

Finding Truth in DNA Mixture Evidence

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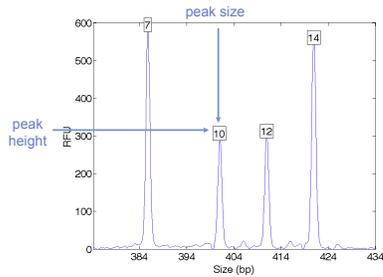


Cybergenetics

Cybergenetics © 2003-2013

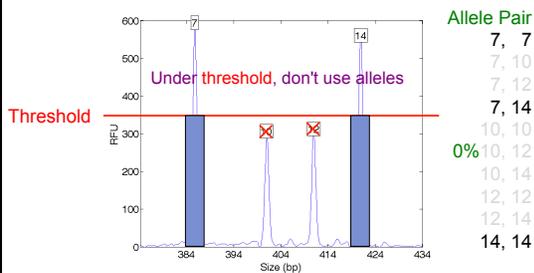
DNA Mixture Data

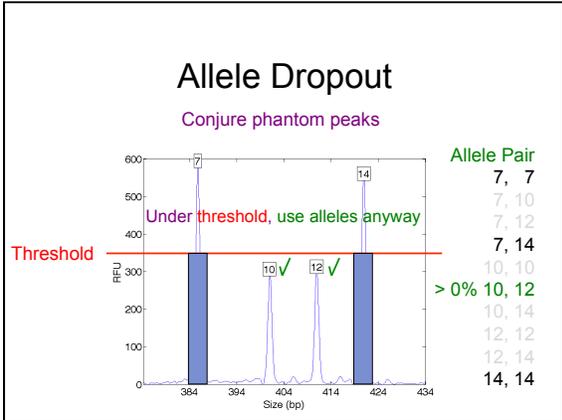
Quantitative peak heights at a locus



Peak Thresholds

Simplify data for human review





Human Interpretation Issues

Evidence

- call good data inconclusive
- peaks are too low for them
- too many contributors to handle
- potential examination bias

Database

- hit by association, not by match
- comparison: make false hits
- restrict upload: lose true hits

TrueAllele® Casework

Evidence

- preserve data information
- use all peaks, high or low
- any number of contributors
- entirely objective, no bias

Database

- hit based on LR match statistic
- sensitive: find true hits
- specific: only true hits

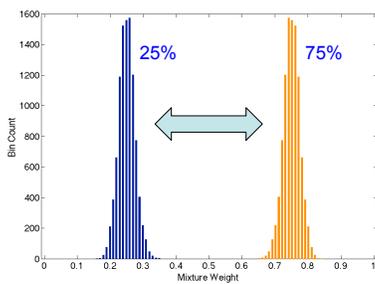
Validation Studies

Perlin MW, Sinenikov A. [An information gap in DNA evidence interpretation](#). *PLoS ONE*. 2009;4(12):e8327.

Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. [Validating TrueAllele® DNA mixture interpretation](#). *Journal of Forensic Sciences*. 2011;56(6):1430-47.

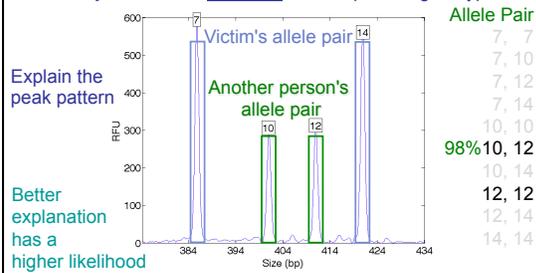
Perlin MW, Belrose JL, Duceman BW. [New York State TrueAllele® Casework validation study](#). *Journal of Forensic Sciences*. 2013;58(6):in press.

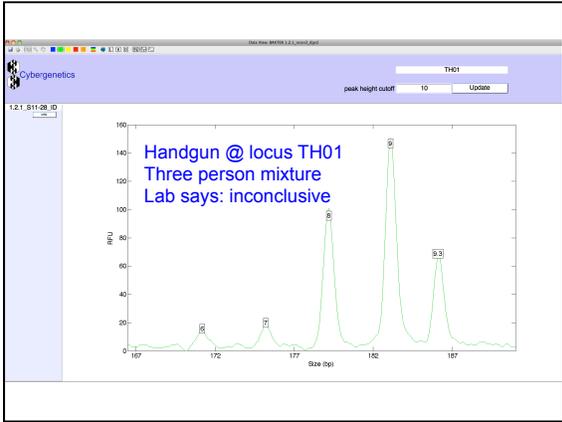
Separate Mixture Contributors

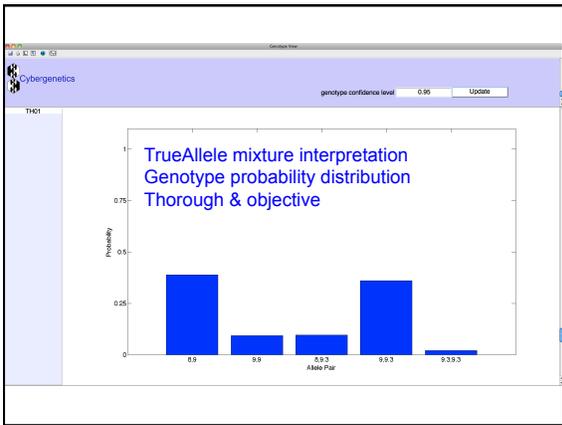


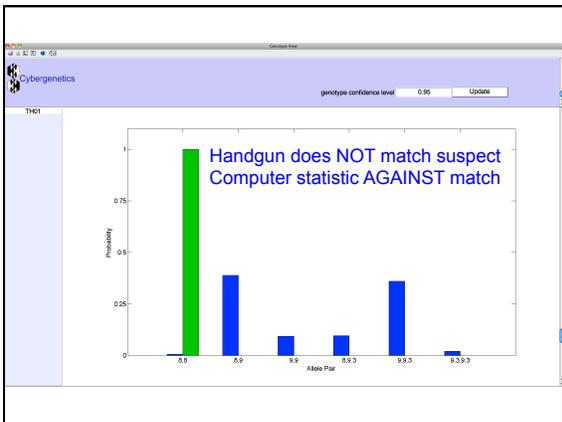
Genotype

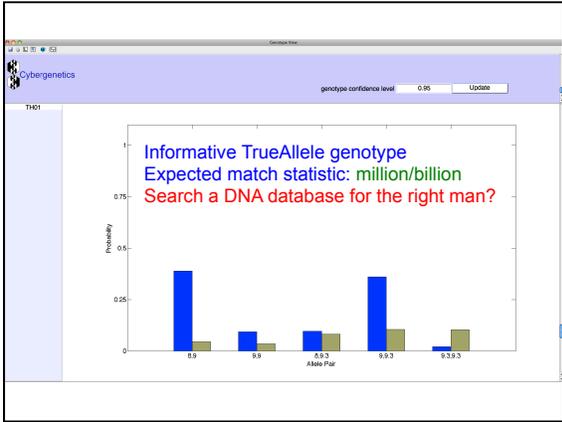
Thorough: consider every possible genotype solution
Objective: does not know the comparison genotype











The Search for Truth

M. W. Perlin, "When good DNA goes bad," *Journal of Forensic Research*, S11:003, 2013.

M. W. Perlin, "DNA Identification Science," in *Forensic Sciences*, volume 3. C. H. Wecht, Ed., Albany, NY: LexisNexis Matthew Bender, Chapter 37C, 2012.

M. W. Perlin. "Forensic science in the information age." *Forensic Magazine*, 9(2):17-21, 2012.

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