



abc 2020

Interpretation errors in DNA profiling

Dan E. Krane, Wright State University, Dayton, OH

Forensic Bioinformatics
(www.bioforensics.com)

A controversial idea:

Analysts should arrive at conclusions about evidence samples before looking at references.

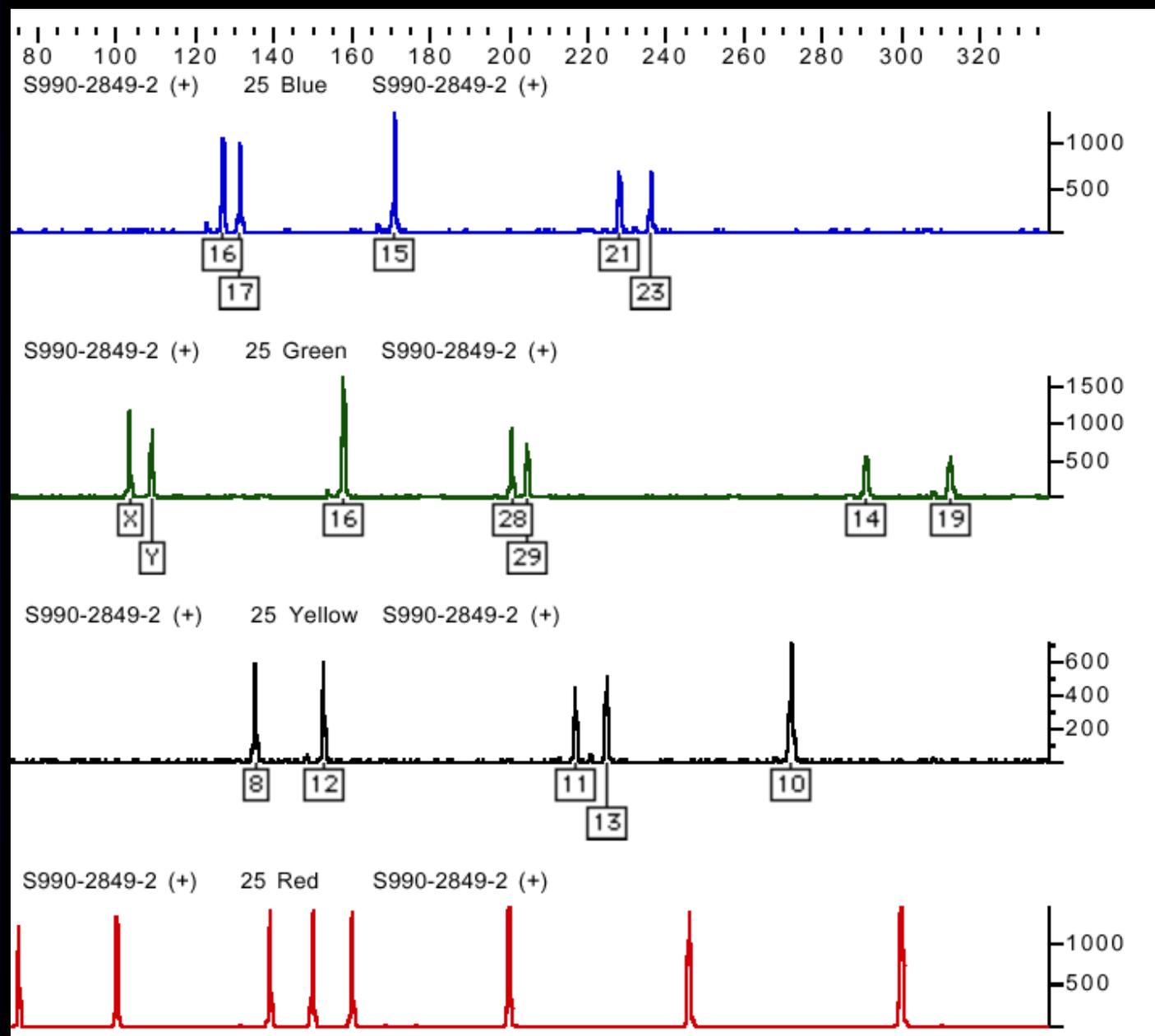
Krane, D. E., S. Ford, J. R. Gilder, K. Inman, A. Jamieson, R. Koppl, I. L. Kornfield, D. M. Risinger, N. Rudin, M. S. Taylor, W. C. Thompson. 2008. Sequential unmasking: A means of minimizing observer effects in forensic DNA interpretation. *Journal of Forensic Sciences*, **53**(4):1006-1007.

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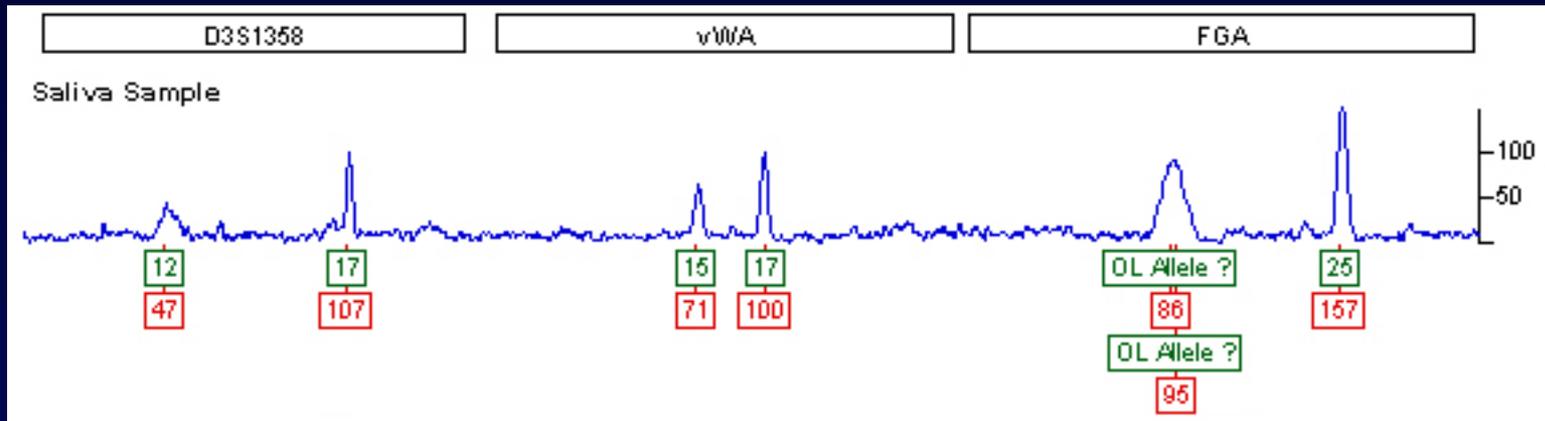
Analysts should arrive at conclusions about evidence samples before looking at references – and write those conclusions down.

Dror, I. E., W. C. Thompson, C. A. Meissner, I. Kornfield, D. Krane, M. Saks, and M. Risinger. 2015. Context management toolbox: A linear sequential unmasking (LSU) approach for minimizing cognitive bias in forensic decision making. *Journal of Forensic Sciences*, **60**(4):1111-1112.

Doesn't someone either match or not?



Opportunities for subjective interpretation?



Can "Tom" be excluded?

Suspect

Tom

D3

17, 17

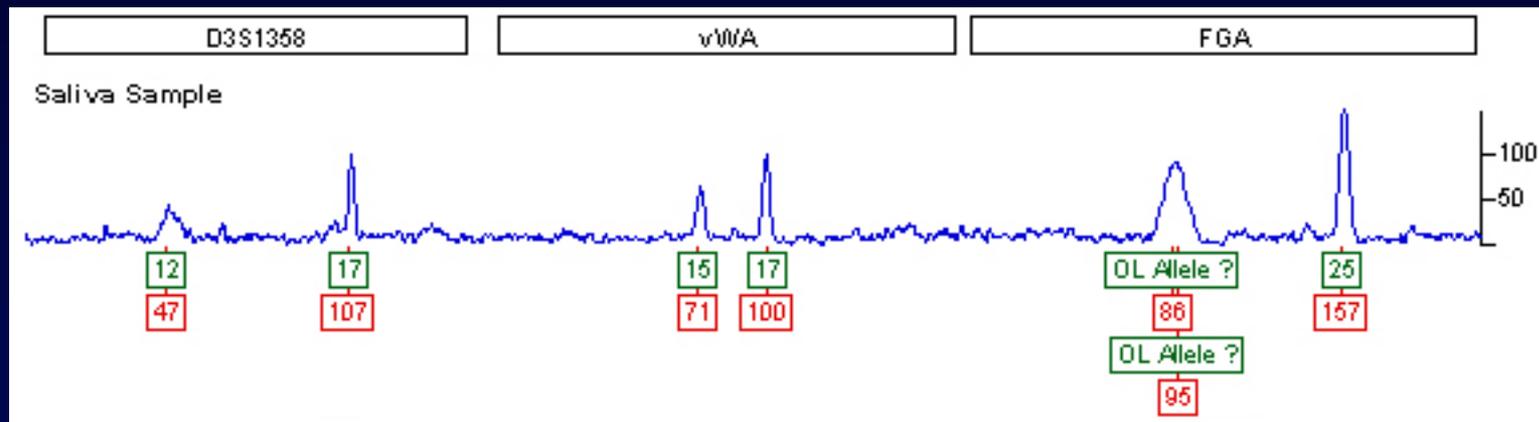
vWA

15, 17

FGA

25, 25

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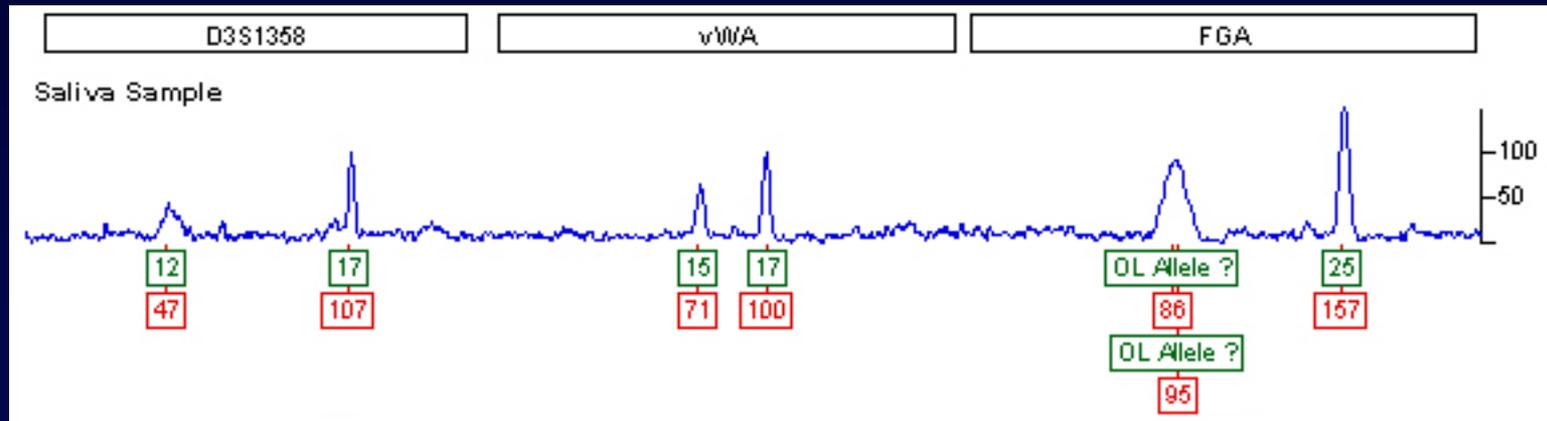


Can “Tom” be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25

No -- the additional alleles at D3 and FGA are “technical artifacts.”

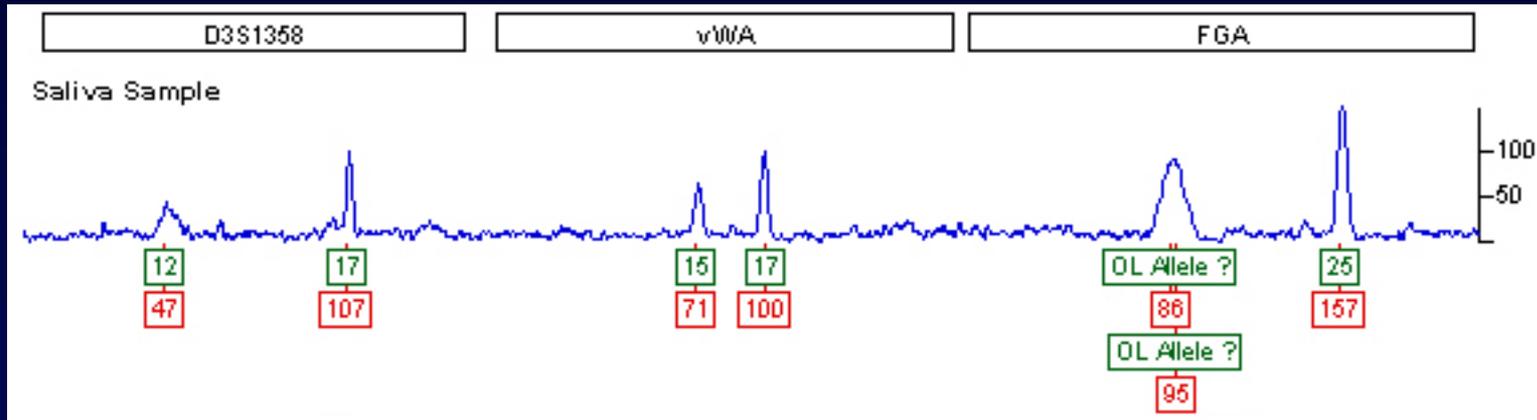
Opportunities for subjective interpretation?



Can “Dick” be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25

Opportunities for subjective interpretation?

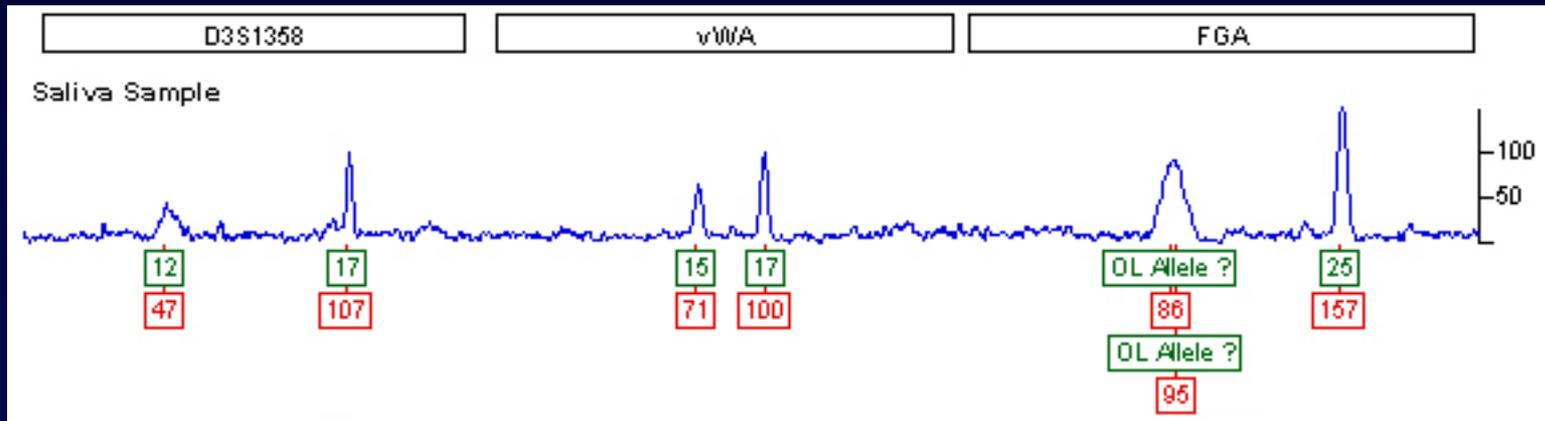


Can “Dick” be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25

No -- stochastic effects explain peak height disparity in D3; blob in FGA masks 20 allele.

Opportunities for subjective interpretation?

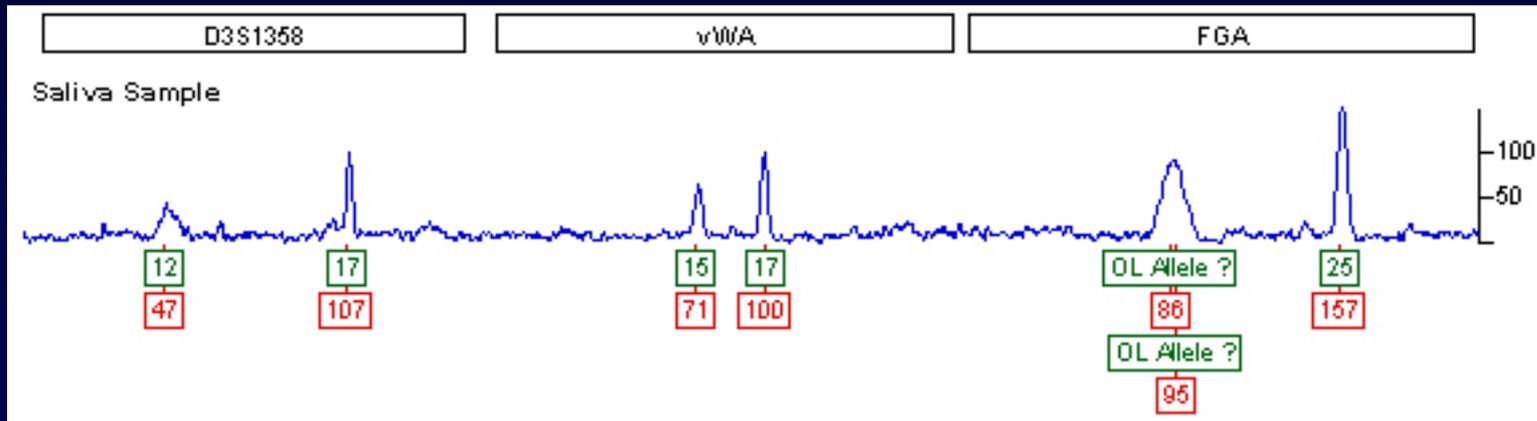


Can “Harry” be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25
Harry	14, 17	15, 17	20, 25

No -- the 14 allele at D3 may be missing due to “allelic drop out”; FGA blob masks the 20 allele.

Opportunities for subjective interpretation?



Can “Sally” be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25
Harry	14, 17	15, 17	20, 25
Sally	12, 17	15, 15	20, 22

No -- there must be a second contributor; degradation explains the “missing” FGA allele.

Observer effects, aka context effect

- *--the tendency to interpret data in a manner consistent with expectations or prior theories (sometimes called “examiner bias”)*
- Most influential when:
 - Data being evaluated are ambiguous or subject to alternate interpretations
 - Analyst is motivated to find a particular result

Analyst often have strong expectations about the data

DNA Lab Notes

*– “Suspect-known crip gang member--keeps ‘skating’ on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. Miller [deputy DA] wants to connect this guy to scene w/DNA
”
... ”*

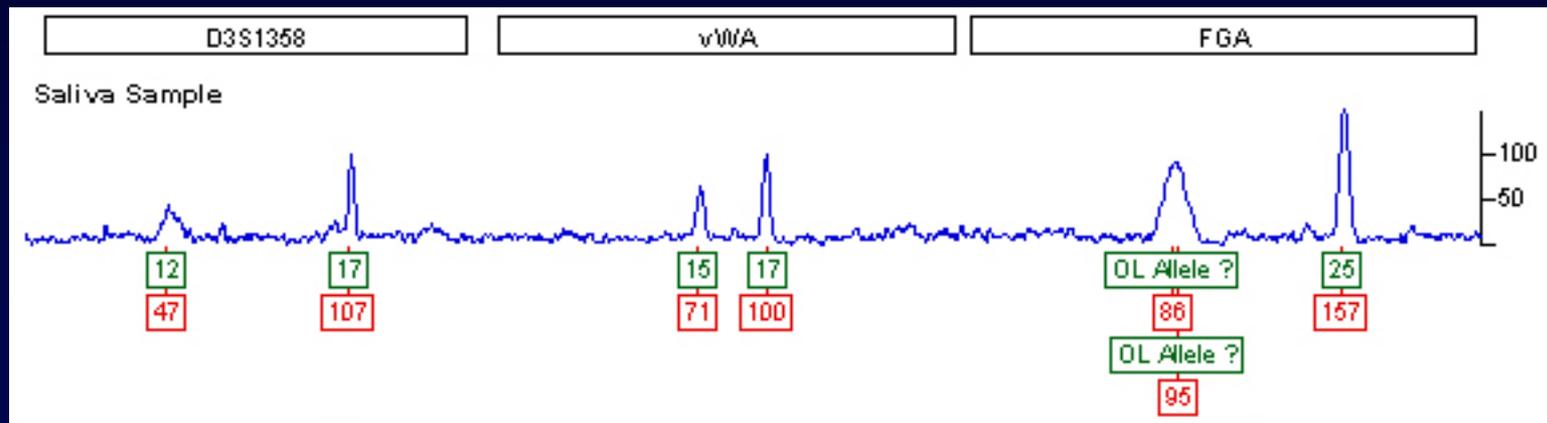
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– “Suspect-known crip gang member--keeps ‘skating’ on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. Miller [deputy DA] wants to connect this guy to scene w/DNA ...”

“Death penalty case! Need to eliminate Item #57 [name of individual] as a possible suspect”

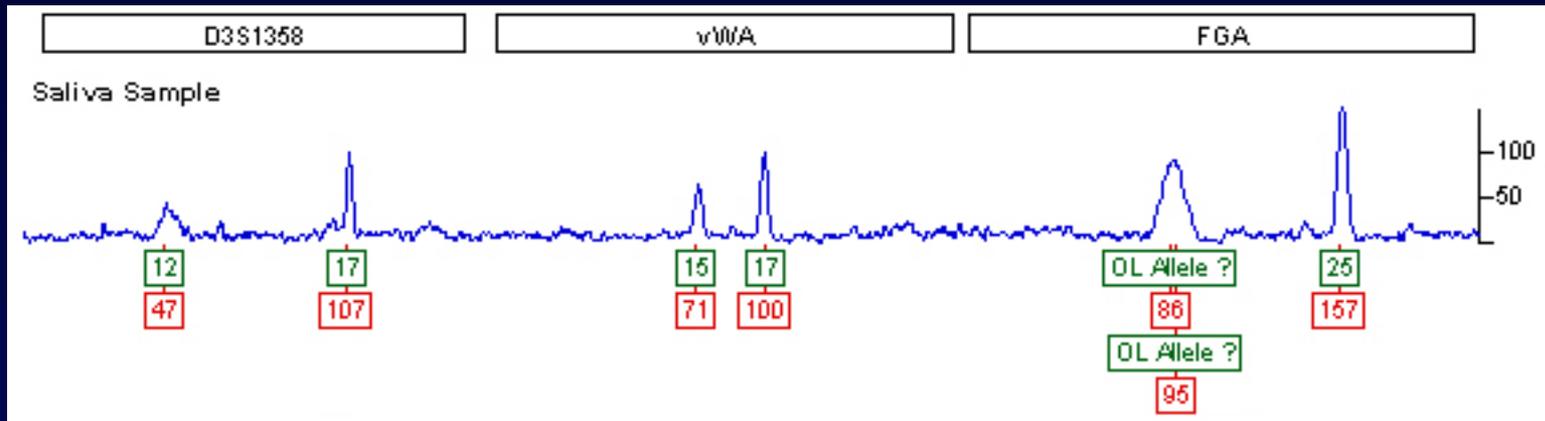
Opportunities for subjective interpretation?



Who can be excluded?

<u>Suspect</u>	<u>D3</u>	<u>vWA</u>	<u>FGA</u>
Tom	17, 17	15, 17	25, 25
Dick	12, 17	15, 17	20, 25
Harry	14, 17	15, 17	20, 25
Sally	12, 17	15, 15	20, 22

Opportunities for subjective interpretation?



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“Suspect-known crip gang member--keeps ‘skating’ on charges-never serves time. This robbery he gets hit in head with bar stool--left blood trail. Miller [deputy DA] wants to connect this guy to scene w/DNA”

Lies, damned lies and

- “A well-known lawyer, now a judge, once grouped witnesses into three classes: simple liars, damned liars, and experts.”
 - *Nature*, p. 74, November 26, 1885.

Blind testing may not be enough.

Are analysts motivated to see single contributors in mixed samples?

Statistics do not lie.

But, you have to pay close attention to the questions they are addressing.

What is the chance that a randomly chosen, unrelated individual from a given population would have the same DNA profile observed in a sample?

Single source statistics:

Random Match Probability (RMP)

Statistical estimates: the product rule

Single source samples

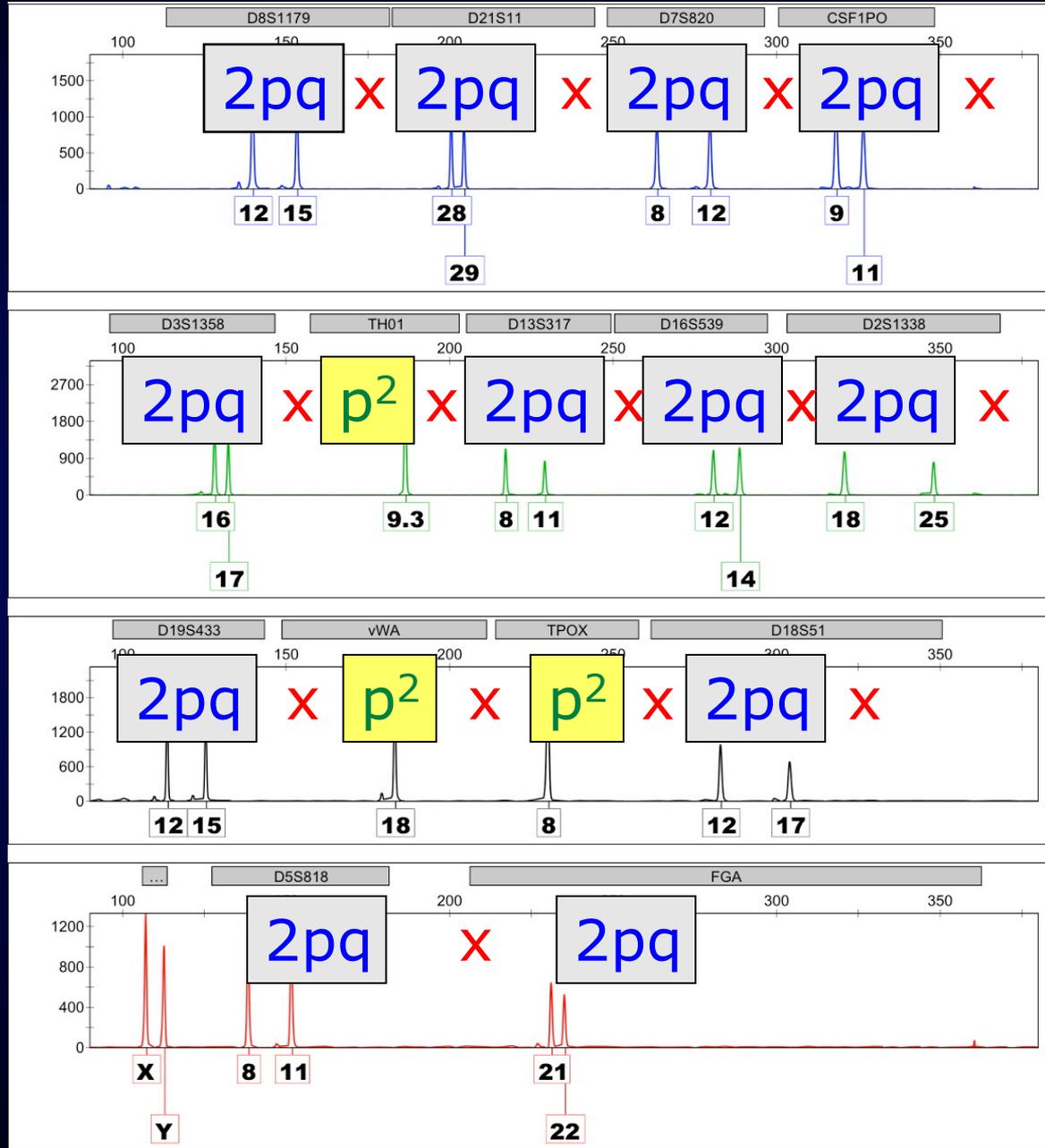
Formulae for RMNE:

At a locus:

Heterozygotes: $2pq$

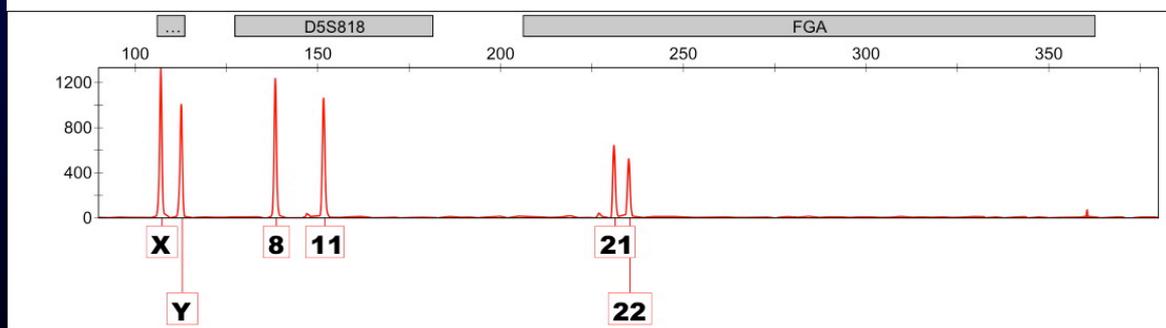
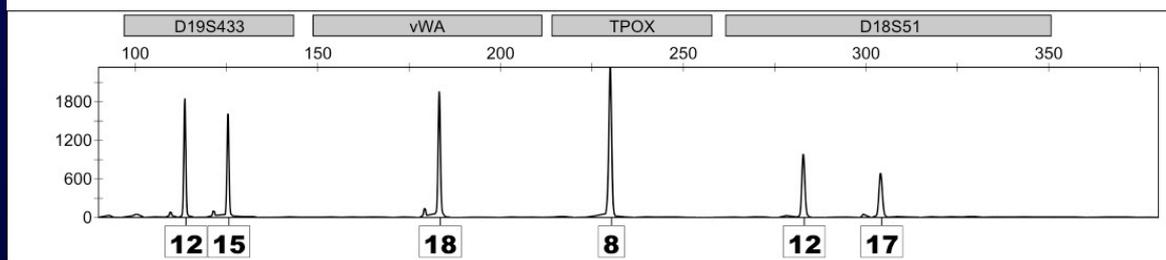
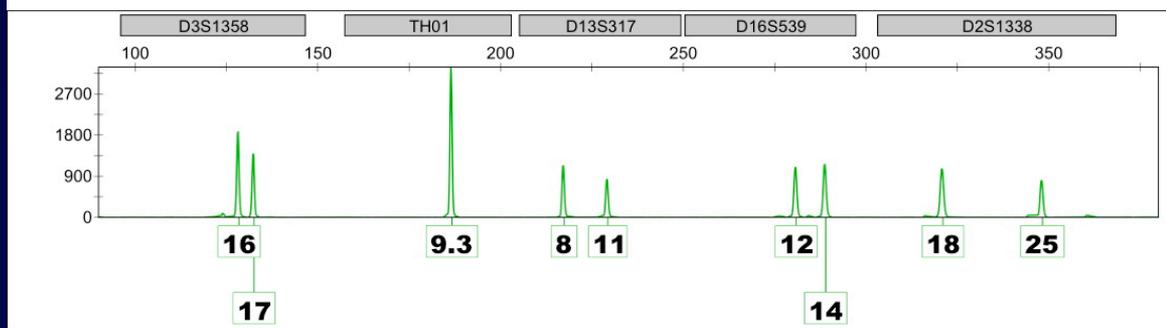
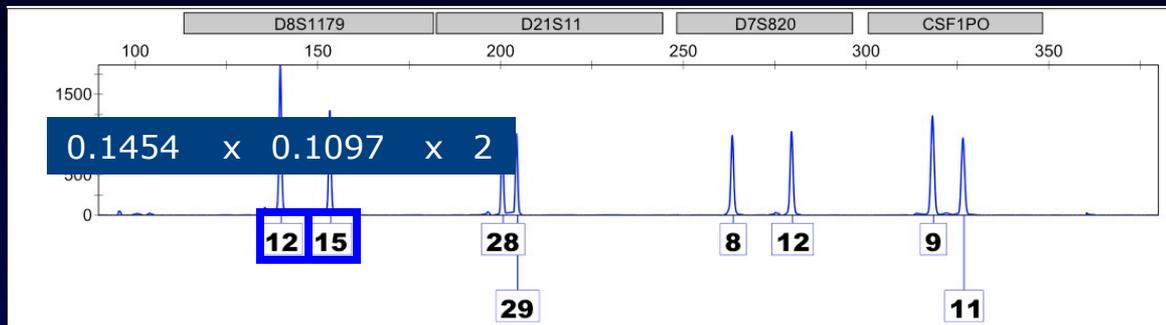
Homozygotes: p^2

Multiply across all loci



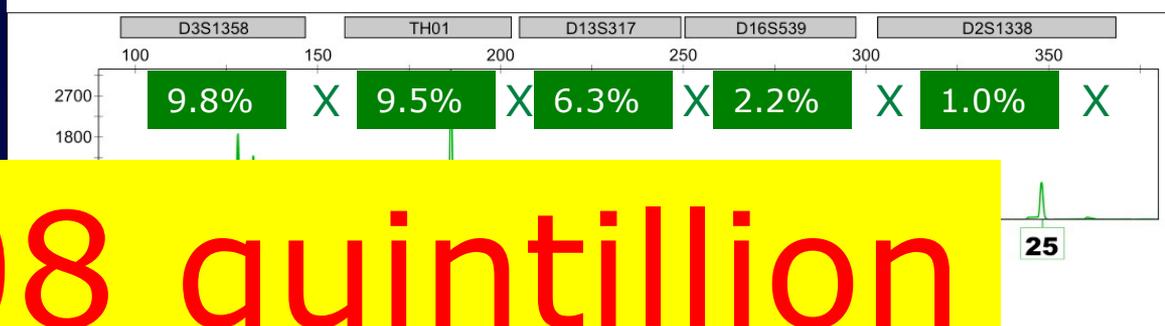
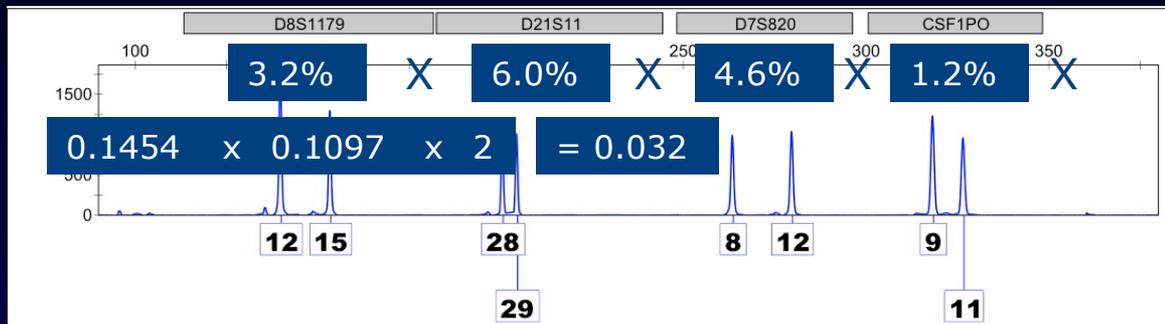
Statistical estimate: Single source sample

D8S1179	Caucasian (N=196)
<9	1.786
9	1.020
10	10.204
11	5.867
12	14.541
13	33.929
14	20.153
15	10.969
16	1.276
17	0.255
18	0.000

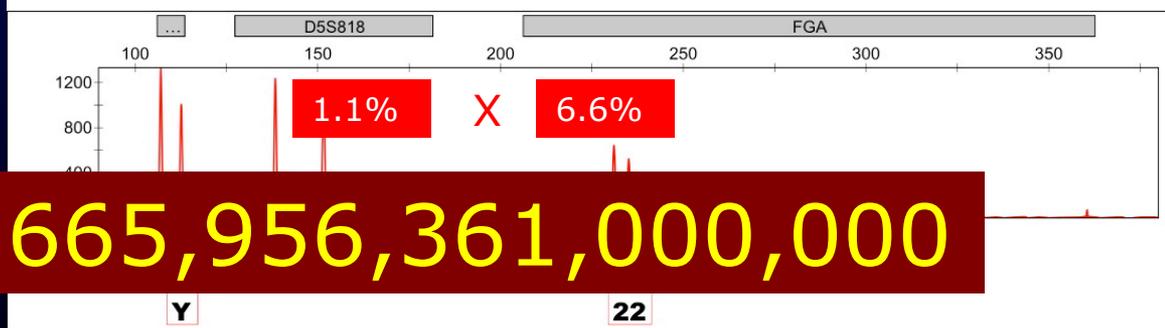
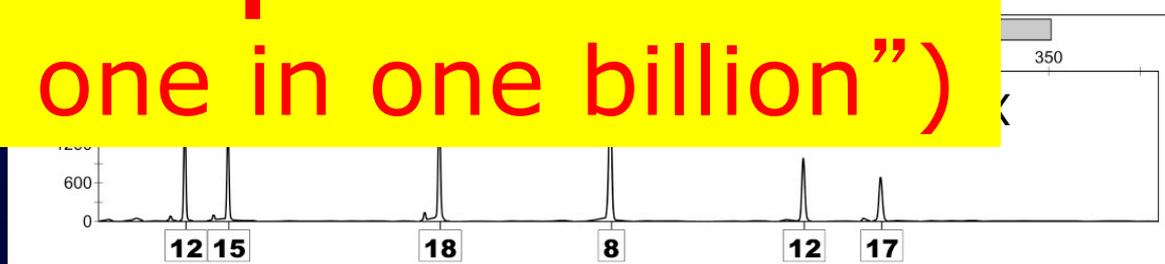


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1 in 608 quintillion
 (“less than one in one billion”)



1 in 608,961,665,956,361,000,000

Are analysts motivated to see single contributors in mixed samples?

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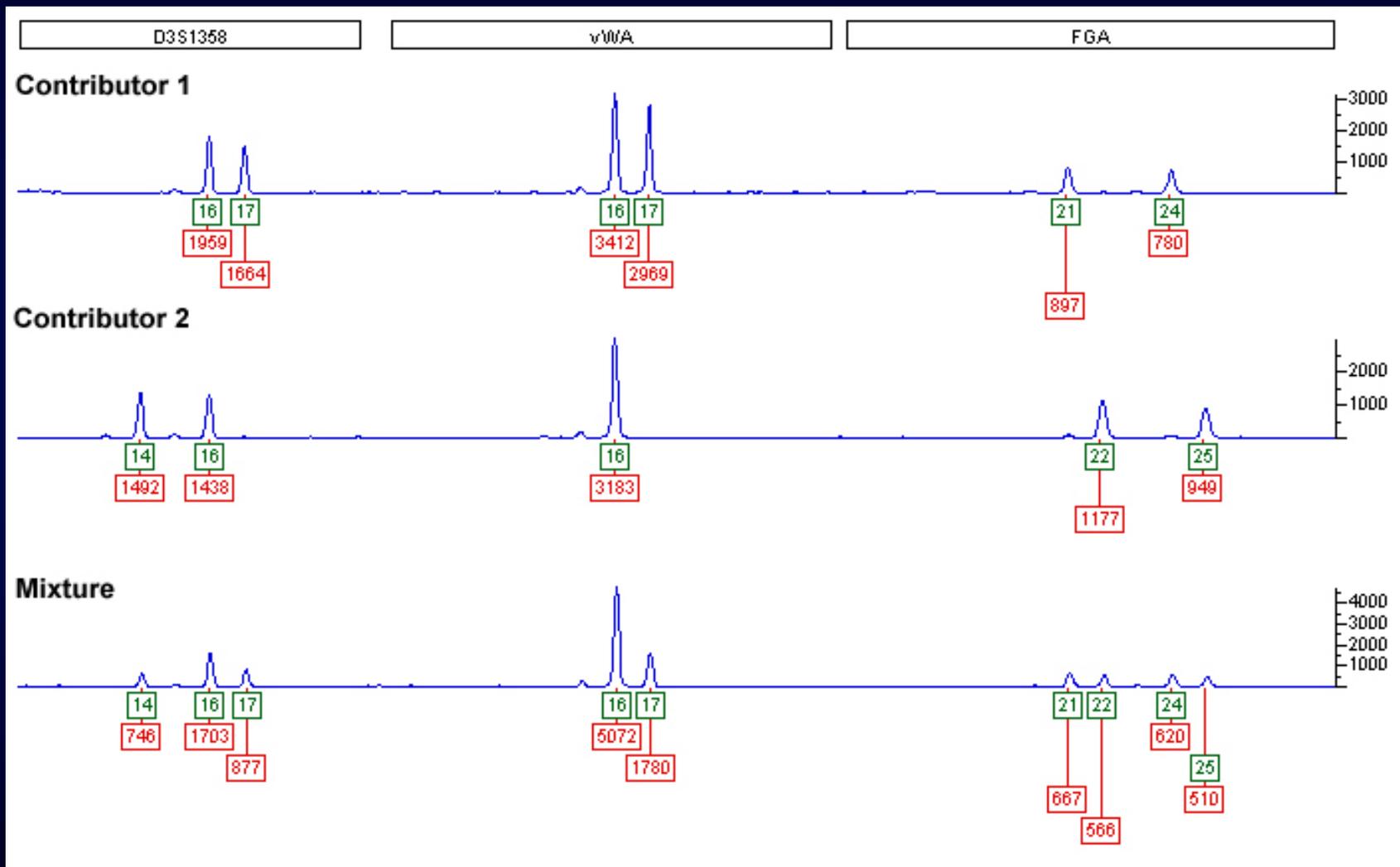
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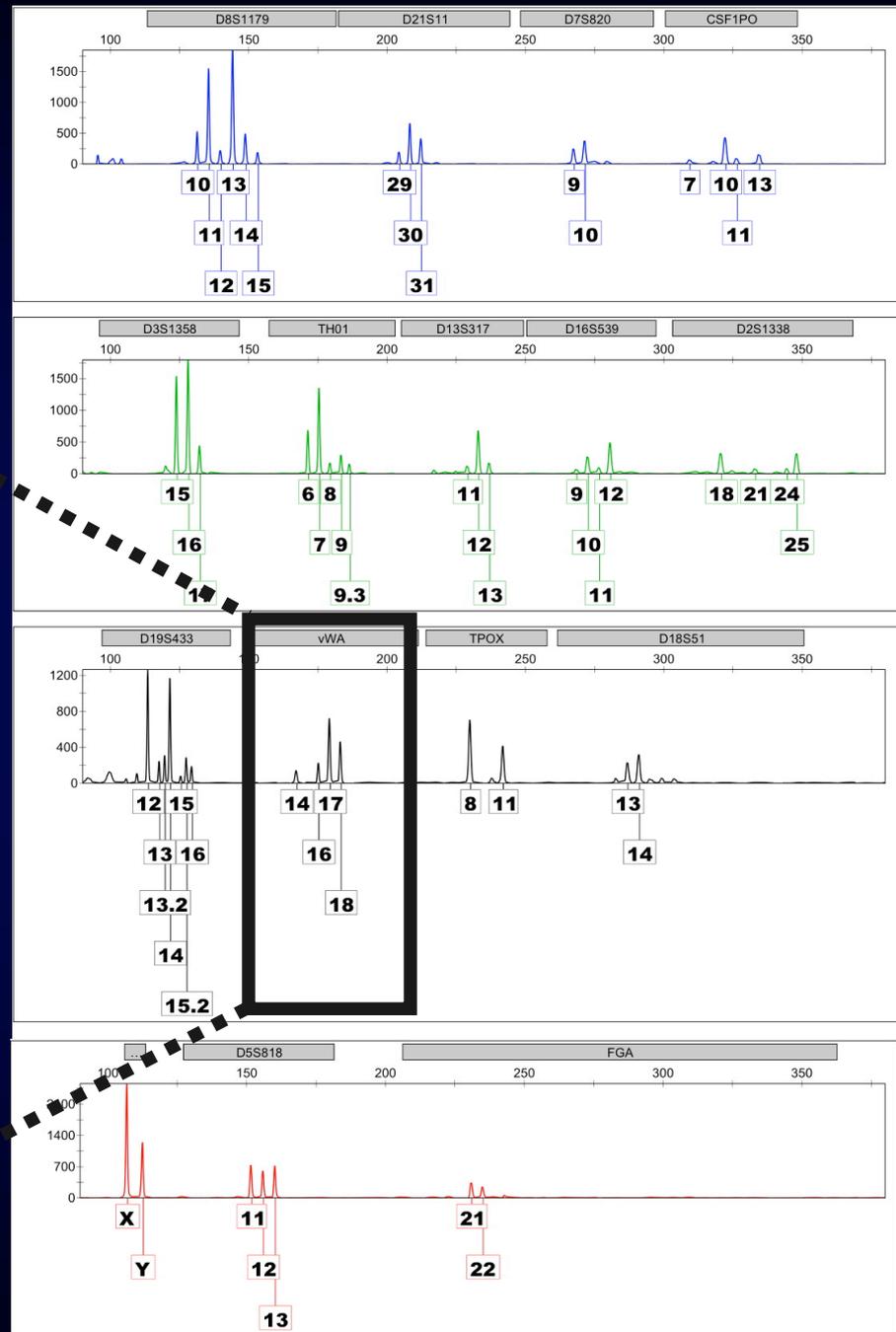
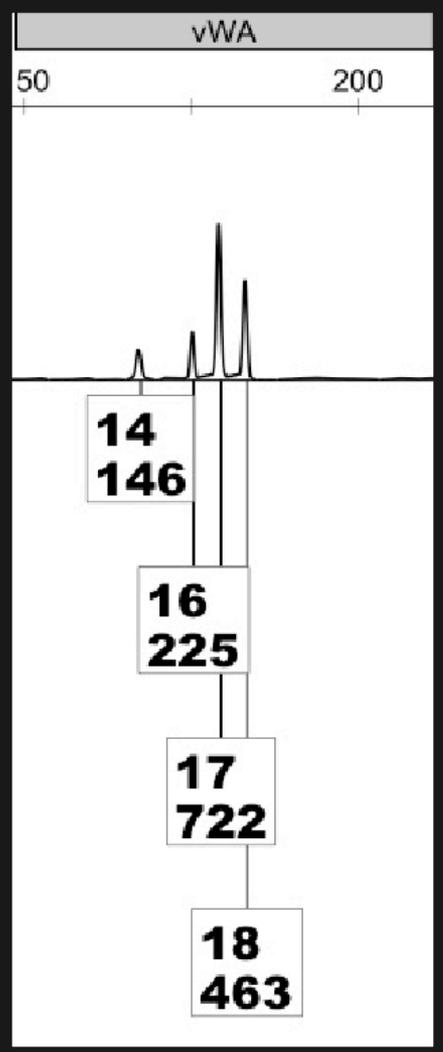
Mixture statistics:

Combined Probability of
Inclusion (CPI)

Mixed DNA samples



CPI statistics



CPI statistics

Combined Probability of Inclusion

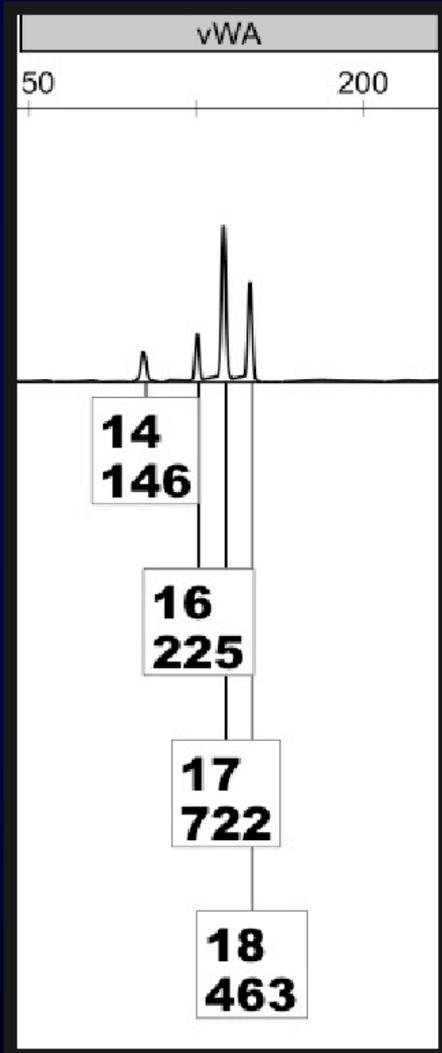
- Probability that a random, unrelated person could be included as a possible contributor to a mixed profile
- For a mixed profile with the alleles 14, 16, 17, 18; contributors could have any of 10 genotypes:

14, 14	14, 16	14, 17	14, 18
	16, 16	16, 17	16, 18
		17, 17	17, 18
			18, 18

Probability works out as:

$$\text{CPI} = (p_{[14]} + p_{[16]} + p_{[17]} + p_{[18]})^2$$

$$(0.102 + 0.202 + 0.263 + 0.222)^2 = 0.621$$



Lies, damned lies and

MO v Cecil McBenge, St. Charles, MO, October, 2014.



<http://stories.frontline.org/dna> (The Surprisingly Imperfect Science of DNA Testing, by Katie Worth)

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- A database match probability calculated by the defense was 1 in 2.5.

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Lies, damned lies and

*R v. Joel Ofori, Central Criminal Court, London,
May, 2015.*



Issachan Nichols, a rapper known as "Nasty" was stabbed to death in 2010 because he was in the wrong post code (E3 vs E14). 17 people were arrested.

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- Joel Ofori was not excluded as a partial, minor contributor to the handle of a knife found in a park.

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- $H_d = 10^{-38.916}$
- $H_p = 10^{-36.328}$

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*US v. Rashawn Smalls, US District Court,
Eastern District of New York, June, 2015.*



http://www.nj.com/hudson/index.ssf/2015/01/jersey_city_man_charged_with_attempting_to_murder.html

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- FST has not been validated (and should not be used) for mixtures of more than three individuals.
- 90% of known four-person mixtures would be mischaracterized as three-person mixtures if the locus with the most alleles was ignored.

Lies, damned lies and

VA vs. Jens Soering, Bedford Cty, Virginia, 1990



<https://www.washingtonpost.com/lifestyle/magazine/>
(In 1985, a gruesome double murder rocked Virginia)

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- Their daughter, Elizabeth, and her boyfriend, Jens Soering, were convicted of the murders in 1990 despite alibis and conflicting evidence.
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- Samples 2FE and 6FE were blood type O, like Soering.
- 2FE and 6FE had the same DNA profile as Derek Haysom – but he was blood type A.

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- “A well-known lawyer, now a judge, once grouped witnesses into three classes: simple liars, damned liars, and experts.”
- “He did not mean that the expert uttered things which he knew to be untrue, but that by the emphasis which he laid on certain statements, and by what has been defined as a highly cultivated faculty of evasion, the effect was actually worse than if he had.”
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