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## Studies of Models of Striated Marks Generated by Random Processes

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**ABSTRACT:** Computer-aided studies of the degree of similarity of striated marks are described. Digitized image data on 40 grinding marks were fed into a minicomputer, and the position values of the lines were determined semiautomatically. Idealized models were defined for an objective comparison of striated marks and then applied to the grinding mark data. Necessary conditions of the models were tested by comparing them with actual, measured properties of the marks. Results of the model calculations are presented and the properties of the models discussed.

**KEYWORDS:** criminalistics, striations, computers

The comparison of striated marks is of great importance in the forensic sciences. Examiners magnify the marks by microscope and decide, on the basis of their experience, whether the degree of similarity is sufficient for an identification. One aim of scientific research is to develop methods to make possible objective and reproducible results. Several authors [1-4] have attempted to develop such methods to evaluate the degree of match of striated marks. Furthermore, those research efforts have investigated some aspects of automating the comparison of marks. This paper studies several probability theory models and describes the results obtained from a total of 40 impressions of grinding marks. Digitized image data were fed into a minicomputer and reduced semiautomatically to the relevant information.

### Experimental Setup

Special equipment and a computerized image data processing system were developed [5,6] and are described in the following sections.

### Generation of Marks

The edges of multiple-purpose shears were passed by hand along a grindstone (average roughness depth of the shears, 10  $\mu\text{m}$ ). This process caused surface wear of the grindstone. Various areas of the grindstone were used as the shears were passed along it. Therefore it is assumed that in each case a different configuration of the surface of the grindstone created the patterns on the shears. When metal is cut, those patterns are impressed onto the cut surface of the metal. Two impressions each from 20 shears were made into lead.

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### *Image Preparation and Scanning*

A 1.2-mm section of the marks was magnified with a light microscope and photographed (illustration scale on the negatives, 10:1). The negatives were mounted on a computer-controlled scanning table and scanned line by line by a microscope photometer (Leitz MPV II). The data were digitized with a ten-bit analog to digital converter and fed into a computer (Honeywell H316). The distance between two image points was 20  $\mu\text{m}$ .

### *Software*

A program system for the acquisition, reduction, and comparison of data on striations has been developed. It consists of a series of FORTRAN IV and Assembler programs. A block diagram of the system is shown in Fig. 1. The programs for the acquisition and reduction of data are run on the H316 computer under the operating system BOS. The programs for the comparison of the marks and the display of results (Tektronix 4014) are run on a PDP11/70 (Digital Equipment) with the operating system RSX11M because of its faster speed of calculation.

For control purposes the digital image data are transferred to a gray-level display system (Ramtek GX100B) after the data acquisition. The area to be evaluated and the defective parts to be disregarded are communicated to the computer interactively ("trackball"). Subsequently, all scans of the image data are averaged. Because of the high redundancy in the images of the striations, the average photometric curve contains the essential information and is reduced to line diagrams after a seven-point smoothing. Only that information extracted from the position of the mark elements (called lines) has been used. The position of the lines corresponds to that of the bright stripes in the photograph shown in Fig. 2.

It may be possible to eliminate the image-processing part of the program system. Alternatively, striated line position values that have been measured manually on a photograph or under a microscope can be fed into the computer via a terminal. This input mode is foreseen for future applications.

### **Probability Theory Models**

A high degree of similarity between two sets of marks is not sufficient to identify a tool if it is highly probable that the similarity may occur by chance. For this reason, the following question has been studied: Given two patterns that are similar to a certain degree, what is the probability that such a similarity or an even greater one occurs at random? To answer this question, models were constructed. Different model approaches were studied, and the necessary assumptions were checked as far as possible.

### *General Aspects of the Models*

To examine the models, a total of 40 images of marks generated by shears were available, and these patterns were compared with each other. An attempt was made to derive from the collected data those model parameters that are specific to this type of grinding marks and to use those parameters to calculate probabilities for the various comparisons. This attempt was abandoned. Apparently the process of generating these marks differs from one pair of shears to the next; the number of lines of the various patterns varies, for instance, within a defined section to a greater extent than is to be expected on the basis of statistics.

An attempt was then made to derive the data required for the model calculations directly from the line diagrams to be compared. The two patterns of equal length to be compared were lined up and then one was moved. That part of the second pattern that jutted out at one end after the shift was transposed to the beginning of the pattern, so that both patterns were always directly aligned (Fig. 3). This method corresponds also to the way of proceeding in

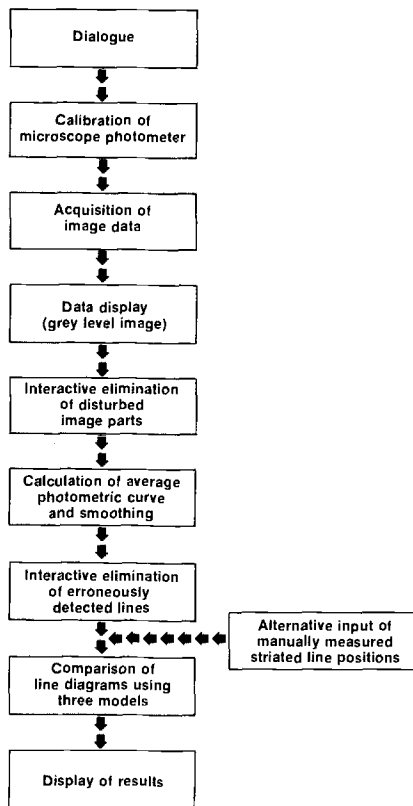


FIG. 1—Block diagram of the program system for the acquisition and evaluation of data from striations.

relation to the cyclic cross correlation. The random pattern arrays generated by the shifting were compared.

After each shift the number of matching striae of the two patterns was counted. Each line of the first pattern was framed. If a line of the second pattern fell within this frame, it was counted as a match. Because of the variation of the positions of the striations generated repeatedly by one tool, a finite width for the frames must be assumed. This width was about twice the maximum difference between the positions of corresponding striae. By the cyclic shifting process information about the random occurrence of certain numbers of matches and about the distribution of the distances between the matching striae was obtained. These frequency distributions were needed for the model studies. Figure 4 gives an idea of the statistical fluctuations in the numbers of matches. It shows probability values that correspond to the numbers of matches that depend on the shifting of the patterns. Shift number 0 signifies an excellent match of the two patterns generated by the same pair of shears.

The construction of models is always based on certain assumptions. The common assumptions for the models described in this paper are these:

1. Random processes generate the patterns on the tools.
2. The different patterns on tools produced by the same machine are independent. This means that specific striation groups are not transferred onto a series of tools when they are manufactured.
3. The probability of the occurrence of a line is independent of its position.

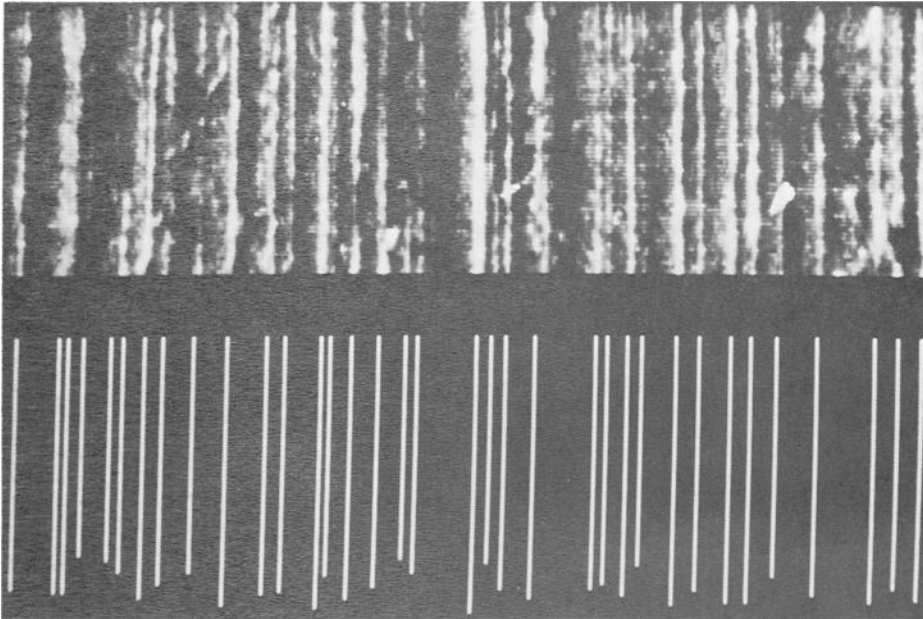


FIG. 2—Representation of the impression of grindstone-marked shears in lead and the corresponding diagram on the display system (64 gray levels).

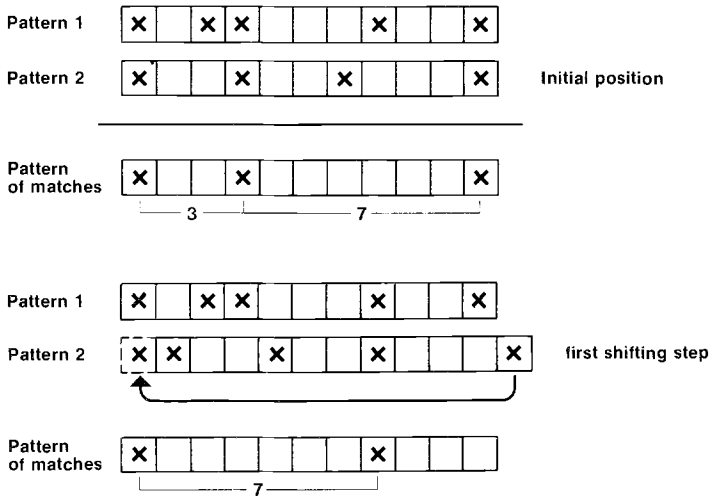


FIG. 3—Explanation of the cyclic shifting process (interval length, one scanning unit; step width, 1).

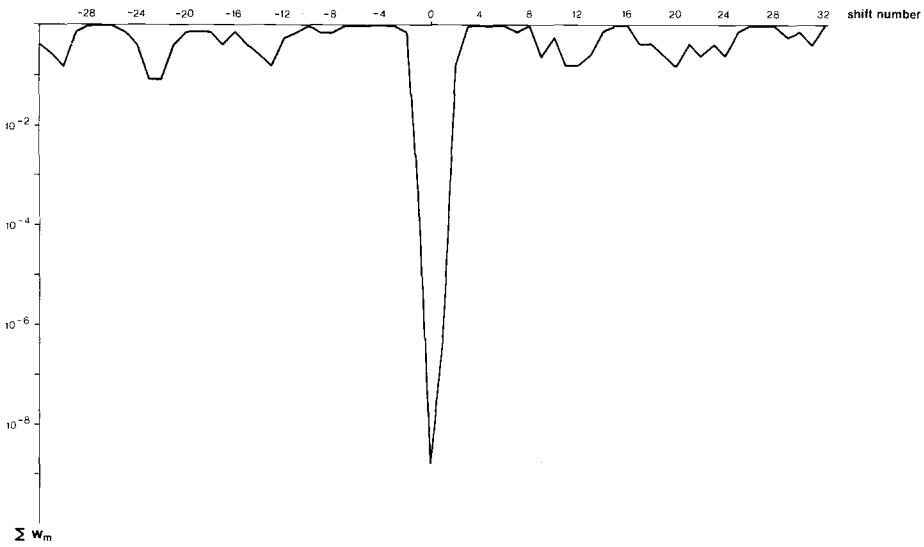


FIG. 4—Statistical fluctuations with part of the cyclic shifting process. Probability values are calculated with the binomial function fit (section, 800  $\mu\text{m}$ ; number of intervals, 133; interval length, three scanning units; step width, 1).

4. The density of the striae is constant across the studied section of the pattern. Consequently, the different segments of the pattern have the same degree of roughness.

The grinding marks that are subject of this study meet these requirements.

*Description of the Models*

*Combinatorial Model*—Given a set of patterns of equal length with  $k$  lines, the patterns can be divided into  $n$  intervals, with the size of each interval equaling the size of the frames mentioned in the previous paragraph. Each interval may contain at most one line. Then

$$\binom{n}{k}$$

different striation arrangements are possible. It is assumed that all pattern arrangements occur with the same probability. Then the probability that any pattern should be identical to a given pattern is equal to

$$1/\binom{n}{k}$$

In practice, however, it often happens that not all of the striations of two marks generated by the same tool match and that the number of striae of the two patterns differs. In that case one has to determine the probability of two patterns having a certain degree of random match. The extension of the combinatorial approach leads to the hypergeometric distribu-

tion [7]. It permits the calculation of the probability  $w_m$  that  $m$  lines of two patterns match at random, if the first pattern comprises  $k_1$  and the second pattern  $k_2$  lines:

$$w_m = \frac{\binom{k_1}{m} \cdot \binom{n - k_1}{k_2 - m}}{\binom{n}{k_2}} = \frac{\binom{k_2}{m} \cdot \binom{n - k_2}{k_1 - m}}{\binom{n}{k_1}}$$

The sum

$$\sum_{i \geq m} w_i$$

indicates the probability that at least  $m$  striae of two samples match. This probability value is also used with the other models.

*Renewal Theory Model*—Two striated diagrams to be compared are shifted along each other at full length, and after each shift the matching striae are determined and the distances between successive line matches are calculated (Fig. 3). Thus one gets a distribution of the distances between the random line matches, which is the starting point for the renewal theory model. If two patterns generated by the same tool are placed next to each other, a very high degree of match occurs with shifting number 0 (initial position). This high degree of match does not occur at random, since the marks were generated by the same tool. Therefore this shifting region is disregarded when the distance distribution is determined. On the basis of this distribution the probability is calculated that  $m$  striae fall at random within a given number of intervals [ $\delta$ ]. If  $g_i$  represents the probability that the distance between two matching lines is equal to the width of  $i$  intervals, then the probability that the  $r$ th match falls within the  $i$ th interval is expressed by the following formula:

$$g_i^{(r)} = g_1 \cdot g_{i-1}^{(r-1)} + g_2 \cdot g_{i-2}^{(r-1)} + \dots + g_{i-1} \cdot g_1^{(r-1)}$$

The probability that  $m$  striae fall within  $n$  intervals is then calculated as follows:

$$w_m = \sum_{i=m}^n g_i^{(m)} \cdot (1 - G_{n-1})$$

where  $G_0 = 0$  and

$$G_k = \sum_{j=i}^k g_j$$

A necessary condition for this model is that the distances between successive coincidences are independent of each other.

*Binomial Function Fit*—Two patterns are compared, and the number of matches is counted. Consequently, one gets a frequency distribution of the random match numbers by the cyclic shift. This permits the calculation of the probability  $p$  that a coincidence falls within a certain interval. The probability of the occurrence of a certain number of line matches is calculated on the basis of the binomial distribution:

$$w_m = \binom{n}{m} \cdot p^m \cdot q^{n-m}$$

wherein  $q = 1 - p$ . The extrapolation of the binomial function makes possible statements about the probability of higher degrees of match. The necessary condition for this model is

that for a given number of coincidences all possible patterns of those coincidences are equally probable.

### **Application of the Models**

The models were applied to a total of 40 impressions of grinding marks, each being 1.2 mm long. These 40 sets permitted the performance of a total of 820 cyclic shifts.

#### *Determination of the Interval Length*

Calculations based on diagrams generated by the same shears led to the result that, for all models, an average interval length of three scanning units (together equal to an object-related width of 6  $\mu\text{m}$ ) delivered the smallest probability values (Table 1). When other diagrams were compared, however, other interval lengths ranging from two to five scanning units produced smaller probability values. Therefore it was not possible to define the interval length unambiguously. All additional examinations were performed with an interval length of three scanning units.

#### *Checking Assumptions*

Probabilities of highly infrequent events such as the complete match of two patterns cannot be checked since for practical reasons the sample size cannot be made sufficiently large. Assumptions of the probability calculations can, however, be tested with frequent events. For this purpose the statistical fluctuations of the random match numbers obtained during the cyclic shift are analyzed. With the aid of the model parameters it is possible to predict this distribution of the random match numbers or, alternatively, the parameters are fitted to this distribution. In either case, the quality of the adaptation can be estimated by means of a  $\chi^2$  test, and in this way one can check on whether or not an extrapolation aiming at greater numbers of matches appears to be justified (Fig. 5). In most cases the  $\chi^2$  test indicated a still satisfactory adaptation; however, the distribution of the calculated  $\chi^2$  values was somewhat wider than expected.

Another type of test takes advantage of the fact that by the cyclic shift of the patterns a large group of comparisons is obtained. Thus the number of comparisons made during a cyclic shifting process equals the number of the intervals (200 at most). The frequency of infrequent events with regard to the various model calculations can be counted and compared with the numerical values to be expected. Table 2 indicates the expected frequencies for various intervals of probability and the actually counted absolute and relative frequencies.

The renewal theory model and the binomial function fit use statistical fluctuations in connection with the random matches to compute the probability of occurrence of certain numbers of line matches. These fluctuations may be determined by the fact (1) that a given pattern is compared with itself, or (2) that two different patterns generated by the same tool are compared to each other, or (3) that two patterns generated by different tools are compared to each other. The experimental results showed a good agreement among these three distributions.

### **Results of the Probability Theory Models**

Figure 6 shows the results of the probability calculations for the comparisons of the 40 line diagrams for different pattern lengths, each diagram being compared with itself (100% match). The end points of the strokes indicate the highest and lowest values of the respective series. The combinatorial model produces the smallest and the binomial function fit the greatest probabilities. For a given pattern length the binomial function fit results in the narrowest range of probability values. A pattern 1.2 mm long contains an average of 36 striae.

TABLE 1—Effect of the interval length on probability values (0.4-mm sections).

Interval Length	Number of Intervals	Combinatorial Model	Binomial Function Fit	Renewal Theory Model
1	200	$0.82 \times 10^{-1}$	$0.87 \times 10^{-1}$	$0.55 \times 10^{-1}$
2	100	$0.82 \times 10^{-2}$	$0.17 \times 10^{-1}$	$0.55 \times 10^{-2}$
3	67	$0.98 \times 10^{-4}$	$0.16 \times 10^{-2}$	$0.15 \times 10^{-3}$
4	50	$0.12 \times 10^{-3}$	$0.32 \times 10^{-2}$	$0.33 \times 10^{-3}$
5	40	$0.60 \times 10^{-3}$	$0.99 \times 10^{-2}$	$0.16 \times 10^{-2}$

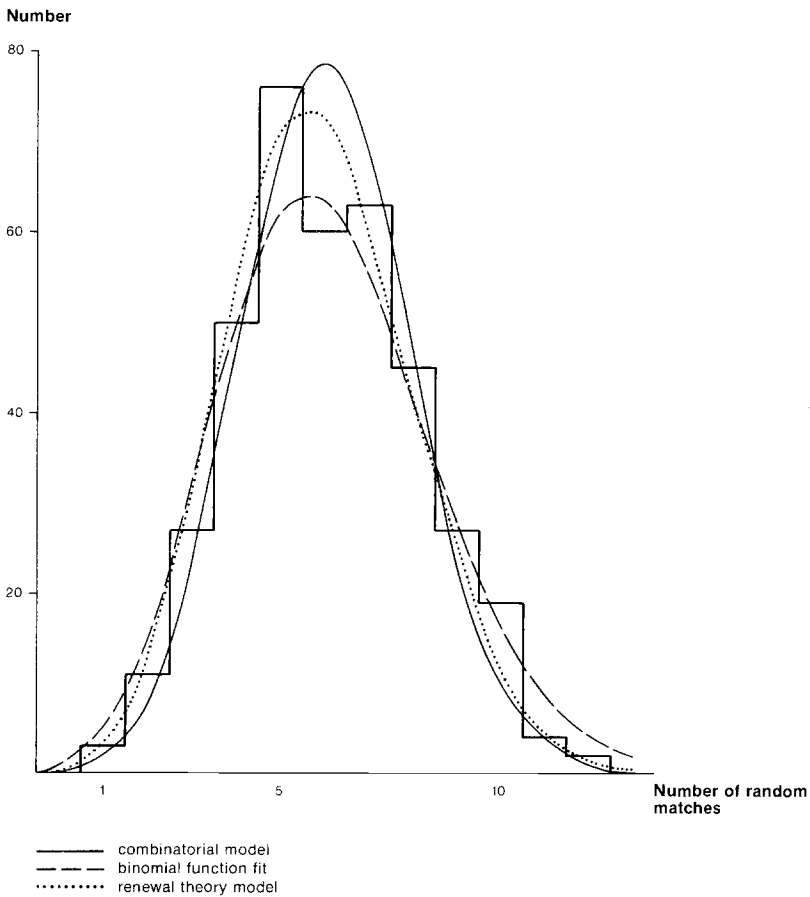


FIG. 5—Frequency distribution of the random matches resulting from the cyclic shifting process with different adaptations (section,  $800 \mu\text{m}$ ; number of intervals, 133; interval length, three scanning units; step width, 1).

### Combinatorial Model

The combinatorial model is based on the assumption that all conceivable patterns are equally probable given a defined number of intervals and striae. In this case one expects an exponential distribution of the distances between successive striations [5]. Figure 7 shows the



TABLE 2—Frequencies of the values of  $\Sigma w_m$  obtained by the cyclic shifting process for random matches (number of intervals, 200; interval length, three scanning units; section, 1.2 mm; step width, 3).

Regions for $\Sigma w_m$	Frequency with the Combinatorial Model		Frequency with the Binomial Function Fit		Frequency with the Renewal Theory Model	
	Absolute	Relative	Absolute	Relative	Absolute	Relative
1 to $10^{-1}$	150 738	0.92	155 477	0.95	151 089	0.92
$10^{-1}$ to $10^{-2}$	11 601	$0.71 \times 10^{-1}$	8 014	$0.49 \times 10^{-1}$	11 743	$0.72 \times 10^{-1}$
$10^{-2}$ to $10^{-3}$	1 298	$0.79 \times 10^{-2}$	315	$0.19 \times 10^{-2}$	912	$0.56 \times 10^{-2}$
$10^{-3}$ to $10^{-4}$	162	$0.99 \times 10^{-3}$	14	$0.85 \times 10^{-4}$	69	$0.42 \times 10^{-3}$
$10^{-4}$ to $10^{-5}$	17	$1.04 \times 10^{-4}$	0	0.0	7	$0.43 \times 10^{-4}$
$< 10^{-5}$	4	$2.44 \times 10^{-5}$	0	0.0	0	0.0

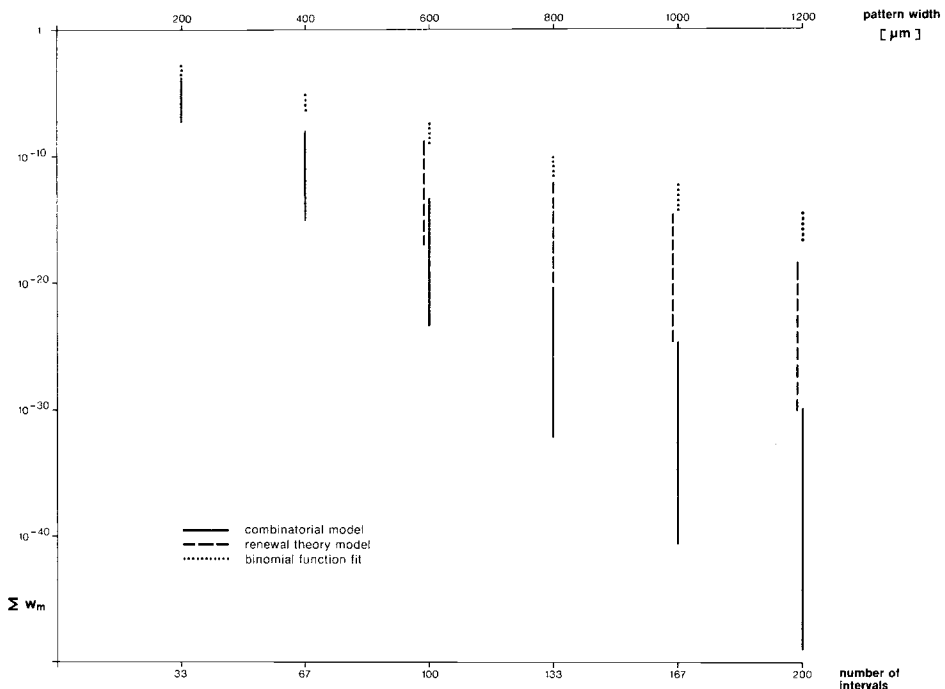


FIG. 6—Ranges of probability values resulting from the comparisons of patterns with themselves (40 diagrams; interval length, three scanning units; step width, 3).

actual distribution of distances measured on the total of 40 tool marks. This distribution deviates considerably from the exponential one. Thus this requirement of the combinatorial model is not fulfilled. On the other hand, Table 2 shows that the actual and expected frequencies with regard to the various probability intervals still agree satisfactorily. Consequently the combinatorial model provided a reasonable range of probability for not-too-high degrees of pattern match. However, for very infrequent events this model calculated too low a probability.

#### *Renewal Theory Model*

The starting point for the probability calculations of the renewal theory model is the distribution of distances of successive random matches (Fig. 8). When very short pattern sections are compared this distribution cannot be determined with adequate statistics, so that the model computation is not applicable and, therefore, values for 200- and 400- $\mu\text{m}$ -long patterns calculated by this model have been omitted from Fig. 6. Table 2 shows that small probability values do not occur at random more frequently than is to be expected. The necessary condition that the distances between successive coincidences are independent of each other was tested and it was found that there is no correlation between the length of spaces between successive coincidences.

#### *Binomial Function Fit*

The condition for the binomial function fit model is that given a certain number of line matches the probability is the same for all possible patterns with this given number of ele-

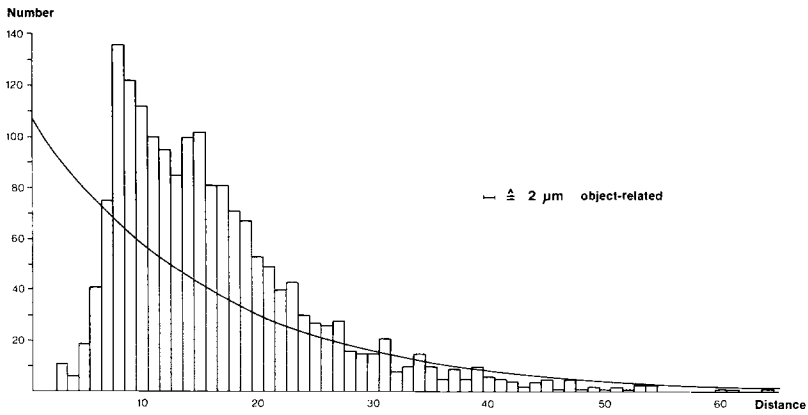


FIG. 7—Frequency distribution of the distances between successive striae of grinding marks (40 diagrams).

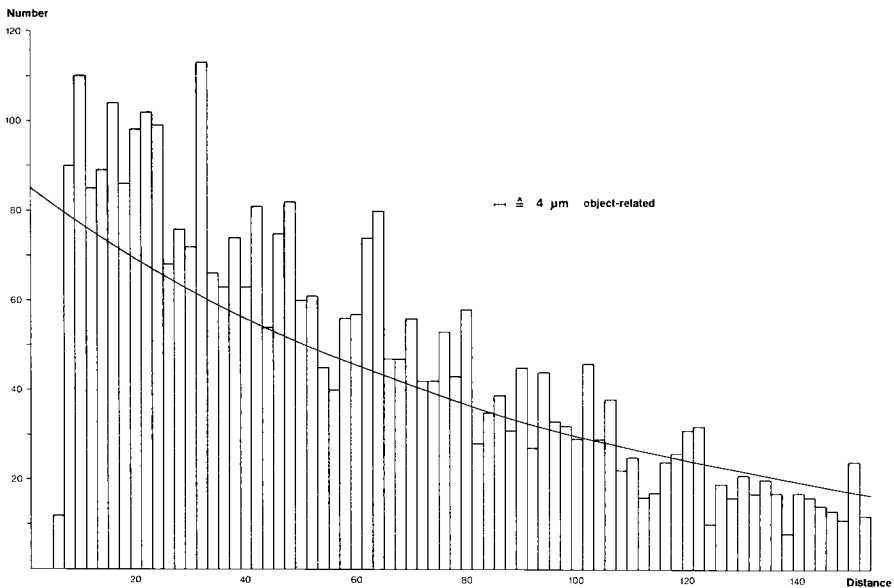


FIG. 8—Distribution of distances between successive random matches (760 comparisons; 40 diagrams; interval length, three scanning units; no cyclic shifting process).

ments. This requires an exponential distribution of the distances between random line matches. The actual distribution obtained by the addition of the results of 760 comparisons shows considerable deviations for only small distances (Fig. 8). It may be expected that the distribution of the numbers of matches resulting from the comparisons of different patterns is narrower than the fitted binomial function. This has been observed. Extrapolation with the binomial function should therefore deliver probabilities that are too high for large num-

bers of matches. This conclusion is supported by counting the frequency of the occurrence of low probability values, which is smaller than expected (Table 2).

**Run Distribution Model**

Examinations were performed with respect to the run distribution model described by Brackett [3]. He found that run distributions of striated mark comparisons obey the relationship:

$$N/p^* = s_1 (1 + 2/r + 3/rr' + 4/rr'r'' \dots)$$

where

$N$  = total striae (counting each matching striation as one, and each nonmatching striation as one),

$p^*$  = the reciprocal of the probability of match,

$r = s_1/s_2$ ,

$r' = s_2/s_3$ , and so forth, and

$s_i$  = the number of runs of size  $i$ .

Figure 9 shows the experimentally obtained run distribution of 760 comparisons obtained by applying the cyclic shifting process. The ideal distribution equation with  $p^* = r = r' = r'' \dots$  is not fulfilled. A good fit of the data is given with  $r = r' = r'' \dots$  ( $p^* = 10.2$ ;  $r = 5.0$ ). Probability calculations for the comparisons of the patterns with themselves with

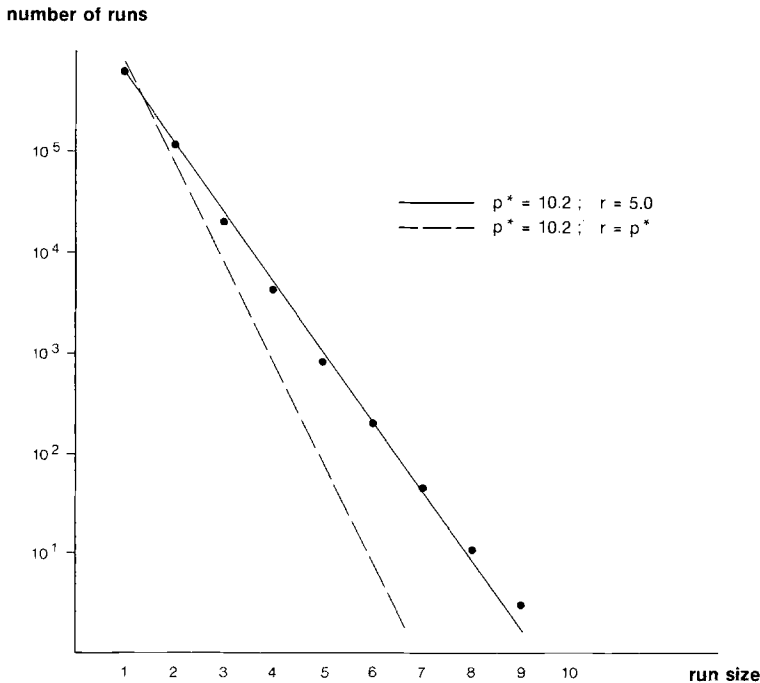


FIG. 9—Run distribution resulting from the cyclic shifting process (760 comparisons; 40 diagrams; number of intervals, 200; interval length, three scanning units; total striae,  $9.911 \times 10^6$ ).

these constants delivered values usually lying between those of the combinatorial and the binomial function fit models.

### Summary

Different model approaches were used to calculate the probability of the random occurrence of matches when 40 striated marks were compared. The requirement needed for the combinatorial model that the probability of all possible patterns should be the same is not fulfilled. The combinatorial model, under the conditions tested here, gives estimates that are too low for very low values of probability. With the binomial function fit to the distribution of the random match numbers, in most cases, the actual distribution is somewhat narrower than the fitted function, so that in general the extrapolated probabilities are too high. The renewal theory model can be applied to fairly long patterns, since short patterns allow only an inaccurate determination of the distribution of the distances between random matches. Furthermore, statistical parameters in respect to the run distribution model are determined.

For a high degree of match, the probabilities provided by the models are so small that they cannot be statistically ascertained. Additional pattern configurations could be generated by means of a cyclic shifting process. By using 1.2-mm-wide marks, with more than  $10^5$  comparisons, the frequency of probability values down to  $10^{-5}$  could be ascertained by counting.

If the manufacturing process produces machining marks on the tools, admitting the possibility of a false line match being mistaken for a true one, the model requirements are not fulfilled. However, the numerical values computed with the aid of the models permit an evaluation of the degree of similarity. For automation of pattern comparisons a preselection is possible, but any probability-related statements require additional studies and examinations.

## APPENDIX

### Comparison of Two Striations Differing in Width

In the text the assumption was made that two patterns of the same length are available for comparison. In practice, however, it often happens that the comparative mark (Pattern 1) is wider than the mark (Pattern 2) found at the scene of a crime, and therefore the probability calculations have to be modified.

A distinction must be made as to whether or not both patterns show a fixed reference point because of a type-related feature. This comparative feature for the marks left by a pair of shears may, for instance, be the edge generated by the end of the shears. Furthermore, it has to be determined if the good match applies to the entire section of the narrower pattern or only to a continuous partial section. The four cases described below result from these considerations.

#### Case 1

Pattern 1 is wider than Pattern 2 (Fig. A1). The entire region of Pattern 2 shows a good match with part of Pattern 1. A fixed reference point in the form of a type-related feature does not exist.

For the matching region calculations were made to determine the probability

$$w = \sum w_m$$

that the existing degree of match occurs at random. Since a fixed point of reference in the form of a type-related feature does not exist for both patterns, Pattern 2 could be compared with Pattern 1 in other sections as well. There is a total of  $c = n_1 - n_2 + 1$  comparative sec-

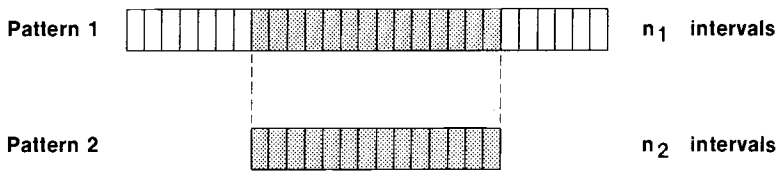


FIG. A1—Diagram of Case 1.

tions, where  $n_1$  and  $n_2$  indicate the total number of intervals of Pattern 1 and Pattern 2, respectively. The probability  $w^*$  that for these comparative sections the existing degree of match occurs at random is calculated by means of the binomial distribution as follows:

$$w^* = \sum_{i=1}^c \binom{c}{i} w^i v^{c-i} = 1 - v^c = 1 - (1 - \sum w_m)^c \quad (1)$$

where  $v = 1 - w$ . Approximately,

$$w^* \approx c \cdot \sum w_m$$

applies, if

$$c \cdot \sum w_m < 1 \quad (2)$$

#### Case 2

Pattern 1 is wider than Pattern 2. Only a continuous part of Pattern 2 shows a good match with Pattern 1. A fixed reference point in the form of a type-related feature enabling orientation does not exist (Fig. A2). To calculate the probability  $w^*$  that a certain degree of match occurs, the number of comparative constellations must be determined. In this case  $c = (n_1 - n + 1)(n_2 - n + 1)$  applies, wherein  $n$  indicates the number of intervals of the matching region. The calculation of  $w^*$  can again be made according to Eqs 1 and 2.

#### Case 3

Pattern 1 is wider than Pattern 2. The entire region of Pattern 2 shows a good match with part of Pattern 1. A fixed reference point for both patterns in the form of a type-related feature exists (Fig. A3). In this case there is only one comparative constellation:  $c = 1$ . Consequently, the following equation applies:

$$w^* = \sum w_m$$

#### Case 4

Pattern 1 is wider than Pattern 2. A partial region of Pattern 2 with  $n$  intervals shows a good match with Pattern 1. A reference point enabling the mutual orientation of the patterns exists (Fig. A4). In this case there are  $c = n_2 - n + 1$  comparative constellations and  $w^*$  is calculated according to Eqs 1 and 2.

The values for  $c$  obtained from the calculations of the number of comparative constellations are somewhat too high, since neighboring constellations of comparisons are correlated with each other. Thus the computation of  $w^*$  is conservative.

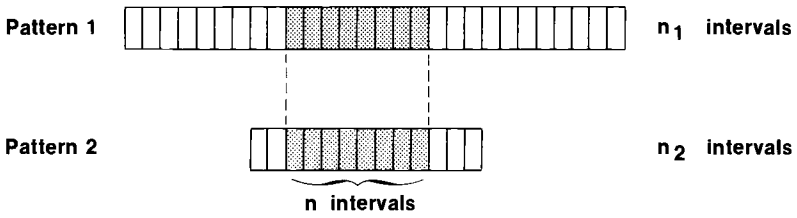


FIG. A2—Diagram of Case 2.

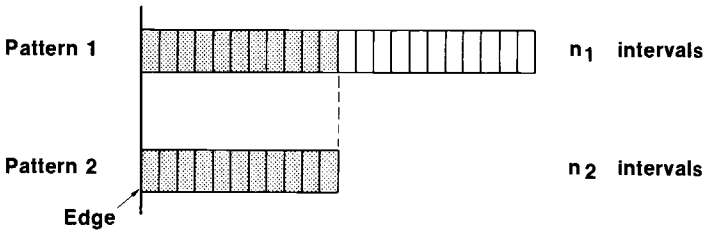


FIG. A3—Diagram of Case 3.

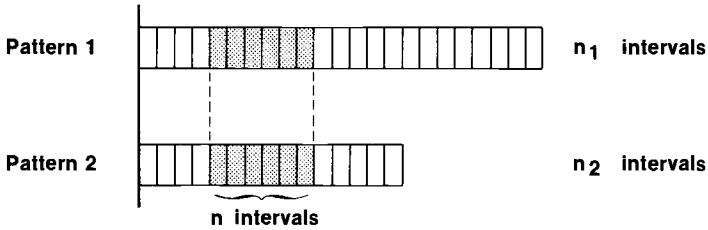


FIG. A4—Diagram of Case 4.

**Examples of the Model Calculations**

In the following two examples, model calculations will be presented. Two striated line diagrams of grinding marks produced by the same tool are given in each case to be compared to each other.

*Longer Patterns*

Given two patterns, each being 720  $\mu\text{m}$  long (360 scanning units), with  $k_1 = 26$  and  $k_2 = 25$  lines, the position values in scanning units are:

Diagram 1: 7, 18, 31, 37, 44, 54, 64, 86, 103, 106, 125, 141, 165, 175, 199, 211, 225, 241, 261, 271, 285, 308, 322, 330, 341, 352.

Diagram 2: 10, 19, 31, 36, 44, 54, 85, 102, 124, 141, 154, 165, 174, 198, 212, 225, 241, 261, 271, 292, 309, 322, 330, 340, 353.

Let the interval length be three scanning units. Then the number of intervals is  $n = 120$ , and the number of matching lines is  $m = 22$ . The probability that an accidental coincidence is within a certain interval is  $p = 0.0446$ . The model calculations brought the following results:

Combinatorial model:  $\Sigma w_m = 4.8 \times 10^{-17}$

Renewal theory model:  $\Sigma w_m = 1.1 \times 10^{-12}$

Binomial function fit:  $\Sigma w_m = 1.7 \times 10^{-8}$

### Shorter Patterns

Only the first halves of the former patterns are evaluated:

Length: 360  $\mu\text{m}$  (180 scanning units),  $k_1 = 14$ ,  $k_2 = 13$

Interval length: three scanning units,  $n = 60$

Diagram 1: 7, 18, 31, 37, 44, 54, 64, 86, 103, 106, 125, 141, 165, 175

Diagram 2: 10, 19, 31, 36, 44, 54, 85, 102, 124, 141, 154, 165, 174

$m = 11$ ,  $p = 0.0494$

Combinatorial model:  $\Sigma w_m = 7.4 \times 10^{-8}$

Renewal theory model:  $\Sigma w_m = 2.4 \times 10^{-6}$

Binomial function fit:  $\Sigma w_m = 1.5 \times 10^{-4}$

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