How TrueAllele® Works (Part 2) Degraded DNA and Allele Dropout

Cybergenetics Webinar November, 2014

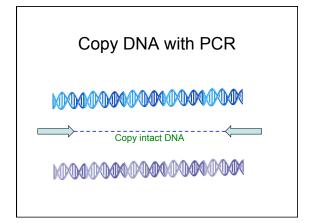
Mark W Perlin, PhD, MD, PhD Cybergenetics, Pittsburgh, PA

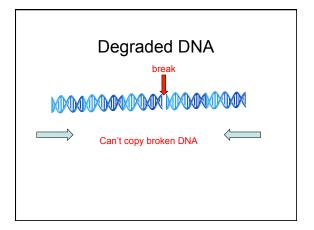


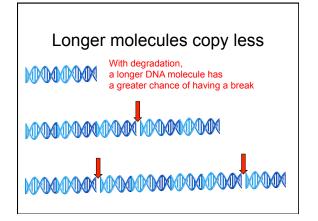
Cybergenetics © 2003-2014



Commonwealth v. Lyons homicide: DNA mixture evidence 70% victim 30% other Victim's blood spatter pulsating spray from severed carotid artery







Break density & copy probability

the break density
p = Pr(break at a nucleotide)

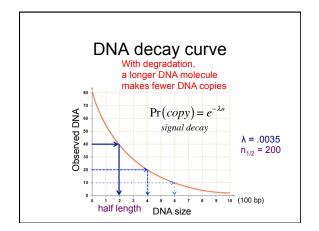
q = Pr(no break at a nucleotide) = 1 - p

qⁿ = Pr(no break in n nucleotides) the copy probability

Decay factor λ

$$q = e^{\ln q} = e^{-\lambda}$$

break density .000 1.000 .000 1.000 1.000 .001 .999 .001 .904 .819 .670 693 .002 .998 .450 .002 .819 .670 346 .005 .995 .005 .606 .367 .135 138 .010 .990 .010 .134 .018 69



Reduced match information

Degraded DNA

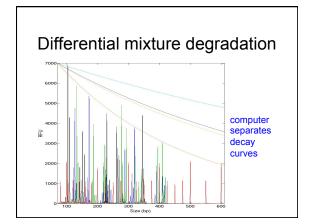
Lower peak height

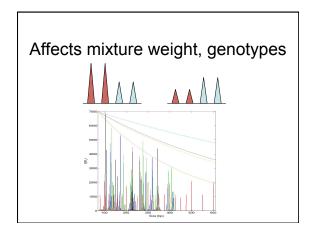
Greater data variation

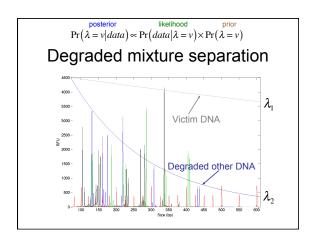
More genotype uncertainty

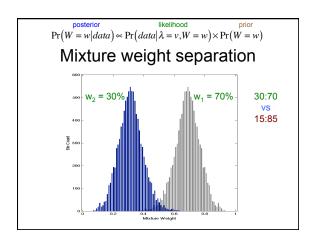
Diffused genotype probability

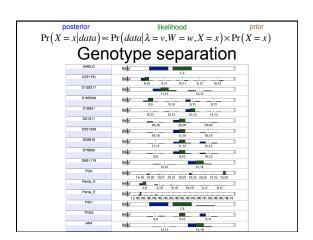
Reduced match information











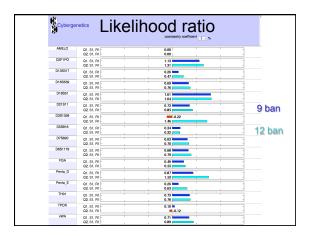
Information comparison

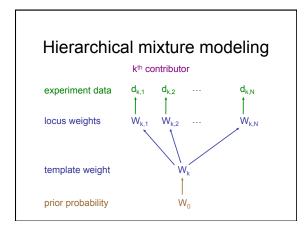
Combined probability of inclusion of 42 thousand. (Human review with thresholds)

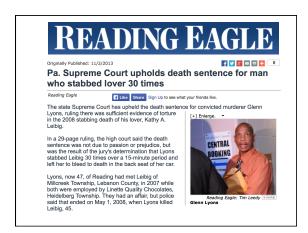
A match between the suspect and the evidence is a billion times more probable than coincidence.

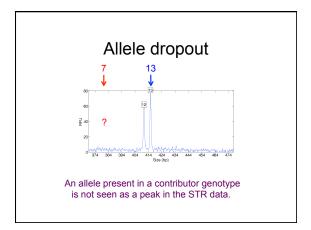
(TrueAllele not solving for degradation)

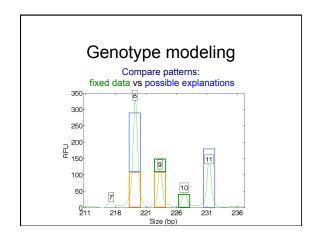
A match between the suspect and the evidence is a trillion times more probable than coincidence. (TrueAllele solving for degradation)

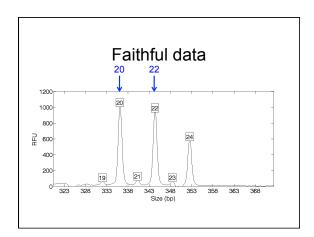


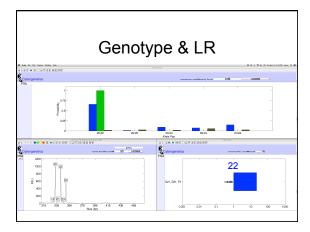


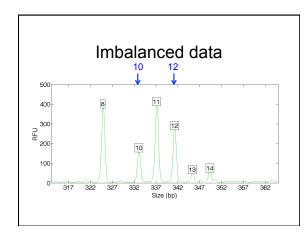


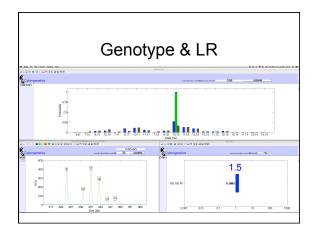


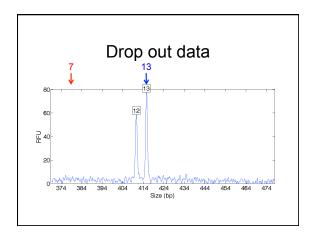


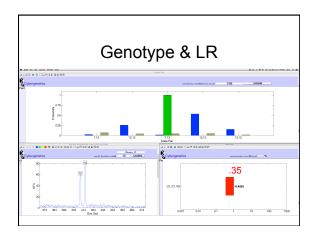


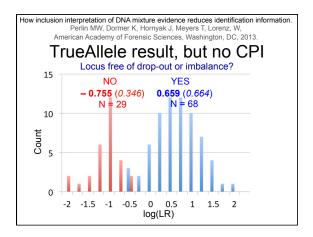


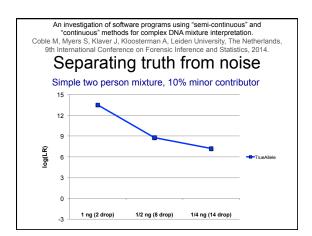


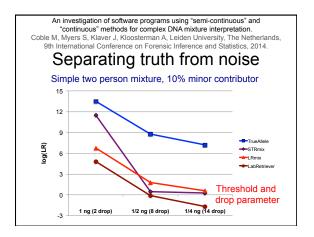












How TrueAllele Works

Part 1, 16-Oct-2014 Genotype modeling and the likelihood ratio

Part 2, 20-Nov-2014 Degraded DNA and allele dropout

Part 3, 18-Dec-2014 Kinship, paternity and missing persons

http://www.cybgen.com/information/webinar/page.shtml



perlin@cybgen.com