Transparency in DNA Evidence

**President's Council of Advisors
on Science and Technology**
November, 2016
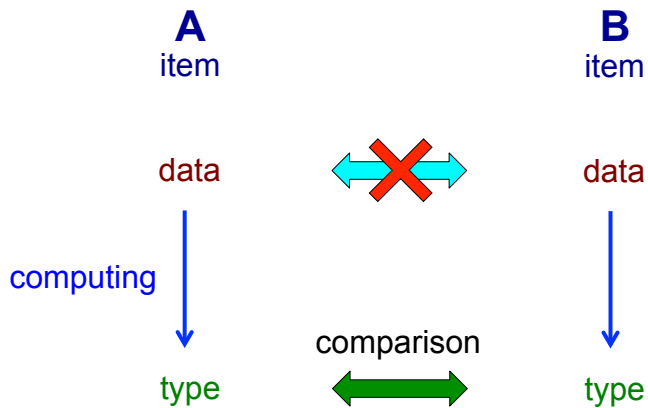**Washington, DC**

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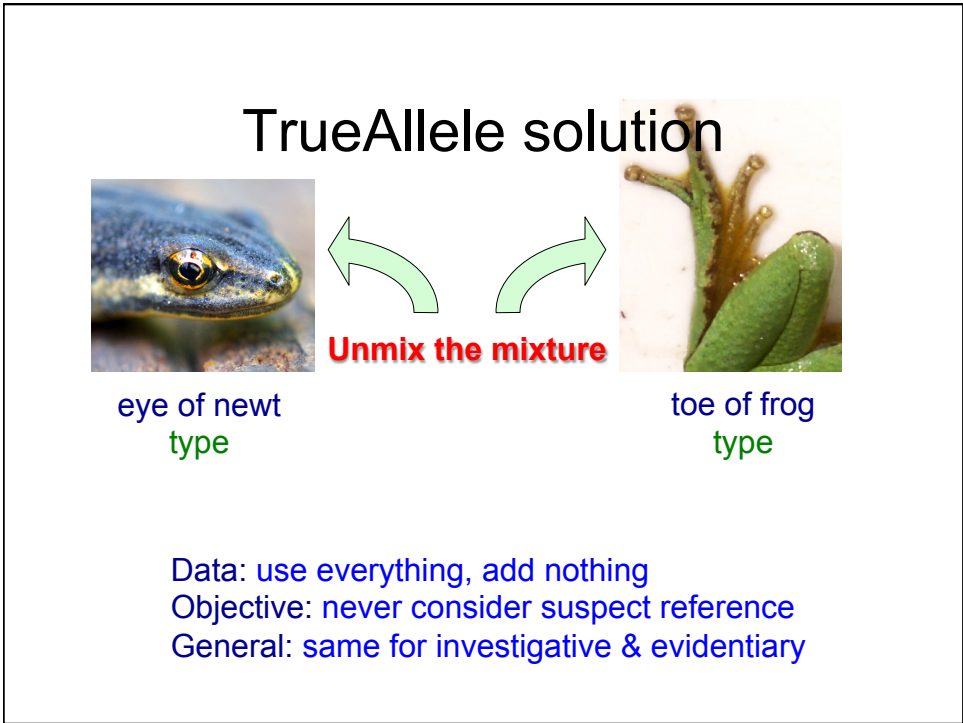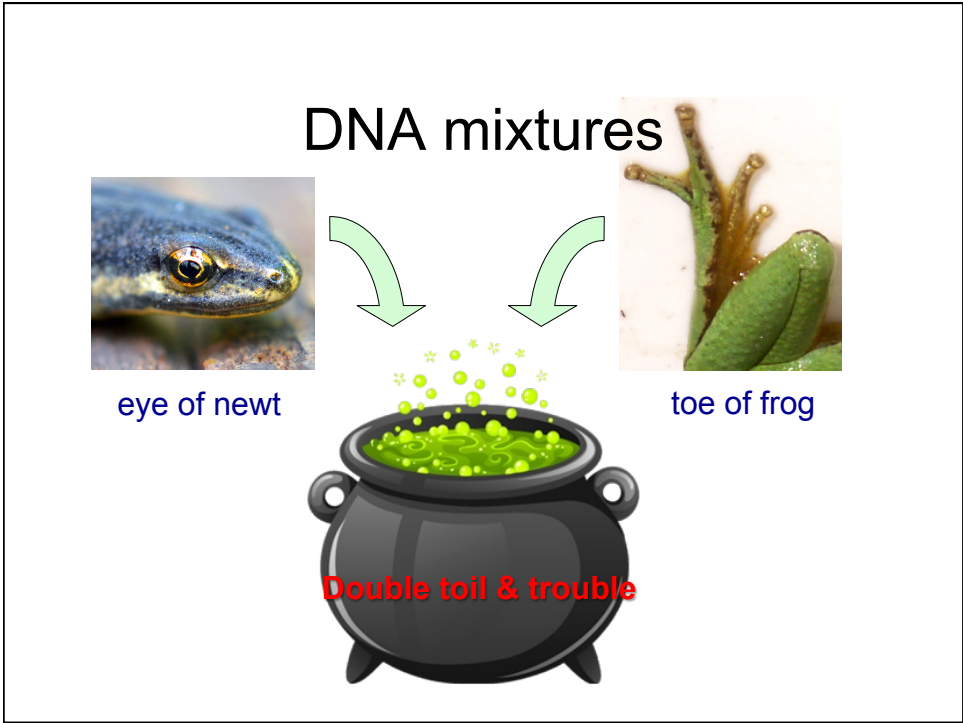**Cybergenetics, Pittsburgh, PA**

Cybergenetics

Cybergenetics © 2003-2016

Pattern evidence

A
item

B
item

data

data

computing

comparison

type

type

DNA mixtures

eye of newt

Double toil & trouble

toe of frog

TrueAllele solution

eye of newt
type

Unmix the mixture

toe of frog
type

Data: use everything, add nothing
Objective: never consider suspect reference
General: same for investigative & evidentiary

Validation studies

PAPER

CRIMINALISTICS

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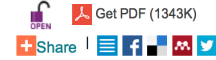
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TrueAllele® Genotype Identification on DNA Mixtures Containing up to Five Unknown Contributors*

ABSTRACT: Computer methods have been developed for mathematically interpreting mixed and low-template DNA. The genotype modeling approach computationally separates out the contributors to a mixture, with uncertainty represented through probability. Comparison of inferred genotypes calculates a likelihood ratio (LR), which measures identification information. This study statistically examined the genotype modeling performance of Cybergenetics TrueAllele® computer system. High- and low-template DNA mixtures of known randomized composition containing 2, 3, 4, and 5 contributors were tested. Sensitivity, specificity, and reproducibility were established through LR quantification in each of these eight groups. Covariance analysis found LR behavior to be relatively invariant to DNA amount or contributor number. Analysis of variance found that consistent solutions were produced, once a sufficient number of contributors were considered. This study demonstrates the reliability of TrueAllele interpretation on complex DNA mixtures of representative casework composition. The results can help predict an information outcome for a DNA mixture analysis.

KEYWORDS: forensic science, DNA mixture, genotype modeling, validation study, likelihood ratio, probabilistic genotyping

Linear relationship
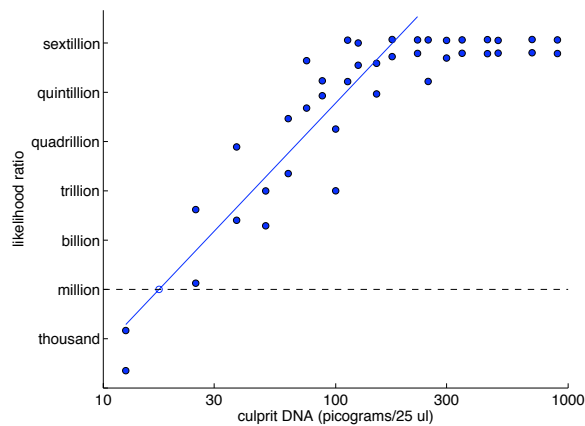
Inclusion probability

2005 NIST study

Some Differences in Reporting Statistics

			Case1	
LabID	Kits Used	Caucasians	African Americans	Hispanics
90	ProPlus/Cofiler	1.18E+15	2.13E+14	3.09E+15
34	ProPlus/Cofiler	2.40E+11	7.00E+03	9.80E+10
33	ProPlus/Cofiler	2.94E+08	1.12E+08	1.74E+09
6	ProPlus/Cofiler	40,000,000	3,500,000	280,000,000
9	ProPlus/Cofiler	1.14E+07	1.97E+07	1.54E+08
79	ProPlus/Cofiler	930,000	47,900	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

Remember that these labs are interpreting the same MIX05 electropherograms

When not "inconclusive":

213 trillion (14)

31 thousand (4)

Government failure

Random counting

J Pathol Inform

Research Article

Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information

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Peer review

Funding sources for articles listed on Dr. Eric Lander's website

https://biology.mit.edu/people/eric_lander#selected_publications

Genome of the marsupial Monodelphis domestica reveals innovation in non-coding sequences

Generation of the Monodelphis domestica sequence at the Broad Institute of MIT and Harvard was supported by grants from the National Human Genome Research Institute (NHGRI).

For work from other members of the Opossum Genome Sequencing Consortium, we acknowledge the support of the National Institutes of Health (NHGRI, NIAID, NLM),

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the UK Medical Research Council and the Australian Research Council.

Justice

April 25, 2016

Transparency

- open crime lab data to outside scrutiny
- open CODIS database to everyone
- DNA mixtures solved ten years ago
- no more money for failed government
- replace bad government with good science