

Computer Interpretation of Uncertain DNA Evidence

National Institute of Justice
Computer v. Human

June, 2011
Arlington, VA

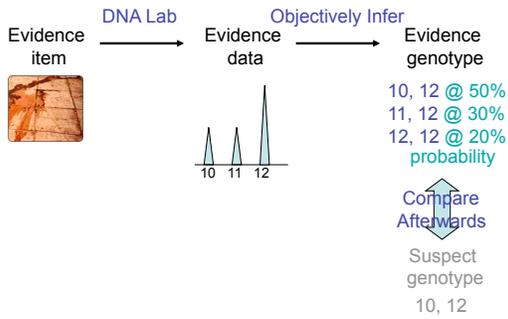
Mark W Perlin, PhD, MD, PhD
Cybergenetics, Pittsburgh, PA



Cybergenetics

Cybergenetics © 2003-2011

Uncertain DNA Evidence



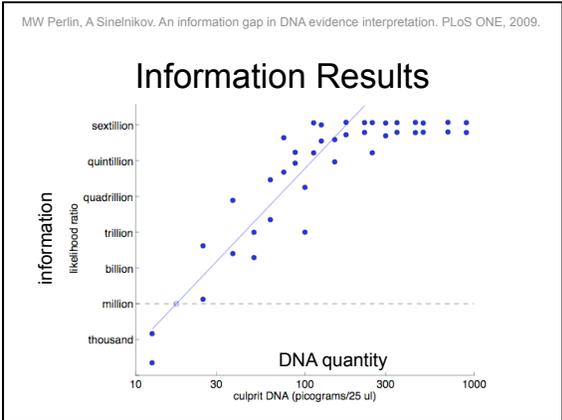
Automated STR Mixture Analysis NIJ Award 2001-IJ-CX-K003

Provide quantitative DNA mixture analysis
on a wide range of data.

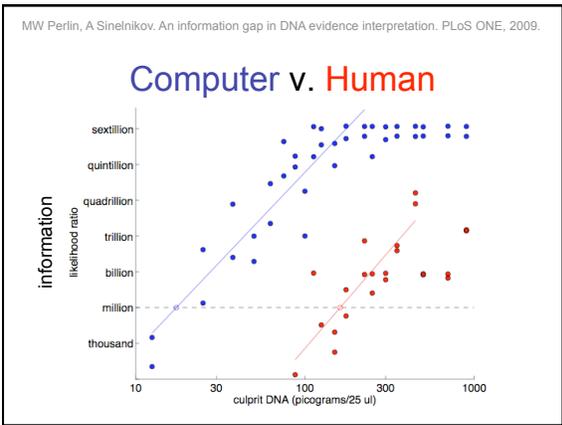
Handle known STR artifacts and
adapt to new marker technologies.

Interact well with users, including
DNA analysts and reporting
officers.

MW Perlin, A Sinelnikov. An information gap in DNA evidence interpretation. PLoS ONE, 2009.



MW Perlin, A Sinelnikov. An information gap in DNA evidence interpretation. PLoS ONE, 2009.



The DNA Investigator™ Newsletter, 2009
Same Data, More Information – Murder, Match and DNA

Commonwealth v. Foley

homicide: 7% DNA mixture fingernail evidence

ScoreMethod

13 thousand threshold

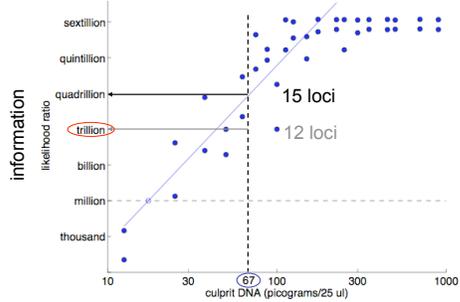
23 million use victim

189 billion quantitative

- probability modeling preserves information
- peak threshold discards information

MW Perlin, A Sineelnikov. An information gap in DNA evidence interpretation. PLoS ONE, 2009.

Predictably Preserves Information

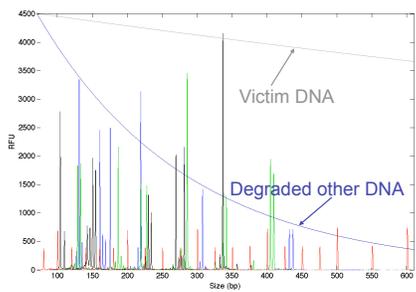


Commonwealth v. Lyons

homicide: DNA mixture evidence



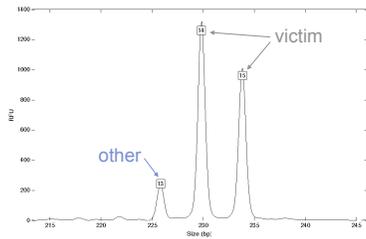
Degraded DNA Mixture



Perlin MW, Szabady B. Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. Journal of Forensic Sciences, 2001.

Quantitative Mixture Evidence

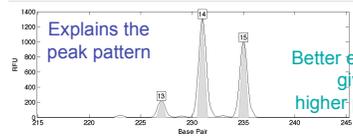
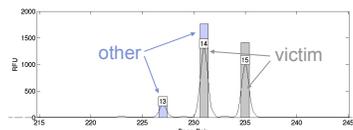
Quantitative peak heights at locus D8S1179



MW Perlin, MM Legler, CE Spencer, JL Smith, WP Allen, JL Belrose, BW Duceman. Validating TrueAllele DNA mixture interpretation. Journal of Forensic Sciences, 2011.

How the Computer Thinks

Considers every possible genotype solution



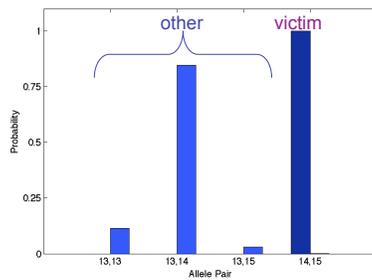
Explains the peak pattern

Better explanation gives a higher probability



MW Perlin, MM Legler, CE Spencer, JL Smith, WP Allen, JL Belrose, BW Duceman. Validating TrueAllele DNA mixture interpretation. Journal of Forensic Sciences, 2011.

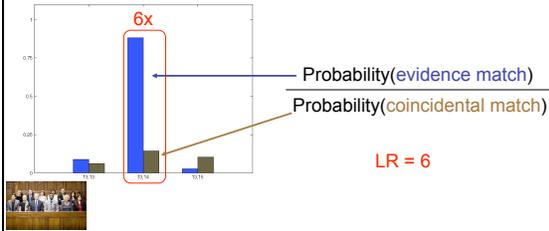
Objectively Infer Genotype



MW Perlin. Explaining the likelihood ratio in DNA mixture interpretation. Proceedings of Promega's 21st International Symposium on Human Identification, 2010.

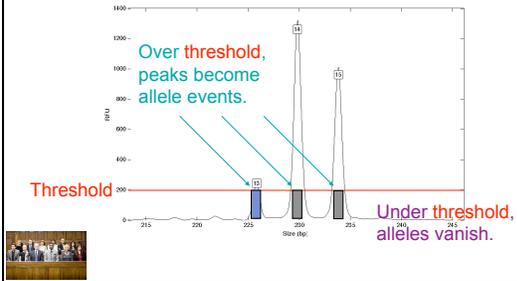
DNA Match Information

How much more does the suspect match the evidence than a random person?



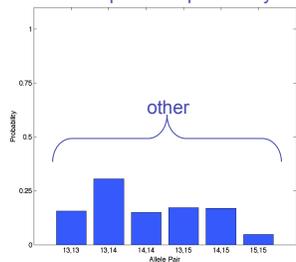
Thresholds Discard Data

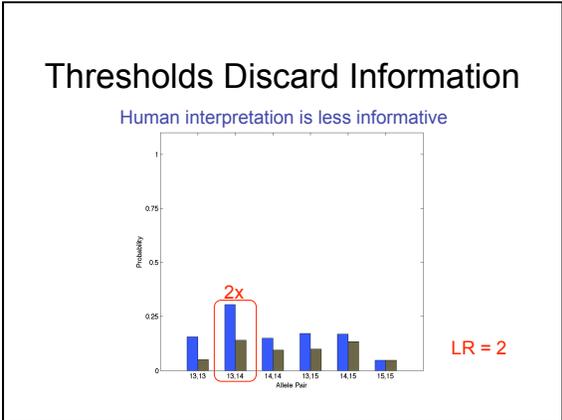
All-or-none allele peaks; ignore victim genotype



Thresholds Disperse Genotype

Human mixture interpretation probability distribution



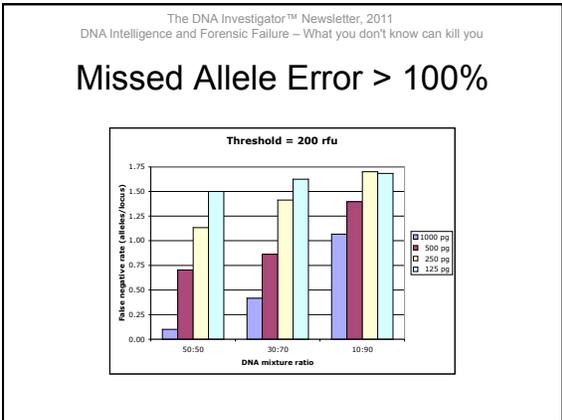


MW Perlin, Explaining the likelihood ratio in DNA mixture interpretation. Proceedings of Promega's 21st International Symposium on Human Identification, 2010.

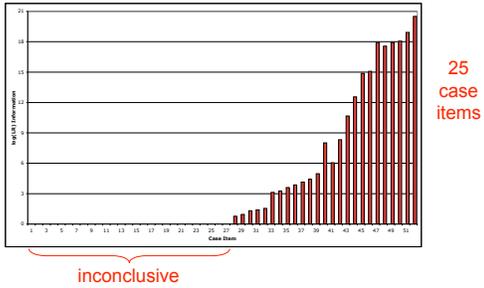
Likelihood Ratio Simple Statement

A match between the suspect and the evidence is 9.5 trillion times more probable than coincidence.

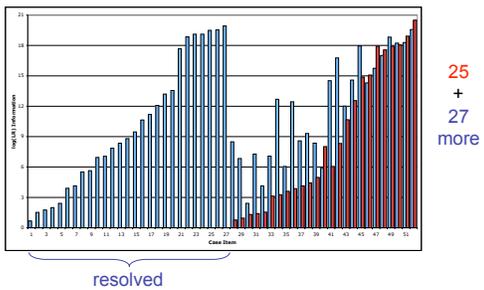
Computer	9,500,000,000,000
Human	42,000



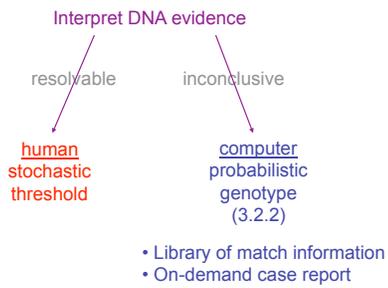
Human Information



Computer Information



SWGAM Triage



Computer v. Human

No competition

• information	1,000,000x
• reproducible	Validated
• mixture resolution	1, 2, 3, 4, ...
• degraded DNA	Quantified
• unsolved cases	Solved
• complex cases	Automated
• interpretation	Easy & fast
• likelihood ratio	Explained
• crime impact	Maximized

People use computer tools to do a better job

Learning More

The science of quantitative DNA mixture interpretation

www.cybgen.com/information

- **Newsletters**
gentle introduction to ideas
- **Courses**
for scientists and lawyers
- **Presentations**
handouts, movies, transcripts
- **Publications**
abstracts, manuscripts
