A Pipeline for Cartridge Case Comparisons

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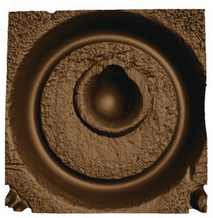
Get hands-on with the algorithm.

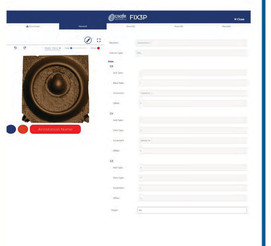
Project Rationale & Goals

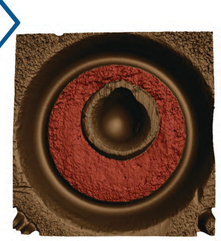
- Develop an open-source implementation of a cartridge case comparison algorithm.
- Utilize a modularized pipeline structure of the package to ease reproducibility, enable experimentation, and support rapid development of new research.
- Measure the effect of sub-procedures on results compared to previously-developed pipelines.



Data Collection

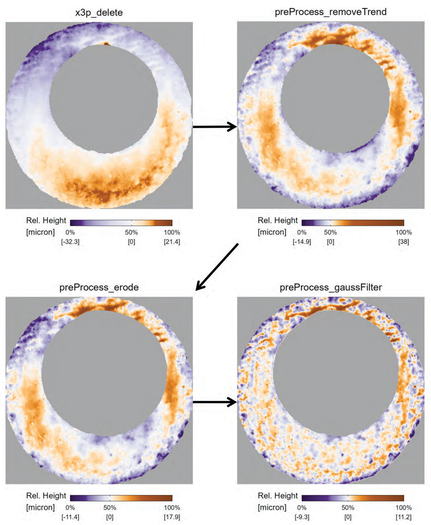
Collect a fired cartridge case and scan it using the TopMatch-3D High-Capacity Scanner from Cadre Forensics.





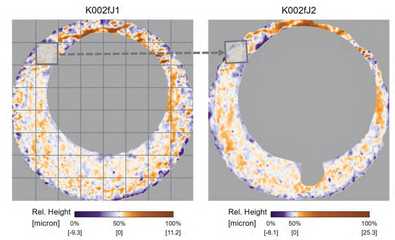
BF Identification

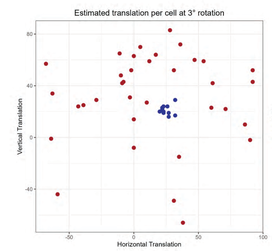
Manually identify the breech face region of the cartridge case scan using the FiX3P software.



Pre-processing

Highlight the breech face impressions by isolating the manually-identified region, removing global trend from scan, eroding primer edge to mitigate roll-off effects, and applying a Gaussian filter.

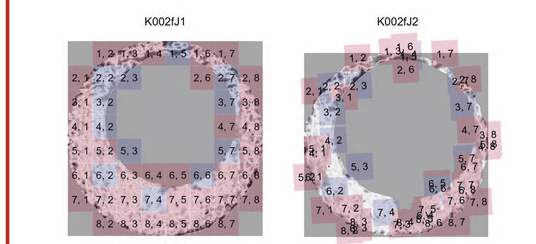




Comparison

Compare two pre-processed scans by dividing one scan into a grid of cells and calculating the registration (translation & rotation) that maximizes the cross-correlation function per cell.

Apply Density-Based Spatial Clustering of Applications with Noise (DBSCAN) to the estimated registrations to identify cells that agree on registration (blue cells in plot above). Treat the center of this cluster as the estimated registration for the two scans.



$$\bar{C} = \frac{1}{2}(C_1 + C_2)$$

$$\Delta_\theta = |\hat{\theta}_1 + \hat{\theta}_2|$$

$$\Delta_{trans.} = \sqrt{(\widehat{dx}_1 + \widehat{dx}_2)^2 + (\widehat{dy}_1 + \widehat{dy}_2)^2}$$

Similarity Features

Perform the comparison procedure to identify the cluster points and estimated registration in both directions.

Consider blue cluster point cells as Congruent Matching Cells (CMCs; the plot above shows CMCs for one direction).

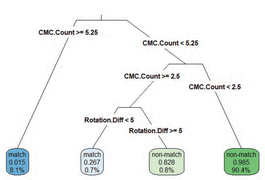
Calculate the average number of CMCs and the difference in the estimated registration across both comparison directions. Train a Decision Tree model using these as similarity features.

References

- J. Maiers. (2022, March 29). *AAFS 2022 recap: An internal validation study of the TOPMATCH 3D scanner for cartridge cases*. Center for Statistics and Applications in Forensic Evidence. URL https://forensicstats.org/blog/2022/03/29/aafs-2022-recap-an-internal-validation-study-of-the-topmatch-3d-scanner-for-cartridge-cases/
- J. Zemmels, H. Hofmann, S. VanderPlas. (2022). cmcR: An Implementation of the 'Congruent Matching Cells' Method. R package version 0.1.9.
- J. Song. Proposed "NIST Ballistics Identification System (NBIS)" Based on 3D Topography Measurements on Correlation Cells. American Firearm and Tool Mark Examiners Journal, 45(2):11, 2013. URL https://tsapps.nist.gov/publication/get_pdf.cfm?pub_id=910868.
- J. Song, W. Chu, M. Tong, and J. Soons. 3D topography measurements on correlation cells—a new approach to forensic ballistics identifications. Measurement Science and Technology, 25(6):064005, June 2014. ISSN 0957-0233, 1361-6501. URL https://doi.org/10.1088/0957-0233/25/6/064005.
- J. Song, T. V. Vorburger, W. Chu, J. Yen, J. A. Soons, D. B. Ott, and N. F. Zhang. Estimating error rates for firearm evidence identifications in forensic science. Forensic Science International, 284:15–32, Mar. 2018. ISSN 03790738. URL https://doi.org/10.1016/j.forsciint.2017.12.013.
- A. Millard. (2016, February 20). *5 reasons you're bad with a handgun*. Realtree Camo. URL https://www.realtree.com/guns-and-camo/5-reasons-youre-bad-with-a-handgun

Results

- Based on 21,945 pairwise comparisons, we have the following trained Decision Tree & Confusion Matrix.



% Confusion Matrix	Pred. Match	Pred. Non-match	Row Total
Actual Match	85.9% (1,868)	14.1% (331)	2,199
Actual Non-match	0.3% (66)	99.7% (19,680)	19,926

- Test CART model using 44,850 pairwise comparisons.

% Confusion Matrix	Pred. Match	Pred. Non-match	Row Total
Actual Match	84.7% (2,609)	15.3% (472)	3,081
Actual Non-match	0.4% (149)	99.6% (41,620)	41,769

- Compare results to the CMC method implementation from Zemmels et al. (2022) with different parameter settings using the same 300 scans.

Method	False Positive (%)	False Negative (%)	Error Rate (%)
CMC w/ Song et al. (2014) parameters	0.06	53.3	3.7
CMC w/ Song et al. (2018) parameters	0.6	36.1	3.1
DBSCAN CART	0.4	15.3	1.4

Discussion & Conclusion

- Modularization of the pipeline allows sub-procedures to be "swapped out" for others.
- Experimentation with variations of the pipeline can be performed in a coherent, unified framework.
- The modularized pipeline can be better understood overall by practitioners and lay-people.

- We introduce novel sub-procedures in the pre-processing, comparison, and similarity feature steps.
- These sub-procedures result in an improved error rate compared to our implementation of the CMC method (with various parameter settings) while also requiring fewer parameters.
- The fitted Decision Tree model is easily interpretable.

- Improvements upon sensitivity of the pipeline may come in the form of better pre-processing procedures or more informative similarity features.

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