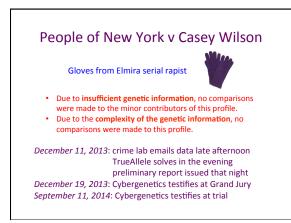


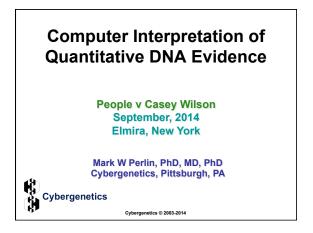
Elmira, New York

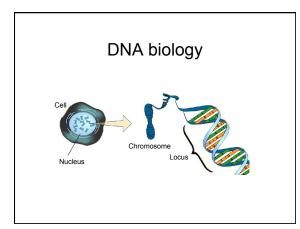
On June 15, 2011, a man broke into a woman's apartment. Wielding a knife and wearing a bandana, he raped her. The victim recognized Casey Wilson by his voice and height.

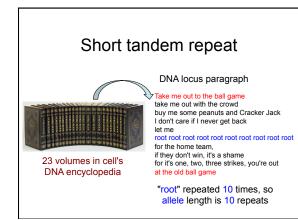
On September 29, 2013, a man broke into another woman's apartment. With a knife, he raped and robbed her, and then tried to eliminate evidence of the sex crimes. Wilson was again recognized by his voice and height.

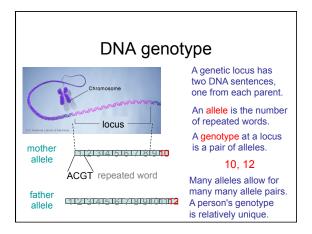
Surveillance video showed a masked man wearing gloves leaving the second victim's apartment. Later surveillance placed him in the same clothes near Wilson's Mt. Zoar home.











DNA evidence interpretation

data

Evidence

genotype 10, 12

Compare

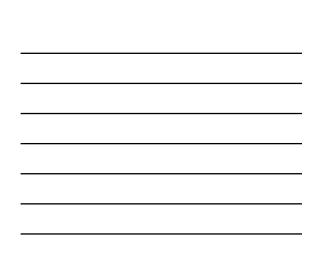
Known genotype 10, 12

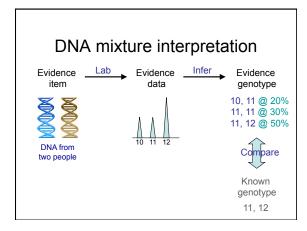
Evidence Lab Evidence Infer

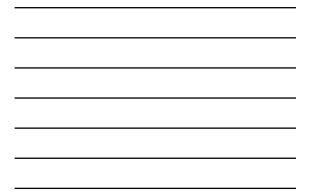
item

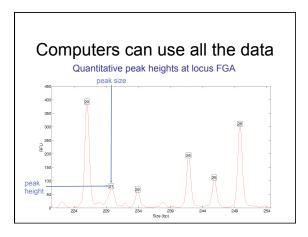
DNA from

one person

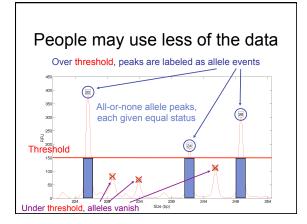




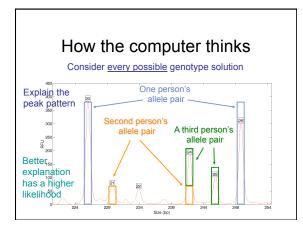


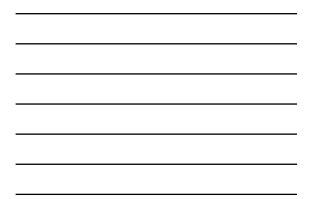


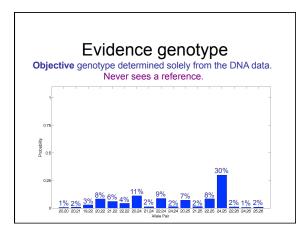




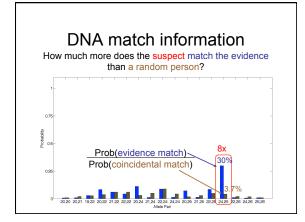




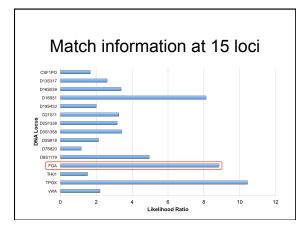




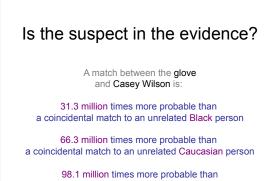








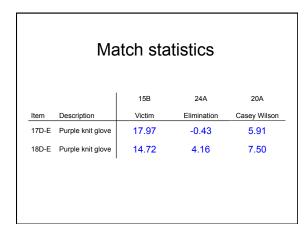


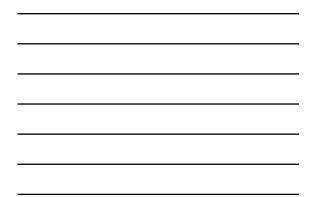


a coincidental match to an unrelated Hispanic person

Match statistics				
	15B	24A	20A	
Description	Victim	Elimination	Casey Wilson	
Purple knit glove	930 quadrillion	1/2.72	817 thousand	
Purple knit glove	520 trillion	14.6 thousand	31.3 million	
	Description Purple knit glove	15B Description Victim Purple knit glove 930 quadrillion	15B 24A Description Victim Elimination Purple knit glove 930 quadrillion 1/2.72	

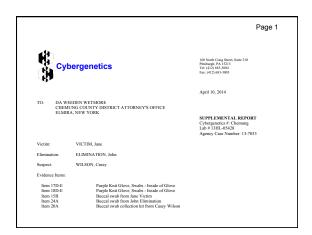


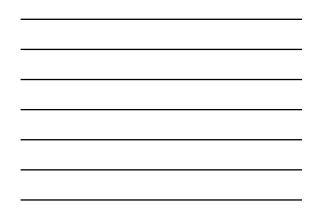


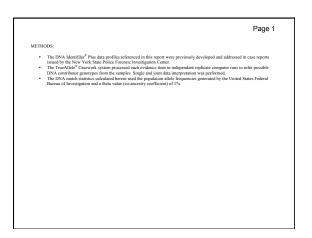












Page 1

METHODS:

- The DNA Identifiler[®] Plus data profiles referenced in this report were previously developed and addressed in case reports issued by the New York State Police Ferensic Investigation Center.
 The TrancHiefe Casework system proceeds each evolution the interpretation was performed.
 The TrancHiefe Assistive calculates herein using hep-patient adjust data interpretation was performed.
 The DNA Hep-tastistic calculates herein using hep-patient allele frequencies generated by the United States Federal Bureau of Investigation and a theta value (co-ancestry coefficient) of 1%.

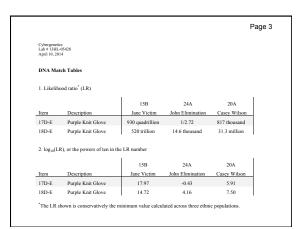
RESULTS:

Item 17D-E

TrueAllel assumed that the evidence sample data (Item 17D-E) contained three and four unknown contributors, and objectively inferred evidence genotypes solely from these data. The victim and elimination genotypes were assumed in some calculations. Following genotype inference, the computed a genotype from this evidence into provided reference (Items 15B, 24A and 20A) genotypes, relative to reference populations, to compute LR DNA match statistics. Based on these results:

- between the glove (Item 17D-E) and Jane Victim (Item 15B) is: 35.9 quintillion times: more probable than a coincidental match to a unrelated Black person, 10.1 quintillion times; more probable than a coincidental match to a unrelated Caucasian person, and 90 quadrillion times; more probable than a coincidental match to a unrelated Hispanic person.
- atch between the glove (Item 17D-E) and John Elimination (Item 24A) is: 272 times less probable than a coincidental match to an unrelated Black person, 1.44 times meer probable than a coincidental match to a nureltated accussion person, and 1.71 times less probable than a coincidental match to an unrelated Hispanic person.
- h between the glove (Item 17D-E) and Casey Wilson (Item 20A) is: 817 ducasad times more probable than a coincidental match to an unrelated Black person, 5.25 million times more probable than a coincidental match to an unrelated Caucasian person, and 2.49 million times more probable than a coincidental match to an unrelated Hispanic person.

		Page 2
Item 18D-E		
inferred evidence genoty Following genotype infe	pes solely from these data. The victin rence, the computer then compared a) contained three and four unknown contributors, and objectively and elimination genotypes were assumed in some calculations. enotype from this evidence item to provided reference (Items 15B, 24 ute LR DNA match statistics. Based on these results:
3.33 quadrillion 2.64 quadrillion		tal match to an unrelated Black person, tal match to an unrelated Caucasian person, and
	ve (Item 18D-E) and John Elimination	
35.7 thousand t		I match to an unrelated Black person, I match to an unrelated Caucasian person, and I match to an unrelated Hispanic person.
	ve (Item 18D-E) and Casey Wilson (Ites more probable than a coincidental	
		match to an unrelated Caucasian person, and match to an unrelated Hispanic person.
		Mark W. Perlin, PhD, MD, PhD Chief Scientific Officer. Cybergenetics





Cybergenetics Lab # 13HL-05428 April 10, 2014

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Page 4

TrueAllele[®] Casework Method

Computer interpretation of DNA evidence

A definite genotype can be determined when a person's DNA produces unambiguous data. However, when the data signals are less definitive, or when there are multiple contributors to the evidence, uncertainty arises. This uncertainty is expressed in the resulting genotype, which may describe different genetic identity possibilities. Such genotype uncertainty may translate into reduced identification information when a comparison is made with a suspect.

The DPM (distification indic can thus be anderstood as a to wedge process: b) closelscole by descript geospice from exclusion, also accessing of a table pair uncertainty using probability, and 2 subsequently matching geospice, rome exclusion, also specification to a population, to express the strength of association using probability. The match strength is reported as a single number, the likelihood ratio (LR), which quantifies the change in identification information produced by having cannot due DAN evidence.

The TrueAllele Casework system is a computer implementation of this two-step DNA identification inference approach. The computer objectively infers genotyces from DNA data through statistical modeling, without reference to a known compurison genotype. To represent the identification information present in the data, the system represents genotype uncertainty using probability These probability cannot be added and a statistical modeling and the system strength and the system provides evidentiary infinited infinition infinitement. Subsequent comparison with suspects provides evidentiary the probability cannot be added and and a strength and the system strength and the system provides evidentiary the system of the system strength and the system provides and the system strength and the

Many TransMede validation studies have been conducted to establish the reliability of the model [1]. Five of these studies have been published in process-mosed scientific gammals, no abel spatiatic [2, 3] and caresoved [4, 5, 6] data: Conducting such validations test consistent with the 2010 Scientific Working Group on DNA Analysis Methods (SWGDAM) interpretation guidelines [7] (paragraph 3.2.).

Validation papers 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):103-114.

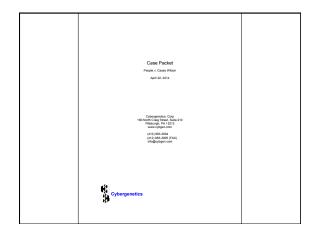
Perlin MW, Hornyak J, Sugimoto G, Miller K. TrueAllele® genotype identification on DNA mixtures containing up to five unknown contributors. *Journal of Forensic Sciences*. 2015;60(4):857-868.

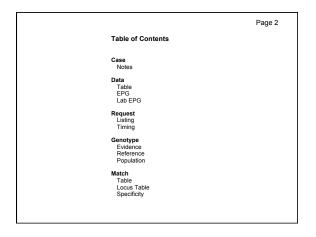
Greenspoon SA, Schiermeier-Wood L, Jenkins BC. Establishing the limits of TrueAllele® Casework: a validation study. *Journal of Forensic Sciences*. 2015;60(5):1263-1276.

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):1430-1447.

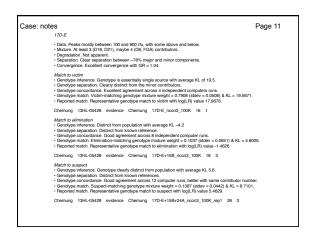
Perlin MW, Belrose JL, Duceman BW. New York State TrueAllele® Casework validation study. Journal of Forensic Sciences. 2013;58(6):1458-1466.

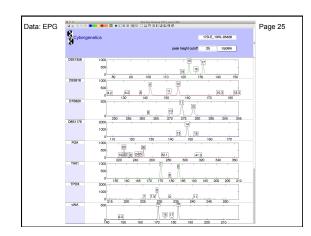
Perlin MW, Dormer K, Homyak J, Schiermeier-Wood L, Greenspoon S. TrueAllele® Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases. *PLOS ONE*. 2014;(9)3:e92837.













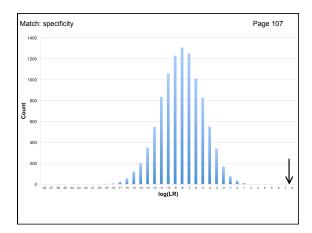
equest: listing	Name	Contributors	Known	Options	Cycles Page 34
	17D-E_ncon3_100K	3			100K
	17D-E_ncon3_100K_rep1	3			100K
	17D-E+15B_ncon3_100K	3	15B		100K
	17D-E+15B_ncon3_100K_rep1	3	15B		100K
	17D-E+15B+24A_ncon3_100K	3	15B, 24A		100K
	17D-E+15B+24A_ncon3_100K_rep1	3	15B, 24A		100K
	17D-E+15B+24A ncon3 100K rep2	3	15B, 24A		100K
	17D-E ncon4 100K	4			100K
	17D-E ncon4 100K rep1	4			100K
	17D-E+15B ncon4 100K	4	15B		100K
	17D-E+15B_ncon4_100K_rep1	4	15B		100K
	17D-E+15B+24A_ncon4_100K	4	15B, 24A		100K
	17D-E+15B+24A_ncon4_100K_rep1	4	15B, 24A		100K
	18D-E ncon3 100K	3			100K
	18D-E_ncon3_100K_rep1	3			100K
	18D-E+15B_ncon3_100K	3	15B		100K
	18D-E+15B_ncon3_100K_rep1	3	15B		100K
	18D-E+15B+24A_ncon3_100K	3	15B, 24A		100K
	18D-E+15B+24A_ncon3_100K_rep1	3	15B, 24A		100K
	18D-E_ncon4_100K	4			100K
	18D-E_ncon4_100K_rep1	4			100K
	18D-E+15B ncon4 100K	4	15B		100K
	18D-E+15B ncon4 100K rep1	4	15B		100K
	18D-E+15B+24A ncon4 100K	4	15B, 24A		100K
	18D-E+15B+24A_ncon4_100K_rep1	4	15B, 24A		100K
	17D-E+18D-E_ncon3_100K	3			100K
	17D-E+18D-E_ncon3_100K_rep1	3			100K
	17D-E+18D-E+15B_ncon3_100K	3	15B		100K
	17D-E+18D-E+15B ncon3 100K rep1	3	15B		100K
	17D-E+18D-E+15B+24A ncon3 100K	3	15B, 24A		100K
	17D-E+18D-E+15B+24A ncon3 100K rep1	3	15B. 24A		100K



Item 18D-E v	s suspect 20A			-
18D-E+15B+2	24A_ncon4_100k	contributor	4	
locus	allele 1	allele 2	probability	
AMELO	1	1	0.6354	
	1	2	0.3646	
CSF1PO	11	12	0.4260	
	10	11	0.1203	
	11	11	0.1012	
	10	12	0.0872	
	12	12	0.0437	
	10	10	0.0358	
	11	13	0.0250	
	7	11	0.0248	
	10	13	0.0234	
	9	11	0.0233	
	7	12	0.0197	
	9	10	0.0135	
	12	13	0.0134	
	9	12	0.0117	
	7	10	0.0104	
	9	13	0.0076	
	7	13	0.0042	

Match: locus table	18D-E vs suspect 20A 18D-E+15B+24A_ncon4_100K contributor 4 vs. 20A				Page 105
	locus	US BLK FBI	US CAU FBI	US HIS FRI	
	CSF1PO	0.2210			
	D13S317	0.4160	0.4650	0.5155	
	D16S539	0.5292	0.6055	0.4936	
	D18S51	0.9098			
	D19S433	0.3001	0.0527	0.2465	
	D21S11	0.5127	0.4024	0.2766	
	D2S1338	0.4998	0.3737	0.5187	
	D3S1358	0.5328	0.5826	0.6931	
	D5S818	0.3266	0.1828	0.2171	
	D7S820	0.0639	0.1107	0.1432	
	D8S1179	0.6948	0.8062	0.8043	
	FGA	0.9469	1.0298	0.9890	
	TH01	0.1797	0.5681	0.3726	
	TPOX	1.0183	1.0035	1.0085	
	vWA	0.3438	0.3831	0.3087	
	Total	7.4953	7.8218	7.9915	
	Joint	31283563	66349092	98066703	
	Words	31.3 million	66.3 million	98.1 million	









General YouTube talks

M.W. Perlin, "Challenging DNA Evidence", *Allegheny County Courthouse - Continuing Legal Education*, Pittsburgh, PA, 27-Feb-2015.

M.W. Perlin. "Objective DNA Mixture Information in the Courtroom: Relevance, Reliability and Acceptance", *National Institute of Standards and Technology*, Arlington, VA, 22-July-2015.

M.W. Perlin. "Forensic Science and Criminal Law: Cutting Edge DNA Strategies", *Pennsylvania Association of Criminal Defense Lawyers*, Pittsburgh, PA, 25-Sep-2015.

