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Validation of Tool Mark Comparisons Obtained Using a Quantitative, Comparative, Statistical Algorithm

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Validation of Tool mark Comparisons Obtained Using a Quantitative, Comparative, Statistical Algorithm

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ABSTRACT: A statistical analysis and computational algorithm for comparing pairs of tool marks via profilometry data is described. This analysis is superior to *ad hoc* comparisons based on maximized correlation values, described in Faden et al. (2007). Empirical validation of the method is established through experiments based on tool marks made at selected fixed angles from fifty sequentially manufactured screwdriver tips that had yet to see use. Further comparisons between scores produced by the algorithm and visual assessments of the same tool mark pairs by professional tool mark examiners in a blind study in general shows good agreement between the algorithm and human experts. In a limited number of cases where the algorithm had difficulty in assessing a particular comparison pair, results obtained during the visual assessment and in discussion with professional examiners suggest ways in which algorithm performance may be further enhanced.

KEYWORDS: forensic science, tool mark comparison, comparison microscope, screwdriver, statistics, striae

In the fifteen years since the 1993 Daubert vs. State of Florida decision, increasing attacks have been aimed at firearm and tool mark examiners by defense attorneys via motions to exclude evidence based on expert testimony. Such motions claim that the study of tool marks has no scientific basis, that error rates are unknown and incalculable, and that comparisons are subjective and prejudicial. Often persuasive, these motions skillfully blend truth with unsupported assertions or assumptions in a number of ways. Firstly, the claim that scientific evidence is lacking in tool mark examinations ignores the numerous studies that have been conducted, especially in the area of firearms [1-4], to investigate the reproducibility and durability of markings. These studies have shown time and again that while matching of cartridges cannot be universally applied to all makes and models of guns using all types of ammunition, the characteristic markings produced are often quite durable and a high percentage can be successfully identified using optical microscopy. Secondly, the claims that error rates are unknown, and that the probability of different guns having identical markings has not been established, are true. However, it must be understood that establishing error rates and probabilities in the area of tool marks is fundamentally different than in an area such as genetic matching involving DNA. When considering genetic matching, all the variables and parameters of a DNA strand are known and error rates can be calculated with a high degree of accuracy. This is not the case in tool marks where the variables of force, angle of attack, motion of the tool, surface finish of the tool, past history of use, etc. are not known or cannot be determined, and the possibility for variation is always increasing as the population under study continues to increase and change. For practical purposes, this may indeed mean that realistic error rates cannot be completely characterized, but experiments based on sequentially manufactured tools may lead to

useful approximations and/or bounds.

Finally, it is also true that an examiner necessarily offers a subjective opinion when rendering a decision. However, the pattern on which that decision is based consists of striations that can be characterized and quantified in an objective, mathematical manner. The proposition that tool marks must necessarily have a quantifiable basis is the principle upon which the Integrated Ballistics Imaging System (IBIS) developed and manufactured by Forensic Technology, Inc. for bullets and cartridge cases operates. IBIS uses fixed lighting and an image capture system to obtain a standard digital image file of the bullet or cartridge case. The contrast displayed in the image is reduced to a digital signal that can then be used for rapid comparisons to other files in a search mode. The latest version of IBIS uses the actual surface roughness as measured by a confocal microscope to generate a comparison file. The results are displayed in a manner analogous to a web search engine, where possibilities are listed in order with numbers associated with each possibility. An experienced tool mark examiner must then review the list of possibilities to make a judgment as to whether a match does, in fact, exist. In instances where a match is declared, it is quite common for the match not to be the first possibility displayed by IBIS, but to be further down the list. In other words, while the analysis/algorithm employed by FTI produces the numbers associated with each match, these numbers carry no clear statistical relevance or interpretation related to the quality or probability-of-match of any given comparison [5]. However, since the marks under investigation can be quantified, there appears to be a significant potential for advancement in analyses of such data. An objective method of analysis should be possible for any given type of tool mark, and (at least in principle) an error rate

established for comparisons made between any given subset of marks within a larger population of similar marks.

Researchers at Iowa State University have developed a computer-based data analysis technique that allows rapid comparison of large numbers of data files of the type that might be produced when studying striated tool marks. A major aim of the research reported here is to construct well-defined numerical indices, based upon the information contained within the tool mark itself, that are useful in establishing error rates for objective tool mark matching. While this error rate may only be practically achievable for a particular set of experimental conditions, it should serve as a benchmark error rate for subsequent studies. Initial results [6] indicated that simple statistics computed from the quantitative data produced by a surface profilometer, namely, maximized data correlations over short data segments, supported the empirical assertions of forensic examiners concerning comparisons of tool marks generated on lead plates by consecutively manufactured screwdriver tips. One drawback in using maximized correlations is that there is no clear standard against which they can be objectively compared. In some cases, maximized correlations may be high, implying a high degree of linear agreement between data pairs, but not necessarily implying strong similarity between the tool mark patterns. In others, the linear correlations over short data segments may be smaller, but the overall tool mark patterns are convincingly similar and would be declared a positive identification by a practicing examiner. One situation in which this shortcoming is especially troublesome is in poorly marked samples where striations may not be present across the entire surface of the lead plates used for making the tool marks. For example, consider the possibility where two dissimilar tools are used to mark

two plates. Suppose that in both cases the screwdriver tip does not adequately mark the surface. In such cases the similar unmarked sections of the plates may produce very high correlation values, even though the marked sections are entirely dissimilar. For these and many other reasons, a simple maximized correlation coefficient is not a reliable index of match quality.

This paper presents a description of a matching analysis and algorithm that overcomes many of these difficulties, and summarizes experimental data collected to characterize algorithm performance. The index produced by the algorithm provides a more statistically meaningful comparison than maximized correlation. Experiments involving comparisons of samples obtained from a single tool to each other, and to samples produced from other similar sequentially manufactured tools, show that the analysis can fairly reliably separate sample pairs that are known matches from the same tool from pairs obtained from different tools. Additionally, the index provides a means of calculating estimates of error rates within the narrow and specific setting of this study.

For the sake of clarity, a brief summary of how the algorithm operates and the assumptions upon which it is based is given below. This discussion is necessary in order to understand the algorithm results in comparison to those obtained by human subjects. Agreement between algorithm results and examiner evaluations was assessed at the 2008 Association of Firearms and Tool mark Examiners Training Meeting held in Honolulu, Hawaii. Results obtained from this blind study in which practicing tool mark examiners were asked to compare the same samples will be presented. Comparison of the results obtained by human examiners to those of the

algorithm provides interesting insights that hopefully will lead to algorithm performance improvements.

Statistics

An earlier work [7], described a statistical analysis and algorithm for comparing two-dimensional images of tool marks. The algorithm described here is similar in construction, although it is restricted only to matching along one-dimensional profilometer data traces, and so is lacking some of the steps required to deal with two-dimensional data arrays. The data examined in this analysis are of the type collected by a surface profilometer that records surface height (z) as a function of distance (x) along a linear trace taken perpendicular to the striations present in a typical tool mark. Important assumptions in the analysis are that the values of z are reported at equal increments of distance along the trace and that the traces are taken as nearly perpendicular to the striations as possible. The algorithm then allows comparison of two such linear traces.

The first step taken by the algorithm, referred to as Optimization, is to identify a region of best agreement in each of the two data sets for the specified size of the comparison window (which is user-defined). This is determined by the maximum correlation statistic, hereafter referenced as an “R-value”, and described in [6]. By way of illustration, two different possibilities are shown in Figure 1. The schematic of Figure 1a shows the comparison of a true match, i.e. profilometer recordings from two specimens made with the same tool, while Figure 1b shows data from a true

nonmatch pair of specimens (i.e. two marks from two different tools). In each case, the matched regions marked with solid rectangles are the comparison windows denoting the trace segments over which the ordinary linear correlation coefficient is largest. Note that in both cases the R-value returned is very close to 1, the largest numerical value a correlation coefficient can take. In the first instance this is so because a match does in fact exist, and the algorithm has succeeded in finding trace segments that were made by a common section of the tool surface. In the second case, the large R-value is primarily a result of the very large number of correlations calculated in finding the best match. Even for true nonmatches, there will be short trace segments that will be very similar, and it is almost inevitable that the algorithm will find at least one pair of such segments when computing the R-value. It is primarily for this reason that the R-values cannot be interpreted in the same way that simple correlations are generally evaluated in most statistical settings.

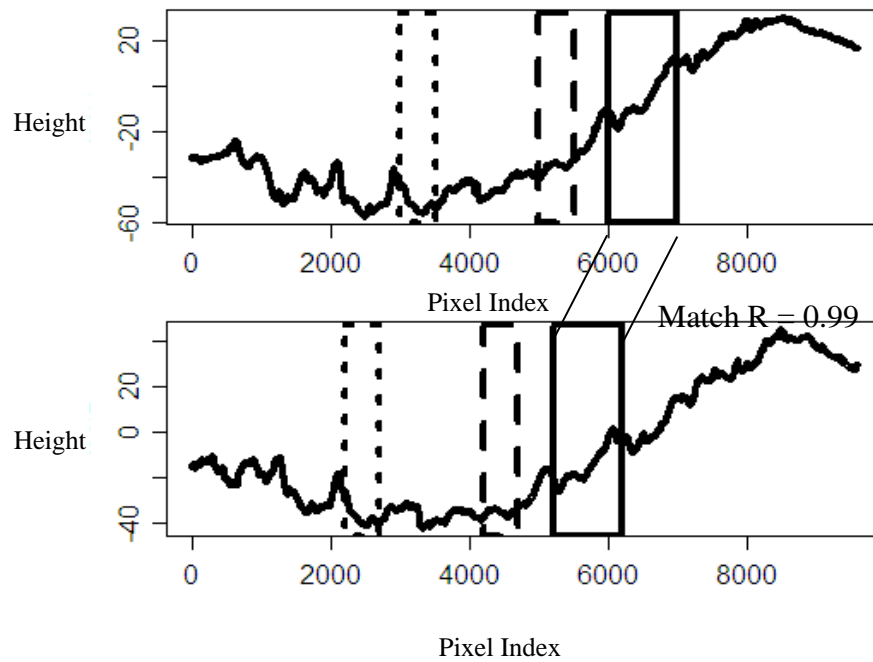
For the reasons described above, the algorithm now conducts a second step in the comparison process called Validation. In this step a series of corresponding windows of equal size are selected at randomly chosen, but common distances from the previously identified regions of best fit. For example, a randomly determined shift of 326 pixels to the left, corresponding to the dashed rectangles in Figure 1a, might be selected. The correlation for this pair of corresponding regions is now determined. Note that this correlation must be lower than the R-value, since the latter has already been determined as being the largest of all possible correlations determined in the Optimization step. The assumption behind the Validation step is that if a match truly does exist, correlations between these shifted window pairs will also be reasonably large because they

will correspond to common sections of the tool surface. In other words, if a match exists at one point along the scan length (high R-value), there should be fairly large correlations between corresponding pairs of windows along their entire length. However, if a high R-value is found between the comparison windows of two nonmatch samples simply by accident, there is no reason to believe that the accidental match will hold up at other points along the scan length. In this case rigid-shift pairs of windows will likely not result in especially large correlation values.

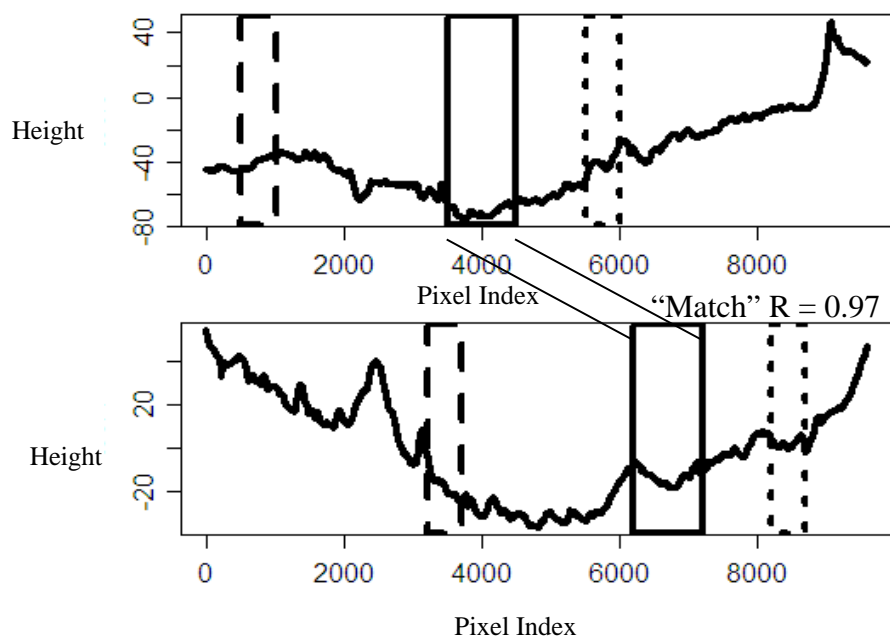
During the Validation step a fixed number of such segment pairs is identified, corresponding to a number of different randomly drawn shifts, and the correlation coefficient for each pair is computed. Dotted and dashed rectangles displayed in Figure 1 illustrate schematically the selection of two such pairs of shifted data segments; in actual operation the algorithm chooses many such pairs. In the case of the true match the regions within the corresponding dashed windows of Figure 1a do appear somewhat similar, and can be expected to return fairly large correlation values. However, when similar corresponding pairs of windows are taken from the nonmatch comparison of Figure 1b, the shape of the scans within the windows is seen to differ drastically. Lower correlation values will be obtained in this case.

The correlation values computed from these segment-pairs can be judged to be “large” or “small” only if a baseline can be established for each of the sample comparisons. This is achieved by identifying a second set of paired windows (i.e. data segments), again randomly selected along the length of each trace, but in this case, without the constraint that they represent equal rigid-shifts from their respective regions of best fit. In other words, for this second set of

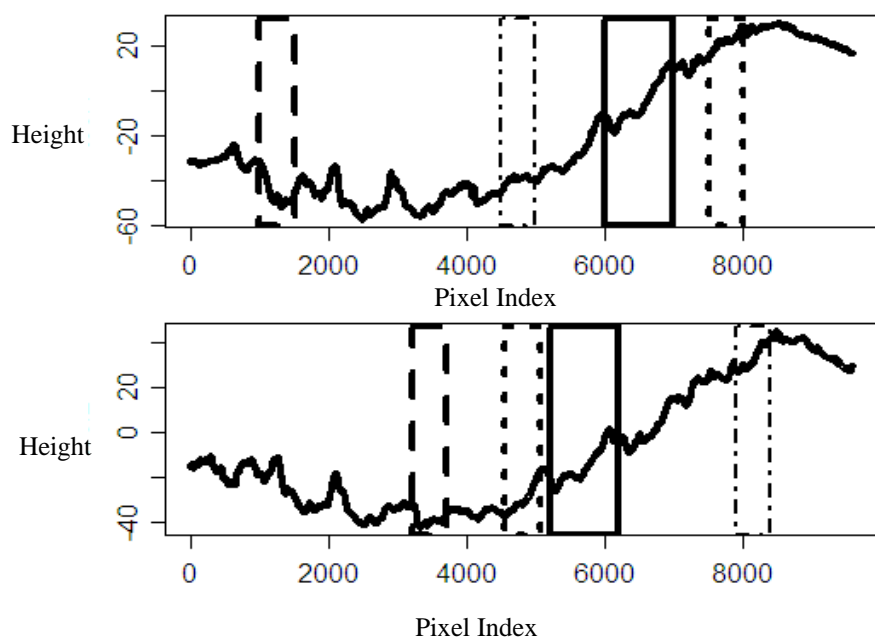
comparisons the shifts are selected at random and independently from each other – any segment of the selected length from one specimen has an equal probability of being compared to any segment from the other. This is illustrated in Figure 1c for three pairs of windows, denoted by the dashed rectangles, the dotted rectangles, and the dot-and-dash rectangles.



a.



b.



c.

Figure 1: a) Comparison pair showing a true match. Best region of fit shown in solid rectangle with corresponding R value. Note the similarity of the regions within the two possible sets of validation windows (dashed and dotted rectangles). b) Comparison pair showing a true nonmatch. While a high R value is still found between “Match” segments, the validation windows are distinctly different from one another. c) Validation windows (dashed, dotted, and dot-and-dash rectangles) selected at random for the comparison pair shown in a) to establish a baseline value.

The Validation step concludes with a comparison of the two sets of correlation values just described, one set from windows of common random rigid-shifts from their respective regions of best agreement, and one set from the independently selected windows. If the assumption of similarity between corresponding points for a match is true the correlation values of the first set of windows should tend to be larger than those in the second. In other words, the rigid-shift window pairs should result in higher correlation values than the independently selected, totally random pairs. In the case of a nonmatch, since the identification of a region of best agreement is simply a random event and there truly is no similarity between corresponding points along the trace, the correlations in the two comparison sets should be very similar.

A nonparametric Mann-Whitney U-statistic (referred to in this paper as T1), computed from the joint ranks of all correlations computed from both samples, is generated for the comparison. Where the correlation values of the two comparison sets are similar, T1 takes values near zero,

supporting a null hypothesis of “no match”. If the correlations from the first rigid-shift sample are systematically larger than the independently selected shifts, the resulting values of T1 are larger, supporting an alternative hypothesis of “match”.

Method

The test set for this study is the same as described in [6], namely, a series of 50 sequentially manufactured screwdriver tips were obtained and used to make tool marks at angles of 30, 60 and 85 degrees on flat lead plates. The surface roughness of the resultant striae was measured using a surface profilometer and the measurements saved as a series of data files detailing z height as a function of x direction. All details of data collection are given in [6].

In order to compare the effectiveness of the algorithm to human examiners, and potentially identify areas where the algorithm might be enhanced or improved, a double-blind study was conducted during the 2008 Association of Forearms and Tool mark Examiners Training Seminar. During the course of this meeting 50 different volunteers rendered over 250 opinions on some of the sample pairs used for this study and evaluated by the algorithm.

A series of 20 comparison pairs covering a range of T1 values from low to high were selected from the tool marks produced at the 85 degree comparison angle. Of the twenty comparison

pairs, five were from samples where the algorithm correctly identified a matched set (high T1); five were correctly eliminated nonmatch comparisons (low T1); five were incorrectly eliminated matched sets (T1 values in the low or inconclusive range); and five were incorrectly identified nonmatches (intermediate or high T1). Examiners were asked to assess each pair of samples twice. For the initial observation, paper blinders were placed on the samples so that examiners were restricted in their view to the same general area where the profilometer data were collected, Figure 2. After making an initial assessment, the blinders were removed and the examiner was given the opportunity to make a second assessment based on a view the entire sample. In each case, examiners were asked to render an opinion as to whether they were viewing a positive identification, a positive elimination, or inconclusive, for reasons that will become apparent.

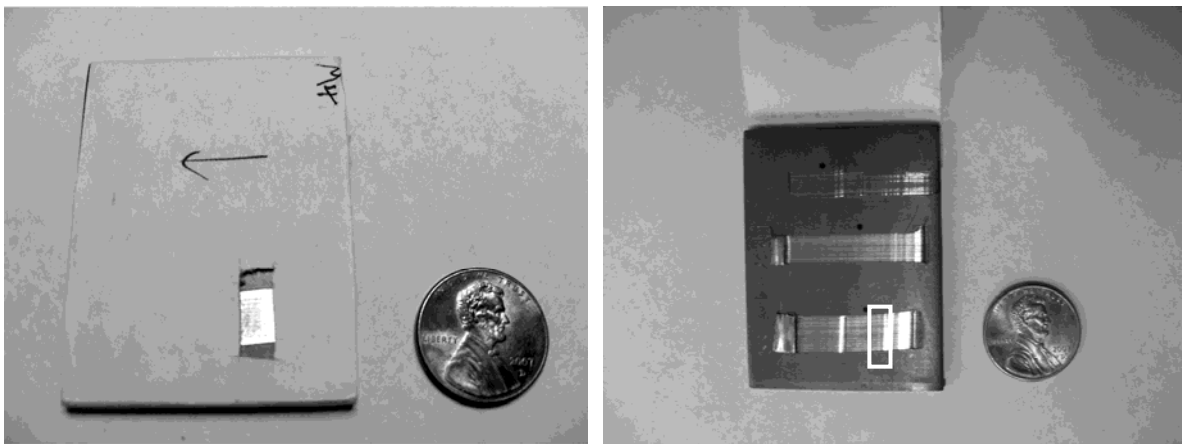


Figure 2: Image of a tool marked plate with a) blinder in place and b) removed, showing the entire mark. Area shown in a) indicated by white rectangle.

Names of examiners were not recorded, although demographic data was collected concerning the experience and training of the volunteers. Of the 50 volunteers all except five were court qualified firearm and tool mark examiners. Of the remaining five, two were firearms (but not tool mark) qualified, two were in training, and one was a foreign national where a court qualification rating does not exist. Volunteers were required to do a minimum of two comparison pairs, and could do as many as they wished. Several chose to do the maximum number of comparisons possible. Numbers were assigned to identify each volunteer during data collection; afterwards the ID numbers were randomly mixed to preserve anonymity.

Examiners were asked to use whatever methodology they employed in their respective labs. This caused some confusion initially and placed constraints on the volunteers since some labs never use the term “positive elimination”, while others are reluctant to use the term “positive identification” unless the examiner personally either makes the marks or knows more information about them than what could be supplied in this study. After understanding this the examiners were told the direction of the tool when making the mark and that the tool marks were all made at the same angle from similar, sequentially made, flat blade screwdriver tips. Also, examiners were told that for the purposes of the study they could consider the terms of “positive elimination” or “inconclusive” to be essentially interchangeable.

Results and Discussion

Algorithm Performance

The data obtained from the profilometer was used to test a series of hypotheses that are held as being true by tool mark examiners, Figure 3. The first and most fundamental assumption, that all tool marks are unique, was tested by a comparison of marks made by different screwdriver tips at the angles of 30, 60 and 85 degrees with respect to horizontal. The T1 statistic values are shown in Figure 4 as a function of angular comparison. The data is plotted as box plots, the boxes indicating where 50% of the data falls with the spread of the outlying 25% at each end of the distribution shown as dashed lines. As stated previously, when using a T1 statistic a value relatively close to 0 indicates that there is essentially no evidence in the data to support a relationship between markings. For pairs of samples made with different screwdrivers (Figure 4) the majority of the index T1 values produced by the algorithm fall near the 0 value; only 3 outlier comparisons had a T1 value greater than ± 4 .

- Hypothesis 1:*** *The 50 sequentially produced screwdrivers examined in this study all produce uniquely identifiable tool marks*
- Hypothesis 2:*** *In order to be identifiable, tool marks from an individual screwdriver must be compared at similar angles.*
- Hypothesis 3:*** *Different sides of a flat-bladed screwdriver produce different uniquely identifiable marks.*

Figure 3: Summary of hypotheses tested in this study.

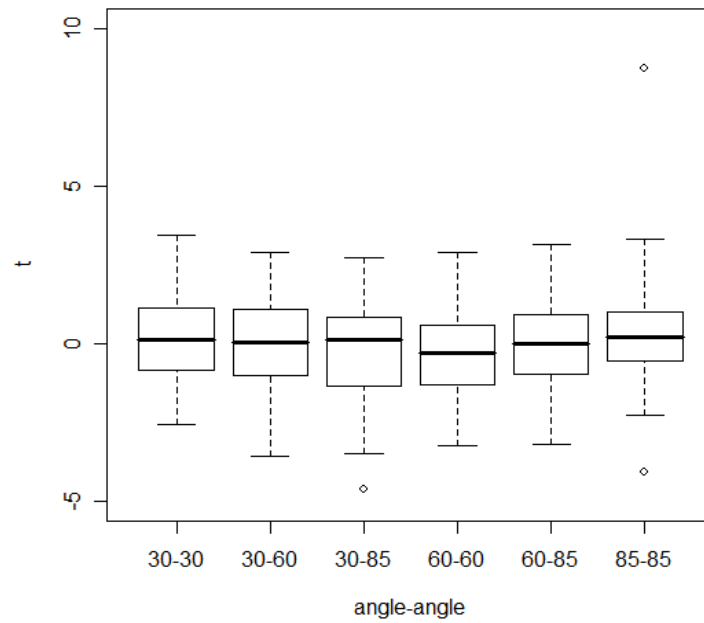


Figure 4: Box plots showing T1 results when comparing marks from different screwdrivers.

In comparison, Figure 5 displays indices computed using the algorithm from profilometer scans of marks made by the same side of the same tool and compared as a function of angle. While marks made at different angles still produce index values near 0, the T1 statistic jumps dramatically when marks made at similar angles are considered. Clear separation is seen between the 50% boxes, although overlap still exists when the outliers are considered.

Taken together, Figures 4 and 5 support Hypotheses 1 and 2. When comparing tool marks made at similar angles with different tools, the resulting T1 values cluster near zero (Figure 4), but when the same tool is used to make marks at similar angles, the T1 distributions are on substantially larger values, giving support for Hypothesis 1. Support for Hypothesis 2 is

demonstrated by Figure 5 alone, since even among same-tool marks, only those made at the same angle produce large T1 values.

The last hypothesis considered was that when comparing tool marks made from screwdriver tips, the marks must be made from the same side of the screwdriver; marks made using different sides of the screwdriver appear as if they have come from two different screwdrivers. These results are shown in Figure 6. The hypothesis is again supported because, as in Figure 4, the T1 values cluster around 0 regardless of the angles used in making the marks, indicating no relationship between the samples.

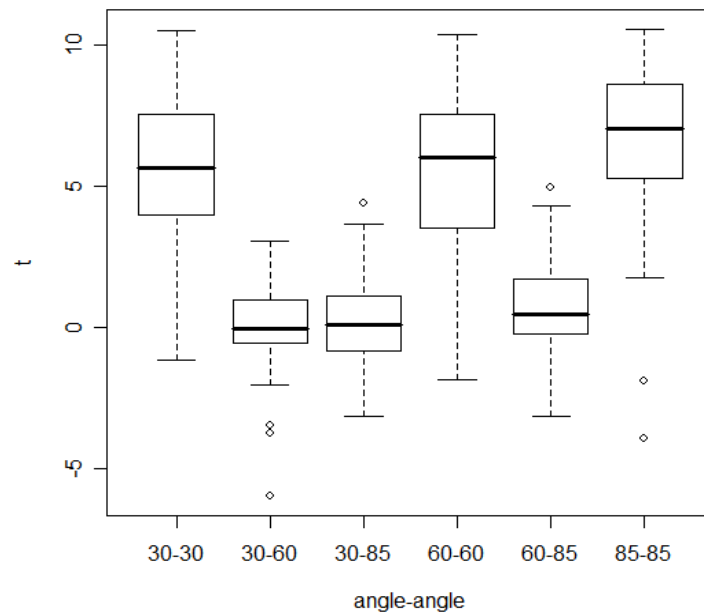


Figure 5: Box plots showing T1 results when comparing marks obtained from the same side of the same screwdrivers.

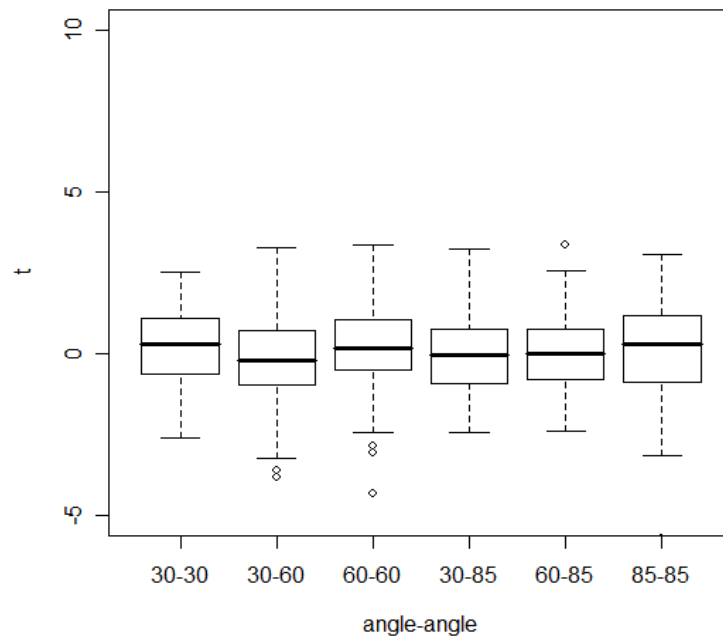


Figure 6: Box plots showing T1 results when comparing marks made from different sides of the same screwdrivers.

The T1 values summarized in Figures 4 and 5 are individually replotted in Figure 7, with the y-axis randomly varied (known as jittering) to create an artificial vertical separation that makes it easier to view the data points. Known comparisons that should match and produce high T1 values are shown in black. Known “nonmatches” that should have T1 values near zero are shown in gray.

Examination of these plots indicates that the algorithm operates best using data obtained at higher angles than lower angles, i.e. the spread of black and gray spots is more defined for the 85 degree data than, for example, the 30 degree data. This is believed related to the quality of the

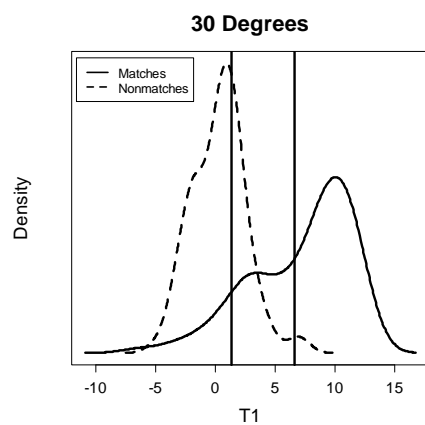
mark. As the angle of attack of the screwdriver with the plate increased the quality of the mark increased. It was common to obtain marks that represented the entire screwdriver tip at high angles, while marks at lower angles were often incomplete [5]. Algorithm performance also appears more efficient at reducing false positives than it does in eliminating false negatives. At all angles known matches were found with very low T1 values, while nonmatches with high T1 values were very limited.

While T1 is a much more stable index of match quality than R-value, problems still remain in establishing an effective, objective standard for separating true matches from nonmatches. Ideally, when employing standard U-statistic theory the critical T1 values separating the regions of known matches (black data points) and known nonmatches (gray data points) should remain constant for all data sets. Examination of Figure 7 shows that this is not the case. For example, reasonable separation for the 30 and 60 degree data appears to be somewhere around a T1 value less than 5, but rises to approximately 7 for the 85 degree data. This variation is most likely due to lack of complete independence among the correlations computed in each sample, arising from the finite length of each profilometer trace.

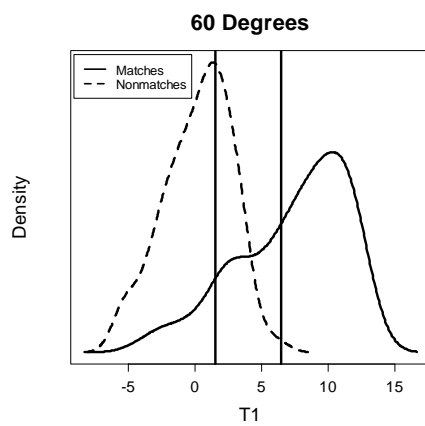
For the reasons discussed above, assigned threshold values indicating “Positive ID” and “Positive Elimination,” and denoted by black lines on the graphs of Figure 7, were chosen based on a K-fold cross validation using 95% one-sided Bayes credible intervals. Specifically, the lower threshold is a lower 95% bound on the 5th percentile of T1 values associated with nonmatching specimen pairs, and the upper threshold is an upper 95% bound on the 95th

percentile of T1 values associated with matching specimen pairs. The region between these two threshold values is labeled “Inconclusive”. A Markov Chain-Monte Carlo simulation was used to determine potential error rates.

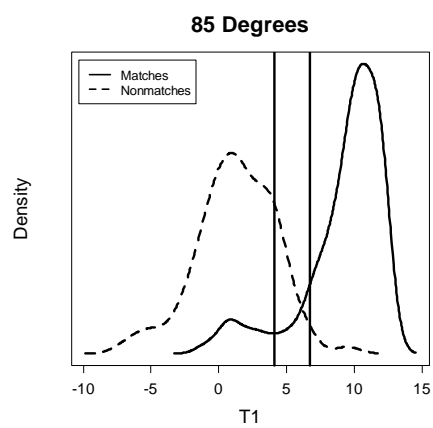
Using this method the estimated error rates are as follow. For comparisons made at 30 degrees the estimated probability of a false positive (i.e. a high T1 value for a known nonmatch comparison) is 0.023. In other words there is a possibility of slightly over two false positives for approximately every 100 comparisons. The estimated probability of a false negative is 0.089, or almost 9 true matches having a low T1 value per every 100 comparisons. The cross-validation method used ensures that all the data have similar error rates, and the rates found for the 60 and 85 degree data are approximately 0.01 and 0.09 for false positives and false negatives, respectively. What is most noticeable is that the T1 lower threshold value for the 85 degree data is much larger than for the 30 and 60 degree data, being 4.10 vs 1.34 and 1.51, respectively. This suggests that a more distinct difference is required to classify nonmatches for the 30 and 60 degree cases than is true for the 85 degree case. This, in turn, results in a corresponding increase for the estimated inconclusive error rates, which are 0.103, 0.298, and 0.295 for the 85, 60 and 30 degree data, respectively. It would, of course, be possible to shift these error rates, i.e. produce fewer false negatives at the expense of more false positives, by altering the percentiles used in our estimation procedure.



a.



b.



c.

Figure 7: Summation of the T1 values from comparisons made at a) 30 degrees; b) 60 degrees; and c) 85 degrees.

Association of Firearm and Tool mark Examiners Study

Results of the computerized analysis of specimen pairs was compared to expert evaluations of the same samples made by volunteer examiners at the 2008 Association of Firearm and Tool mark Examiners seminar. However, before the algorithm performance can be discussed in comparison to the data obtained at the Association of Firearm and Tool mark Examiners seminar using human volunteers, a brief consideration of the constraints experienced by the examiners is in order. Firstly, it should be recognized that the conditions under which the examiners rendered an opinion would ordinarily be regarded as restrictive or even professionally unacceptable.

Without having the tool in hand, or without being permitted to make the actual mark for comparison, tool mark examiners were forced to make assumptions they would not make in an actual investigation. For example, without having the screwdriver tip in hand the examiners did not know whether the mark they observed represented the entire width or only a portion of the screwdriver blade. Secondly, given this uncertainty about how the specimen was made, examiners tended to be more conservative in their willingness to declare a positive identification or elimination. During the course of the Association of Firearm and Tool mark Examiners study several examiners commented that typical lab protocol would require them to have physical access to the subject tool before rendering a “positive identification” judgment. Finally, examiners do not typically employ the terms used to denote the three regions identified for error

analysis. Thus, while privately saying they felt a comparison was a “positive elimination” (given their knowledge of the test being conducted), lab protocol required an opinion of “inconclusive” to be rendered. Such policies are put in place since the signature of a tool may so change during use that a mark made at one point in time may not resemble a mark made with the same tool at a different point in time, e.g., after the tip has been broken and/or re-ground. In such cases positive elimination is only allowed if the class characteristics of the marks are different.

When viewed in light of these constraints, some interesting observations concerning the algorithm performance are apparent. In a small number of cases (12 out of 252 comparisons), when examining the entire tool mark after first viewing only the restricted area where the profilometer scans were obtained, examiners changed their opinion from inconclusive to either positive ID or positive elimination. This indicates that algorithm performance might be improved simply by increasing the amount of data processed. This may be achieved, for example, by ensuring that the profilometer scans span the entire width of the mark or possibly by considering a number of scans taken at locations dispersed along the entire length of the available mark.

In a slightly smaller number of cases, comparisons between specimens made by the same screwdriver that were not conclusively identified as such by the algorithm also presented problems for the examiners. Five true matches that received low T1 values and were classified as a positive elimination by the algorithm were examined during the Association of Firearm and Tool mark Examiners study. Three of the five were given ratings of “inconclusive” or “positive

elimination” on one occasion, and one particular comparison sample (designated MW4) was rated this way seven times. Thus, while examiners in general were vastly superior to the algorithm in picking out the matches, both the algorithm and the examiners had more trouble with some true matches than with others.

Close examination of the sample that was most often problematic for examiners (i.e. MW4) was conducted and the images obtained are shown in Figure 8. Figure 8a shows the side-by-side comparison of the marks, where no match is seen. Note that the mark width matches extremely well, and the entire mark seems to be present. Figure 8b shows the samples positioned where the true match is evident. It can be seen that each mark only represents a portion of the screwdriver blade width, predominately from the two sides of the tip. A match is only possible if the marks are offset, allowing the opposing “edge” sections (which actually were produced by the middle of the screwdriver blade) to be viewed side-by-side.

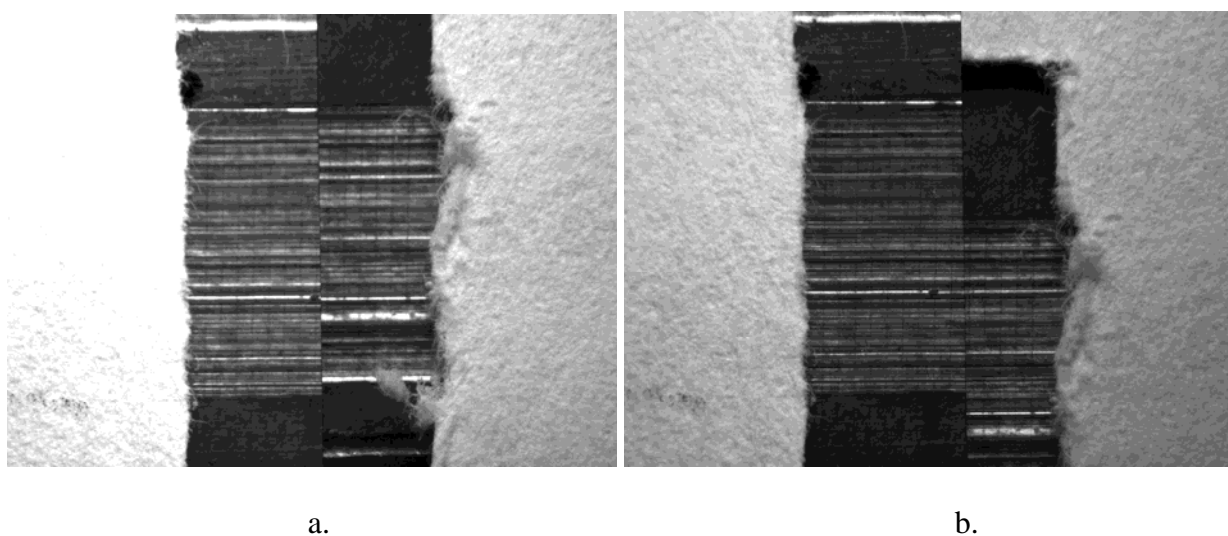


Figure 8: Sample MW4. a) Tool marks placed so that assumed edges align. B) Correct placement required for positive identification.

This sample points out weaknesses in the study conducted at Association of Firearm and Tool mark Examiners as well as in the laboratory tests of the algorithm. In a screwdriver mark comparison it is common for examiners to use the edges of the marks as initial registration points for the start of an examination. Since examiners make the comparison marks themselves they are well aware of the edge markings, if not for the evidence marks, at least for the marks they produced. In the Association of Firearm and Tool mark Examiners study, such information was not provided and may have led to some false assumptions. For example, in the majority of cases the volunteers were under some pressure to quickly conduct a comparison before, e.g. the next meeting session started, or so that another examiner could use the equipment, etc. Due to these time constraints, samples often were placed on the stages of the comparison microscope for the volunteer, giving the examiner little or no time to observe the macroscopic appearance of the mark. Without the benefit of seeing the size of the entire mark, and given the identical widths of the two partial marks for sample MW4 when initially viewed using the comparison microscope, the assumption that the entire width of the screwdriver blade was represented would be a natural one. However, such an assumption could easily lead to an inconclusive or positive elimination conclusion, especially if the examiner was being conservative due to lack of information concerning the sample.

The problem described above essentially relates to the examiners having a lack of a point of reference or registry of the mark for the comparison. The same could be said of the algorithm and the manner in which it performs, since no point of registry exists to indicate when the data being acquired is actually coming from a tool-marked region or from the unmarked plate. All of the profilometer scans analyzed by the algorithm were run using the same set of sampling parameters. However, the initial positioning of the stylus was inexact. For incomplete marks, large regions of the unaffected lead plate were also scanned in order to keep the file sizes consistent and this lack of registry could have affected algorithm performance. This is not immediately evident if one examines the raw profilometer traces, Figure 9. In this figure the top and bottom traces show the entire scans while the two middle traces show the matched details found within the two corresponding solid rectangles superimposed on the top and bottom traces. At first sight the two scans do appear quite different, as the offset in the scans, revealed during examination at Association of Firearm and Tool mark Examiners, is not immediately evident in the data files. Given observation of Figure 8, one can mark the approximate location of the region that is common between the two traces; this is shown in Figure 9 by the dashed rectangles. In this case, paired validation windows, displaced equal amounts in either direction may return a low T1 value since the majority of either scan is not held in common with the other. In other words, there is a high probability that the validation windows fall in regions where no correspondence between plates exists (see Figure 8b). Thus, what should be a match is rated as a nonmatch.

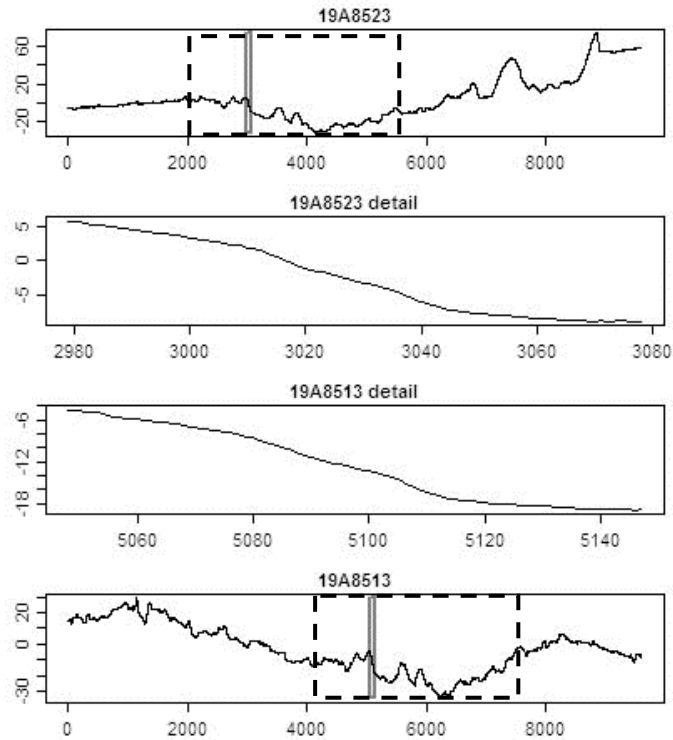


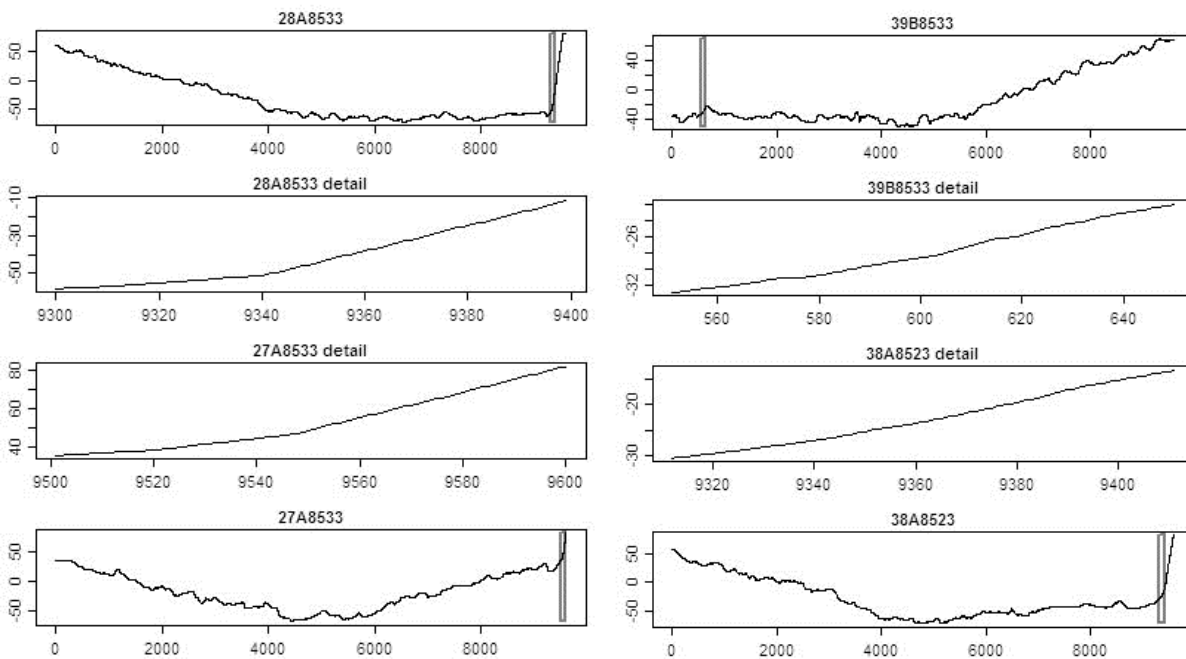
Figure 9: Profilometer data showing results from comparison MW4. The match region is shown by the solid rectangle. Dashed rectangles show the approximate location of the common region revealed in Figure 8.

A somewhat different problem is revealed when traces from true nonmatch samples are examined, Figure 10. In these instances, the optimization step may identify windows at extreme edges of the two traces as being most similar. Given the nearness of the match to the ends of the traces, the random selection of paired, rigid-shift windows during the validation step is severely constrained. For the example shown in Figure 10a the match region (denoted by solid rectangles) falls at the extreme right ends of the data files. This means that the rigid translations

taken for each pair of verification windows must always fall to the left of the match region.

While this may be less than desirable, the entire mark is still available for validation and a large number of rigid-shift windows spaced across the entire length of the file should be sufficient to produce good separation between this accidental match and the T1 values of a true match.

However, this is not true for the true non-match shown in Figure 10b. In this case the windows identified in the optimization step as being most similar are at opposite ends of the compared data traces. The distances of possible rigid translations are constrained to a short distance to the left of the top profile and a short distance to the right of the bottom profile. Thus, the majority of the mark cannot be used in the validation step for this accidental match. If the regions in the immediate vicinity of the accidental match are also similar, high T1 values may be returned due to the constrained sampling parameters, giving results that cannot be separated from a true match.



a.

b.

Figure 10: Comparisons of traces obtained from four different screwdrivers that were rated as possible matches by the algorithm. Match areas denoted by thin rectangles. Good agreement found at a) similar and b) opposite ends of the traces resulted in high T1 numbers for known non-matching pairs.

The above discussion suggests that further development of the algorithm to incorporate additional data concerning the region of the profilometer trace that is actually tool-marked and/or the location of the tool edge might improve its performance. While tool mark examiners do not directly use features such as these as a basis for identification, they do use it indirectly in establishing a context for the comparison. Such information, routinely and quickly noted by a human examiner, is unavailable to the current algorithm. The algorithm treats all possible pairs of trace windows the same way and functions under the assumption that all marks analyzed are essentially the same, i.e., it assumes the screwdriver tip has completely marked the lead plate and that no unmarked regions exist. This clearly is not the case. At this time it appears the best way to enhance algorithm performance is to ensure that all comparison windows (i.e. Match and Validation) are taken from regions representing the true marked surface of the lead, and that most-similar windows found at the trace edges are used as a basis for match identification only if they are found at the same end of their respective traces.

As a final comment, it should be noted that all types of volunteers (practicing examiners, trainees, retired examiners) were involved in the study, with records kept as to the experience of the participant. Examination of the demographic data in relation to the results showed no significant difference between experienced examiners and rather newly qualified examiners or those in training; all performed equally well.

Summary and Conclusions

The analysis described here for comparing two tool-marked plates is a substantial improvement over simply identifying regions of highest correlation. It does this by producing a non-parametric Mann-Whitney statistic, here called T1, obtained through an optimization step followed by a validation step as a measure of evidence for tool mark matching. When used in evaluating the three hypotheses tested, namely, the uniqueness of tool marks, the necessity of comparing marks at similar angles, and the uniqueness of different sides of screwdriver blades, the T1 statistic results constitute support for the experiential knowledge of tool mark examiners. Analysis of algorithm performance in light of actual examiner results reveals deficiencies in algorithm performance that can now be addressed. Increasing the data input, possibly by including more scans spread over a larger tool mark area and incorporating contextual information normally available to examiners, such as the presence of partial scans and reference points from tool edges, may lead to performance improvements. Such changes should, for

example, prohibit the identification of opposite-end windows in the optimization step as potential match segments.

It is clear that examiner performance was much better than the algorithm. While the 20 samples examined at Association of Firearm and Tool mark Examiners represent only a subset of the total comparisons examined using the algorithm, they did contain those samples that were most definitively misclassified by the algorithm. For example, of the 20 true-match pairs shown to the Association of Firearm and Tool mark Examiners volunteers, the algorithm correctly identified 10 of the 20 samples unambiguously; the remaining 10 were listed either as inconclusive or misidentified as a false negative. In comparison, only 11 out of 126 volunteer examinations resulted in false negative classification of true match pairs, primarily from sample MW4 (7 out of 11). Further, the Association of Firearm and Tool mark Examiners volunteers reported no false positives at all. (N.B. The caveat must be added that the terminology used in the previous statements regarding errors is not entirely consistent with examiner protocols and should not be construed by the reader to suggest that the examiners erred. Examiners are trained to render an opinion of positive identification only when no doubt exists in their minds. Thus, a false negative only suggests that the examiner was not fully persuaded.)

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