Automatic Matching of Cartridge Case Impressions

Joseph Zemmels   **Susan VanderPlas**   **Heike Hofmann**
Iowa State University   University of Nebraska - Lincoln   Iowa State University

Abstract

Forensic examinations attempt to solve the binary classification problem of whether two pieces of evidence originated from the same source. A cartridge case found at a crime scene may be compared to a cartridge case fired from a suspect's firearm. Historically, forensic examiners relied on high-powered comparison microscopes, case facts, and their own experience to arrive at a source conclusion. Recently, algorithms that provide an automatic and objective measure of similarity of the evidence have become more prevalent. We introduce a cartridge case comparison algorithm that encompasseses preprocessing, feature extraction, and similarity scoring. We use a train/test split on a data set of 500 cartridge case scans to fit and validate a random forest model. We demonstrate that this random forest model yields improved accuracy compared to predominant algorithms. Finally, we use the random forest model to calculate score-based likelihood ratios that estimate the probative value of the evidence.

Keywords: forensics, forensic statistics, pattern recognition, firearms and toolmarks, R.

1. Introduction

Introduce the problem here. Explain what a cartridge case is. Explain breech face impressions.

The "ground-truth" of a forensic comparison is a binary classification problem. Briefly reference how comparisons are done by examiners currently. Keep focus on firearm and toolmark evidence.

Critics of traditional firearm and toolmark comparisons cite a lack of foundational validity (NAS 2009, PCAST 2016). Discuss what PCAST means by foundational validity and how firearm and toolmark evidence falls short according to NAS & PCAST. Recent studies of examiner proficiency estimate error rates to be low - between % and % according to [Baldwin]. Nonetheless, [NAS] and [PCAST] pushed for the development of "objective image processing algorithms to. . . .[quote PCAST here. . .]." An automatic comparison algorithm could be used as part of an examination to supplement or inform an examiner's opinion [cite Swofford taxonomy paper here].

2. Previous Work

Discuss current state of affairs for algorithmic F&T comparisons.

Cite Hare et al. as a parallel paper to this one applied to bullet data.

Cite Xiao Hui's project.

Cite CMC method as predominant method. Broadly summarize cell-based comparison procedure and CMC method logic. Also reference Zhang et al. (2020) DBSCAN paper here.

Discuss limitations of current cartridge case comparison algorithms. Currently, there is no rigorous procedure for comparing different algorithms. This includes selecting optimal parameters for a specific algorithm. In this work, we introduce a novel validation procedure to learn and validate optimal parameters using a cross-validation procedure.

We introduce a novel set of features to measure the similarity between two cartridge cases. using these features, we train and test a random forest model. We show that this random forest model improves upon the error rate of predominant automatic comparison algorithms. Additionally, we demonstrate how the random forest model can be used to calculate score-based likelihood ratios.

3. Cartridge Case Data

Discuss Baldwin study here. Point out that it was the only appropriately-designed study according to PCAST. Types of cartridge cases, firearms. Design of the experiment (known and questioned samples).

Details of scanning procedure using Cadre 3D-TopMatch High Capacity Scanner. Describe x3p file format and surface matrices.

4. Methods

Include table(s) of calculated features (one for each "type" of feature?)

4.1. Preprocessing

We first use the open-source FiX3P web application to manually annotate the breech face impression region. An example of a manually-annotated cartridge case scan is shown in [Figure]. The FiX3P software includes functionality to "paint" the surface of a cartridge case and save the painted regions to a *mask*. A mask is a 2D array of hexidecimal color values of the same dimension as its associated surface matrix. When initialized, every element of a mask is a shade of brown ("#cd7f32") by default. Any elements that have been painted-over by the user will be replaced with the user's selected color value. In [Figure], the breech face impression region was manually annotated using a shade of [red?] ("#colorValue").

Once read into an R environment, we use sequence of functions available in the [x3ptools] and [cmcR] packages to preprocess the raw scans. [Code] demonstrates how the [magrittr] pipe (`%>%`) operator strings together these functions. [Figure] shows the effect that each function has on the scan surface values. The `x3p_delete` function removes (i.e., replaces with `NA`) values in the scan based on the associated mask. [The other functions do xyz]. The final result is a cartridge case surface matrix with emphasized breech face impressions.

Next, we compute a set of similarity features for two preprocessed cartridge case scans.

4.2. Feature Extraction

In this section, we introduce a set of similarity features for two cartridge case scans. We calculate features at two scales: between two whole scans and between individual cells similar to the CMC method [cite]. Analogous to how a forensic examiner uses a comparison microscope with different magnification levels, this allows us to assess the similarity between two scans at the macro and micro levels.

First, we introduce notation that will be used to define the features. Let A and B denote two surfaces matrices that we wish to compare of dimension $P \times Q$ and $M \times N$, respectively. We use bracket indexing to denote a particular value of a matrix: $A[i, j]$ is the value in the ith row and jth column, starting from the top-left corner, of matrix A.

Registration Estimation

A critical step in comparing A and B is to find a transformation of B such that it aligns best to A (or vice versa). In image processing, this process is called *image registration.* Noting that A and B are essentially grayscale images, we rely on a standard image registration technique [cite Brown, 1992].

In our application, this transformation is composed of a discrete translation by $(m, n) \in \mathbb{Z}^2$ and rotation by $\theta \in [-180°, 180°]$. Under this transformation, the index $[i, j]$ maps to a new index $[i^*, j^*]$ by:

$$\begin{pmatrix} j^* \\ i^* \end{pmatrix} = \begin{pmatrix} n \\ m \end{pmatrix} + \begin{pmatrix} \cos(\theta) & -\sin(\theta) \\ \sin(\theta) & \cos(\theta) \end{pmatrix} \begin{pmatrix} j \\ i \end{pmatrix}.$$

The value that once occupied element $B[i, j]$ now occupies $B[i^*, j^*]$. In practice, we use *nearest-neighbor interpolation* meaning i^* and j^* are rounded to the nearest integer

[cite a nearest-neighbor reference].[1]

To determine the optimal registration, we calculate the *cross-correlation function* (CCF) between A and B. The CCF measures the similarity between A and B for every possible translation of B:

$$(A \star B)[m,n] = \sum_{i=1}^{M} \sum_{j=1}^{N} A[i,j]B[i+m, j+n]$$

where $1 \leq m \leq M + P - 1$ and $1 \leq n \leq N + Q - 1$. $A \star B$ is a 2D array of dimension $M + P - 1 \times N + Q - 1$ where $(A \star B)[m,n]$ quantifies the similarity between A and B after B is translated m elements horizontally and n elements vertically. The CCF is often normalized between -1 and 1 for interpretability.

For large matrices, the above definition of the CCF is computationally taxing. The Cross-Correlation Theorem provides an equivalent expression for the CCF:

$$(A \star B)[m,n] = \mathcal{F}^{-1}\left(\overline{\mathcal{F}(A)} \odot \mathcal{F}(B)\right)[m,n]$$

where $\mathcal{F}$ and $\mathcal{F}^{-1}$ are the discrete Fourier and inverse discrete Fourier transforms, respectively, $\overline{\mathcal{F}(A)}$ is the complex conjugate, and $\odot$ is an element-wise (Hadamard) product [cite Brigham, 1988]. We trade the moving sum computation from the previous CCF expression for two forward Fourier transforms, an element-wise product, and an inverse Fourier transform. The Fast Fourier Transform (FFT) algorithm reduces the computational load considerably [cite Tukey].

Using the CCF as a similarity measure, we estimate the registration by calculating the maximum CCF value across a range of rotations of matrix B. Let B_θ denote B rotated by an angle $\theta \in [-180°, 180°]$. Then the estimated registration (m^*, n^*, θ^*) is:

$$(m^*, n^*, \theta^*) = \arg\max_{m,n,\theta}(A \star B_\theta)[m,n].$$

In practice we consider a discrete grid of rotations $\Theta \subset [-180°, 180°]$. The registration procedure is outlined in algorithm 1.

The overall maximum CCF, $CCF_{\max}$, is a similarity measure between A and B.

Handling Missingness

[Not sure what to do with this section. It needs to be mentioned, but in more or less detail?]

The registration estimation procedure outline above, namely the Fast Fourier Transform algorithm, does not permit missing values in A or B. It is common for cartridge case scans to contain many missing values - the gray regions in [preprocessing Figure] represent structural values in the scan. Thus, when calculating the CCF we impute these missing values with the average non-missing value in the scan.

We wish to measure the similarity between A and B while taking this missingness into account; to measure the similarity between the non-missing intersection of the aligned

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[1]Technical note: We pad the dimensions of matrix B as-needed assuming free boundary conditions (0-padding) so as to not crop-out any of the original values [cite a boundary condition reference here]. For notational simplicity, we'll refer to this padded matrix as B also.

Data: Matrices A, B and rotation grid Θ
Result: Estimated registration of B to A, (m^*, n^*, θ^*), and cross-correlation
function maximum, $CCF_{\max}$

for $\theta \in \Theta$ **do**
    Rotate B by θ to obtain B_θ;
    Calculate $CCF_{\max,\theta} = \max_{m,n}(A \star B_\theta)[m, n]$;
    Calculate translation $[m_\theta^*, n_\theta^*] = \arg\max_{m,n}(A \star B_\theta)[m, n]$
end
Calculate overall maximum correlation $CCF_{\max} = \max_\theta\{CCF_{\max,\theta} : \theta \in \Theta\}$;
Calculate rotation $\theta^* = \arg\max_\theta\{CCF_{\max,\theta} : \theta \in \Theta\}$;
return *Estimated rotation θ^*, translation $m^* = m_{\theta*}^*$ and $n^* = n_{\theta*}^*$, and $CCF_{\max}$*
Algorithm 1: Image Registration Procedure

scans. We compute the *pairwise-complete correlation* using only the complete value pairs, meaning neither value is missing, between A and B.

Whole-Scan Comparison

We first estimate the registration between two full scans A and B using algorithm 1 with a rotation grid $\Theta = \{-30°, -27°, ..., 27°, 30°\}$. This results in an estimated registration (m^*, n^*, θ^*) and similarity measure $CCF_{\max}$. We then apply the registration transformation (m^*, n^*, θ^*) to B to obtain B^* and compute the pairwise-complete correlation, cor_{comp}, between A and B^*.

From this whole-scan comparison procedure we obtain two features summarized in Table 1.

Notation	Feature Description
$CCF_{\max}$	Maximum value of the cross-correlation function across a grid of rotations
cor_{comp}	Pairwise-complete correlation between two aligned scans

Table 1: Two similarity features based on estimating the registration of two whole scans.

Cell-Based Comparison

Following the comparison of A and B^*, we next perform a cell-based comparison procedure. Song (2013) points out that breech face impressions rarely appear uniformly on a cartridge case surface. Rather, distinguishing markings appear in specific, usually small, regions of a scan (the author refers to these as *valid correlation regions*). Calculating a correlation between two whole scans does not necessarily capture the similarity between these regions. Song (2013) proposes partitioning a scan into a rectangular grid of "cells" to isolate the valid correlation regions. [Figure] shows an example of a cartridge case scan partitioned into a grid of 8x8 cells.

The cell-based comparison procedure begins with selecting one of the matrices, say A, as the "reference" matrix to be partitioned into a grid of cells. Each of these reference cells will be compared to the "target" matrix, in this case B^*. Because A and B^* are

already partially aligned based on the course rotation grid $\mathbf{\Theta}$, we compare each reference cell to B^* using a new rotation grid of $\mathbf{\Theta}' = \{\theta^* - 2°, \theta^* - 1°, \theta^*, \theta^* + 1°, \theta^* + 2°\}$.

We now extend the surface matrix notation introduced previously to accommodate cells. Let A_i denote the ith cell of matrix A, $i = 1, ..., T$ where T is the total number of cells containing non-missing values (e.g., in [Figure], $T = 39$).[2]

The cell-based comparison procedure is outlined in algorithm 2.

Data: Reference matrix A, target matrix B^*, $R \times C$ grid size, and rotation grid $\mathbf{\Theta}'$
Result: Estimated translations and $CCF_{\max}$ values per cell, per rotation
Partition A into a grid of $R \times C$ cells;
Discard cells containing only missing values, leaving T remaining cells;
for $\theta \in \mathbf{\Theta}'$ **do**
    Rotate B^* by θ to obtain B^*_θ;
    for $i = 1, ..., T$ **do**
        Calculate $CCF_{\max,\theta,i} = \max_{m,n}(A_i \star B^*_\theta)[m,n]$;
        Calculate translation $[m^*_{\theta,i}, n^*_{\theta,i}] = \arg\max_{m,n}(A_i \star B^*_\theta)[m,n]$
    end
end
return $\{(m^*_{\theta,i}, n^*_{\theta,i}, CCF_{\max,\theta,i}, \theta) : \theta \in \mathbf{\Theta}', i = 1, ..., T\}$
Algorithm 2: Cell-Based Comparison Procedure

Rather than exclusively returning the registration that maximizes the overall CCF as in algorithm 1, algorithm 2 returns the translations and CCF values for each cell and each rotation considered. The following assumption justifies this: if two cartridge cases are truly matching, then we assume that multiple cells will "agree" on a particular translation value at the true rotation.[3] This agreement phenomenon is illustrated in [Figure] where each point represents the translation that maximizes the CCF for a particular cell and rotation. The points appear randomly distributed for most of the rotation values except for $\theta = \#$ where a tight cluster of points forms around translation $[\#, \#]$. This is evidence to suggest that a true registration exists for these two cartridge cases, implying that they match. The task is to determine when cells reach a registration consensus.

Just as with the whole-scan comparison, we calculate the pairwise-complete correlation between each cell A_i and a matrix of the same size extracted from B^*_θ after translating by $[m^*_\theta, n^*_\theta]$. From this we obtain a set of pairwise-complete correlations for each rotation: $\{cor_{\text{comp},\theta,i} : \theta \in \mathbf{\Theta}'\}$. For $i = 1, ..., T$, define the cell-wise maximum CCF and pairwise-complete correlation as:

$$CCF_{\max,i} = \max_\theta\{CCF_{\max,\theta,i} : \theta \in \mathbf{\Theta}'\}$$

$$cor_{\text{comp},i} = \max_\theta\{cor_{\text{comp},\theta,i} : \theta \in \mathbf{\Theta}'\}$$

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[2]In practice, we number the cells in lexicographic order (left-to-right, top-to-bottom) starting from the top-left.
[3]And that cells will not come to such an agreement for a non-matching pair of cartridge cases

We compute the following features using the correlation data:

$$\overline{CCF}_{\text{max},\cdot} = \frac{1}{T}\sum_{i=1}^{T} CCF_{\text{max},i}$$

$$\overline{cor}_{\text{comp},\cdot} = \frac{1}{T}\sum_{i=1}^{T} cor_{\text{comp},i}$$

$$s^2_{CCF} = \frac{1}{T-1}\sum_{i=1}^{T}(CCF_{\text{max},i} - \overline{CCF}_{\text{max},\cdot})^2$$

$$s^2_{cor} = \frac{1}{T-1}\sum_{i=1}^{T}(cor_{\text{comp},i} - \overline{cor}_{\text{comp},\cdot})^2$$

We expect $\overline{CCF}_{\text{max},\cdot}$, $\overline{cor}_{\text{comp},\cdot}$ to be large and s^2_{CCF}, s^2_{cor} small.

For $i = 1, ..., T$, define the estimated translations and rotation for A_i as:

$$\theta_i^* = \arg\max_{\theta}\{CCF_{\text{max},\theta,i} : \theta \in \boldsymbol{\Theta}'\}$$

$$m_i^* = m^*_{\theta_i^*,i}$$

$$n_i^* = n^*_{\theta_i^*,i}$$

We compute the following features using the estimated cell translations and rotations:

$$s^2_{m^*} = \frac{1}{T-1}\sum_{i=1}^{T}(m_i^* - \bar{m}^*_\cdot)^2$$

$$s^2_{n^*} = \frac{1}{T-1}\sum_{i=1}^{T}(n_i^* - \bar{n}^*_\cdot)^2$$

$$s^2_{\theta^*} = \frac{1}{T-1}\sum_{i=1}^{T}(\theta_i^* - \bar{\theta}^*_\cdot)^2$$

where $\bar{m}^*_\cdot = \frac{1}{T}\sum_{i=1}^{T} m_i^*$, $\bar{n}^*_\cdot = \frac{1}{T}\sum_{i=1}^{T} n_i^*$, and $\bar{\theta}^*_\cdot = \frac{1}{T}\sum_{i=1}^{T} \theta_i^*$. We expect $s^2_{m^*}, s^2_{n^*}, s^2_{\theta^*}$ to be small for truly matching cartridge case pairs.

From this cell-based comparison procedure, we obtain seven features summarized in Table 2.

Density-Based Spatial Clustering of Applications with Noise

average cluster size, estimated rotation difference, estimated translation difference

Visual Diagnostic Features

average blob size, blob size sd

4.3. Similarity Scoring

We randomly split the data set into # barrels for training and ## barrels for testing. In our case, this resulted in a training data set of 200 cartridge cases, $\binom{200}{2} = 21,945$

Notation	Feature Description
$\overline{CCF}_{\max,\cdot}$	Average maximum value of the cross-correlation function across all cells and rotations
$\overline{cor}_{\text{comp},\cdot}$	Average pairwise-complete correlation between each reference cell and its paired region in the target matrix at which the CCF is maximized
s^2_{CCF}	Sample variance of the maximum CCF values across all cells
s^2_{cor}	Sample variance of the pairwise-complete correlation values between each reference cell and its paired region in the target matrix at which the CCF is maximized
s^2_{m*}	Sample variance of the estimated vertical (row) translations across all cells
s^2_{n*}	Sample variance of the estimated horizontal (column) translations across all cells
$s^2_{\theta*}$	Sample variance of the estimated rotations across all cells

Table 2: Seven similarity features based on partitioning a reference scan into a grid of cells and comparing each cell to a target scan.

pairwise comparisons, and a testing set of 300 cartridge cases, $\binom{300}{2} = 44,850$ pairwise comparisons.

Describe 10-fold(?) cross-validation procedure here. Cite caret package.

Score-Based Likelihood Ratios

Define prosecution and defense hypotheses, likelihood ratio. Point out that we are solving the common source problem as opposed to the specific source problem.

Then discuss why likelihood ratios aren't usually tractable in pattern evidence. Instead, the high-dimensional feature space is mapped to a low-dimensional, typically univariate, similarity score. In our application, we treat the random forest class probability as the univariate image of the feature space. A predicted class probability close to 0 or 1 is a strong indication that the associated pair of cartridge cases is a non-match or match, respectively.

5. Results

5.1. Cross-Validation Results

5.2. Testing Results

6. Discussion

Provide further details for Baldwin study error rate estimation here. Include false positive and false negative too. Qualify these error rates estimates with a range depending

on how inconclusives are treated (cite Heike, Susan, Alicia paper). Compare these estimates to the algorithmic results.

7. Conclusion

Computational Details

If necessary or useful, information about certain computational details such as version numbers, operating systems, or compilers could be included in an unnumbered section. Also, auxiliary packages (say, for visualizations, maps, tables, . . .) that are not cited in the main text can be credited here.

The results in this paper were obtained using R~3.5.1. R itself and all packages used are available from the Comprehensive R Archive Network (CRAN) at `https://CRAN.R-project.org/`.

Acknowledgments

Affiliation:

Joseph Zemmels
Iowa State University
Center for Statistics and Applications in Forensic Evidence
Iowa State University
195 Durham Center
613 Morrill Road
Ames, IA 50011
E-mail: jzemmels@iastate.edu
URL: https::/jzemmels.github.io

Susan VanderPlas
University of Nebraska - Lincoln
Department of Statistics
University of Nebraska - Lincoln
349A Hardin Hall
3310 Holdrege St
Lincoln, NE 68588
E-mail: susan.vanderplas@unl.edu
URL: https://srvanderplas.netlify.app/

Heike Hofmann
Iowa State University
Center for Statistics and Applications in Forensic Evidence
Iowa State University
195 Durham Center
613 Morrill Road
Ames, IA 50011
E-mail: heike@iastate.edu
URL: https://github.com/heike