identifying the true clusters can be avoided.

There are three advantages in the use of a special hair examination program. First, the obtained results are rarely affected by subjective assessments, since the database is a collection of experiences made by many experts. Second, the examination process possesses a high effectivity because of the speed of computer calculations. Finally, the quality of the derived decisions is high due to the exact consideration of all available information. Moreover, it is possible to compare the evidential value of different hair traces.

It should be noted that the restriction to categorical attributes in the present paper should not be understood as a limitation for future research. Especially, the concentrations of different trace elements represent continuous attributes of hairs which allow a good individualization (see Refs 11 and 12). However, the mathematical treatment of such attributes differs from the one described here. The trace element concentrations must be modeled by normal distributions, so that a continuous version of the Bayes formula is needed.

## APPENDIX

## The Likelihood Ratio for the $r$ Sources Case

In general, Eq 1 holds with

$$
Q=\frac{P\left\{\frac{E}{C}\right\}}{P\left\{\frac{E}{\bar{C}}\right\}}
$$

In the case of $r$ sources, the events $C_{1}, \ldots, C_{r}$ defined in the article represent a disjoint partition of the event $C$. Therefore, the following transformation is valid, where the symbols $\cap$ and $\cup$ stand for the intersection and the union of events, respectively.

$$
\begin{aligned}
P(C) P\{E / C\} & =P(E \cap C) \\
& =P\left(E \cap\left(\bigcup_{i=1}^{r} C_{i}\right)\right) \\
& =P\left(\bigcup_{i=1}^{r}\left(E \cap C_{i}\right)\right) \\
& =\sum_{i=1}^{r} P\left(E \cap C_{i}\right) \\
& =\sum_{i=1}^{r} P\left(C_{i}\right) P\left\{\frac{E}{C_{i}}\right\} \\
& =\sum_{i=1}^{r} P\left(C_{i}\right) \prod_{j=1}^{r} P\left\{\frac{E_{j}}{C_{i}}\right\}
\end{aligned}
$$

The last equality follows from the independence of the $r$ traces. Now, note that

$$
P\left\{\frac{E_{j}}{C_{i}}\right\}=P\left\{\frac{E_{t}}{\bar{C}}\right\}
$$

holds for $j \neq i$. Consequently,

$$
\begin{aligned}
Q & =\frac{\left[\sum_{i=1}^{r} \frac{P\left(C_{i}\right)}{P(C)} P\left\{\frac{E_{i}}{C_{i}}\right\} \prod_{\substack{i=1 \\
j \neq i}}^{r} P\left\{\frac{E_{j}}{\bar{C}}\right\}\right]}{\prod_{i=1}^{r} P\left\{\frac{E_{i}}{\bar{C}}\right\}} \\
& =\sum_{i=1}^{r} \frac{P\left(C_{i}\right)}{P(C)} \frac{P\left\{\frac{E_{i}}{C_{i}}\right\}}{P\left\{\frac{E_{i}}{\bar{C}}\right\}}
\end{aligned}
$$

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