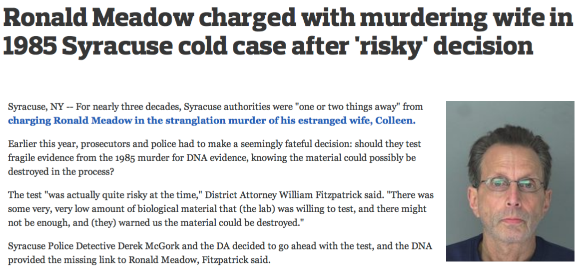
Shedding Light on Inconclusive DNA: TrueAllele® Computer Analysis

Onondaga County District Attorney's Office
November, 2014
Syracuse, NY

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

Cybergenetics

People of New York v Ronald Meadow



Ronald Meadow charged with murdering wife in 1985 Syracuse cold case after 'risky' decision

Syracuse, NY -- For nearly three decades, Syracuse authorities were "one or two things away" from **charging Ronald Meadow in the strangulation murder of his estranged wife, Colleen.**

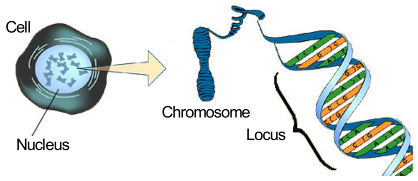
Earlier this year, prosecutors and police had to make a seemingly fateful decision: should they test fragile evidence from the 1985 murder for DNA evidence, knowing the material could possibly be destroyed in the process?

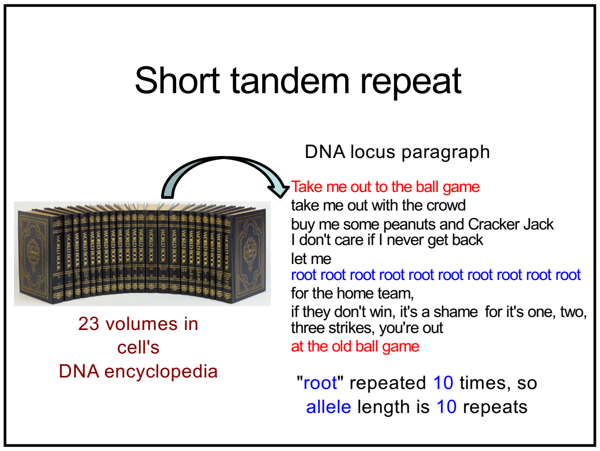
The test "was actually quite risky at the time," District Attorney William Fitzpatrick said. "There was some very, very low amount of biological material that (the lab) was willing to test, and there might not be enough, and (they) warned us the material could be destroyed."

Syracuse Police Detective Derek McGork and the DA decided to go ahead with the test, and the DNA provided the missing link to Ronald Meadow, Fitzpatrick said.

December 12, 2013

DNA biology





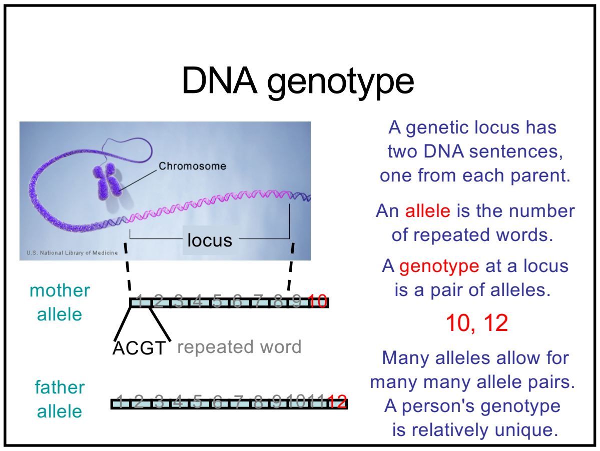
Short tandem repeat

DNA locus paragraph

23 volumes in
cell's
DNA encyclopedia

Take me out to the ball game
take me out with the crowd
buy me some peanuts and Cracker Jack
I don't care if I never get back
let me
root root root root root root root root root root
for the home team,
if they don't win, it's a shame for it's one, two,
three strikes, you're out
at the old ball game

"root" repeated 10 times, so
allele length is 10 repeats



DNA genotype

mother
allele

ACGT repeated word

father
allele

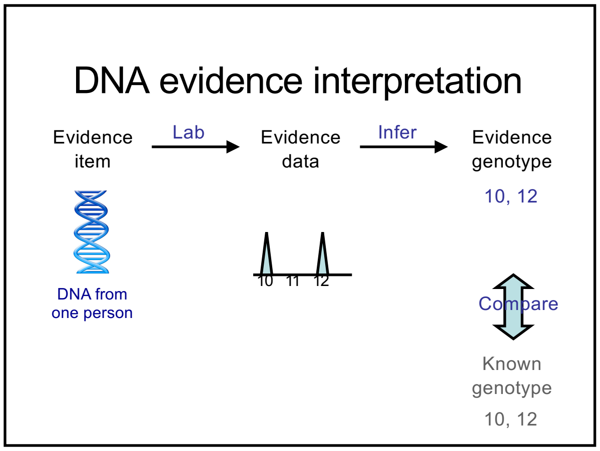
A genetic locus has
two DNA sentences,
one from each parent.

An allele is the number
of repeated words.

A genotype at a locus
is a pair of alleles.

10, 12

Many alleles allow for
many many allele pairs.
A person's genotype
is relatively unique.



DNA evidence interpretation

Evidence item → Lab → Evidence data → Infer → Evidence genotype

10, 12

DNA from
one person

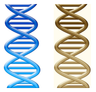
Compare

Known
genotype

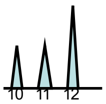
10, 12

DNA mixture interpretation

Evidence item — Lab → Evidence data — Infer → Evidence genotype



DNA from
two people



10, 11 @ 20%
11, 11 @ 30%
11, 12 @ 50%

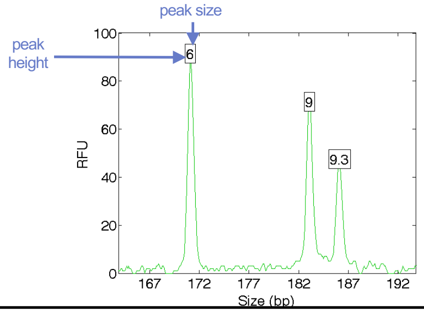
Compare

Known
genotype

11, 12

Computers can use all the data

Quantitative peak heights at locus TH01

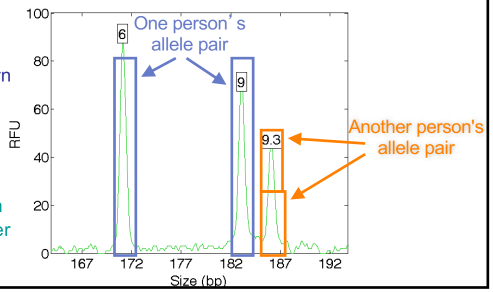


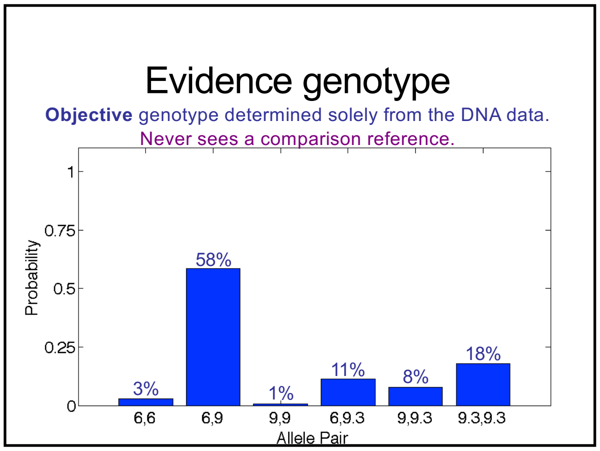
How the computer thinks

Consider every possible genotype solution

Explain the
peak pattern

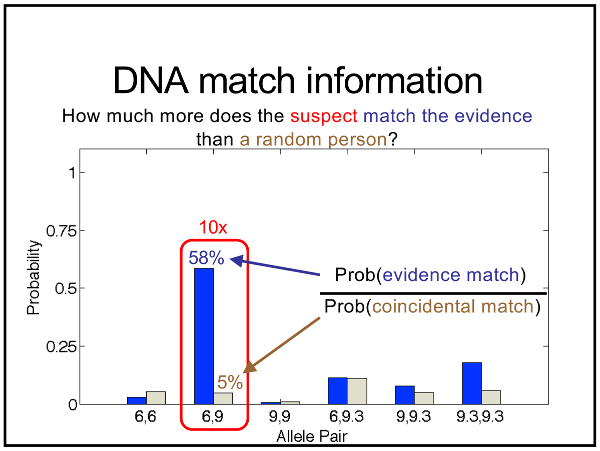
Better
explanation
has a higher
likelihood





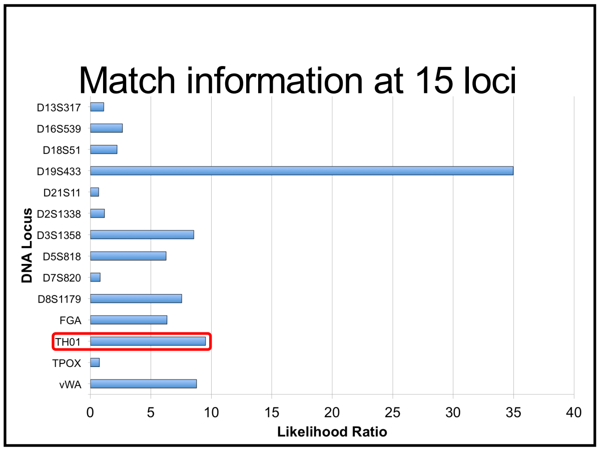
Evidence genotype

Objective genotype determined solely from the DNA data.
Never sees a comparison reference.



DNA match information

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



Match information at 15 loci

Is the suspect in the evidence?

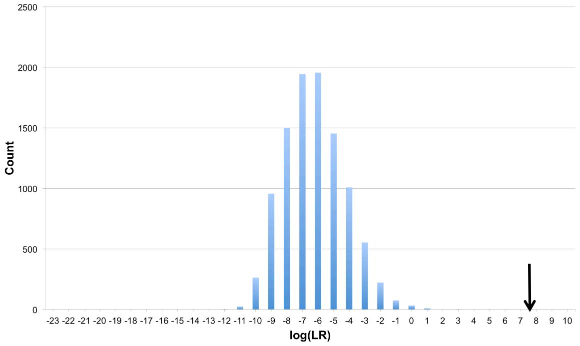
A match between the beer bottle
and Ronald Meadow is:

471 million times more probable than
a coincidental match to an unrelated Black person

28 million times more probable than
a coincidental match to an unrelated Caucasian person

22.6 million times more probable than
a coincidental match to an unrelated Hispanic person

Specificity for Ronald Meadow



People of New York v Ronald Meadow

Ron Meadow found guilty of murdering wife in cold-case trial pitting DA Fitzpatrick and Ed Menkin

Ronald Meadow

Syracuse, NY -- The estranged husband of a woman strangled to death 29 years ago was found guilty this afternoon by an Onondaga County jury.

There was an audible gasp by members of both families as the jury announced its second-degree murder verdict against Ronald Meadow, 62, of Georgia. They deliberated for 6 1/2 hours before rendering a verdict around 1:45 p.m. in the strangulation death of Colleen Meadow in 1985.

Meadow, who had been free on bail, was handcuffed and taken to jail with no bail after the verdict.

November 6, 2014

TrueAllele reinterpretation

The Washington Post

Virginia reevaluates DNA evidence in 375 cases

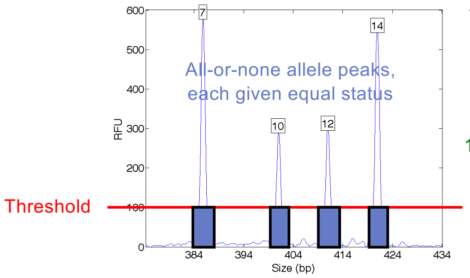
July 16, 2011

"Mixture cases are their own little nightmare," says William Vosburgh, director of the D.C. police's crime lab. "It gets really tricky in a hurry."

"If you show 10 colleagues a mixture, you will probably end up with 10 different answers"
Dr. Peter Gill, Human Identification E-Symposium, 2005

Data summary – "alleles"

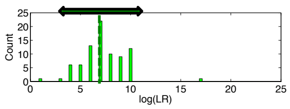
Over threshold, peaks are labeled as allele events



Allele Pair
7, 7
7, 10
7, 12
7, 14
10, 10
10% 10, 12
10, 14
12, 12
12, 14
14, 14

CPI information

6.83
6.68 million



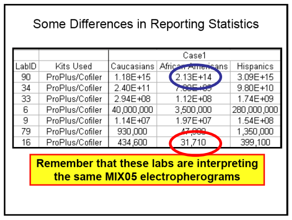
CPI

Combined probability of inclusion

MIX05: Thresholds not reproducible

National Institute of Standards and Technology

Two Contributor Mixture Data, Known Victim



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	[illegible]	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	47,000	1,350,000
16	ProPlus/Cofiler	434,600	31,710	399,100

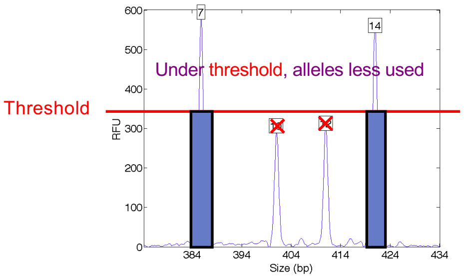
Remember that these labs are interpreting the same MIX05 electropherograms

213 trillion (14)

31 thousand (4)

SWGDAM 2010 guidelines

Higher threshold for human review

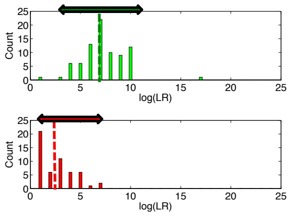


Allele Pair
7,   7
7, 10
7, 12
7, 14
10, 10
0% 10, 12
10, 14
12, 12
12, 14
14, 14

Modified CPI information

6.83
6.68 million

2.15
140



CPI

mCPI

MIX13: An interlaboratory study on the present state of DNA mixture interpretation in the U.S.
Coble M, National Institute of Standards and Technology
5th Annual Prescription for Criminal Justice Forensics, Fordham University School of Law, 2014.

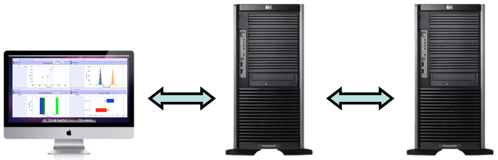
MIX13: Thresholds falsely include

MIX13 Case 5 Outcomes with Suspect C
(whose genotypes were not present in the mixture)

# Labs	Report Conclusions	Reasons given
6	Exclude Suspect C	detailed genotype checks (ID+); TrueAllele negative LR (ID+); assumed major/minor and suspects did not fit (ID+); 3 labs noted Penta E missing allele 15 (PP16HS)
3	Inconclusive with C only (A & B included)	All these labs used PP16HS
21	Inconclusive for A, B, and C	
70	**Include & provide CPI statistics**	*All over the road…*

Range of CPI stats for Caucasian population:
FBI allele frequencies: **1 in 9** to **1 in 344,000**

TrueAllele® Casework



ViewStation
User Client

Database
Server

Interpret/Match
Expansion

Visual User Interface
VUIer™ Software

Parallel Processing Computers

Validated genotyping method

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

Ballantyne J, Hanson EK, Perlin MW. DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: Combining quantitative data for greater identification information. *Science & Justice.* 2013;53(2):103-14.

Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences.* 2015;*in press.*

Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences.* 2015;*in press.*

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):1458-66.

Perlin MW, Dormer K, Hornyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLOS ONE.* 2014;(9)3:e92837.

Sensitivity

The extent to which interpretation identifies the correct person

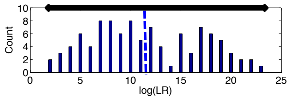
True DNA mixture inclusions

101 reported genotype matches
82 with DNA statistic over a million

TrueAllele sensitivity

log(LR) match distribution

11.05
113 billion

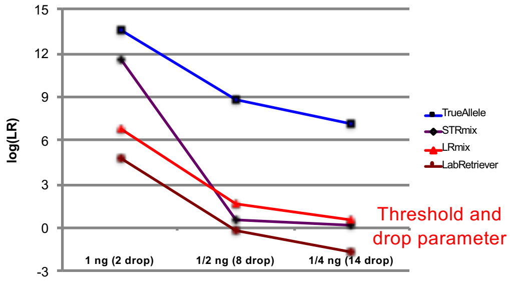


TrueAllele

An investigation of software programs using “semi-continuous” and “continuous” methods for complex DNA mixture interpretation.
Coble M, Myers S, Klaver J, Kloosterman A, Leiden University, The Netherlands, 9th International Conference on Forensic Inference and Statistics, 2014.

Other software loses information

Simple two person mixture, 10% minor contributor



Threshold and drop parameter

Specificity

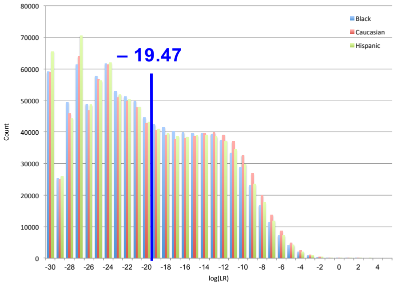
The extent to which interpretation does
not misidentify the wrong person

True exclusions, without false inclusions

101 matching genotypes x 10,000 random references
x 3 ethnic populations,
for over 1,000,000 nonmatching comparisons

TrueAllele specificity

log(LR) mismatch distribution



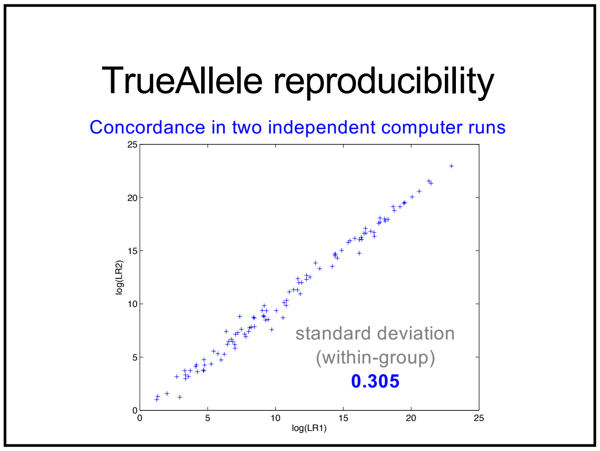
Reproducibility

The extent to which interpretation
gives
the same answer to the same question

MCMC computing has sampling variation

duplicate computer runs
on 101 matching genotypes

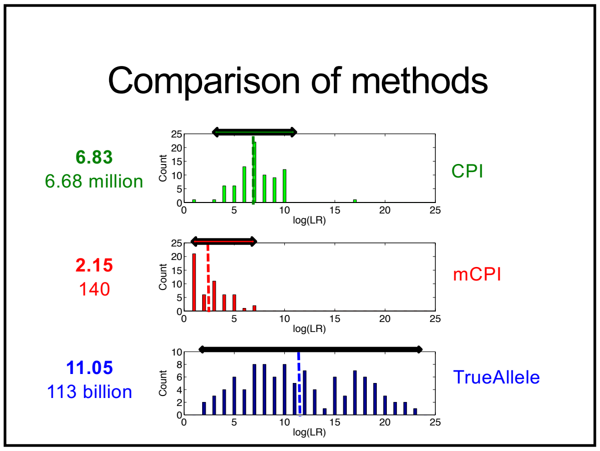
measure log(LR) variation



TrueAllele reproducibility

Concordance in two independent computer runs

standard deviation
(within-group)
0.305

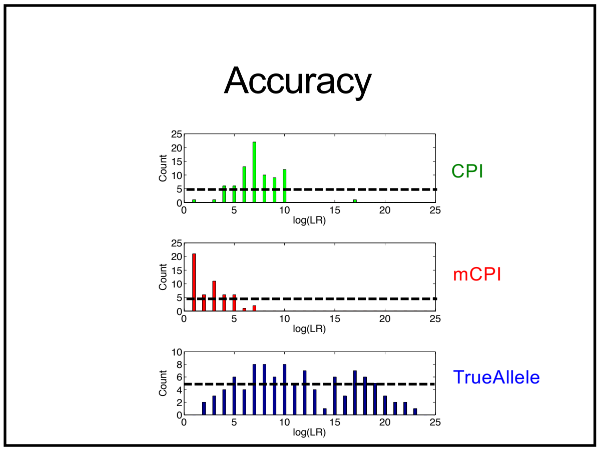


Comparison of methods

6.83
6.68 million
CPI

2.15
140
mCPI

11.05
113 billion
TrueAllele



Accuracy

CPI

mCPI

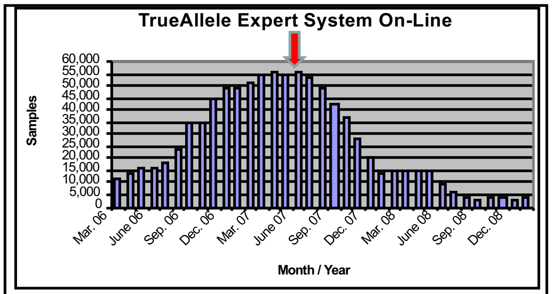
TrueAllele

TrueAllele Virginia outcomes

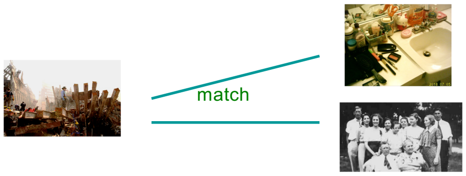
144 cases analyzed
72 case reports – 10 trials

City	Court	Charge	Sentence
Richmond	Federal	Weapon	50 years
Alexandria	Federal	Bank robbery	90 years
Quantico	Military	Rape	3 years
Chesapeake	State	Robbery	26 years
Arlington	State	Molestation	22 years
Richmond	State	Homicide	35 years
Fairfax	State	Abduction	33 years
Norfolk	State	Homicide	8 years
Charlottesville	State	Homicide	15 years
Hampton	State	Home invasion	5 years

Eliminated NYS DNA backlog



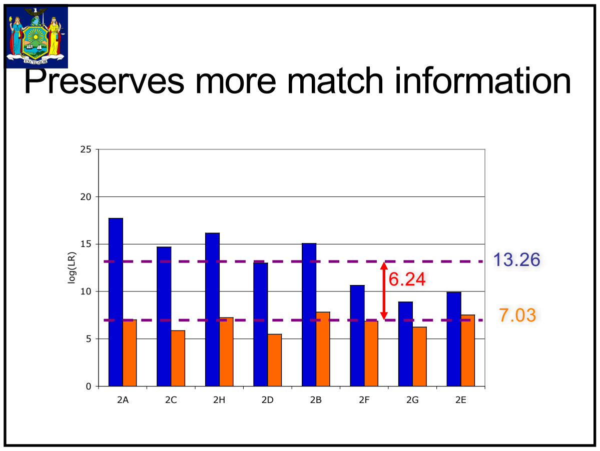
Reanalyzed WTC DNA data



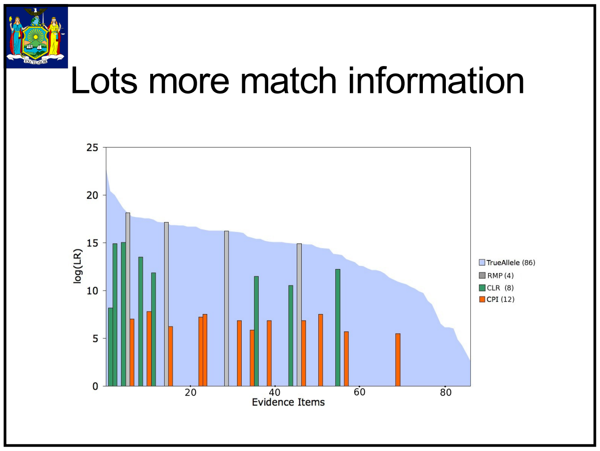
18,000
victim remains

2,700
missing people

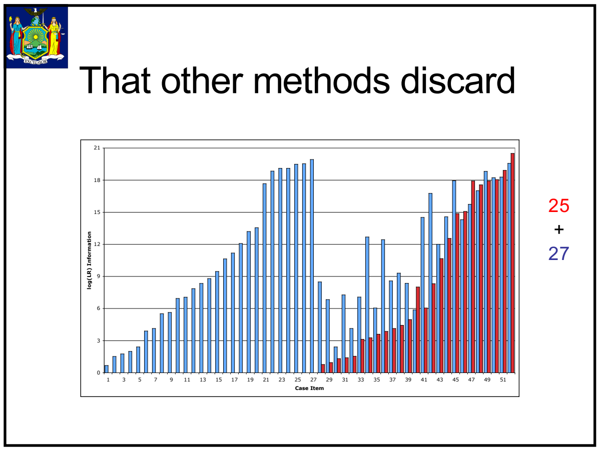
match



Preserves more match information

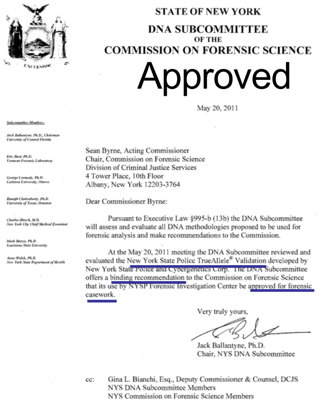


Lots more match information



That other methods discard

Approved



STATE OF NEW YORK
DNA SUBCOMMITTEE
OF THE
COMMISSION ON FORENSIC SCIENCE

May 20, 2011

Subcommittee Members:

Jack Ballantyne, Ph.D., Chairman
University of Central Florida

Eric Buel, Ph.D.
Vermont Forensic Laboratory

George Carmody, Ph.D.
Carleton University, Ottawa

Ranajit Chakraborty, Ph.D.
University of Texas, Houston

Charles Hirsch, M.D.
New York City Chief Medical Examiner

Mark Batzer, Ph.D.
Louisiana State University

Anne Walsh, Ph.D.
New York State Department of Health

Sean Byrne, Acting Commissioner
Chair, Commission on Forensic Science
Division of Criminal Justice Services
4 Tower Place, 10th Floor
Albany, New York 12203-3764

Dear Commissioner Byrne:

Pursuant to Executive Law §995-b (13b) the DNA Subcommittee will assess and evaluate all DNA methodologies proposed to be used for forensic analysis and make recommendations to the Commission.

At the May 20, 2011 meeting the DNA Subcommittee reviewed and evaluated the New York State Police TrueAllele® Validation developed by New York State Police and Cybergenetics Corp. The DNA Subcommittee offers a binding recommendation to the Commission on Forensic Science that its use by NYSP Forensic Investigation Center be approved for forensic casework.

Very truly yours,

Jack Ballantyne, Ph.D.
Chair, NYS DNA Subcommittee

cc: Gina L. Bianchi, Esq., Deputy Commissioner & Counsel, DCJS
NYS DNA Subcommittee Members
NYS Commission on Forensic Science Members

TrueAllele user meeting

California
Louisiana
Maryland
Massachusetts
New York
Pennsylvania
South Carolina
Virginia
Australia
Oman
Prosecutors

Bear Mountain Inn, New York
September, 2014

TrueAllele in New York State

Cybergenetics analyzes DNA case evidence

Counties:
- Cayuga
- Chemung
- Onondaga
- Schenectady
- St. Lawrence
- Tompkins
- Westchester

Crimes:
- murder
- rape

TrueAllele in criminal cases

Used in over 200 cases for DNA evidence

Testimony:
- state
- federal
- military
- foreign

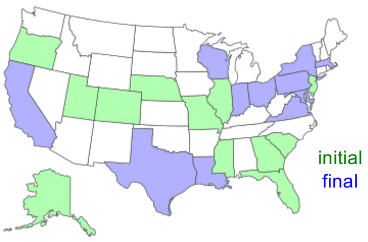
Crimes:
- armed robbery
- child abduction
- child molestation
- murder
- rape
- terrorism
- weapons

TrueAllele admissibility

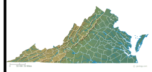
State	Year	Challenge	Outcome
Pennsylvania	2009	Frye	admitted
Pennsylvania	2012	Appellate court	precedent
California	2013	Kelly-Frye	admitted
Virginia	2013	Spencer-Frye	admitted
Ohio	2014	Daubert	admitted
Louisiana	2014	Daubert	admitted
New York	2014	Frye	pending

TrueAllele in the United States

Laboratory systems or case reports in 23 states



DNA mixture crisis



375 cases/year x 4 years = 1,500 cases
320 M in US / 8 M in VA = 40 factor
1,500 cases x 40 factor = 60,000 inconclusive

1,000 cases/year x 4 years = 4,000 cases
320 M in US / 8 M in NY = 40 factor
4,000 cases x 40 factor = 160,000 inconclusive

+ under reporting of DNA match statistics

DNA evidence data in 100,000 cases
Collected, analyzed & paid for – but unused

Turn on the light

TrueAllele Casework at the NYS Police

- Approved
- Installed
- Validated
- Trained
- Certified
- Documented

Forensic Investigation Center
New York State Police
Albany, NY

More TrueAllele information

http://www.cybgen.com/information

- Courses
- Newsletters
- Newsroom
- Presentations
- Publications
- Webinars

http://www.youtube.com/user/TrueAllele
TrueAllele YouTube channel

Cybergenetics

perlin@cybgen.com