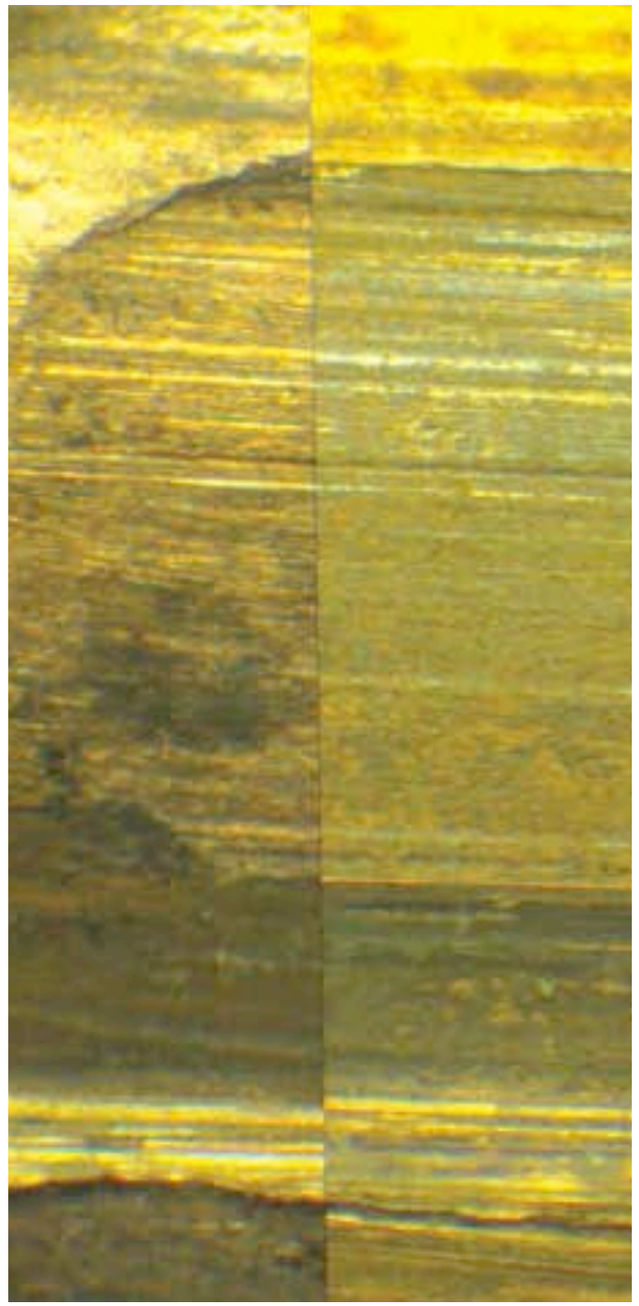
Matching Striae in Bullets

Heike Hofmann, Eric Hare, Alicia Carriquiry
Department of Statistics
Iowa State University

csafe Center for Statistics and Applications in Forensic Evidence

Microscopic alignment

- Match bullets that were fired from the same barrel
- Find a probabilistic quantification of the match
- attempt at quantification:
  CMS (consecutively matching striae)
- concept goes back to Biasotti (1959)
- part of current AFTE practice



From Robert Thompson's "Firearm identification"

James Hamby Study

- Ten consecutively rifled Ruger P-85 pistol barrels used to fire
  - 20 ‘known’ test bullets, 2 from each barrel
  - 15 ‘unknown’ bullets for comparison
- Sets of 35 bullets sent to 507 FEs for examination
- 0 false positive identifications,
  8 inconclusive results (out of 7,605)

Data format

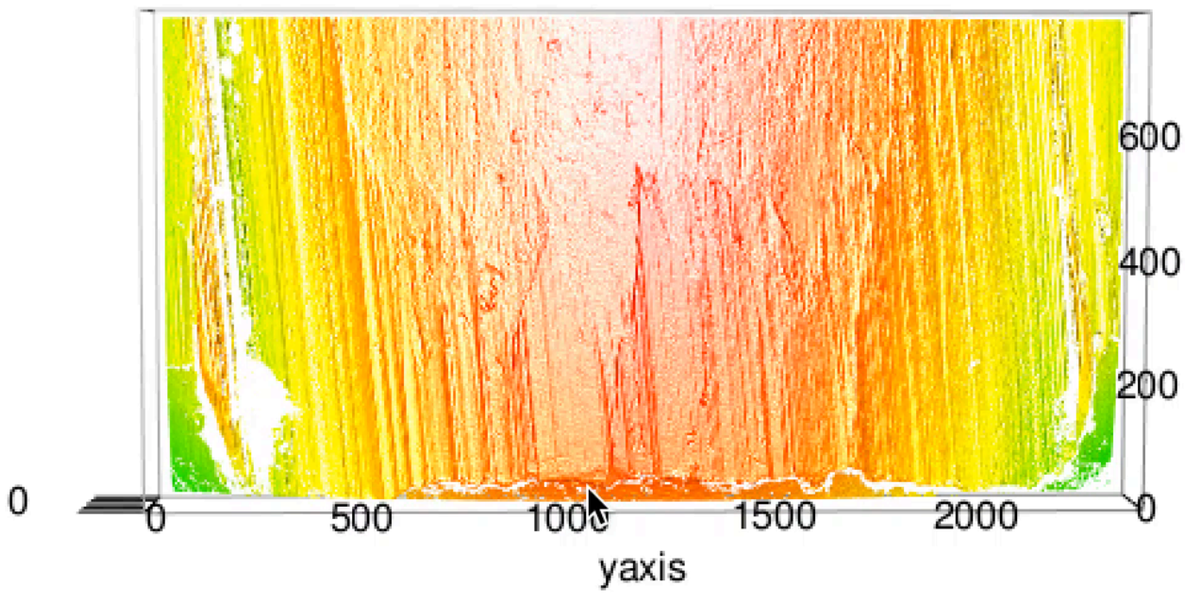
http://www.nist.gov/forensics/ballisticsdb/hamby-consecutively-rifled-barrels.cfm

- 3D topographical images of each bullet
- NanoFocus lens at 20x magnification
- x3p format in ISO5436-2 standard:

header file with meta information

body:

array of surface measurements at 1.5625μm by 1.5625μm



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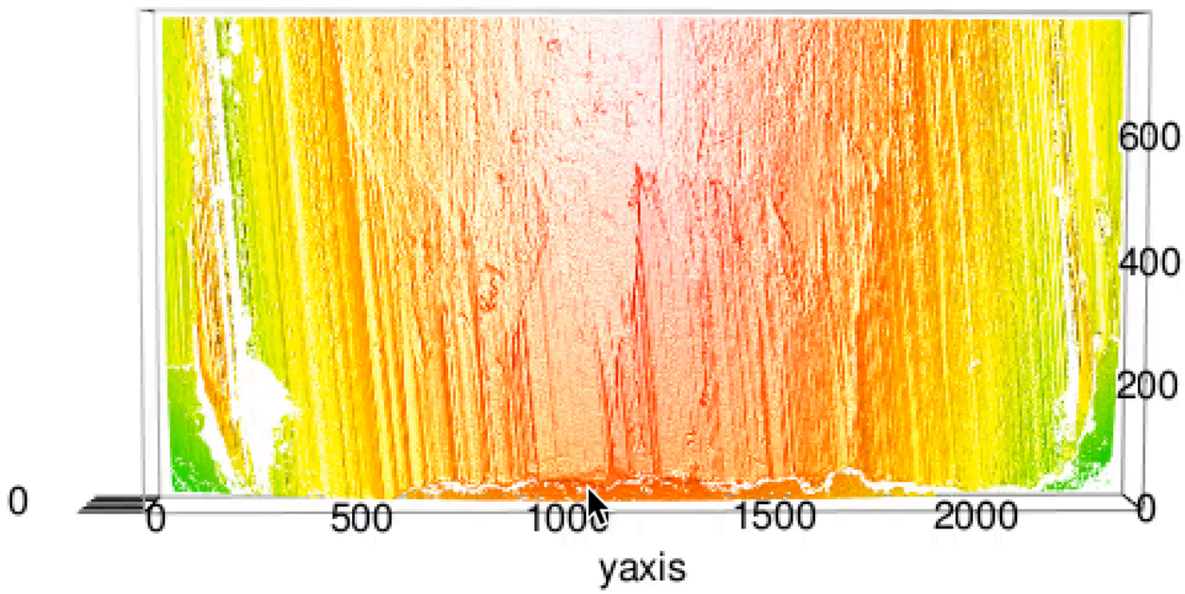
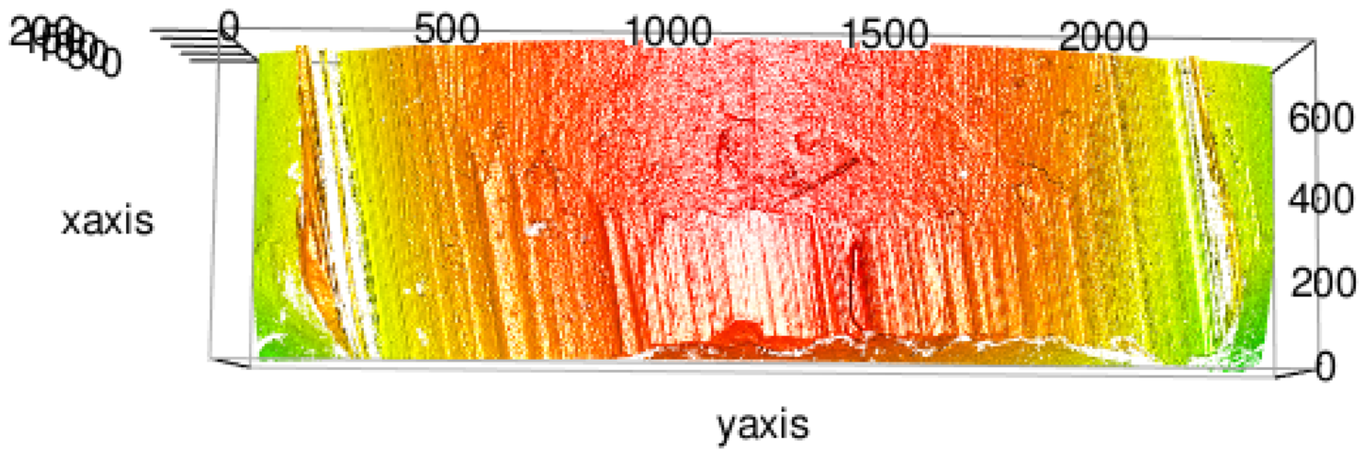


Extracting a signature

- Extract a profile at fixed height



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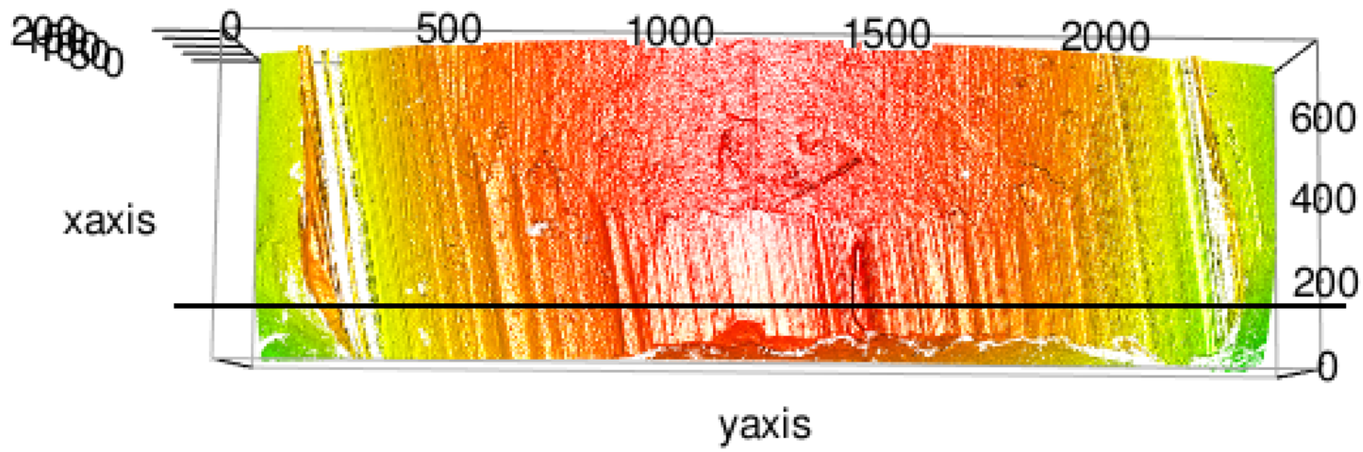

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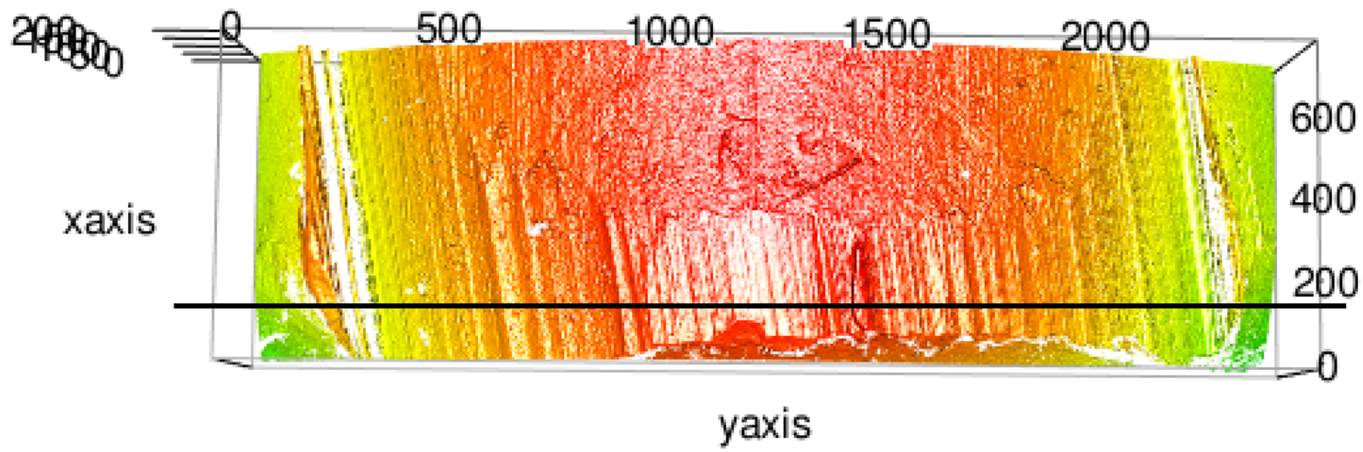

- Profile plot

Extracting a signature

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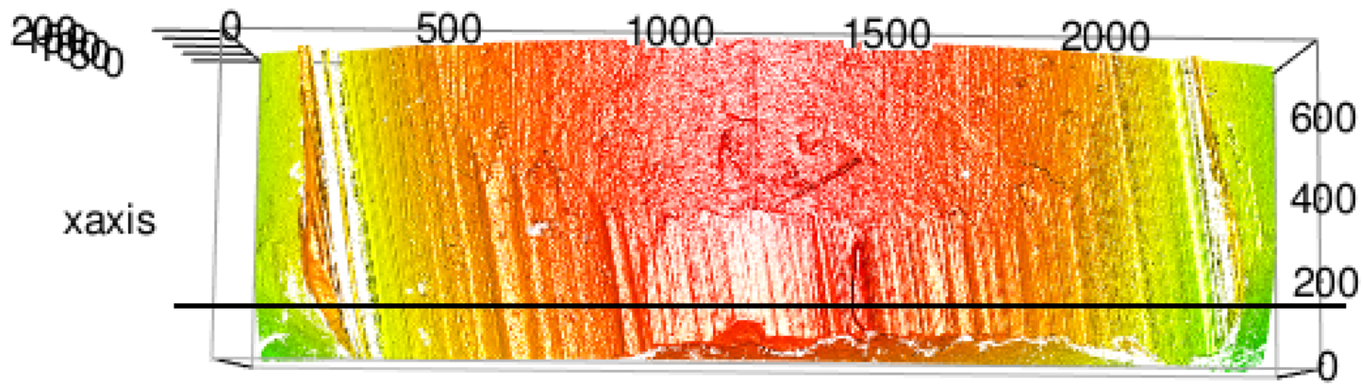

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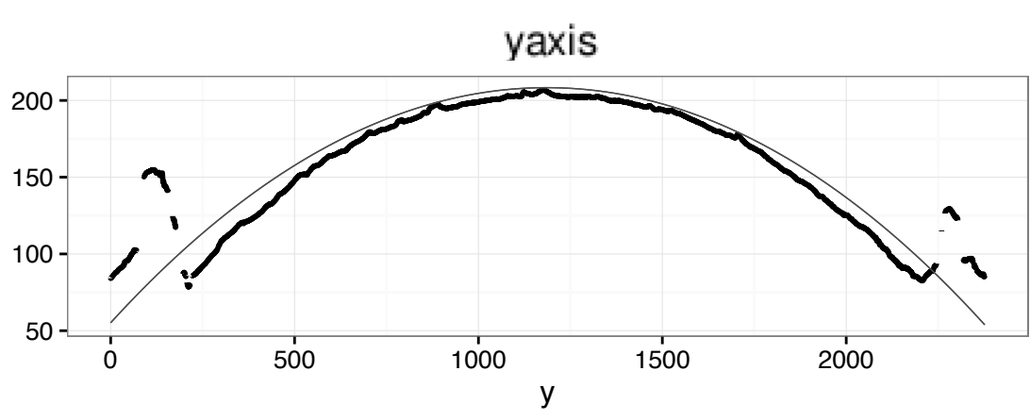

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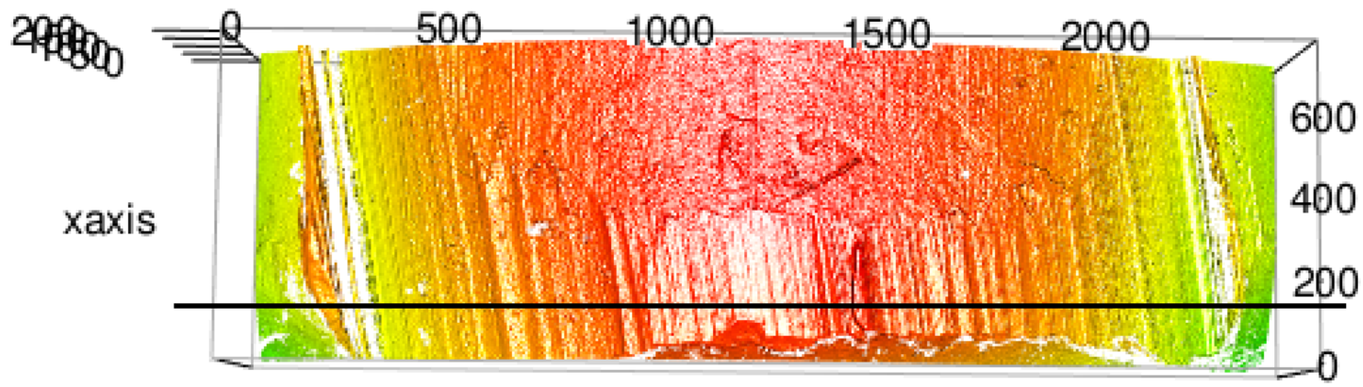
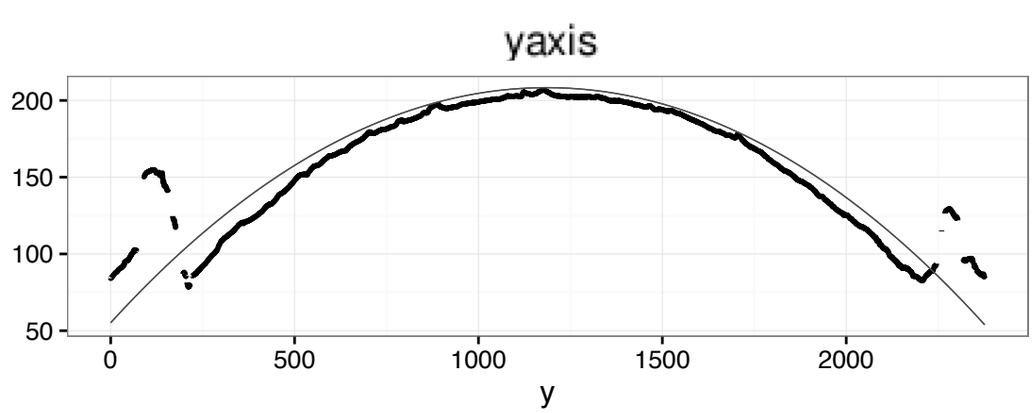


- Profile plot
- Identify grooves



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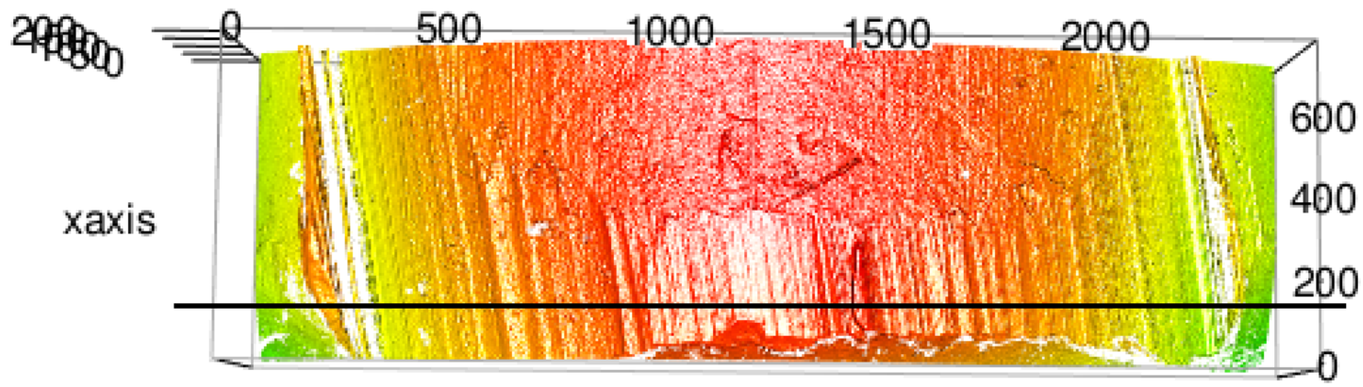

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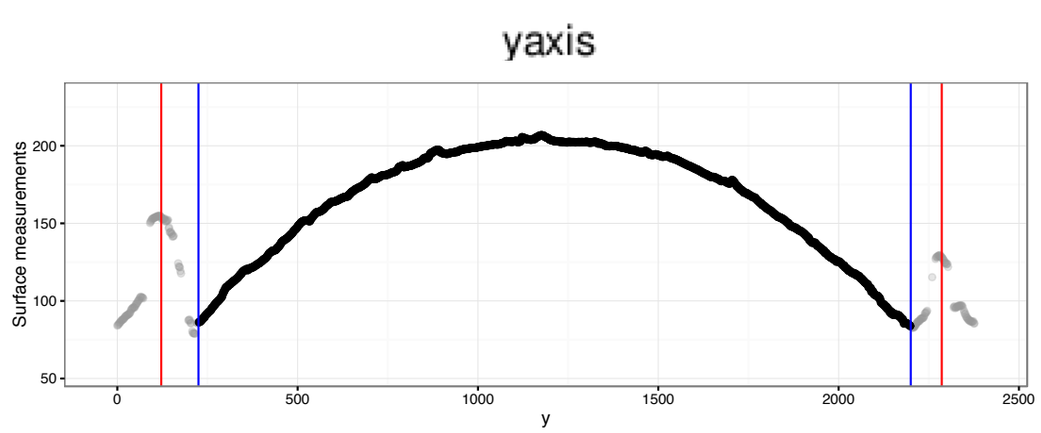

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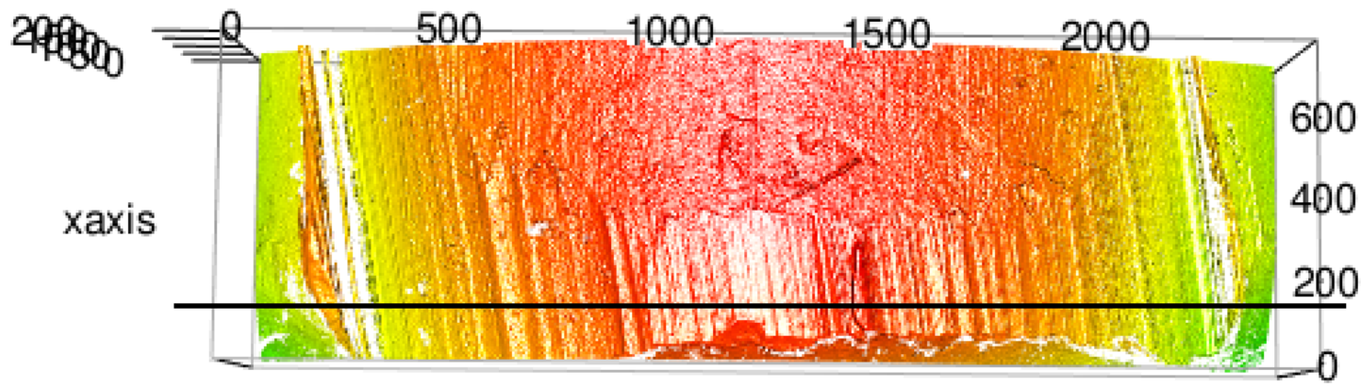
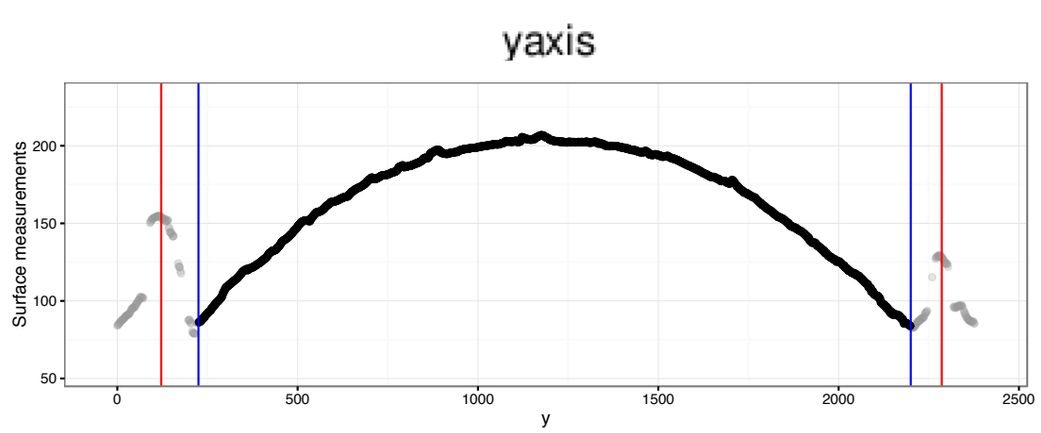


- Profile plot
- Identify grooves
- Get signature from loess fit



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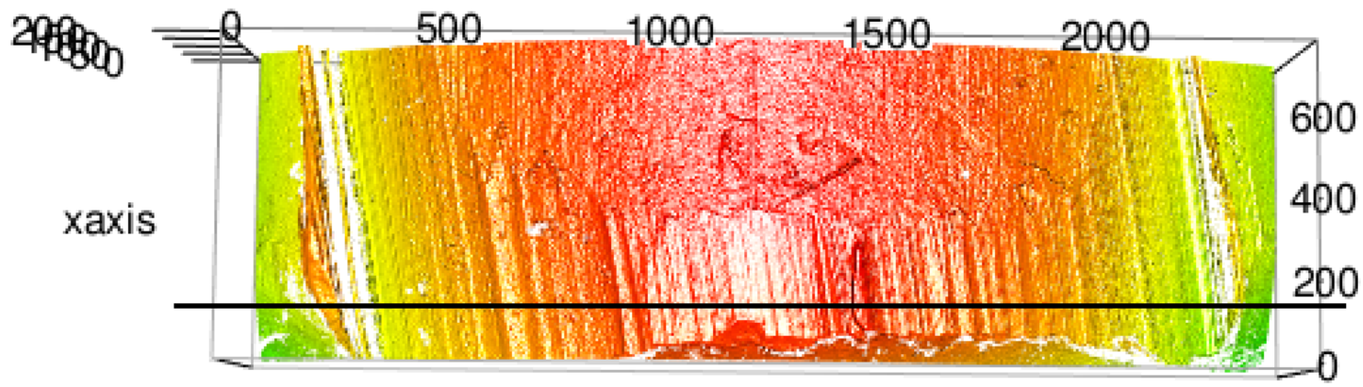

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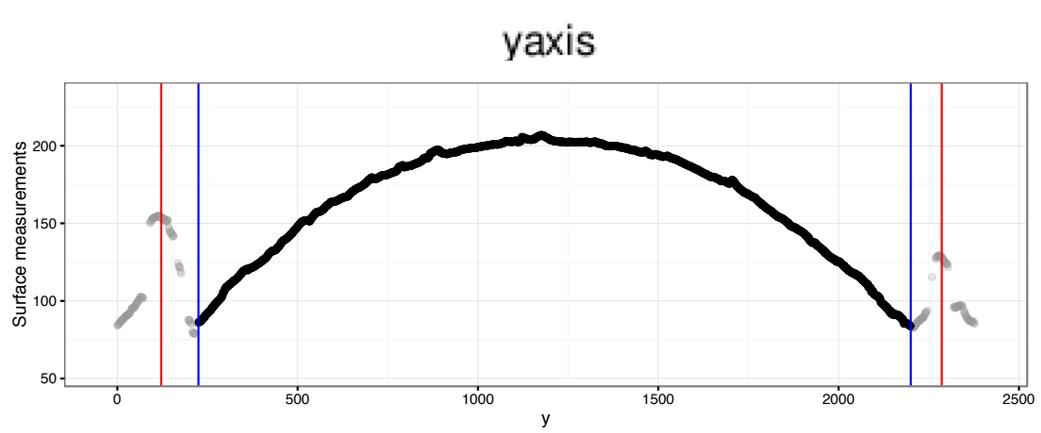
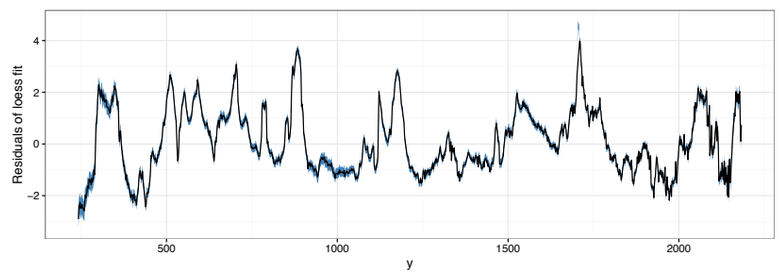
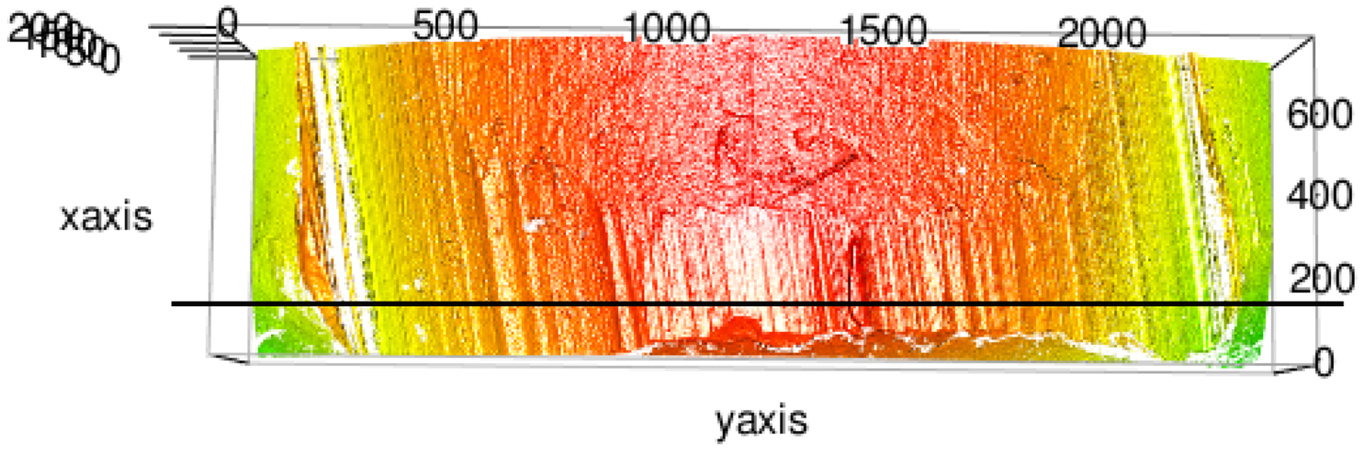




Determining Height

- Want to extract signature at a ‘stable’ region

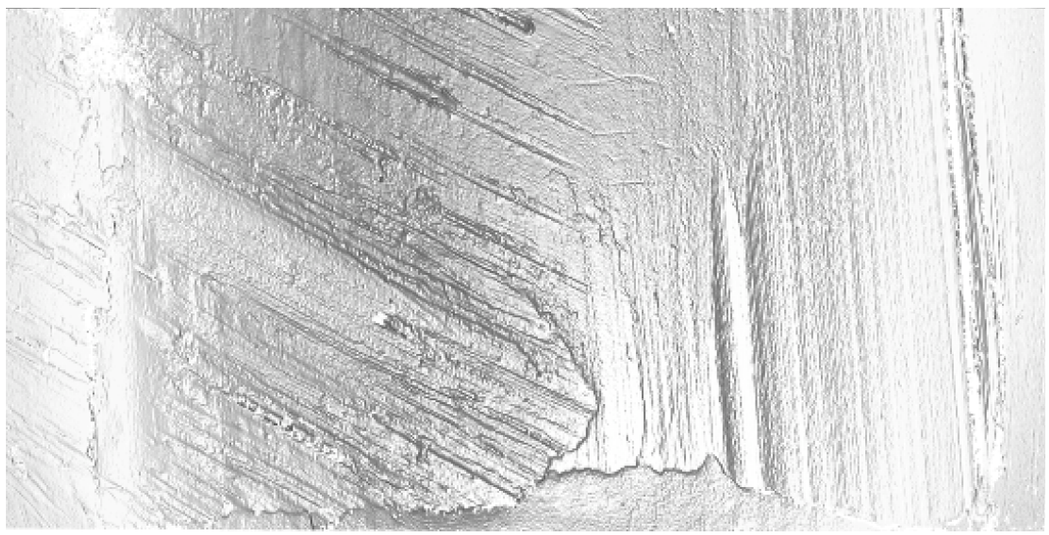


- at the bottom of the bullet: danger of break-off
- at the top: danger of no/low impressions
- Here: extract signatures at intervals of 25µm, use lowest height where signatures have ccf > 0.95
- Also serves as crude automatic quality assessment

CCF test fails

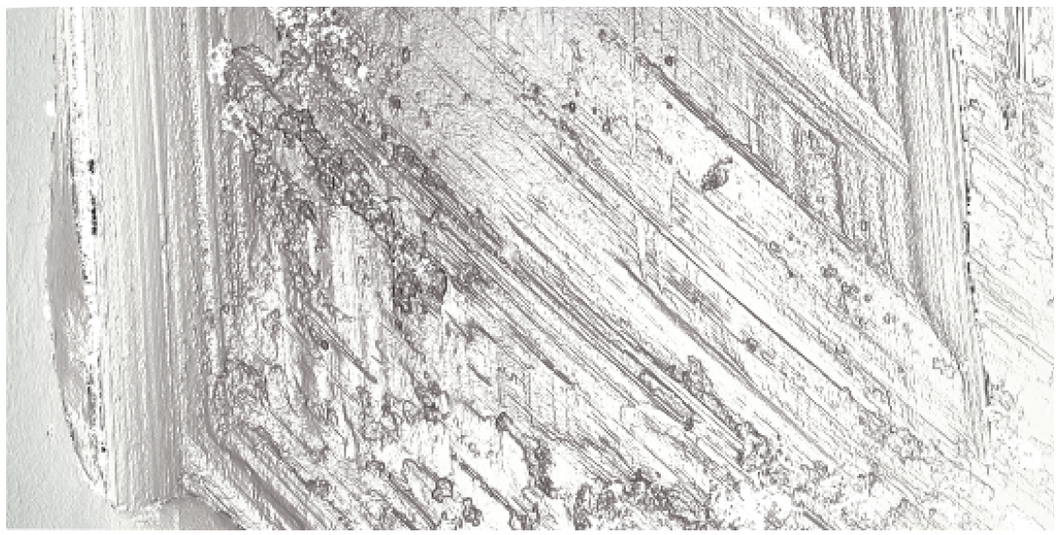
Barrel 6 Bullet 2-1

Barrel 9 Bullet 2-4



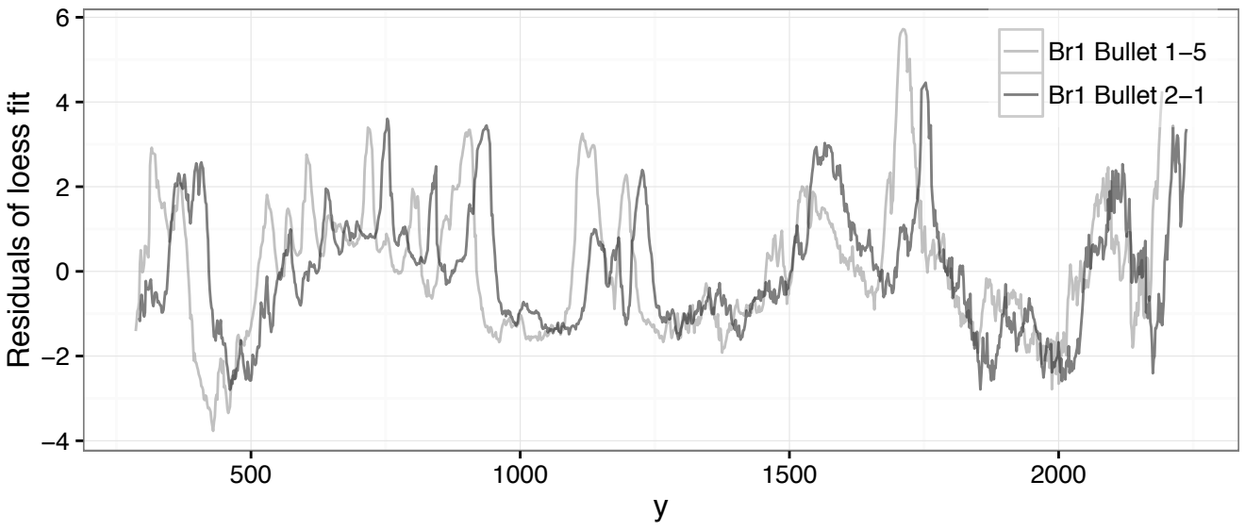
Unknown Bullet B-2

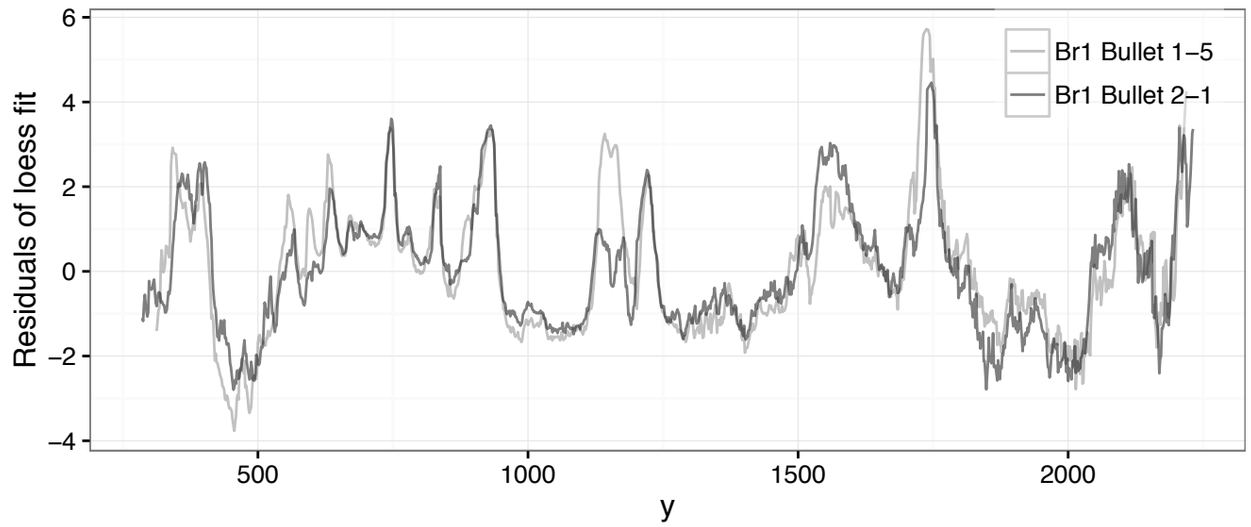
Unknown Bullet Q-4



Aligning Signatures

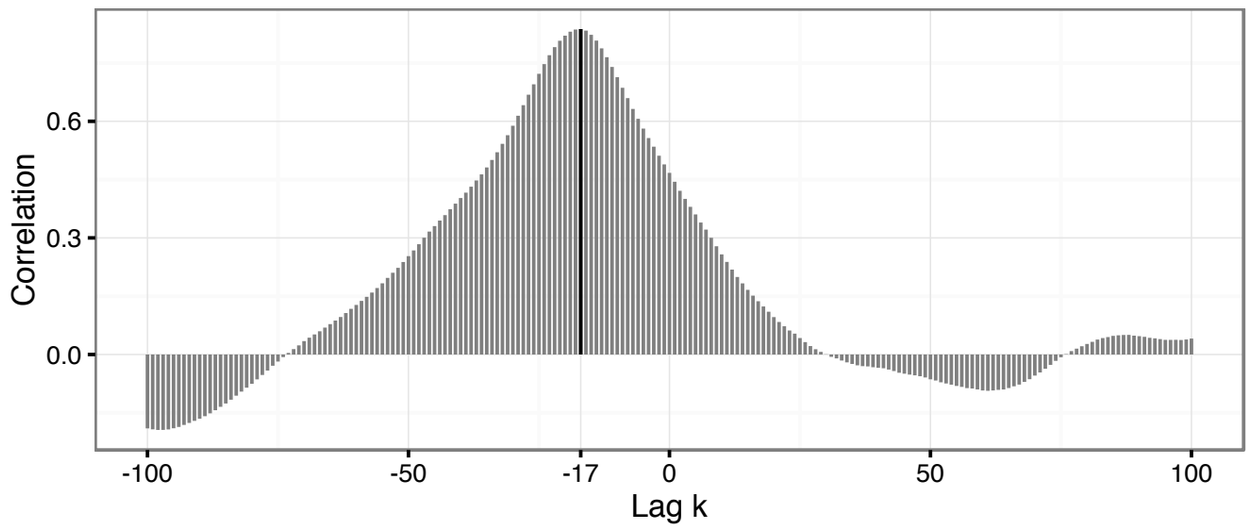
- Raw signatures (left) and aligned signatures (right)





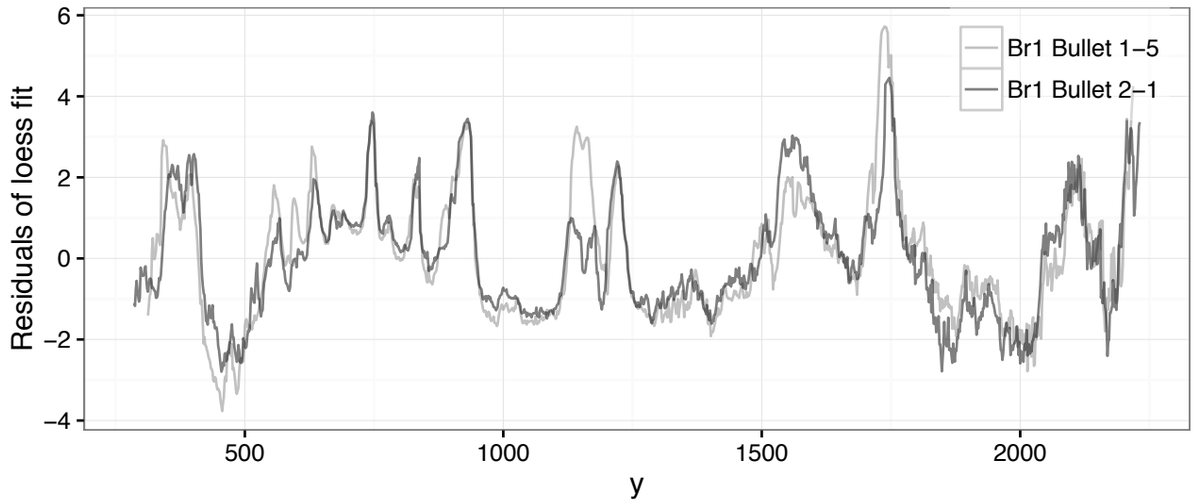
- Alignment is based on cross correlation function(ccf)

$$(f * g)(k) = \sum_t f(t+k)g(t)$$



Feature extraction

- CCF
- lag
- D defined as the average of the vertical distance between f and g:

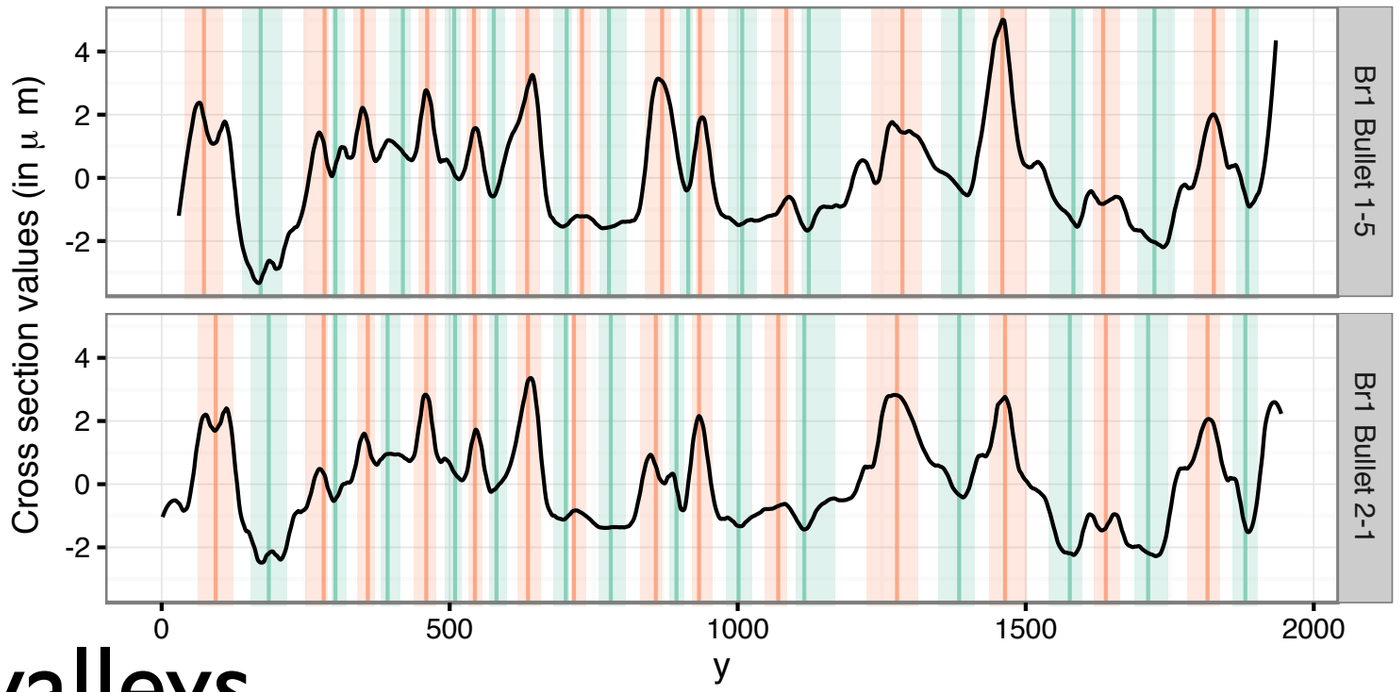


$$D^2 = \frac{1}{\#t} \sum_t (f(t) - g(t))^2$$

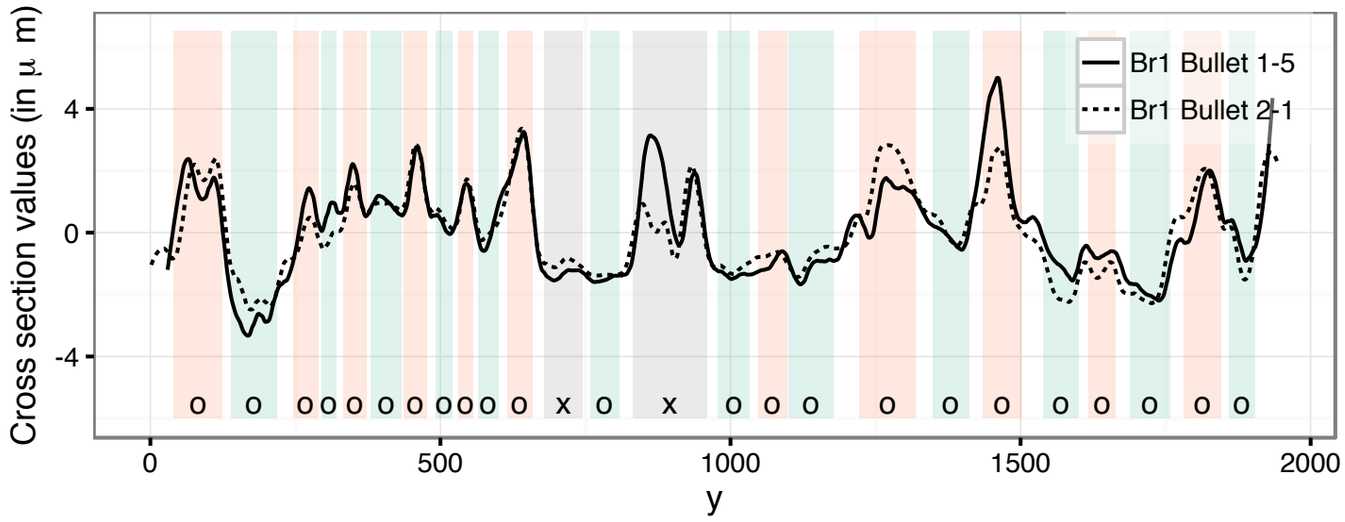
- CMS next …

Peaks and valleys

- Rolling median detects local mins and maxes



- joint peaks and valleys



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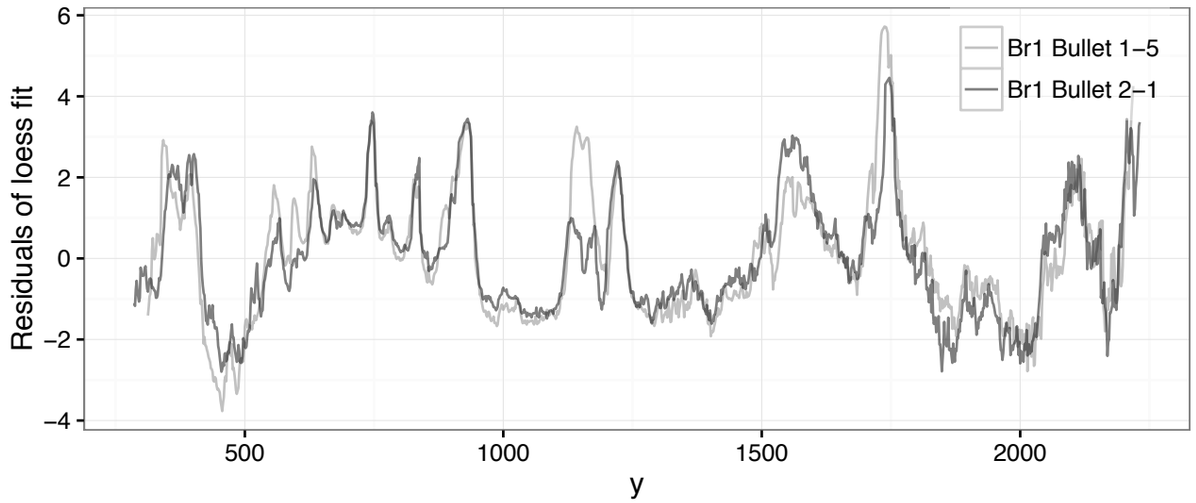


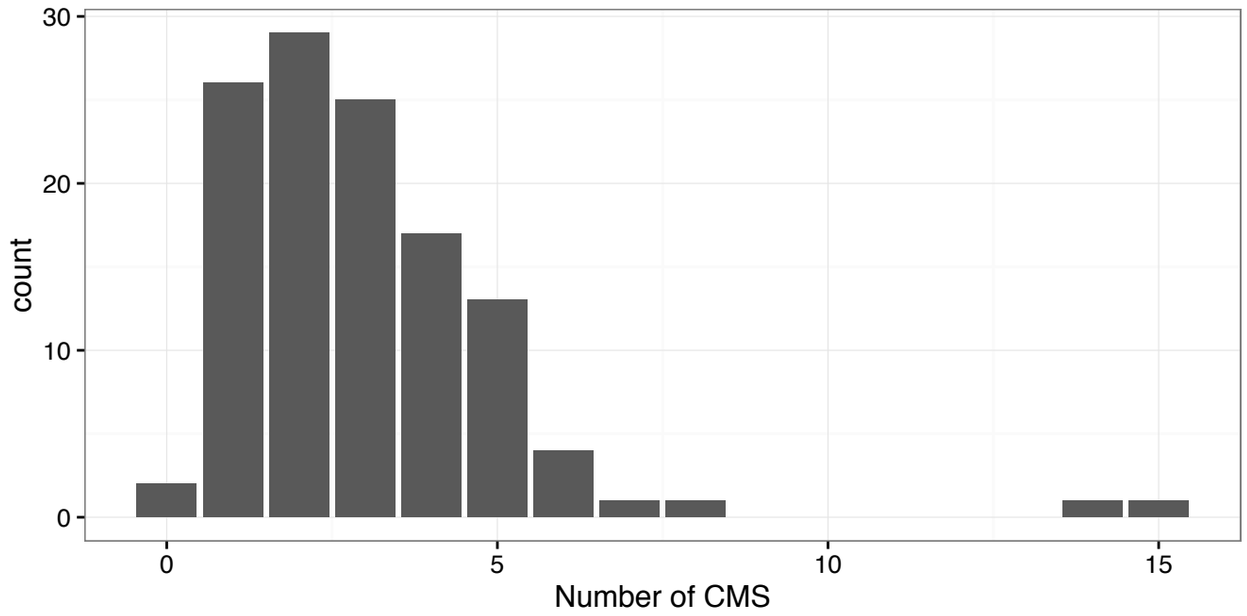
- CMS
- # matched striae, # mis-matched striae
- Consecutively Non-Matching Striae (CNMS)
- S defined as the sum of the (abs) height of matches

Data Extraction

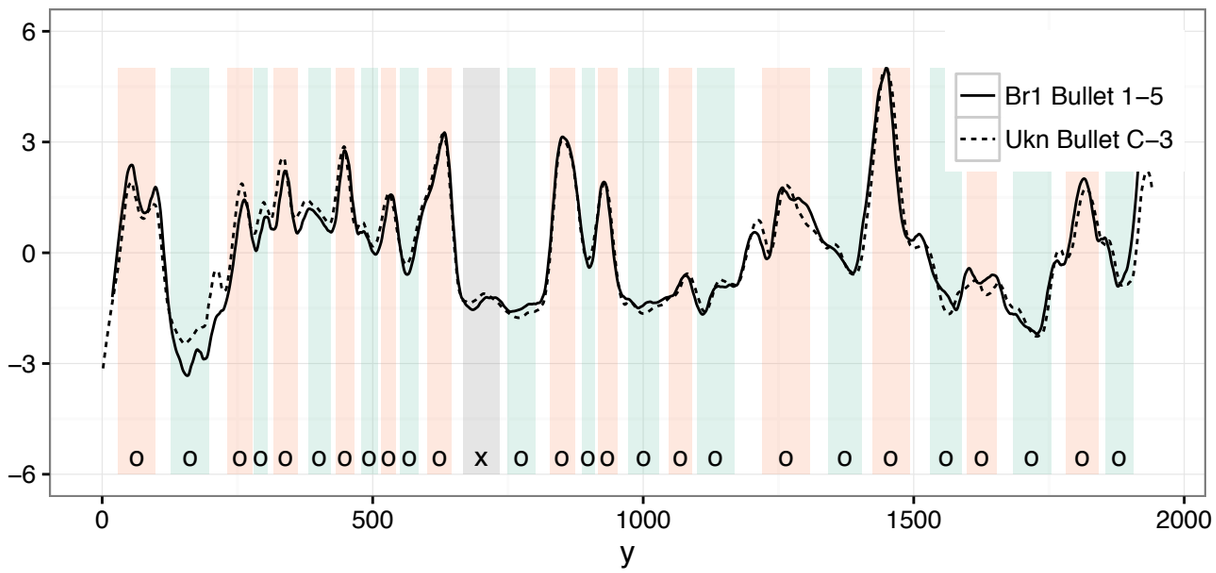
- Extract features from all of the known and unknown bullets of the Hamby study
- Focus on comparisons of unknown lands (88) to known lands (118) of good quality
  88 x 118 = 10,384 land-land comparisons
- 172 land-land comparisons are Known Matches
- Later we will come back to consider all possible land-land comparisons

Example: Unknown Bullet C-3

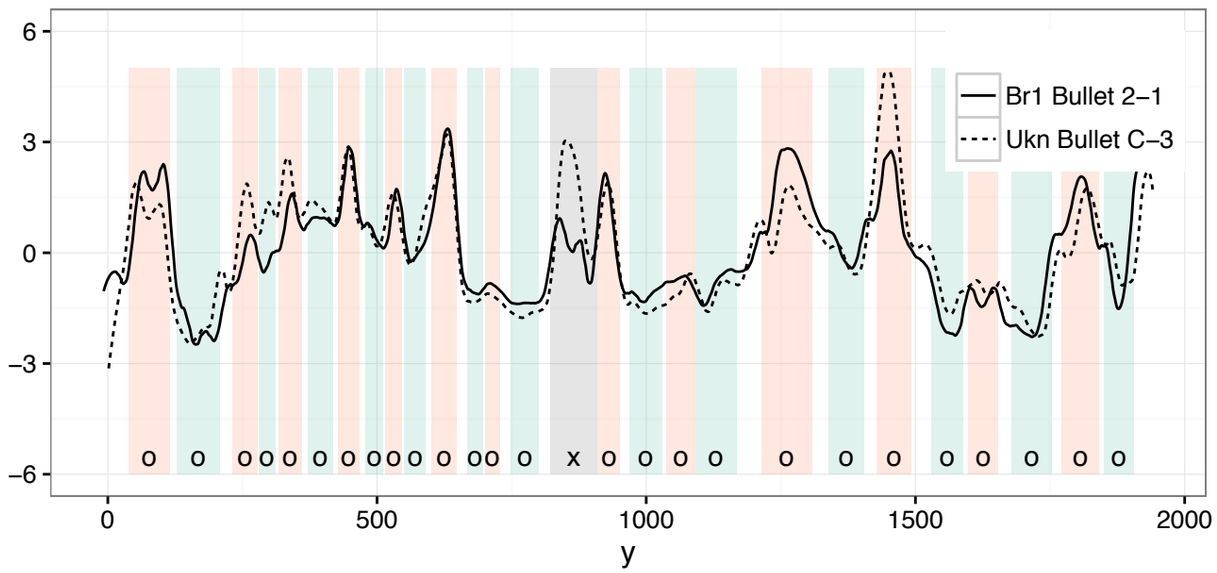
- CMS of C-3 with all known lands



15 CMS

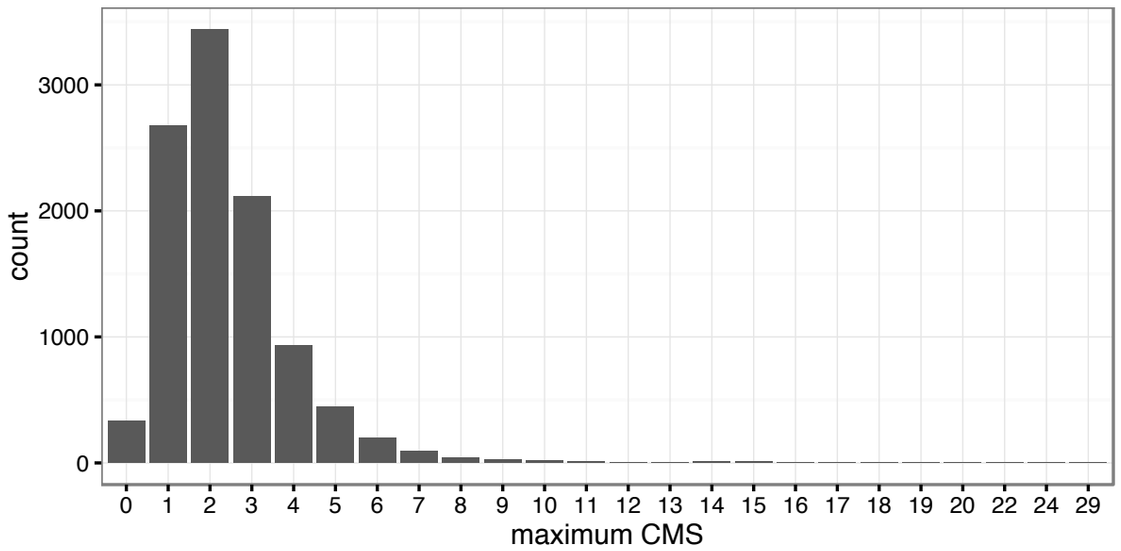


14 CMS

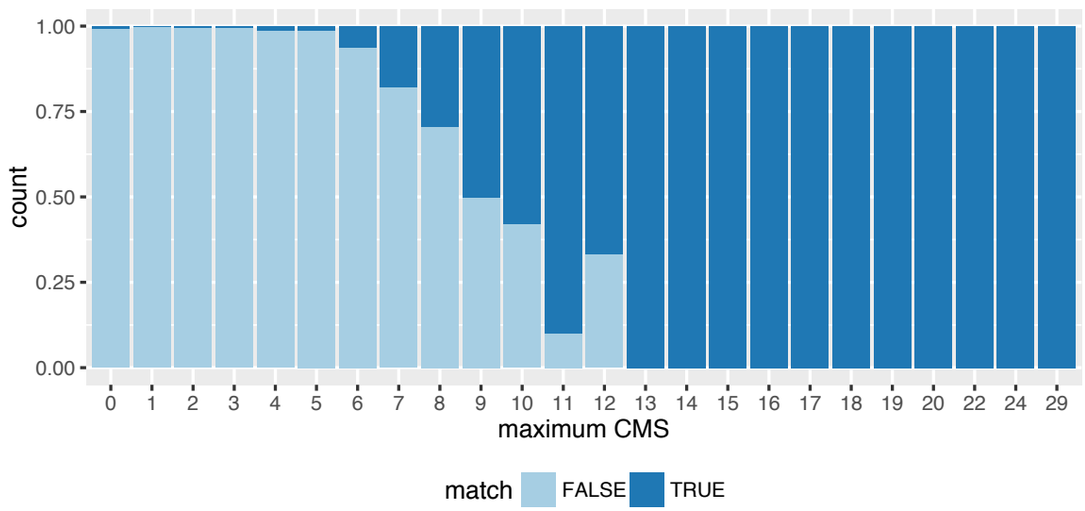


Distribution of CMS

- Marginal distribution of all 10,384 land-land CMS



- Conditional probability of Match/Non-match



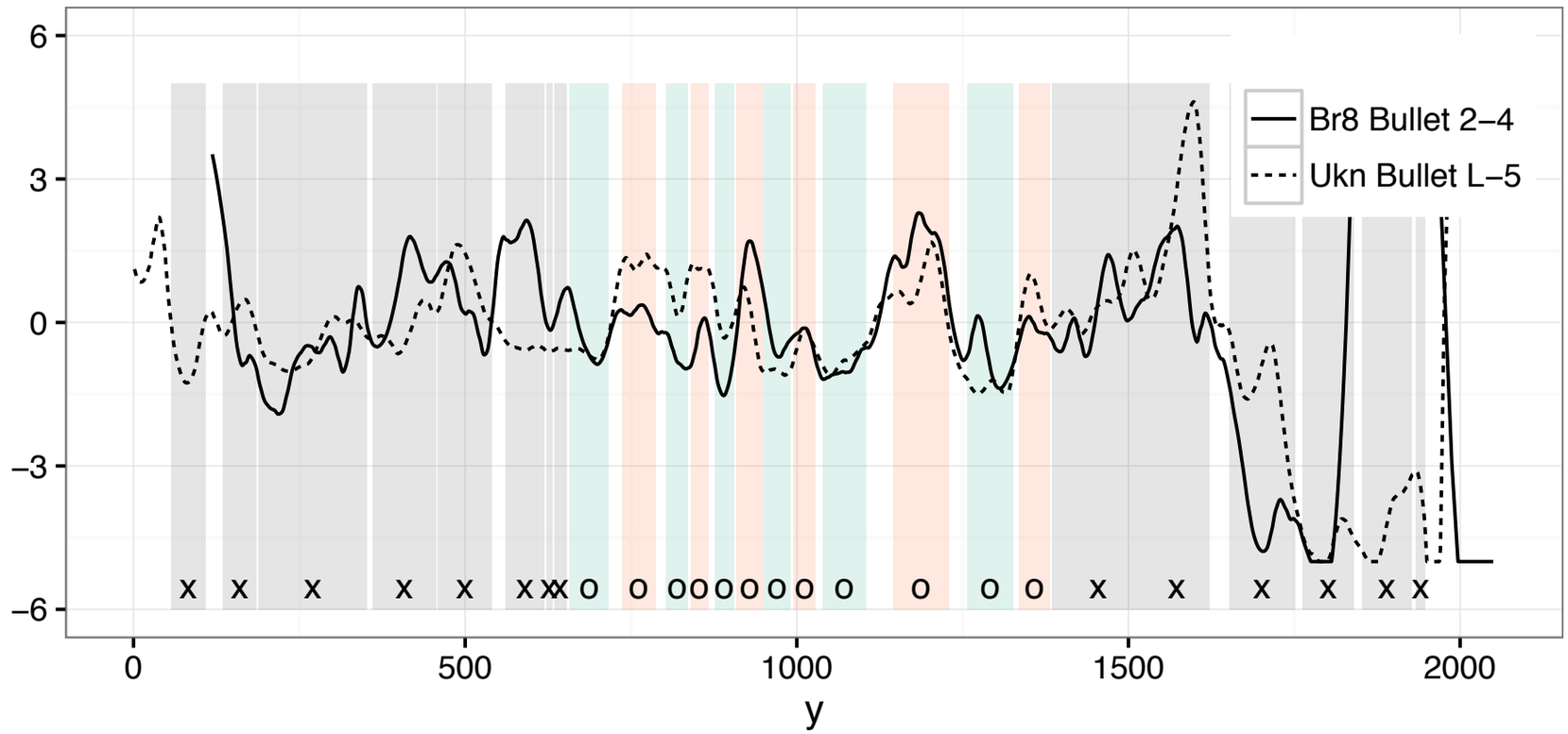
All 42 pairs with CMS > 12 are matches

About half of pairs with CMS = 9 are matches

CMS by itself is not good enough;
this is not a new finding (e.g. Miller, 1998)

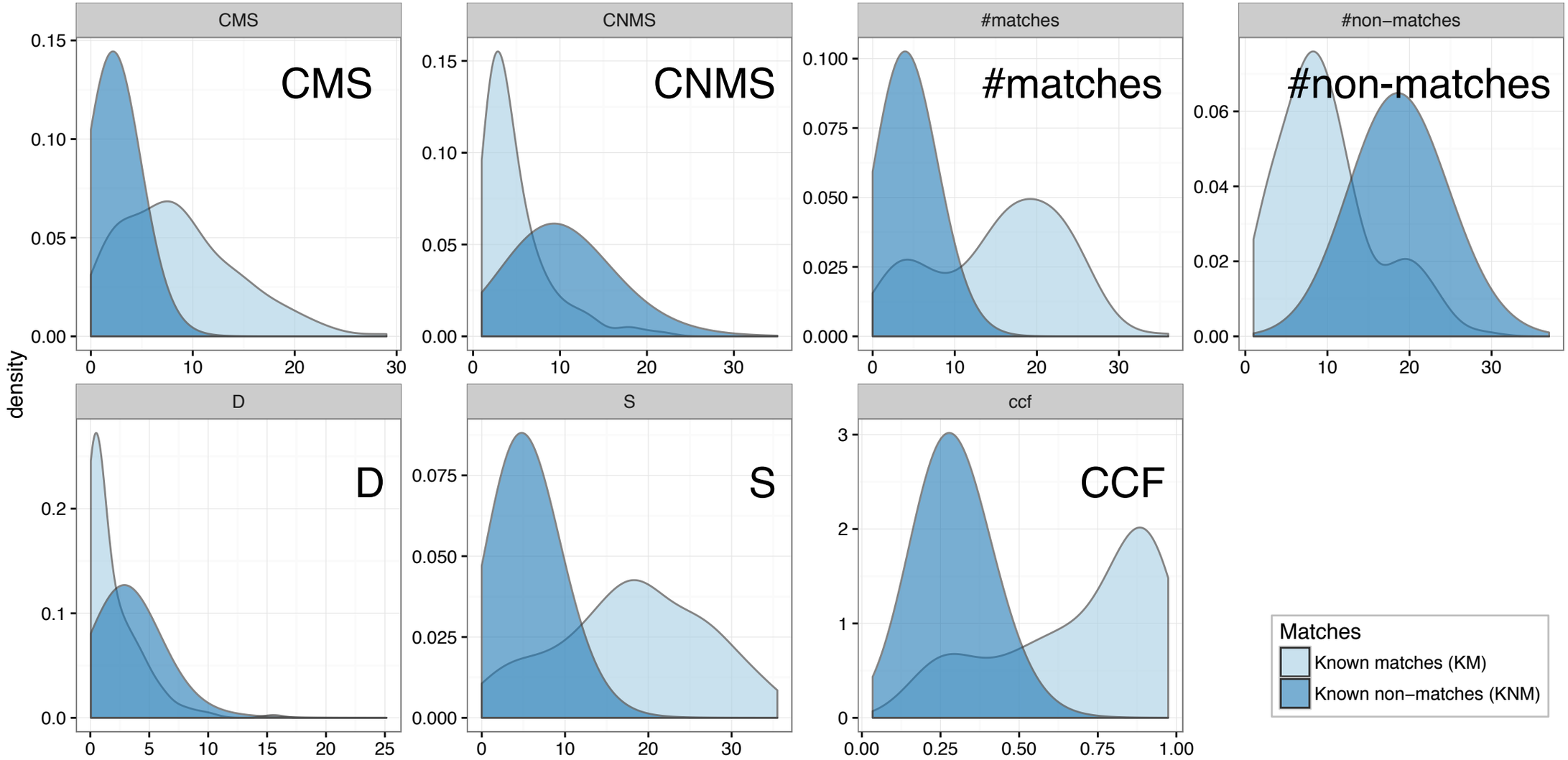
Curious Case of CMS = 12

- Known Non-match with strong agreement in the middle of the lands



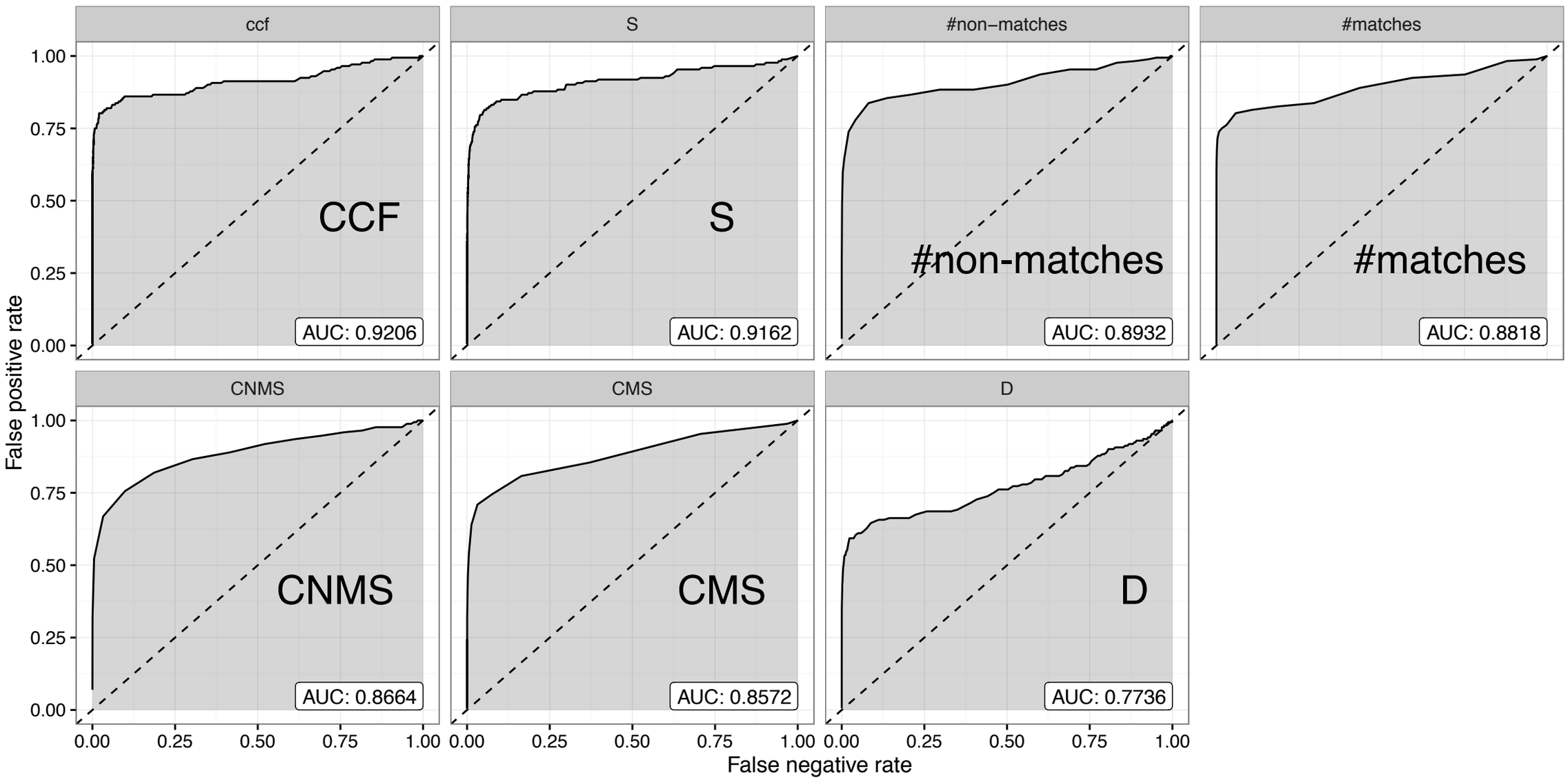
- visually, it is relatively easy to determine the non-match

Feature Densities



- All features show pretty strong differentiation between Known matches (KM) and Known Non-matches (KNM)

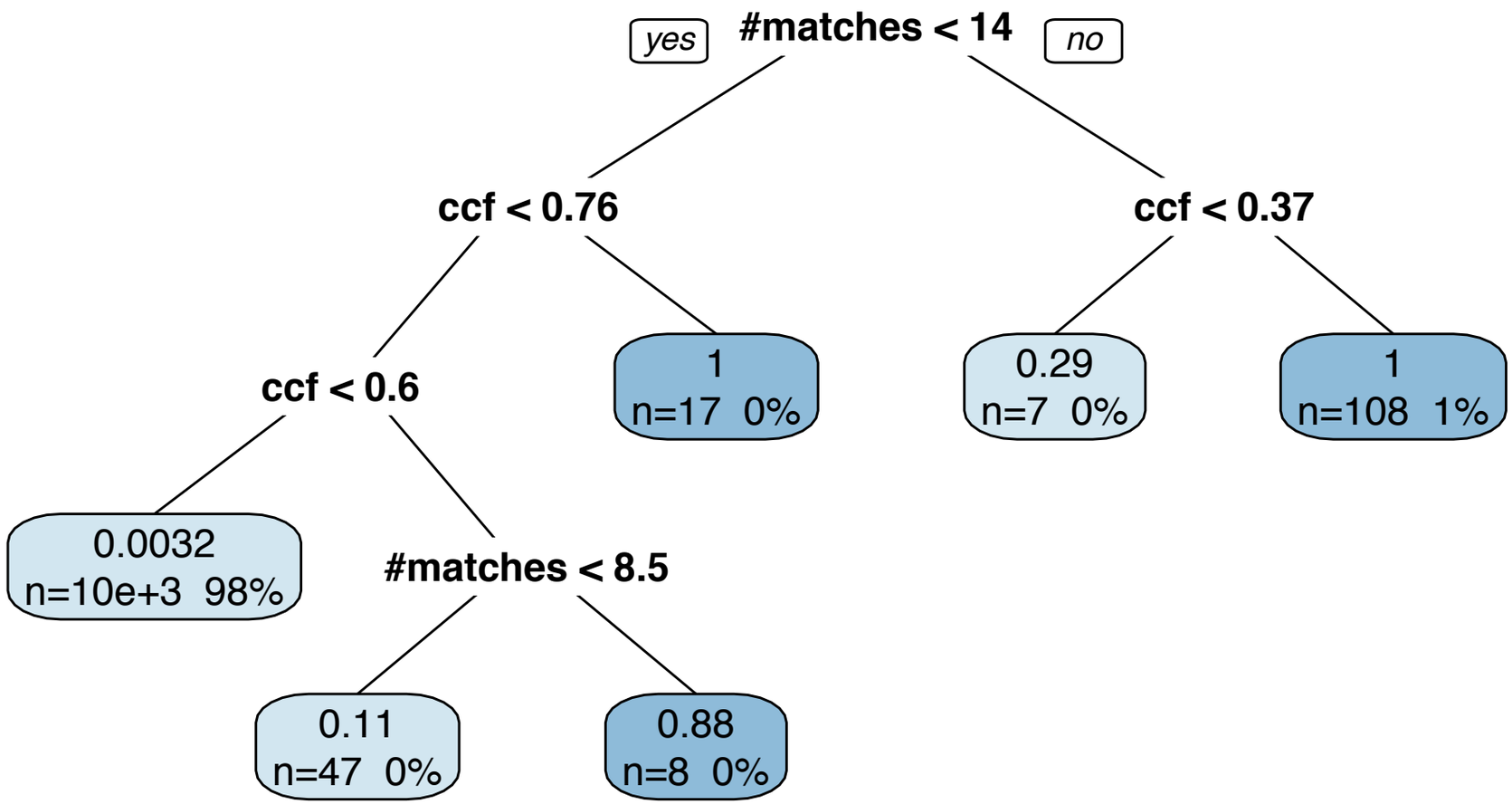
Receiver operating characteristic (ROC) curves



- AUC shows strength of each individual feature for distinguishing between matches and non-matches

Classification Tree

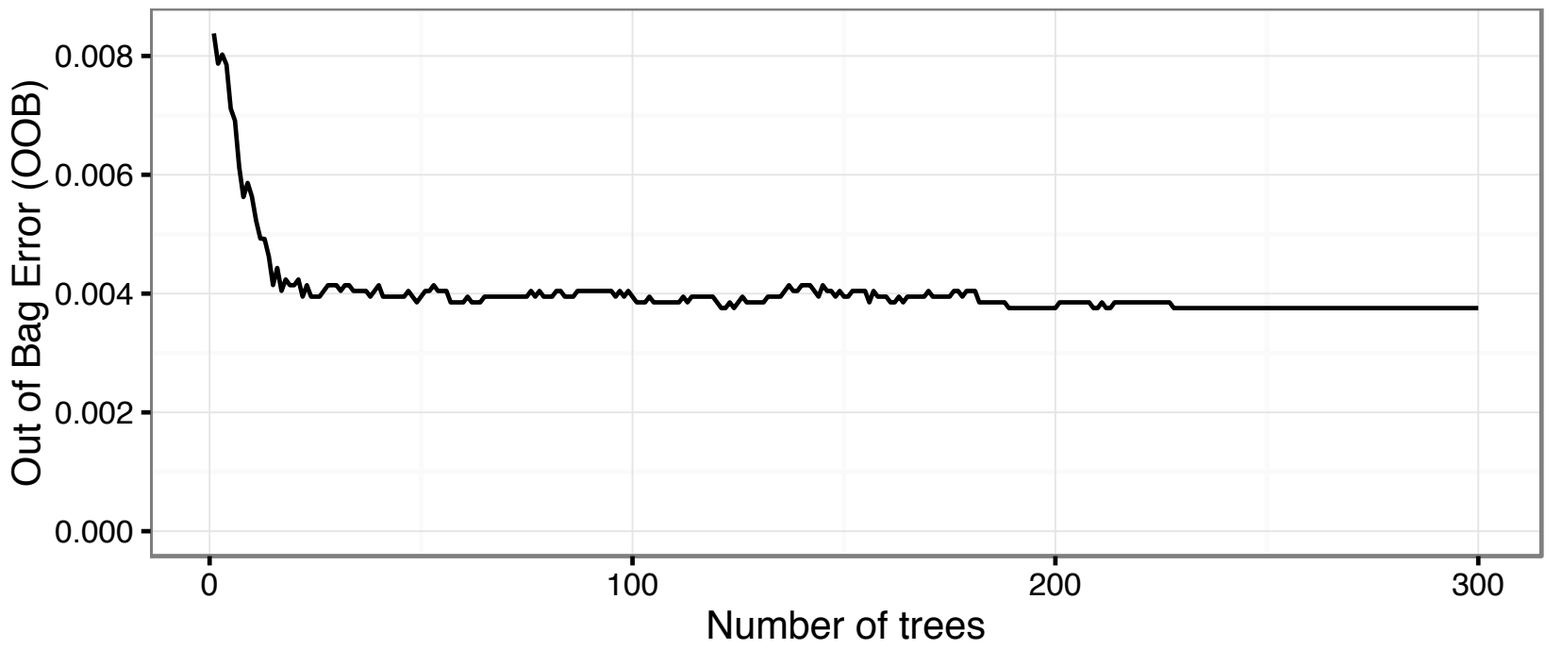
Breiman et al (1984)



- 1 false positive, 40 false negatives (out of 172 KM)
- CMS is not used in the tree at all

Lots of Trees …

- A random forest (Breiman, 2001) is able to correctly predict all matches and non-matches
- OOB error rate is 0.0039 overall (for 300 trees):



- composite of FP of 0.0001 and FN of 0.2267

Larger Forest

- Extract features from all remaining land-land comparisons of the Hamby study
- known-known (6,903) and unknown-unknown (3,828) 10,731 additional land-land comparisons
- Using previously fitted random forest for predictions:
  18 false negatives and 9 false positives
  for FN of 0.19 and FP of 0.00085
- Random forest on ALL land-land comparisons results in OOB error of 0.3% (down from 0.4%)

more data would help considerably!

Conclusions/Further Work

- Overall error rate of Random forest would benefit from more data
- All results on Hamby study only:
  effect of microscope? other type of ammunition? ???
- So far: land-land comparisons
  what, if we use only a fraction of a land (1/2, 1/4, 1/8, …) for a match?
- Web app with implementation of algorithm:
  https://erichare.shinyapps.io/x3prproto