Probability Models for Impression and Pattern Evidence

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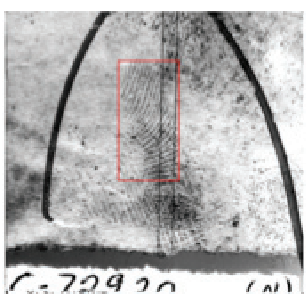
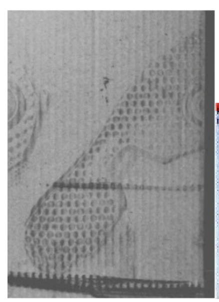
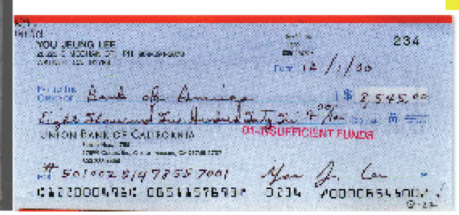
Forensic Modalities

- Forensics
  - Digital
    - Computer
      - Network
      - Database
      - Mobile
    - Multi-media
      - Video
      - Speech
      - Photos
  - Analog
    - Impression/ Pattern Evidence
      - Latent prints
      - QD: Handwriting
      - QD: Printers
      - Footwear
      - Tire tread
      - Fire-arms
      - Tool marks
    - Trace Evidence
      - Genetic
        - DNA
        - Blood
        - Semen
        - Hair
        - Saliva
      - Other
        - Pollen
        - Dust
        - Paint
        - Glass
        - Fiber
        - Arson
        - Voltage







Forensic Opinion

- Courts allow Latent Print Examiner to opine on ultimate question of individualization
  - Evidence is attributed to a single individual and no other
- Three possible opinions
  - The evidence
    - Individualizes
      - No other individual on earth
    - Inconclusive
    - Excludes
      - Definitely not this individual

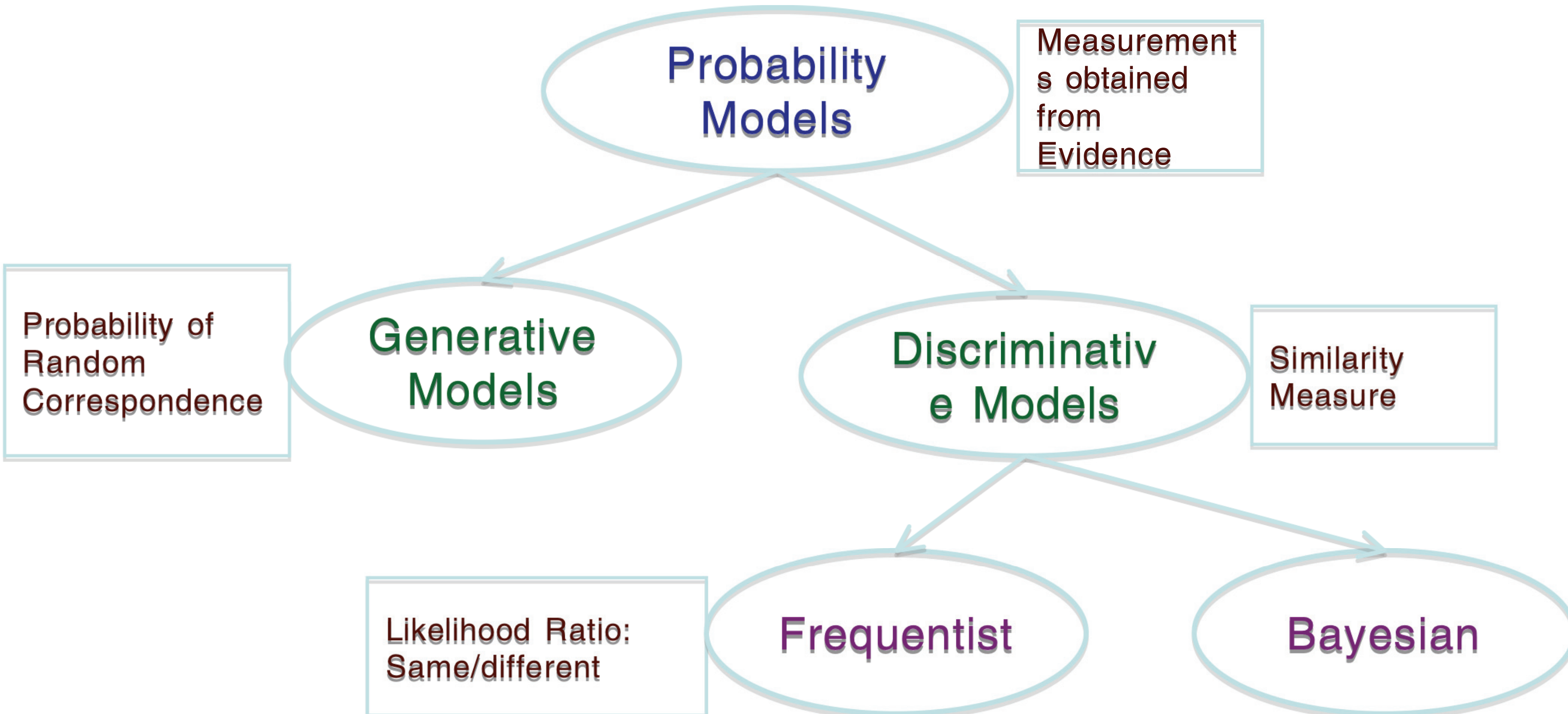
Madrid Bombing Case

Latent Fingerprint
on bag of detonator

Brandon Mayfield
Identified by FBI

Algerian National
Identified by SNP

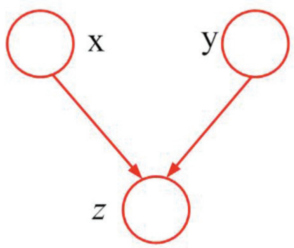
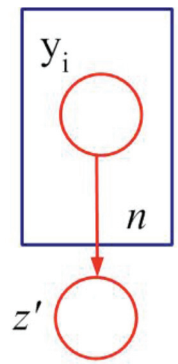
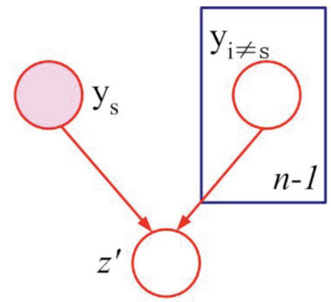
Methods for Expressing Uncertainty



How to Compute Uncertainty?

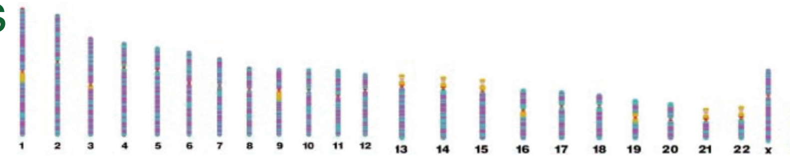
- Discrete Variables
  - Birthdays
  - DNA
- Continuous Variables
  - Heights
  - Pattern/Impression evidence (Ongoing Research)
    - 5 or 9-point scale suggested by SWGs-- no guidelines
    - New statistical models being developed

Generative Models: Several Probabilities

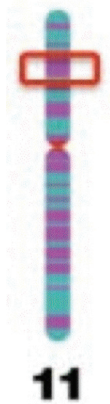
	Random two have same birthday (n=2)	Some two among n have same birthday	A specific birthday among n
	PRC	nPRC	Specific nPRC
Graphical Model	 (a) $z = \{1,0\}$	 (b) $z' = \{1,0\}$	 (c) $z' = \{1,0\}$
Inference	$p(z) = \sum_{\mathbf{x}} \sum_{\mathbf{y}} p(z \mid \mathbf{x}, \mathbf{y}) p(\mathbf{x}) p(\mathbf{y})$ PRC is $\rho = p(z=1)$	$\rho[n] = 1 - (1 - \rho)^{\frac{n(n-1)}{2}}$	$p(z' \mid \mathbf{y}_s) = \sum_{\mathbf{Y}'} p(z', \mathbf{Y}' \mid \mathbf{y}_s) = \sum_{\mathbf{Y}'} p(z' \mid \mathbf{y}_s, \mathbf{Y}') p(\mathbf{Y}')$

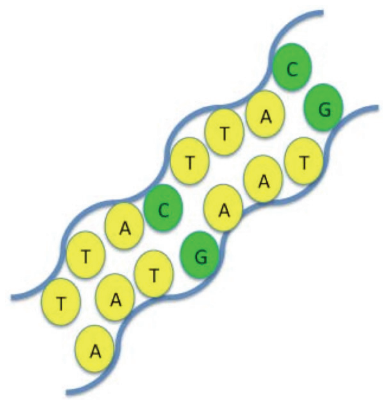
Generative Model: DNA

Genome: sequence of $3x10^9$ base-pairs (nucleotides A,C,G,T)
Represents full set of chromosomes



Actual Electron photomicrograph





Single Chromosome: $\sim 10^8$ base-pairs

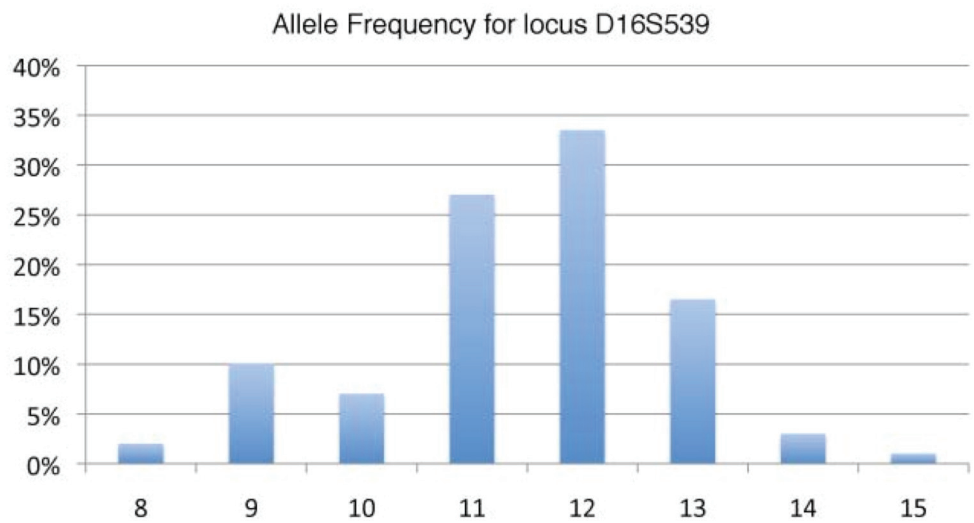
Genome has 46 chromosomes
(22 are repeated plus XX and XY)

Large portions of DNA have no survival function (98.5%) and have variations
useful for identification

TH01 is a location on short arm of chromosome 11:
short tandem repeats (STR) of same base pair AATG
Variant forms (alleles) different for different individuals

Generative Model: DNA

Allele Frequency of single locus for 200 individuals



DNA profile of 13 loci:

Average match probability (PRC) is 0.1 per locus, 10^{-13} for a profile

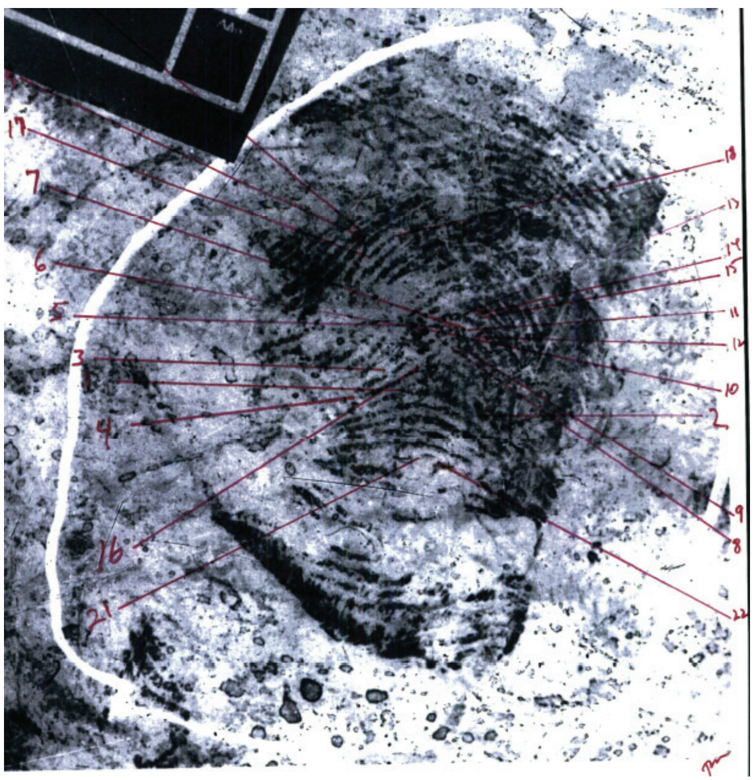
If database has 1 million entries,

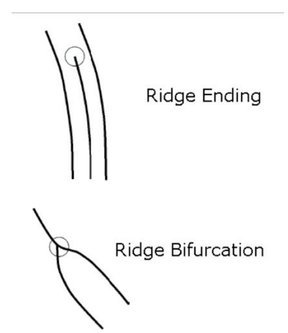
since there are 500 billion pair-wise matches, $nPRC = 0.05$

However specific $nPRC$ can be much lower

Generative Models: Fingerprints

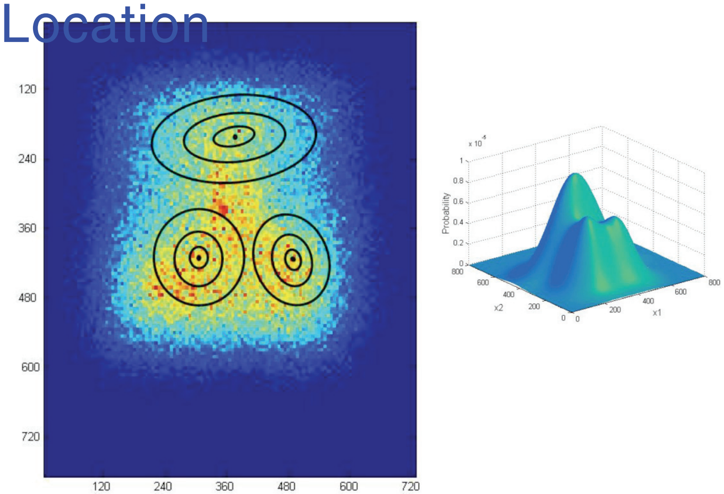
- Fingerprints are characterized by ridges and minutiae



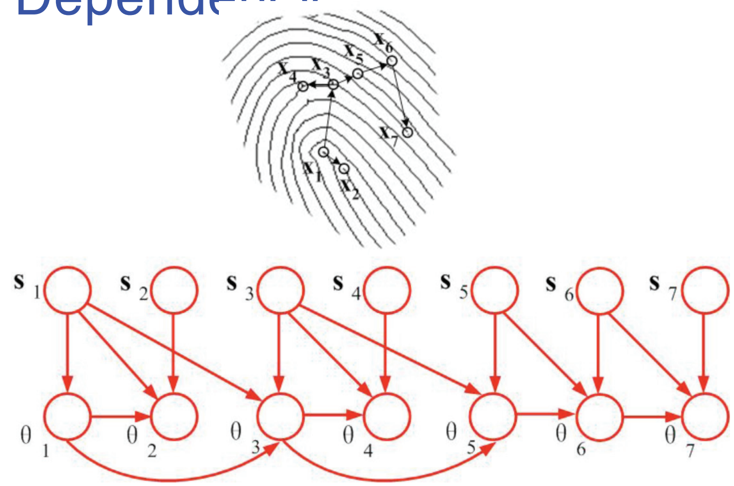


Generative Model: Minutiae

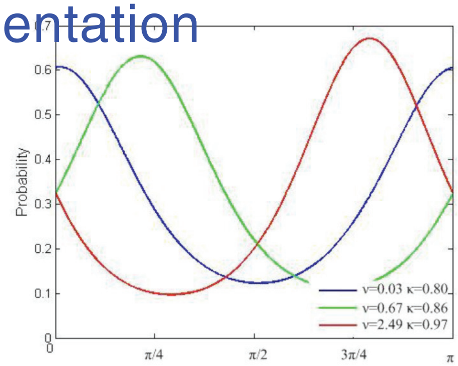
1. Distribution of Minutia Location



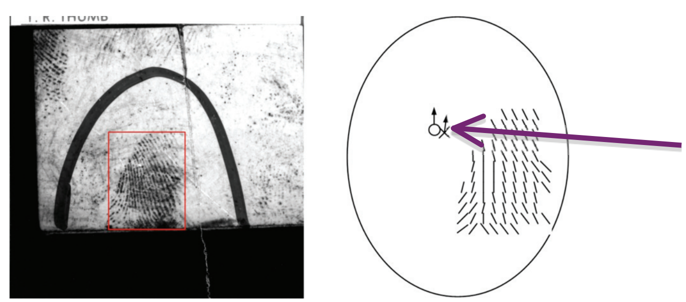
3. Distribution of Minutia Dependency



2. Distribution of Minutia Orientation

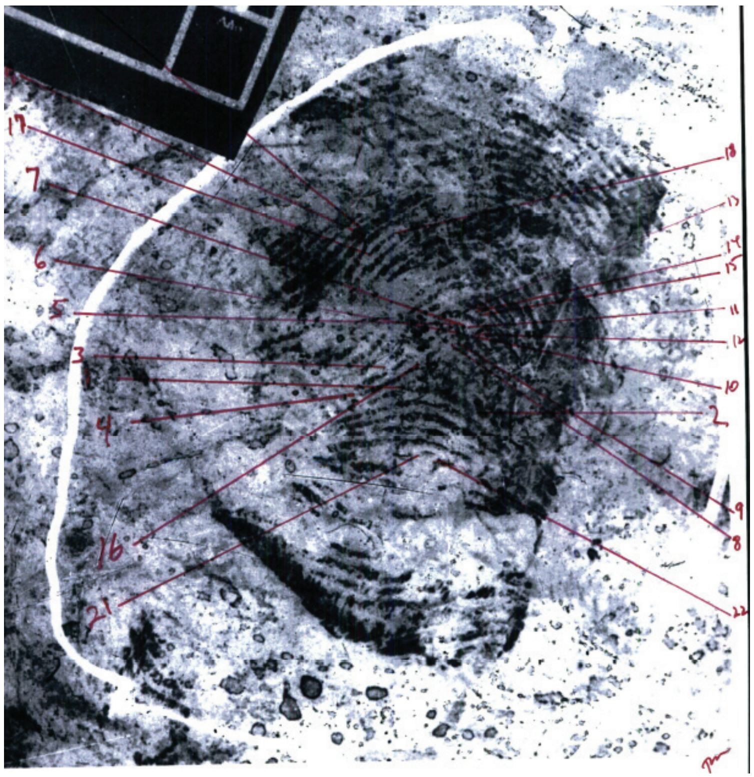


4. Distribution of Minutia Certainty



Core point predicted Using Regression

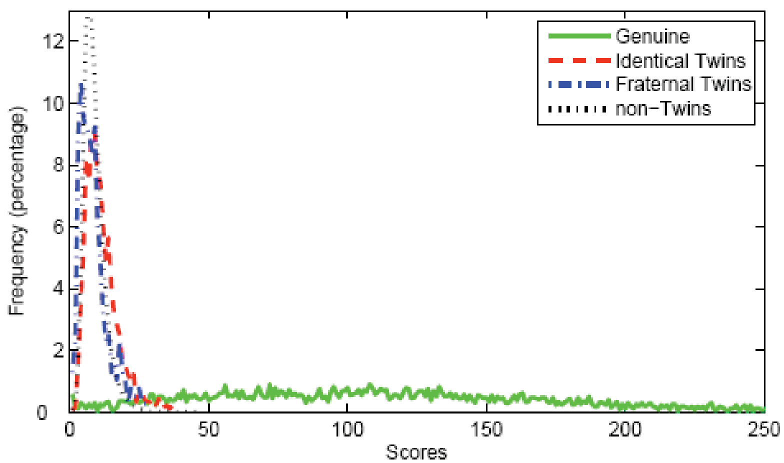
Madrid Bomber Case Revisited



- Madrid Bomber case 22 minutiae identified
- 10 were matched by three FBI experts
- Generative Model
  - 12 of 19 minutiae used for specific nPRC: 1, 2, 3, 4, 7, 8, 9, 10, 11, 12, 17, and 18
  - specific nPRC
    - World population (6.8b) = 0.16
    - US population (330m) = 0.008

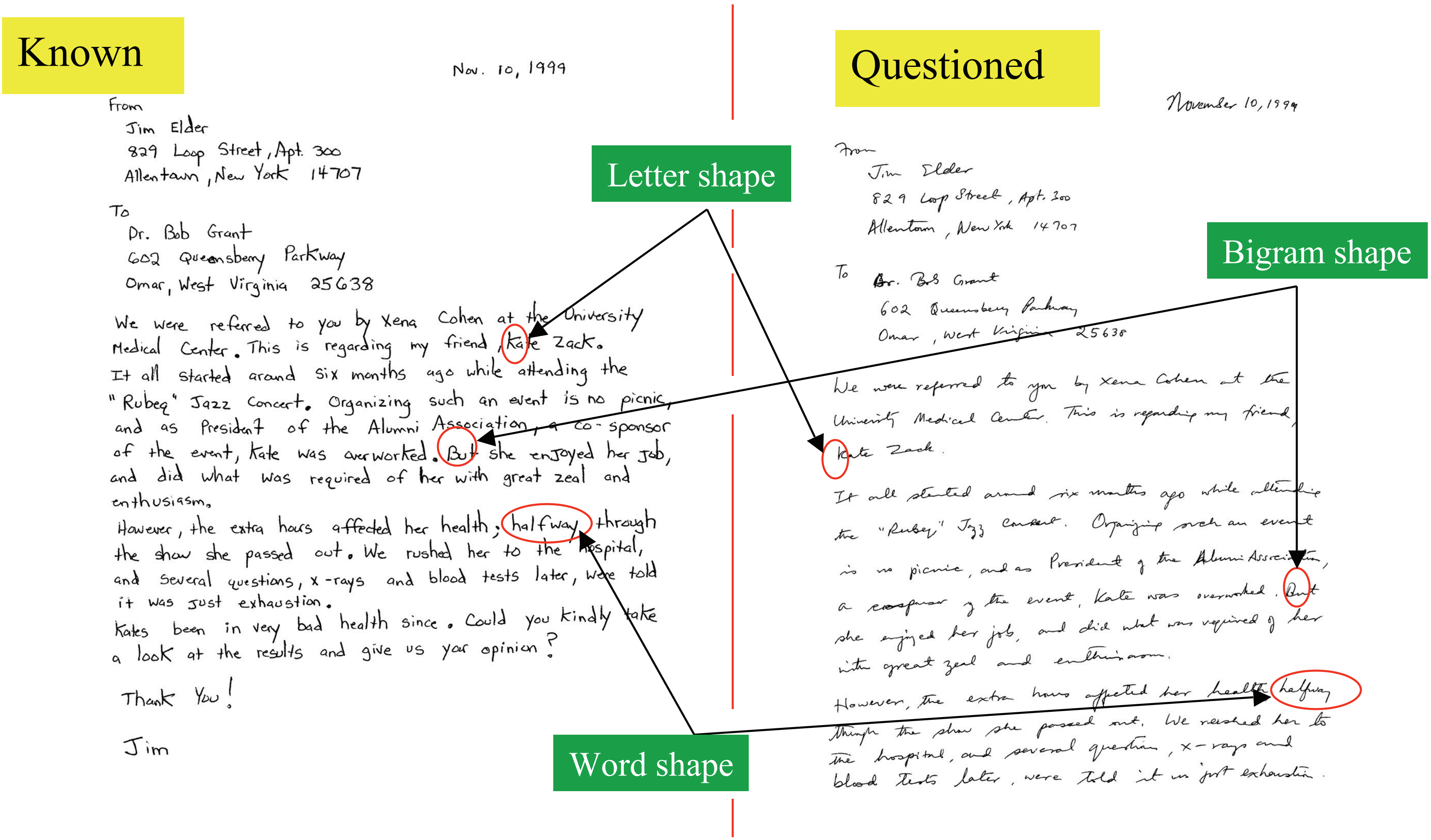
Discriminative Models: Fingerprints

- Need a similarity measure for fingerprints
- AFIS Minutiae Matcher
  - Score distributions give two probabilities
  - Likelihood Ratio
- Error Rates



	EER	EER threshold
Non-Twins	3.33%	19
Fraternal	4.88%	23
Identical	5.09%	25

Discriminative Model: QD

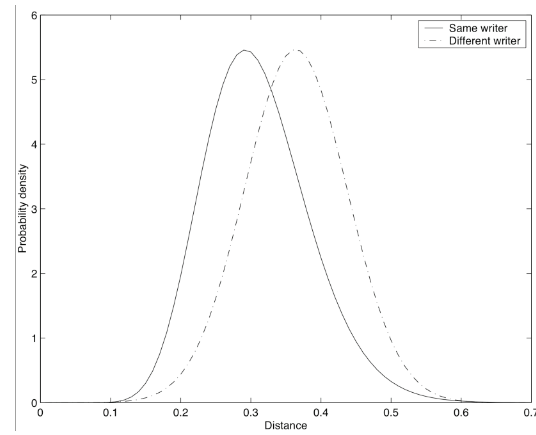


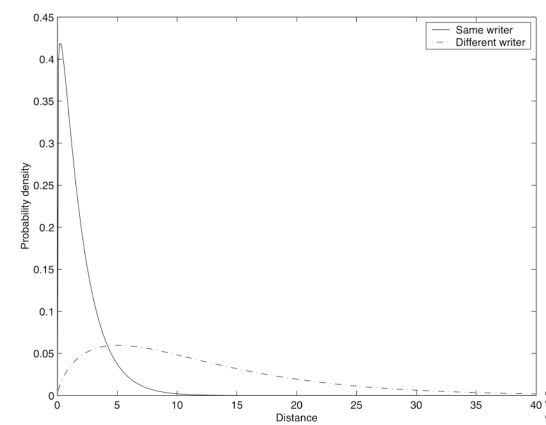
Handwriting Features and Similarities

000000110110000000001100000011100
00000101000000110100001111000000
00001101000011110001010000000110
01100001100011000111000100000100
01000001000000000000000000000100
01100000000001000100000100011000
11000000000000000100101100011000
00000010000000001101000000000001
00000001111010000000001100000000
10100000000000110000001000100100
0000000000000000011000100000100
00000000100010000000000000000001
01110111111100010111001000000000
01010101000100010111001011110010
00000000011001110000000000000000
00000000000000000000000000000000

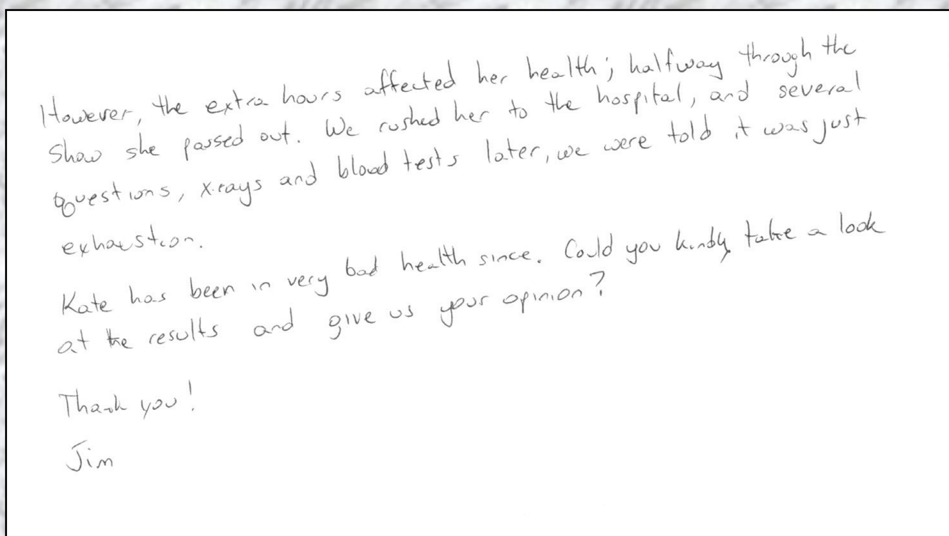
Likelihood Ratio
obtained from
distributions of
similarities
for same and different
origination of evidence

Distributions of Similarities





Discriminative Model for Handwriting

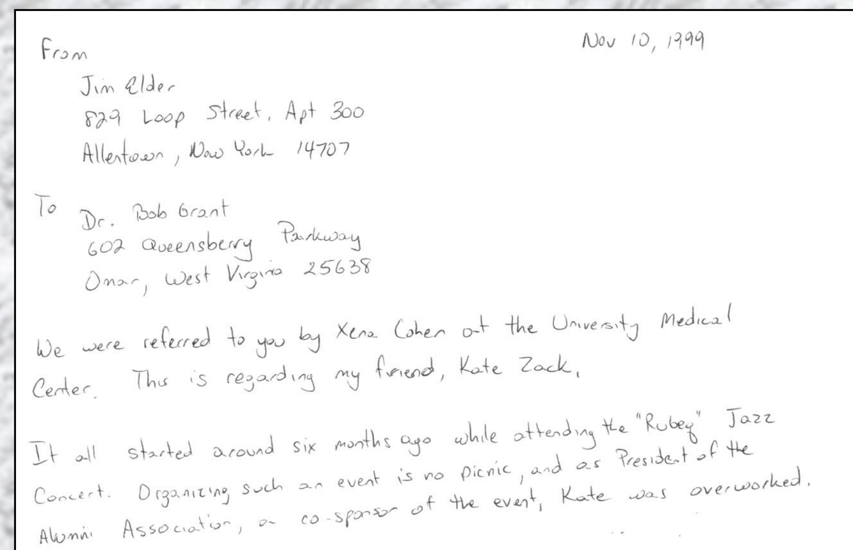


However, the extra hours affected her health; halfway through the
Show she passed out. We rushed her to the hospital, and several
questions, x-rays and blood tests later, we were told it was just
exhaustion.

Kate has been in very bad health since. Could you kindly take a look
at the results and give us your opinion?

Thank you!

Jim



From

Nov 10, 1999

Jim Elder
829 Loop Street, Apt 300
Allentown, New York 14707

To

Dr. Bob Grant
602 Queensberry Parkway
Omar, West Virginia 25638

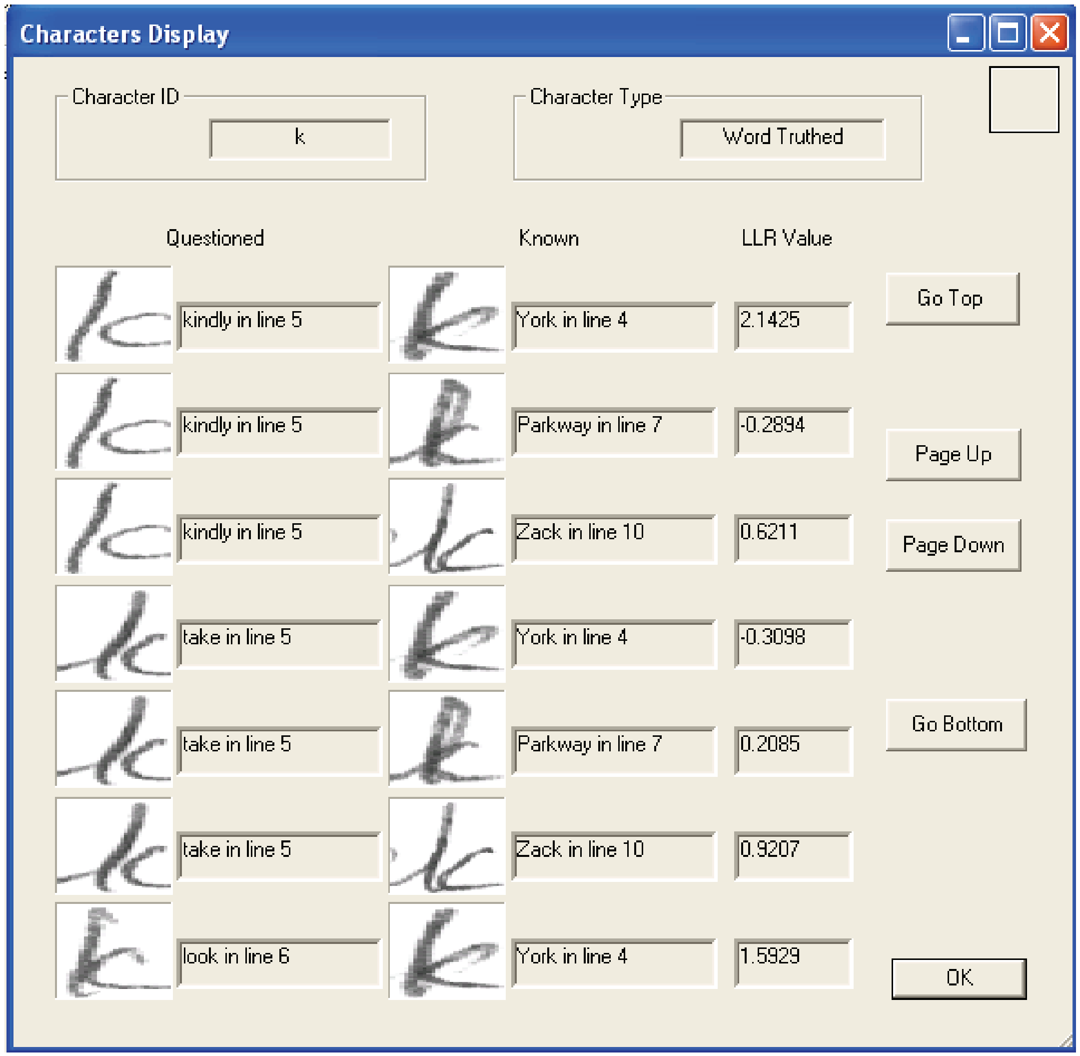
We were referred to you by Xena Cohen at the University Medical
Center. This is regarding my friend, Kate Zack,

It all started around six months ago while attending the "Rubey" Jazz
Concert. Organizing such an event is no picnic, and as President of the
Alumni Association, a co-sponsor of the event, Kate was overworked.

LLR Value for this pair is 41.52
→

1. Identified as same
2. Highly probable same
3. Probably same
4. Indicating same
5. No conclusion
6. Indicating different
7. Probably different
8. Highly probable different
9. Identified as different

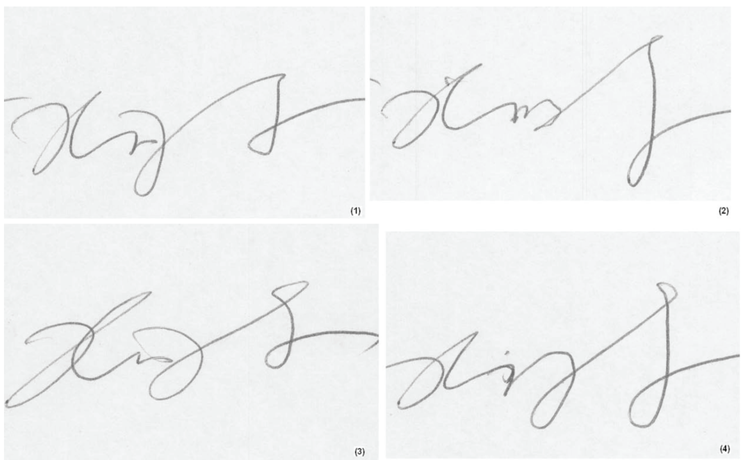
Human-Machine Interface:
Dialog for character image comparison



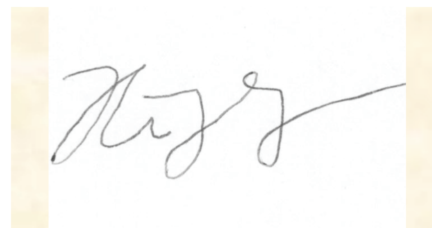
Signatures: Bayesian Adaptation

Wide variability and small learning sets for case at hand

Known Signatures



Questioned Signature

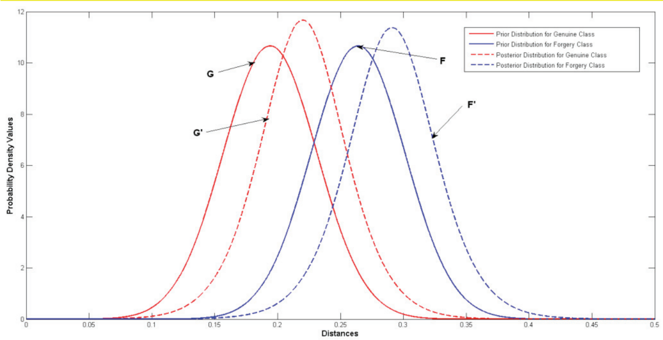


Approach:

Learn hyper-parameters from large data set

Adapt parameters using Bayesian approach

Bayesian Adaptation



	Error Rate
Only Prior	18%
Bayesian Adaptation	11.5% - 14.5%

	After Learning	After Adaptation
Parameter	$\theta_g \sim N(\mu_{g0}, \tau_{g0}^2)$ $\theta_f \sim N(\mu_{f0}, \tau_{f0}^2)$	$P(\theta_g \mid Y_g) \propto N(\theta_g \mid \mu_{g0}, \tau_g^2) \times N(Y_g \mid \theta_g, \sigma_g^2) = N(\mu_g, \tau_g^2)$ $P(\theta_f \mid Y_f) \propto N(\theta_f \mid \mu_{f0}, \tau_f^2) \times N(Y_f \mid \theta_f, \sigma_f^2) = N(\mu_f, \tau_f^2)$
Distance	$P(d_g \mid G) = \int_{-\infty}^{\infty} P(d_g \mid \theta_g) \times P(\theta_g \mid Y_g) d\theta_g = \frac{1}{\sqrt{2\pi(\sigma_g^2+\tau_{g0}^2)}} e^{-\frac{(d_g-\mu_{g0})^2}{2(\sigma_g^2+\tau_{g0}^2)}}$ $P(d_f \mid F) = \int_{-\infty}^{\infty} P(d_g \mid \theta_f) \times P(\theta_f \mid Y_f) d\theta_f = \frac{1}{\sqrt{2\pi(\sigma_f^2+\tau_{f0}^2)}} e^{-\frac{(d_f-\mu_{f0})^2}{2(\sigma_f^2+\tau_{f0}^2)}}$	$p(t/G) = \int_{-\infty}^{\infty} p(t \mid \theta_g) \times p(\theta_g \mid Y_g) d\theta_g = \frac{1}{\sqrt{2\pi(\sigma_g^2 + \tau_g^2)}} e^{-\frac{(t-\mu_g)^2}{2(\sigma_g^2+\tau_g^2)}}$ $p(t/F) = \int_{-\infty}^{\infty} p(t \mid \theta_f) \times p(\theta_f \mid Y_f) d\theta_f = \frac{1}{\sqrt{2\pi(\sigma_f^2 + \tau_f^2)}} e^{-\frac{(t-\mu_f)^2}{2(\sigma_f^2+\tau_f^2)}}$

Summary and Conclusion

- Uncertainty is easily expressed for DNA
  - Discrete counts
- For Impression Evidence it is much harder
  - Continuous features/tolerances
- New Models proposed (being validated)
  - Generative
    - PRC
      - Fingerprints, Handwriting
  - Discriminative (similarity automatically computed)
    - Likelihoods/ Bayesian scores
      - Fingerprints, Handwriting