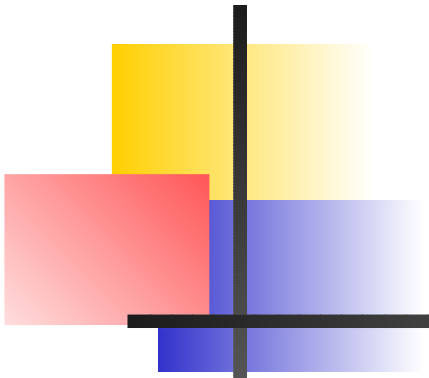


Modeling Fingerprints

MCM Problem A, 2004

Steven Avery, Eric Harley, and Eric Malm

Harvey Mudd College

Fingerprints as Biometrics

Why Fingerprints?

- Almost everyone has them
- Persistent: Fingerprints remain the same throughout a person's lifetime
- Prints are easily (and even unintentionally) made and recorded
- As evidence, accessible and concrete
- Distinguish between family members; even twins!

Fingerprints

Daubert v. Merrill Dow Pharmaceutical (1993) controversy

- New, more stringent criteria for "scientific evidence"
- Motivates analysis of uniqueness claims
- Past models are inadequate:
  - First models divided print with an unnatural square grid
  - Previous models do not consider ridge flow
  - Previous models look at absolute position and orientation of minutiae
  - Previous models do not consider number of comparing minutiae

Model Assumptions

Prints are of ideal quality

Print topologies fall into five mutually exclusive categories

Arch

Right Loop

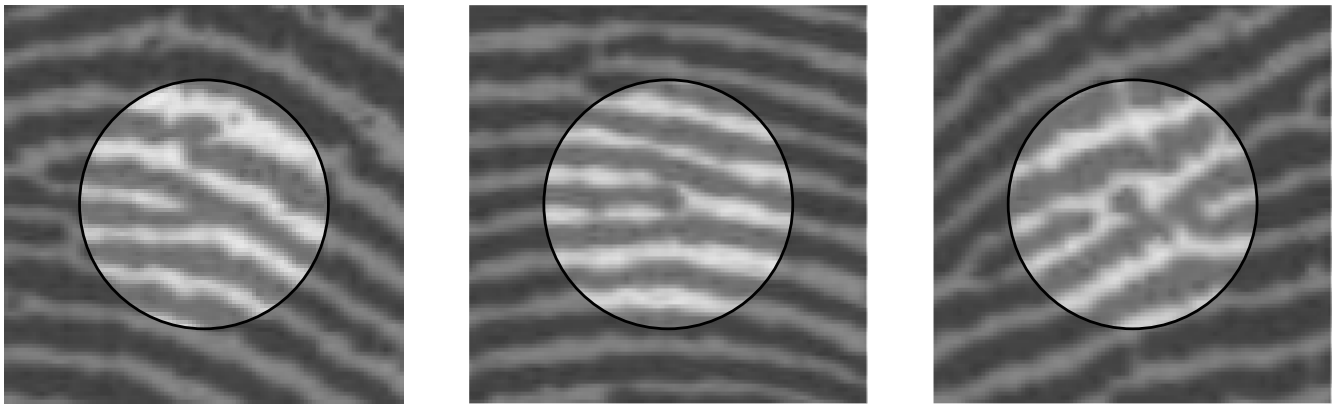
Whorl

Left Loop

Tented Arch

Model Assumptions

Three fundamental types of minutiae



Bifurcation **Termination** **Dot**

Minutiae occur independently of each other

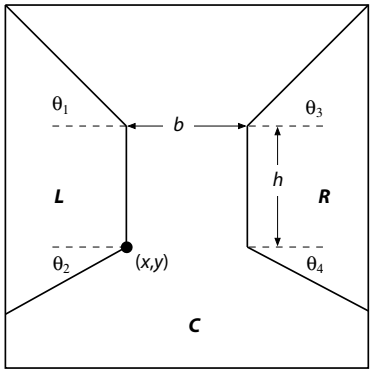
Topology, minutiae structure suffice to characterize print

Model Formulation

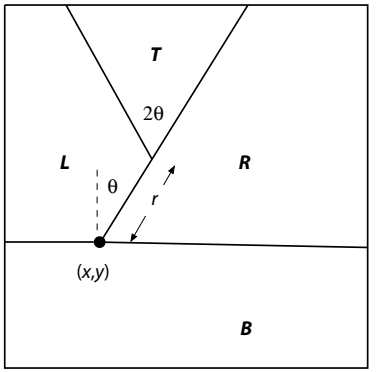
Want to determine probability that a given configuration occurs

- Ridge class structure
- Configuration of regions within ridge structure
- Minutiae probabilities for each region
  - Number in region
  - Spatial configuration
  - Types and orientations

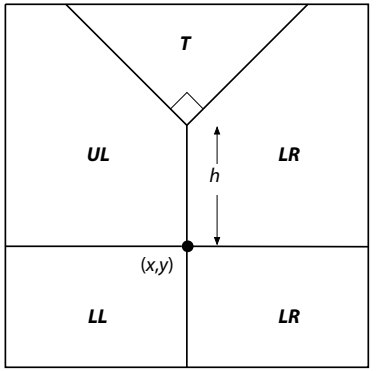
Structural Archetypes



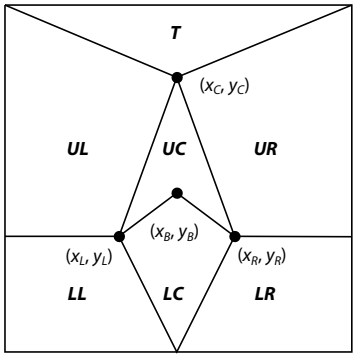
Arch



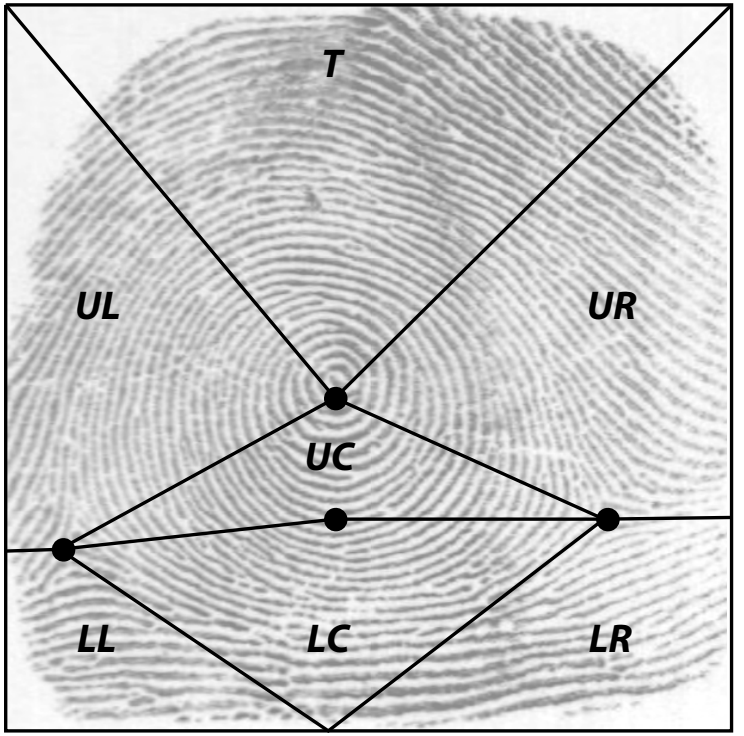
Right Loop



Tented Arch



Whorl



Example Whorl Decomposition

Model Equations

Per-Ridge Minutiae Probabilities:

number $P_n = \binom{l/\delta_2}{k}(\delta_2\lambda)^k(1-\delta_2\lambda)^{l/\delta_2-k}$

configuration $P_c = 1/\binom{l/\delta_2}{k}$

type/orientation $P_{to} = p_b^{k_b} p_t^{k_t} p_d^{k_d} \frac{1}{2^{k_b+k_t}}$

l	ridge length	k	number of minutiae
δ_2	level-2 resolution	λ	linear minutiae density

Probability that a ridge has a given configuration: $P_R = P_n P_c P_{to}$

Parameter Estimates

Key Parameters

- Level-one spatial resolution limit: $\delta_1 = 1.5$ mm
- Level-two spatial resolution limit: $\delta_2 = 1$ mm
- Number of minutiae per print: $\mu = 50 \pm 10$
- Average linear minutiae density: $\lambda = 0.13 \pm 0.03$ min./mm
- Number of people, ever: $N = 10^{11}$

Simplifying Assumptions

More assumptions to afford computational tractability

- Minutiae distribution independent of location, ridge structure
- Eliminate dots
- Bifurcations, terminations equally likely ($p_b = p_t = \frac{1}{2}$)

Analysis

Probability that two people have same print configuration:

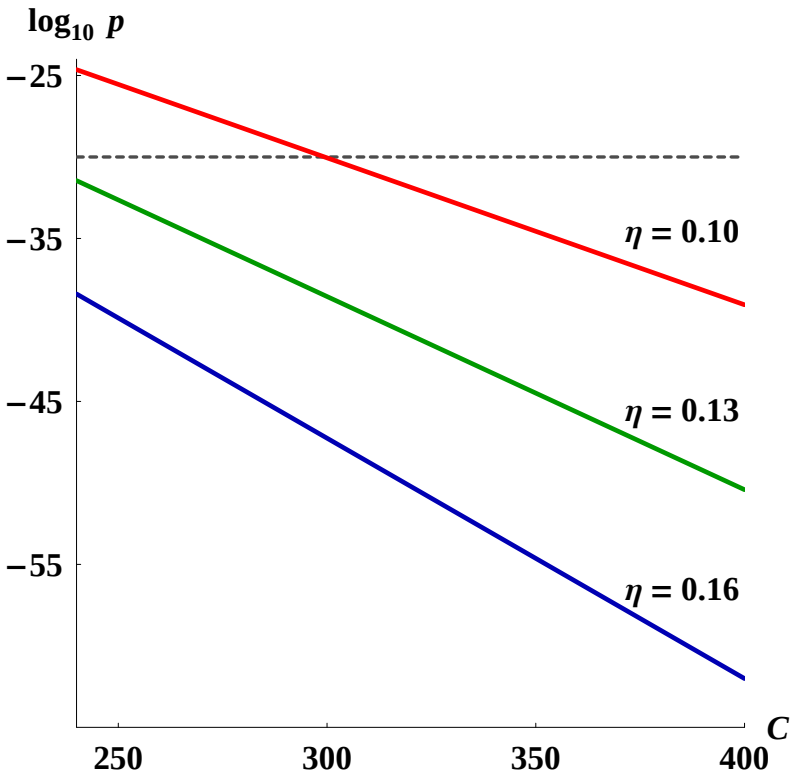
- Sum squares of each configuration probability
- Under uniformity and independence assumptions, total probability p factors into per-level probabilities p_1, p_2
- Level-one probability: $p_1 = \sum_{i \in C_1} p_{c1}^2(i) \approx 0.00044$
- Level-two probability:

$$p_2 = (\tfrac{5}{4}\eta^2 - 2\eta + 1)^C$$

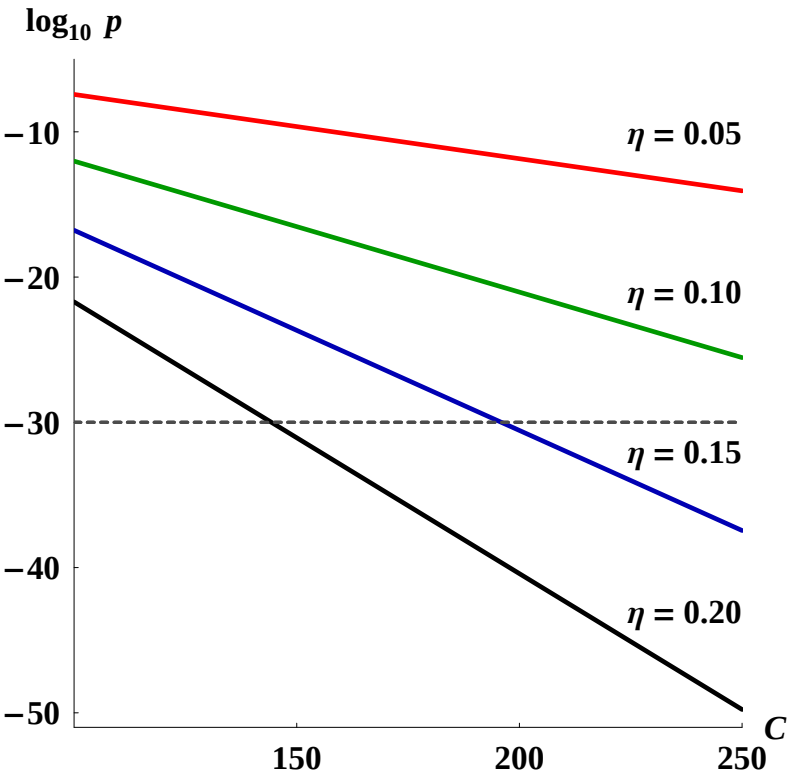
C	number of cells
$\eta = \delta_2 \lambda$	probability of a minutia occurring in a given cell

Analysis: p Estimates

$$p = p_1 p_2(\eta, C)$$



Ideal

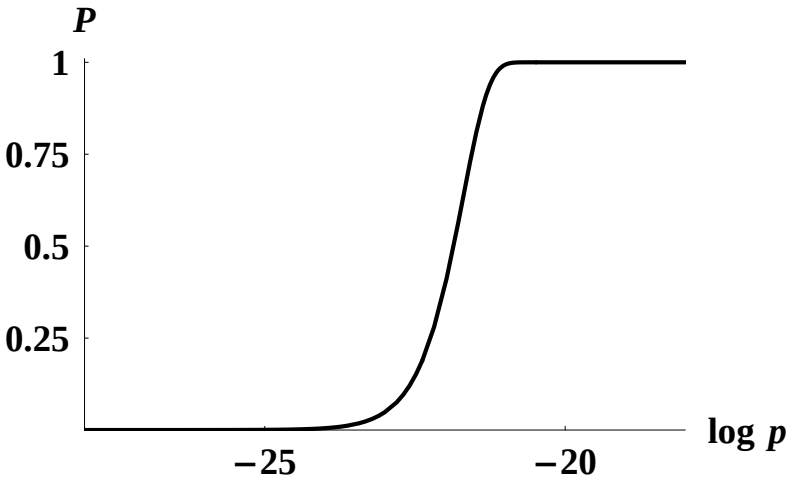


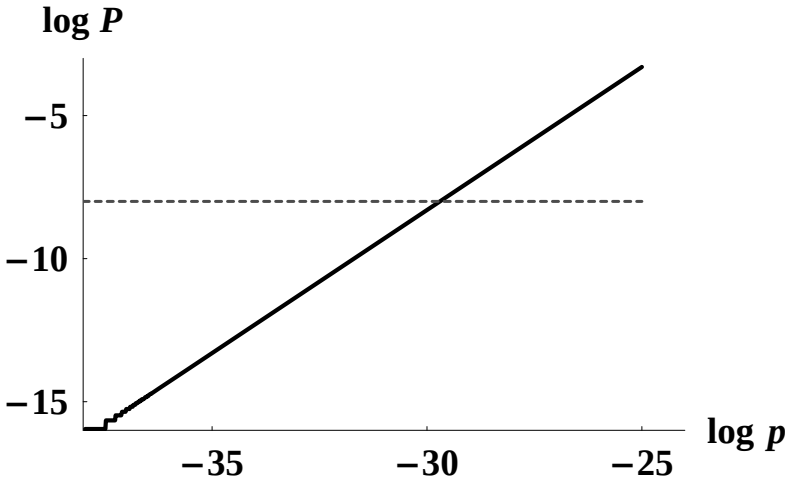
Forensic

Historical Uniqueness

Probability P that two prints throughout history match:

$$P = 1 - (1 - p)^{\binom{N}{2}}$$





$P < 10^{-8}$ for $p < 10^{-30} \Rightarrow$ Uniqueness!

Strengths and Weaknesses

Strengths

- Considers both topological and minutiae data
- Represents minutiae type, orientation accurately
- Allows flexible parameter ranges

Weaknesses

- Poor accounting for ambiguous, smeared, partial prints
- Domain discontinuities
- Simplified distributions

Fingerprints vs. DNA

- DNA "fingerprints" made from Variable Number Tandem Repeats
  - Highly variable sections of genetic material
- Probability of match depends on incidence of VNTRs in population
  - Ranges from 1 in 100 to 1 in 10^{12}
- Example: Monica Lewinsky
  - Probability of DNA match by chance: 7.9×10^{-12}
  - Fingerprints: 12 minutiae gives $p_2 = 1.5 \times 10^{-11}$

Conclusions

Our model:

- Considers both topological structure and fine detail
- Incorporates measurement uncertainities naturally
- Predicts uniqueness of fingerprints throughout history
- Shows fingerprints compare favorably to DNA evidence
- Has room for improvement

Thanks to our advisor, Jon Jacobsen, SIAM, COMAP, and especially Patty's, for their cheap burritos.