Forensic Statistics

15th International Symposium on Human Identification

Calculation of Mixture Statistics

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TOPICS COVERED

- What Constitutes a DNA Mixture?
- Common Mixture Explanations
- Exclusion Probability
- Likelihood Ratio
- Examples

What Constitutes a DNA Mixture?

- ☛ Presence of three or more alleles at several loci typed

Rationale: No more than two alleles can originate from a single individual (occasional exceptions do exist – e.g., Tri-allelic TPOX profiles in single individuals have been found in several populations).

What Constitutes a DNA Mixture?

- ☛ Imbalance of Alleles detected in the sample

Peak height difference, intensity difference, etc. are caused by differential amount of DNA contributed by different contributors in a sample.

What Constitutes a DNA Mixture?

- ☛ Circumstantial Evidence

  Search for foreign DNA in intimate samples, in many cases, may recover traces of DNA of the person who is technically a “substrate” even if attempts to fractionate the DNA are made during the test… incomplete differential extracts, penile swabs, etc

Common Mixture Interpretations

- **Profiles of two or more tested persons explain all alleles detected in the mixture sample,**

- **Mixture contains unexplained alleles beyond the ones present in the profiles of the known persons profiled,**

    - **Unknown persons contributed to the mixture,**
    - **Contamination**

Common Mixture Interpretations

- **Alleles with low intensity consistently belong to specific (known or unknown) persons profiled (i.e., minor and major contributors in the DNA mixture).**

Mixture Interpretation

Alleles that enter into statistical calculations first meet the interpretation guidelines for data analysis

- RFU Threshold
- Peak ratios/percent stutter
- “Match” criteria

But, before we begin…

Calculations based on mixed profiles fall under the same statistical assumptions that we use in the calculation of single source profile statistics

Assumptions

- ☛ Hardy Weinberg Equilibrium
- ☛ No allele dropout
- ☛ Individuals are unrelated
- ☛ Population substructure is negligible
- ☛ Contributors are of the same race

But also,

unlike conventional frequency reporting…

We have to address specific hypotheses

Two common questions are generally asked:

- How often would a random person be excluded as a contributor to the observed mixture ? (**Exclusion Probability**)
- What statistical support is there for any postulated hypothesis of the origin of the mixture? (**Likelihood**)

Exclusion Probability

Exclusion probability addresses the question:

How often a random person would have been excluded as a contributor in the observed DNA mixture?

Exclusion Probability

- This is a measure of how powerful the DNA testing panel is in excluding noncontributory individuals from the analysis
- The statistic is based on the allelic composition of the mixture…not the profiles of potential contributors

Exclusion Probability

The computation of the **exclusion probability** is done exactly as in the parentage testing

Exclusion Probability

For example:

Suppose that the mixture contains i alleles ($A_1, A_2, \ldots, A_i$ at a locus),

whose frequencies are $p_1, p_2, \ldots, p_i$, respectively)

Exclusion Probability

Individuals whose genotypes contain only one or two of the ¿ alleles cannot be excluded as contributors in this mixture.

To be excluded, the person should have at least one allele in his/her genotype not seen in the mixture.

Exclusion Probability

The probability of **inclusion** is given by

$$(p_1 + p_2 + \ldots + p_i)^2$$

and

Exclusion Probability

The compliment of ***Inclusion Probability*** defines the

Exclusion Probability

$$PE = 1 - (p_1 + p_2 + \ldots + p_i)^2$$

Also

Exclusion Probability

In presence of departure from HWE, PE_ℓ can be computed as

$$PE_\ell = 1 - [p^2 + \theta p(1 - p)]$$

where $p = p_1 + p_2 + \ldots + p_i$, and

θ = the population substructure parameter for adjustment of allelic dependence.

Exclusion Probability

When multiple loci are typed, the combined Probability of Exclusion can be computed as

$$PE_{TOT} = 1 - [(1 - PE_1) \times (1 - PE_2) \times \ldots \times (1 - PE_\ell)]$$

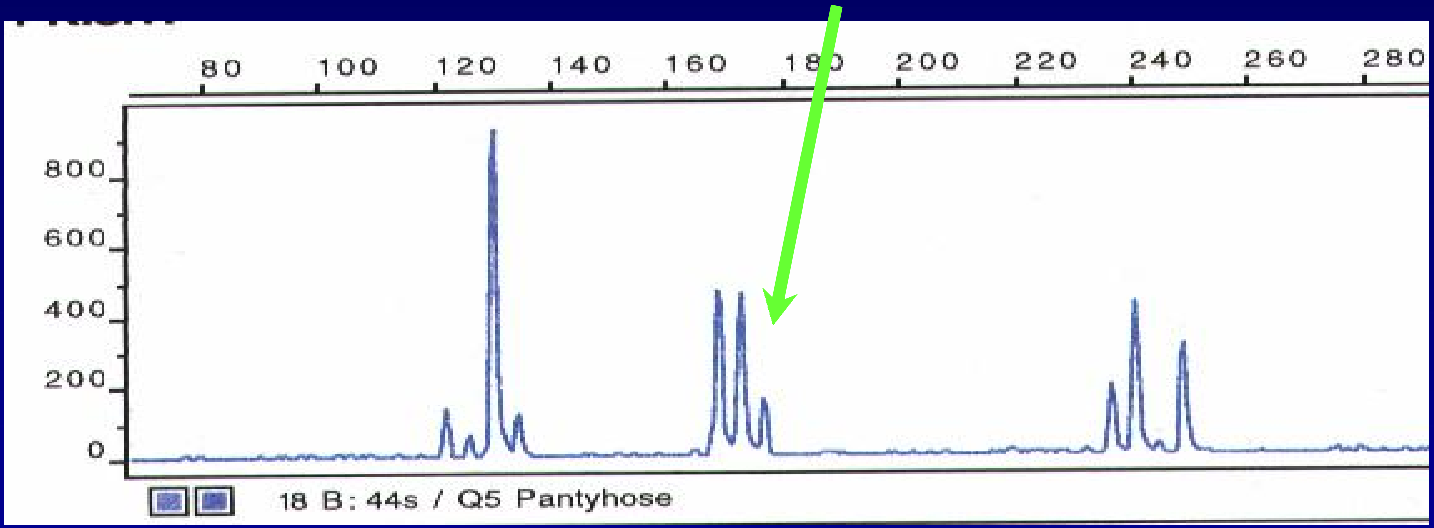
Exclusion Probability

What does this actually tell us???

- Statistical robustness of the testing panel
- Whether the statistical support for any given hypothesis of mixture origin is conservative

How about an example…

A mixture sample shows alleles 7, 8, and 9 at the THO1 locus.



The evidence is from a semen stain found inside the pantyhose of a victim who claimed to have been raped.

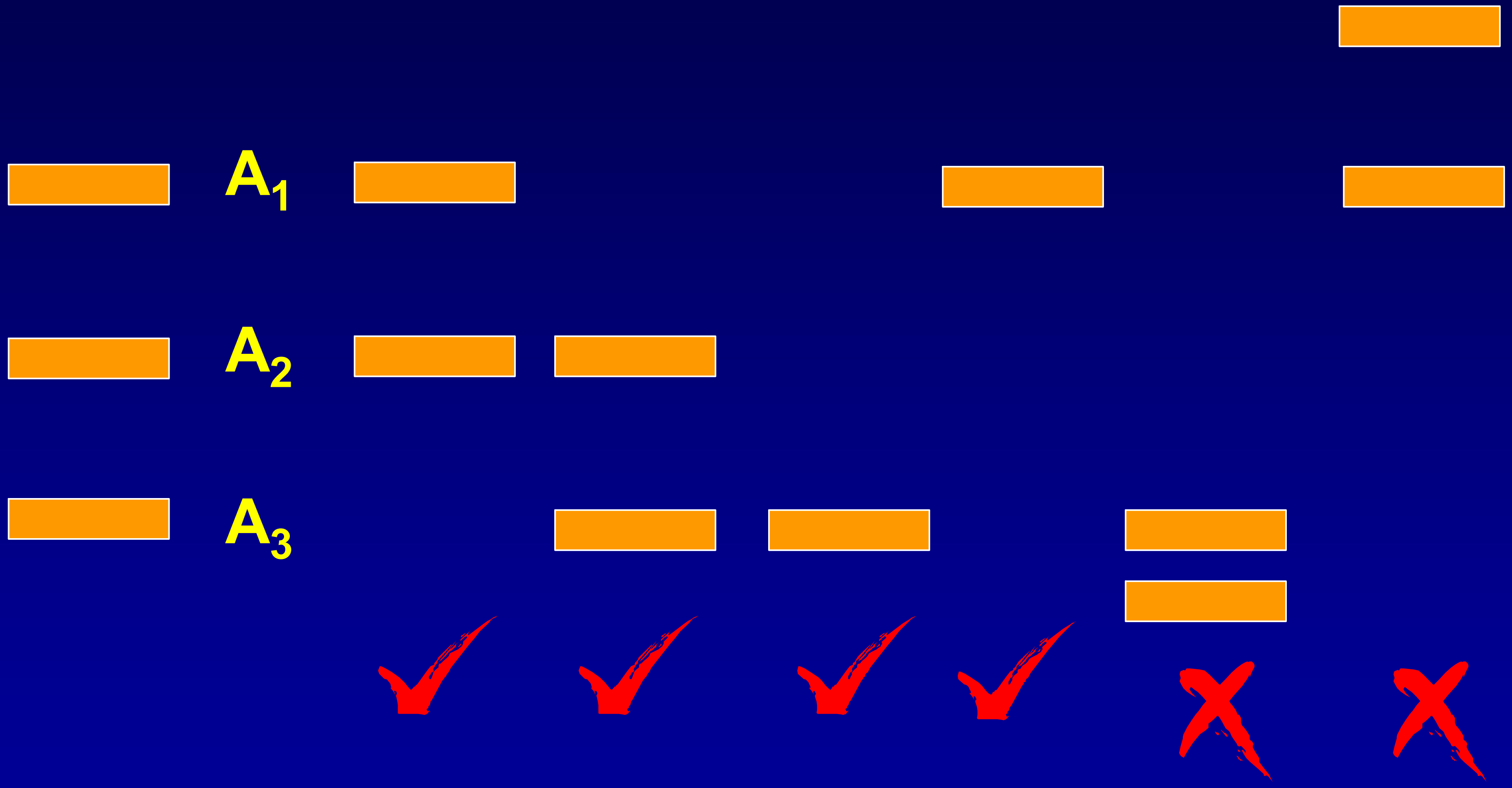
We have the following data:

Mixture Alleles … 7, 8, 9
Victim Alleles … 8, 9
Suspect Alleles … 7, 8

Neither the suspect nor the victim can be excluded as part contributors in the DNA of the mixture

But, who else can?

Evidence



Given that both victim and suspect are of the same race:

frequencies of the alleles are:

$p_7 = 0.1$, $p_8 = 0.2$, and $p_9 = 0.3$

Exclusion Probability would be

$$PE = 1 - (0.1 + 0.2 + 0.3)^2$$
$$= 0.64, \text{ or } 64\%$$

What does this mean???

64% of randomly tested persons would have been excluded as a contributor of the DNA of the mixed sample

WHY??

Says nothing about:

- ☛ Victim or suspect
- ☛ Other potential contributors
- ☛ Ratio of mixture, etc…

What if we couldn't assume H-W?

$$PE_\ell = 1 - [p^2 + \theta p(1 - p)]$$

$$p = p_7 + p_8 + p_9$$

$$p = 0.1 + 0.2 + 0.3$$
$$= 0.6$$

Using a $\theta = 0.01$

$$PE_\ell = 1 - [0.6^2 + 0.01(0.6)(1 - 0.6)]$$
$$= 0.6384$$

What about a $\theta = 0.03$?

$$PE_\ell = 1 - [p^2 + \theta p(1 - p)]$$

$$p = 0.6$$

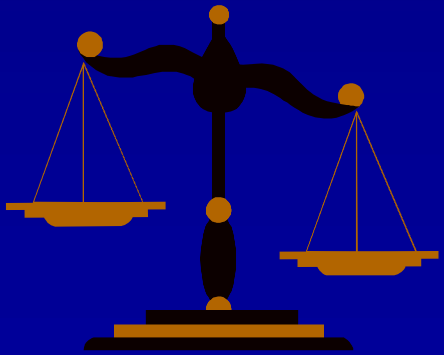
$$PE_\ell = 1 - [0.6^2 + 0.03(0.6)(1 - 0.6)]$$

$$= 0.6328$$

Approximately 1% change in PE

Mixtures and Likelihood Ratios

Likelihood Ratio (LR) is a concept that compares the probabilities of a **given observation** under two mutually exclusive hypotheses.



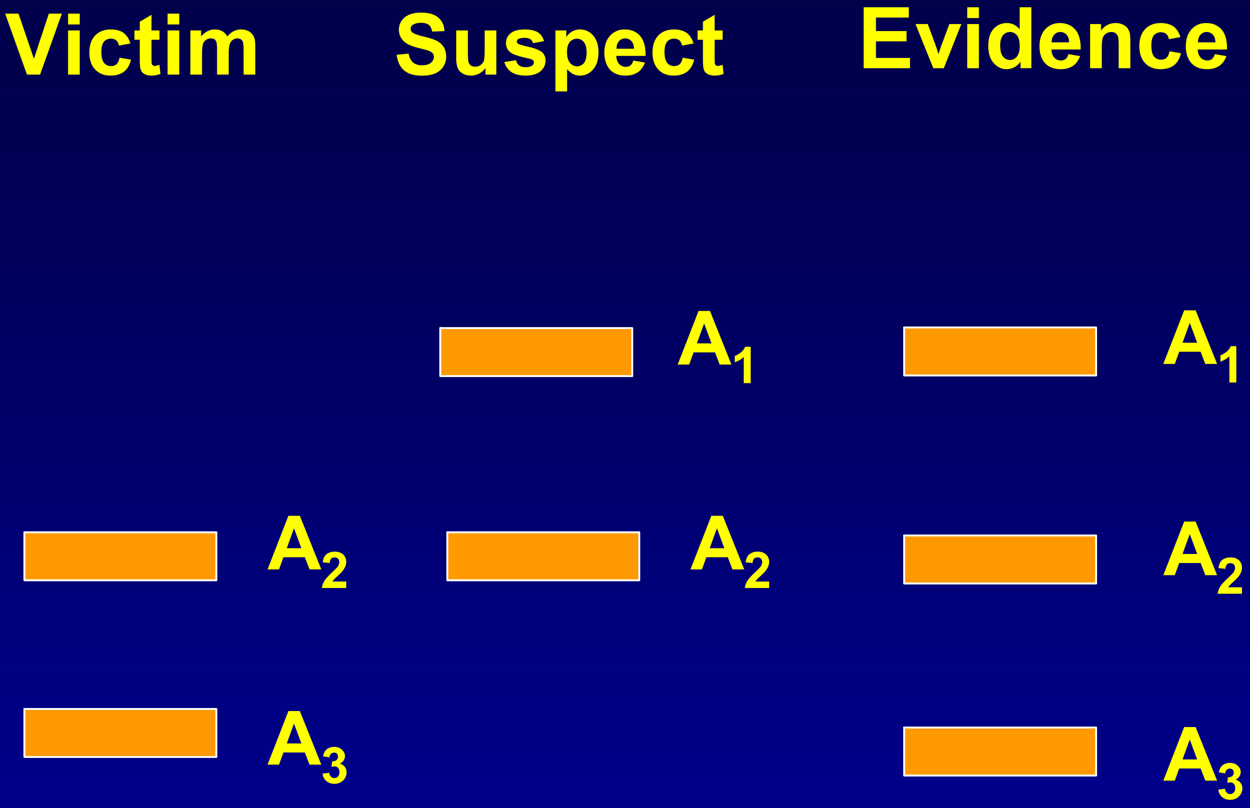
So, now we are including a statement about the circumstances of the case as well as the actual profiles determined for the victim, suspect and evidentiary sample

However, this opens many possibilities… all of which need to be addressed!

Let's use the same example used in the Exclusion Probability calculation for our LR interpretation of a DNA mixture

We have the following data:

Mixture Alleles … 7, 8, 9
Victim Alleles … 8, 9
Suspect Alleles … 7, 8



Victim	Suspect	Evidence
	A_1	A_1
A_2	A_2	A_2
A_3		A_3

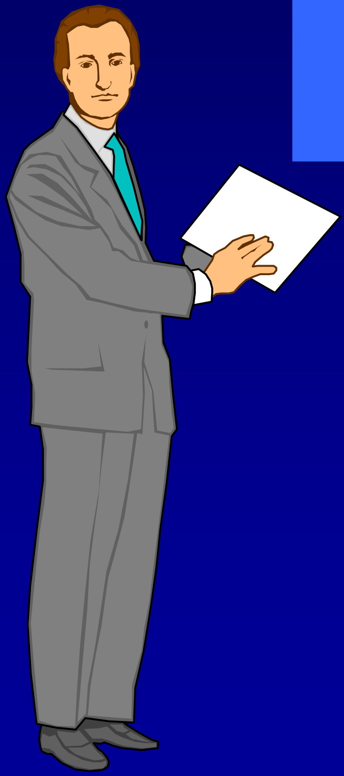
Three Allele Scenario

Three Alleles

Victim is heterozygote - A_2A_3

Suspect is heterozygote- A_1A_2

Mutually Exclusive Hypotheses



Prosecution

DNA is from victim
and suspect

Defense

DNA is from victim
and unknown person

The prosecution may postulate that the victim and the suspect together explain all alleles seen in the mixture.

H_0: The mixture originated from the epithelial cells of the victim and the semen of the suspect

Under this hypothesis,

the only possible mixture profile is 7,8,9

and thus the mixture observation is explained with a probability of **100%.**

BUT…

The defense might argue that the following two alternative hypotheses should also be entertained:

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H_1: The mixture originated from the victim and an unknown person,

The defense might argue that the following two alternative hypotheses should also be entertained:

H_1: The mixture originated from the victim and an unknown person,

and

H_2: The mixture originated from two unknown persons

Let's tackle the first scenario:

So, the Likelihood according to the prosecution's hypothesis (H_0) is **1**

We need to calculate the likelihood according to the defense hypothesis 1…

Since the victim has the profile (8,9), the unknown person can have three possible genotypes:

(7,7), (7,8), or (7,9),

which would explain all alleles in the mixture, in combination with the victim.

Using our allele frequencies from before:

$p_7 = 0.1$, $p_8 = 0.2$, and $p_9 = 0.3$

the probability of observing the mixture profile under the defense hypothesis H_1 is:

$$L_1 = (0.1 \times 0.1) + (2 \times 0.1 \times 0.2) + (2 \times 0.1 \times 0.3) = 0.11$$

Now here is where the “RATIO” in Likelihood Ratio comes into play…

$$LR = H_0/H_1$$

$$1/\ p_1^2 + 2p_1\,p_2 + 2p_1\,p_3$$

$$1.0/0.11 = 9.09$$

So,

Compared with the prosecution's hypothesis (H_0), the defense scenario (H_1) is

9-times **less** well-supported!

Defense hypothesis 2 is a little more involved:

(but then how would YOU explain the victim not being in ***her*** pantyhose!)

Under the hypothesis H_2 all possible genotype combinations will have to be enumerated

Ind 2	Individual 1					
	(7,7)	(7,8)	(7,9)	(8,8)	(8,9)	(9,9)
(7,7)					.0012	
(7,8)			.0024		.0048	.0036
(7,9)		.0024		.0024	.0072	
(8,8)			.0024			
(8,9)	.0012	.0048	.0072			
(9,9)		.0036				

How do we get these probabilities?

Each is the probability of getting Genotype A **and** Genotype B

First individual = (7,7)
Second individual = (8,9)
$= (0.1 \times 0.1) \times (2 \times .2 \times .3)$
$= 0.01 \times 0.12$
= **0.0012**

Ind 2	Individual 1					
	(7,7)	(7,8)	(7,9)	(8,8)	(8,9)	(9,9)
(7,7)					.0012	
(7,8)			.0024		.0048	.0036
(7,9)		.0024		.0024	.0072	
(8,8)			.0024			
(8,9)	.0012	.0048	.0072			
(9,9)		.0036				

Of course…we could incorporate θ here as well:

For homozygotes: $p^2 + p(1 - p)\theta$

with θ = 0.01

First individual = (7,7)
Second individual = (8,9)
$= (0.1^2 + 0.1(1 - 0.1)0.01) \times (2 \times .2 \times .3)$
$= 0.0109 \times 0.12$
= **0.0013**

or

Of course…we could incorporate θ here as well:

For homozygotes: $p^2 + p(1 - p)\theta$

with θ = 0.03

First individual = (7,7)
Second individual = (8,9)
$= (0.1^2 + 0.1(1 - 0.1)0.03) \times (2 \times .2 \times .3)$
$= 0.0127 \times 0.12$
= **0.0015**

Big deal!

What next…

The total probability that two unrelated persons explain the mixture alleles (7,8,9) = Sum of probabilities in the enumerated cells :

Σp = 0.0012 + 0.0024 + … + 0.0036

= **0.0432**

So,

The Defense Hypothesis 2 is:

Approximately **23** times **less** well supported than the Prosecution's Hypothesis

HOW TO EXPRESS THE NUMBERS FROM LIKELIHOOD RATIO COMPUTATIONS

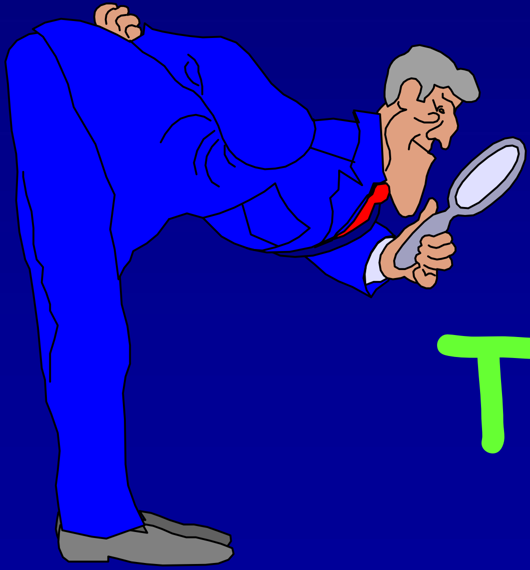
- When making statements on the statistical inferences remember that you are expressing **only the genetic data**
- You are not dealing with issues of **“chance”**
- To do so would involve Bayesian inferences which include Prior Probabilities…for which genetic data offers little assistance.

So, with regard to Defense Hypothesis 1 we could say:

The observed mixture profile is 9-times more likely to occur under the scenario that it is a mixture of DNA from the victim and suspect, as opposed to the scenario that it originated from a mixture of DNA of the victim and an unrelated unknown person.

Conservative

Basic



True!

What this doesn't mean:

With a chance of 1 in 9, an unknown person could have contributed DNA in this mixture

Wrong!!!

Or

The probability (chance) that the suspect contributed DNA to this mixture is 1 in 9.

Wrong Again !!!

And with regard to Defense Hypothesis 2 we could say:

The observed mixture profile is 23-times more likely to occur under the scenario that it is a mixture of DNA from the victim and suspect, as opposed to the scenario that it originated from a mixture of DNA from two unrelated, unknown persons.

Assumptions In Likelihood Computations

Unknown persons are assumed to be unrelated in scenarios, as well as unrelated to the known persons whose contributions are proposed in the mixture.

Assumptions In Likelihood Computations

The different hypotheses of the origin of the mixture assume prescribed number of contributors in the mixture.

Add other potential contributors and you add to the total potential genotypes to be considered

Assumptions In Likelihood Computations

All individuals contributing alleles in the mixture are assumed to be of the same population-origin, so that the same allele frequencies remain applicable to all of them.

Assumptions In Likelihood Computations

The population is assumed to be at H-WE, so that genotype frequencies of one or more persons could be computed by the product rule.

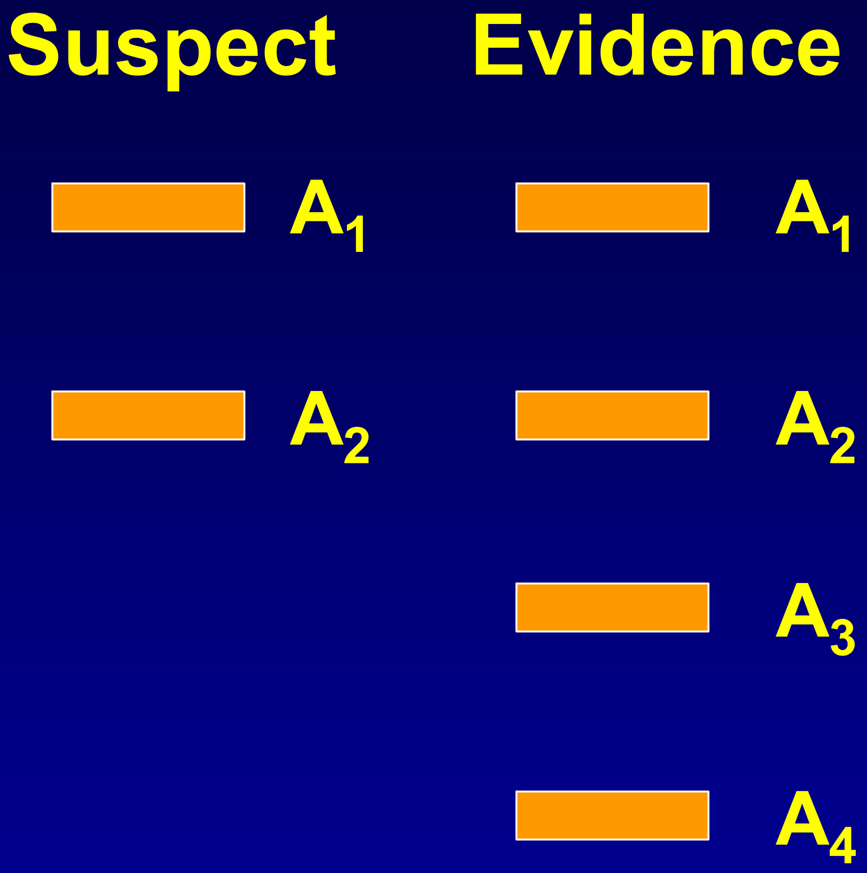
Potential subdivision can be addressed by incorporating appropriate θ values

Lets look at a different scenario

Often you may have evidence that presents a mixture and a suspected contributor…

The question would be:

What is the likelihood of the suspect being a contributor to the evidentiary pattern?



Suspect	Evidence
A_1	A_1
A_2	A_2
	A_3
	A_4

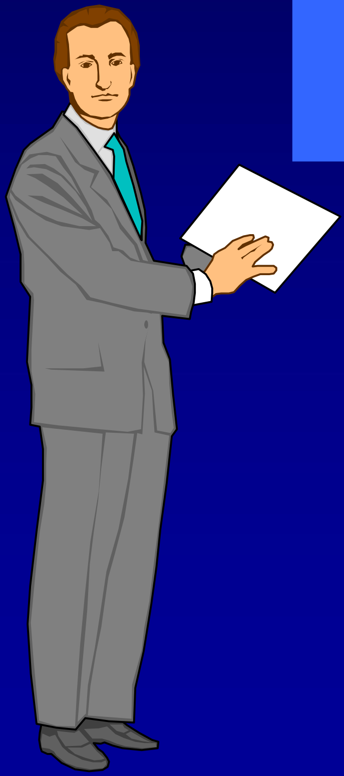
Four Allele Scenario

Two alleles match the suspect - A_1 & A_2

Two alleles match the unknown - A_3 & A_4

Assuming there is only one unknown contributor

Mutually Exclusive Hypotheses



Prosecution

DNA is from suspect and unknown

Defense

DNA is from two unknown persons

The prosecution may postulate that the suspect and and an unknown explain all alleles seen in the mixture.

H_0: The mixture originated from the suspect and an unknown individual

Under this hypothesis,

The components of the mixture are explained with a probability of

$$1 \times 2p_3p_4$$

Probability of the suspect's contribution

Probability of the unknown's contribution

The defense might argue that the following hypothesis should be entertained:

H_1: The mixture originated from two unknown persons

With 4 alleles and 2 contributors the following possible scenarios exist:

Unk 1	**Unk 2**	
A_1A_2	A_3A_4	$2p_1\,p_2 \times 2p_3\,p_4$
A_1A_3	A_2A_4	$2p_1\,p_3 \times 2p_2\,p_4$
A_1A_4	A_2A_3	$2p_1\,p_4 \times 2p_2\,p_3$
A_2A_3	A_1A_4	$2p_2\,p_3 \times 2p_1\,p_4$
A_2A_4	A_1A_3	$2p_2\,p_4 \times 2p_1\,p_3$
A_3A_4	A_1A_2	$2p_3\,p_4 \times 2p_1\,p_2$

$$24p_1\,p_2\,p_3\,p_4$$

The resulting likelihood ratio is:

$$\frac{2p_3p_4}{24p_1\,p_2\,p_3\,p_4}$$

$$\frac{1}{12p_1\,p_2}$$

So, lets throw some numbers at it…

If $p_1 = 0.15$ & $p_2 = 0.2$

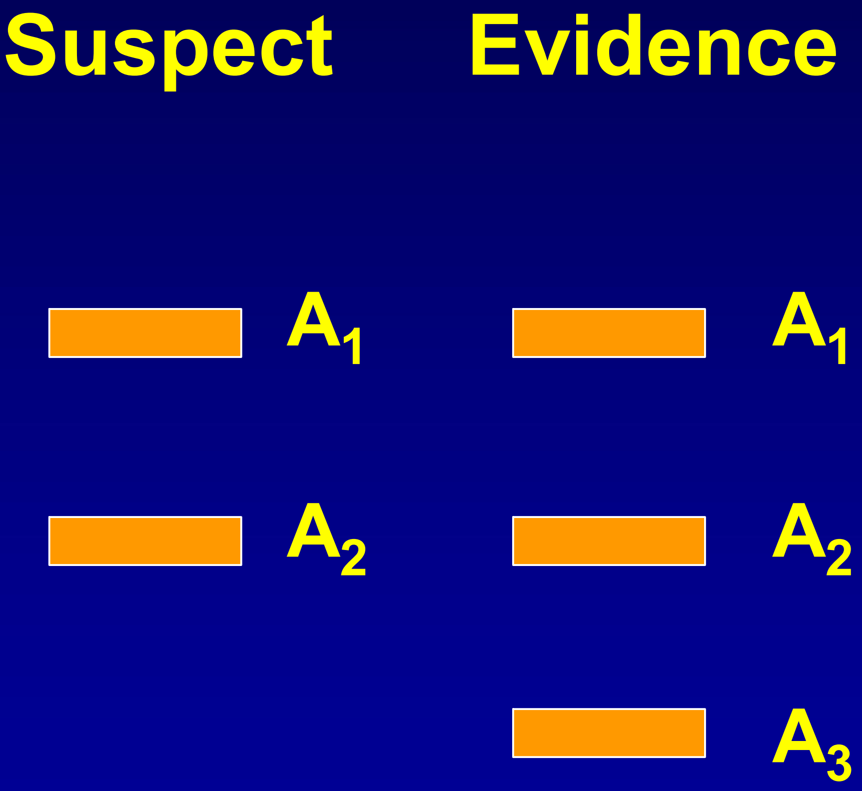
$$\frac{1}{12 p_1 p_2} = \frac{1}{12(0.15)(0.2)}$$

$$\approx 3$$

So, with regard to Defense Hypothesis 1 we could say:

The observed mixture profile is approximately **3-times** more likely to occur under the scenario that it is a mixture of DNA from the suspect and an unknown, as opposed to the scenario that it originated from a mixture of DNA of two unrelated unknown persons.

Now lets really have fun!!



Three Allele Scenario

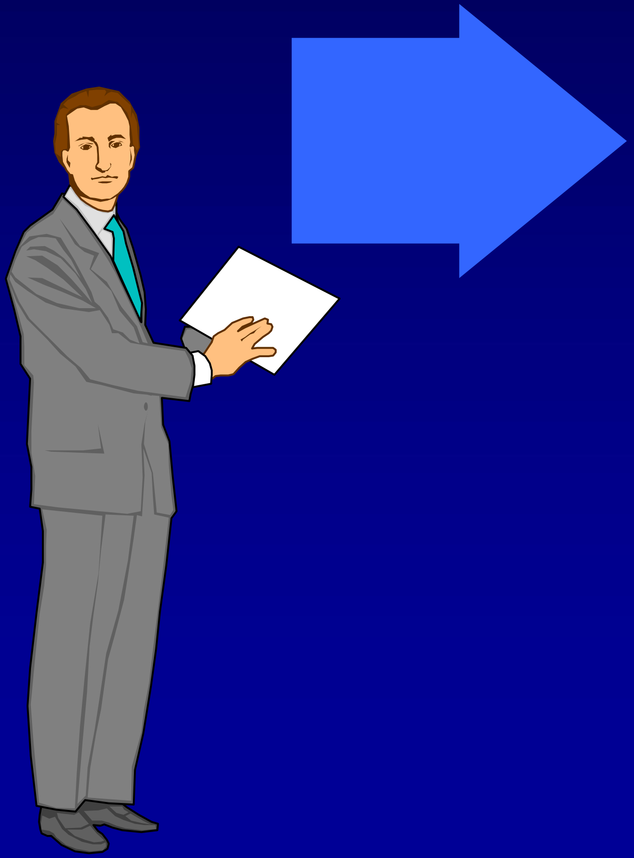
Same question as before but…

Three Alleles

Two match the suspect - A_1A_2

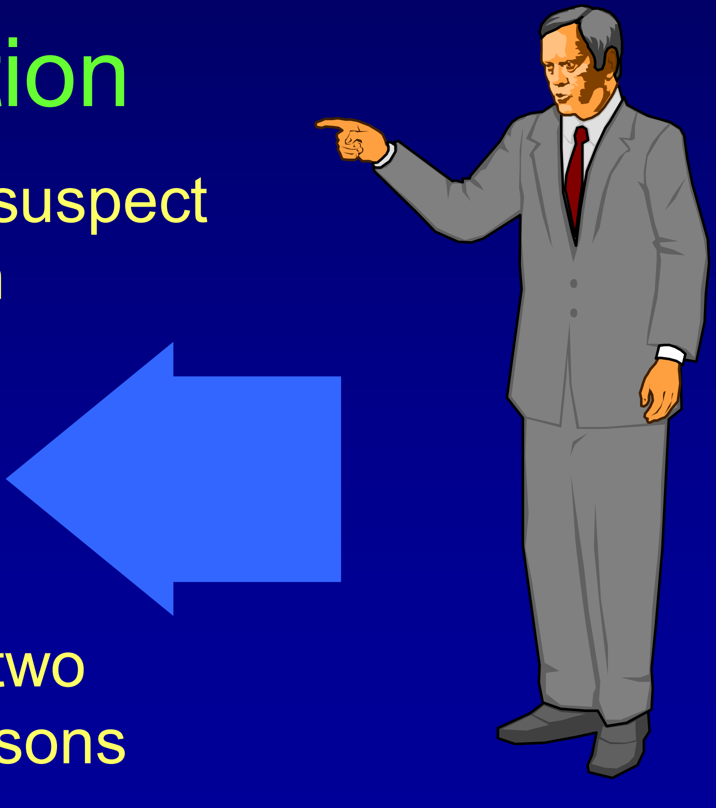
The unknown contributes- at least A_3

Mutually Exclusive Hypotheses



Prosecution

DNA is from suspect and unknown



Defense

DNA is from two unknown persons

Under the Prosecution's hypothesis,

The components of the mixture are explained with a probability of

$$1 \times \overset{A_3A_3}{p_3^2} + \overset{A_1A_3}{2p_1 p_3} + \overset{A_2A_3}{2p_2 p_3}$$

Probability of the suspect's contribution

Probability of the unknown's contribution

Now, the Defense scenario becomes interesting…

Since we don't know if the "unknown" is homozygous or heterozygous…we must cover all bases!

Let's see how this pans out…

Unk 1	Unk 2	
A_1A_2	A_1A_3	$2p_1 p_2 \times 2p_1 p_3$
A_1A_2	A_2A_3	$2p_1 p_2 \times 2p_2 p_3$
A_1A_2	A_3A_3	$2p_1 p_2 \times p_3^2$
A_1A_3	A_1A_2	$2p_1 p_3 \times 2p_1 p_2$
A_1A_3	A_2A_3	$2p_1 p_3 \times 2p_2 p_3$
A_1A_3	A_2A_2	$2p_1 p_3 \times p_2^2$
A_2A_3	A_1A_2	$2p_2 p_3 \times 2p_1 p_2$
A_2A_3	A_1A_3	$2p_2 p_3 \times 2p_1 p_3$
A_2A_3	A_1A_1	$2p_2 p_3 \times p_1^2$

Not done yet!

A_1A_1 A_2A_3 p_3^2 x $2p_2p_3$
A_2A_2 A_1A_3 p_2^2 x $2p_1p_3$
A_3A_3 A_1A_2 p_3^2 x $2p_1p_2$

$$12p_1p_2p_3\,(p_1 + p_2 + p_3)$$

Did you forget anything????

The Likelihood Ratio becomes:

$$\frac{p_3^2 + 2p_1 p_3 + 2p_2 p_3}{12p_1p_2p_3 (p_1 + p_2 + p_3)}$$

or

$$\frac{p_3 + 2p_1 + 2p_2}{12p_1p_2 (p_1 + p_2 + p_3)}$$

So, want to throw some numbers at this…just for a taste?

Using our allele frequencies from before:

Let

$p_1 = 0.1$, $p_2 = 0.2$, and $p_3 = 0.3$

$p_1 = 0.1$, $p_2 = 0.2$, and $p_3 = 0.3$

$$LR = \frac{p_3 + 2p_1 + 2p_2}{12p_1p_2(p_1 + p_2 + p_3)}$$

$$= \frac{0.9}{0.144} = 6.25$$

So,

Compared with the prosecution's hypothesis (H_0), the defense scenario (H_1) is

6-times **less** well-supported!

So, with regard to Defense Hypothesis 1 we could say:

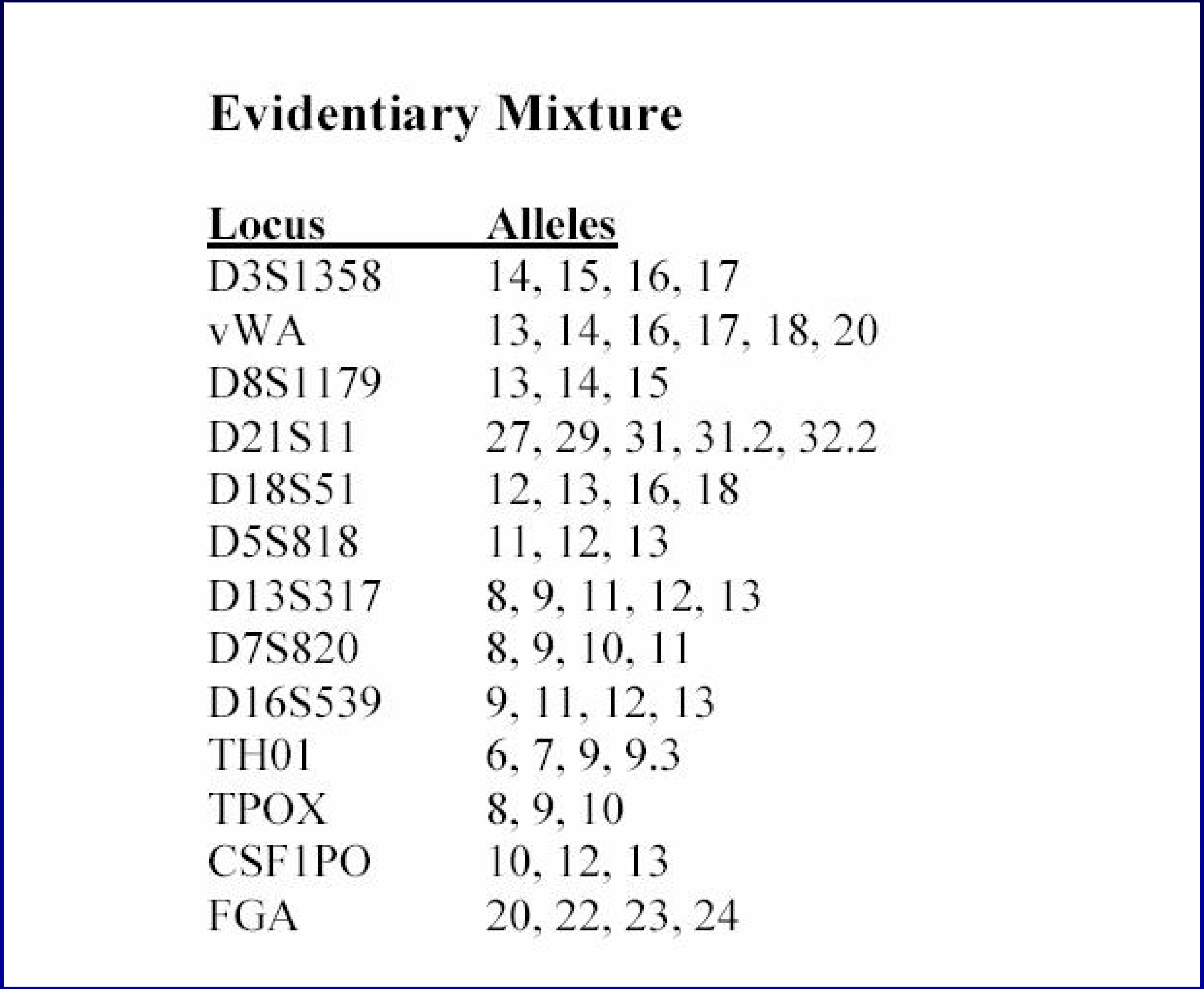
The observed mixture profile is approximately **6-times** more likely to occur under the scenario that it is a mixture of DNA from the suspect and an unknown, as opposed to the scenario that it originated from a mixture of DNA of two unrelated unknown persons.

Now…Let's have some real fun!

Scenario:

Sexual assault case where a mixture was observed on the vaginal swab.

Our data:

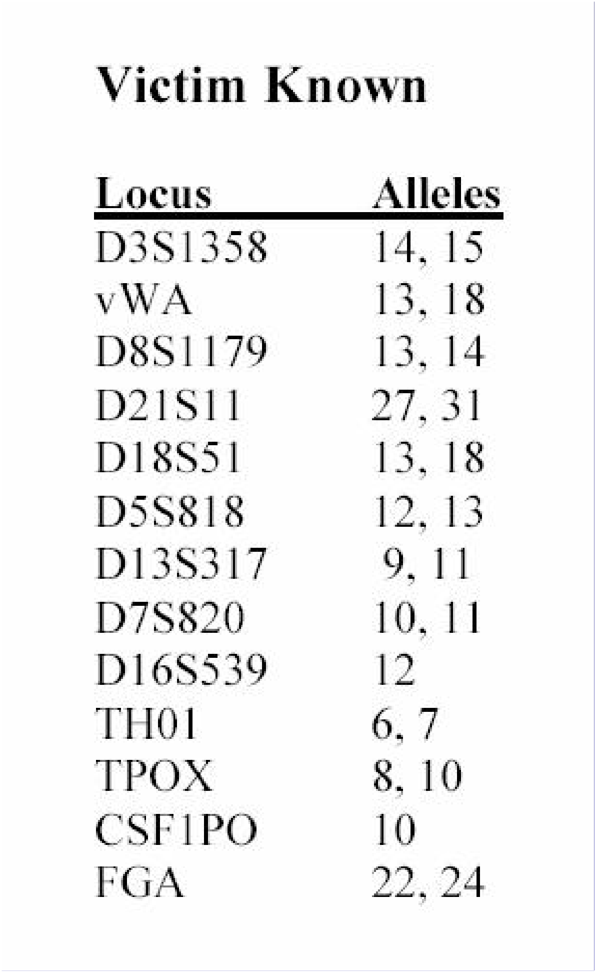


Evidentiary Mixture

Locus	Alleles
D3S1358	14, 15, 16, 17
vWA	13, 14, 16, 17, 18, 20
D8S1179	13, 14, 15
D21S11	27, 29, 31, 31.2, 32.2
D18S51	12, 13, 16, 18
D5S818	11, 12, 13
D13S317	8, 9, 11, 12, 13
D7S820	8, 9, 10, 11
D16S539	9, 11, 12, 13
TH01	6, 7, 9, 9.3
TPOX	8, 9, 10
CSF1PO	10, 12, 13
FGA	20, 22, 23, 24

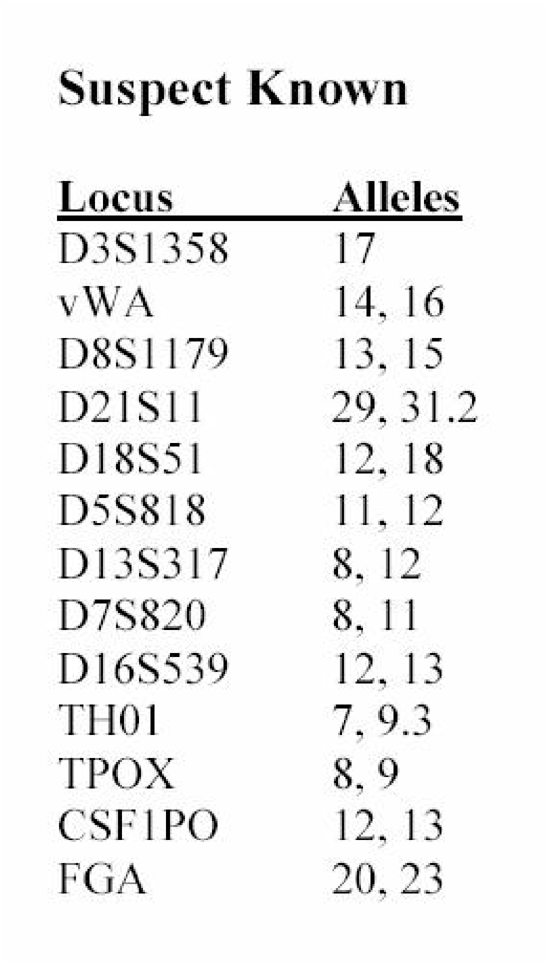
What would you suggest about this mixture??

Our Knowns:



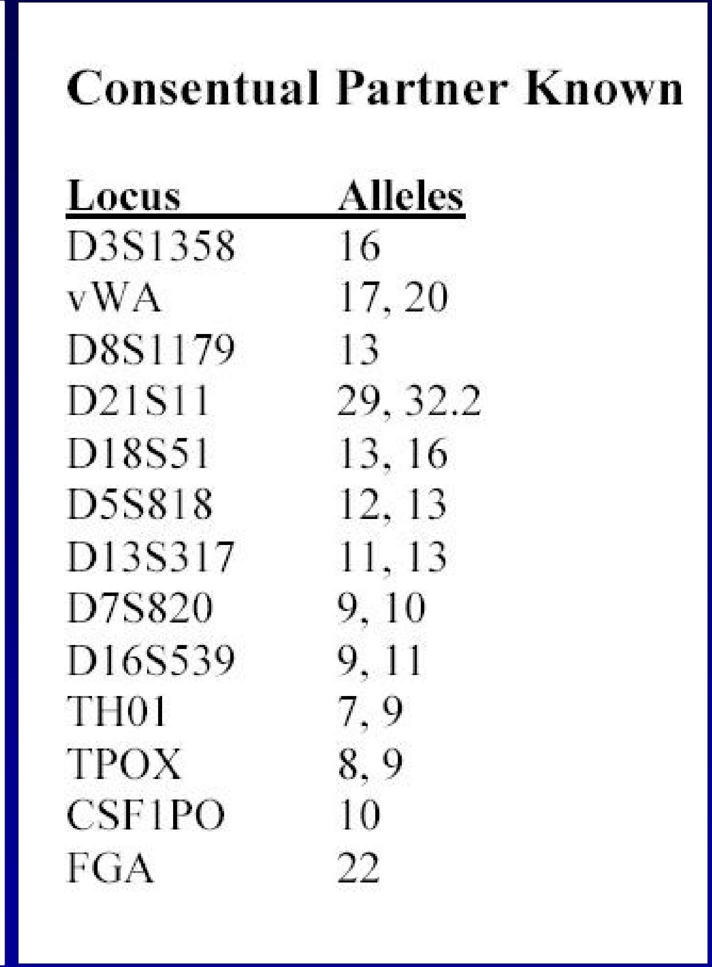
Victim Known

Locus	Alleles
D3S1358	14, 15
vWA	13, 18
D8S1179	13, 14
D21S11	27, 31
D18S51	13, 18
D5S818	12, 13
D13S317	9, 11
D7S820	10, 11
D16S539	12
TH01	6, 7
TPOX	8, 10
CSF1PO	10
FGA	22, 24



Suspect Known

Locus	Alleles
D3S1358	17
vWA	14, 16
D8S1179	13, 15
D21S11	29, 31.2
D18S51	12, 18
D5S818	11, 12
D13S317	8, 12
D7S820	8, 11
D16S539	12, 13
TH01	7, 9.3
TPOX	8, 9
CSF1PO	12, 13
FGA	20, 23

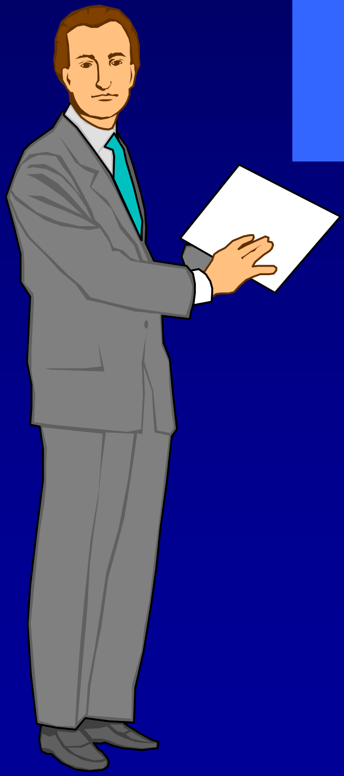


Consentual Partner Known

Locus	Alleles
D3S1358	16
vWA	17, 20
D8S1179	13
D21S11	29, 32.2
D18S51	13, 16
D5S818	12, 13
D13S317	11, 13
D7S820	9, 10
D16S539	9, 11
TH01	7, 9
TPOX	8, 9
CSF1PO	10
FGA	22

Let's see how this scenario effects the statistics

Mutually Exclusive Hypotheses



Prosecution

DNA is from victim, her partner and the suspect

Defense

DNA is from victim, her partner and an unknown person

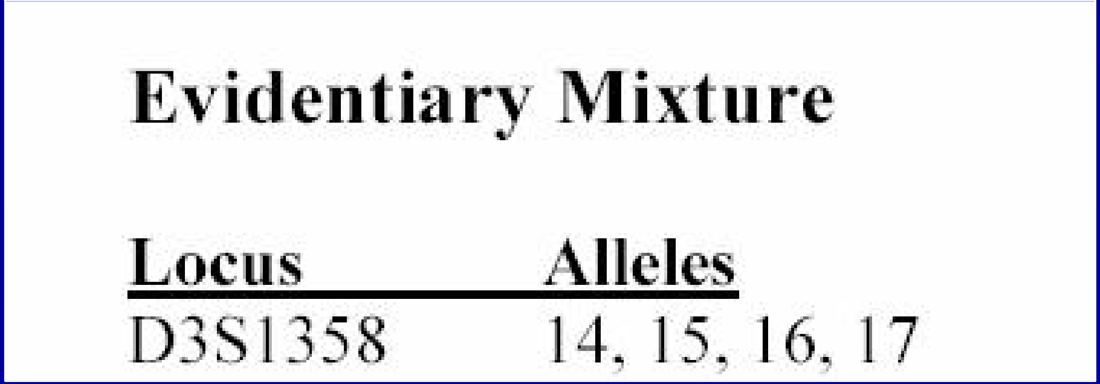
H_o= The results are explained by a mixture of DNA derived from the victim, a consentual partner, and the suspect

H_{a1}= The results are explained by a mixture of DNA derived from the victim, a consentual partner, and an unknown individual

So, in this case, the numerator will be 1

It's the denominator values that you need to think about!

Lets look at a few examples:



Evidentiary Mixture

Locus	Alleles
D3S1358	14, 15, 16, 17

D3

Mixture	Victim	Partner	Unknown
14,15,16,17	14,15	16,16	17

Perpetrator could be:

17,17
14,17
15,17
16,17

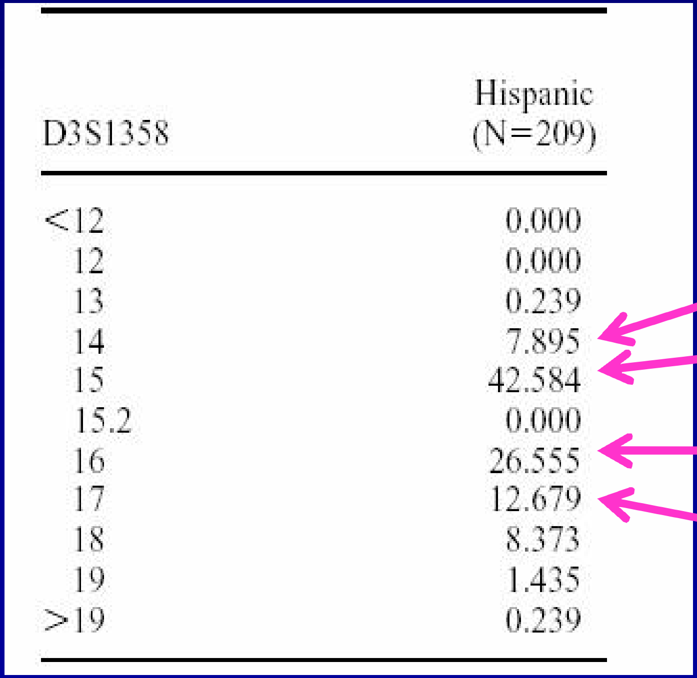
As long as the hypothesis is based on 3 contributors!

Suspect genotype

At this locus the denominator would be:

$$(17)^2 + 2(14)(17) + 2(15)(17) + 2(16)(17)$$

If we used SW Hispanic allele frequencies:



D3S1358	Hispanic (N=209)
<12	0.000
12	0.000
13	0.239
14	7.895
15	42.584
15.2	0.000
16	26.555
17	12.679
18	8.373
19	1.435
>19	0.239

14 = 0.07895

15 = 0.42584

16 = 0.26555

17 = 0.12679

At this locus the denominator would be:

$$(17)^2 + 2(14)(17) + 2(15)(17) + 2(16)(17)$$

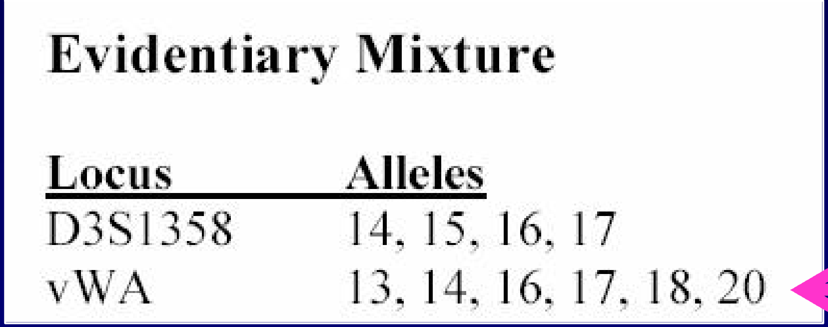
$$(0.12679)^2 + 2(0.07895)(0.12679) + 2(0.42584)(0.12679) + 2(0.26555)(0.12679)$$

$$= 0.21142$$

$$LR = \frac{1}{0.21142} = 4.729$$

The observed mixture profile is approximately **4.5 times** more likely to occur under the scenario that it is a mixture of DNA from the victim, her partner, and the suspect, as opposed to the scenario that it originated from a mixture of DNA from the victim, her partner, and an unrelated, unknown person.

What about this one?



Evidentiary Mixture

Locus	Alleles
D3S1358	14, 15, 16, 17
vWA	13, 14, 16, 17, 18, 20

vWA

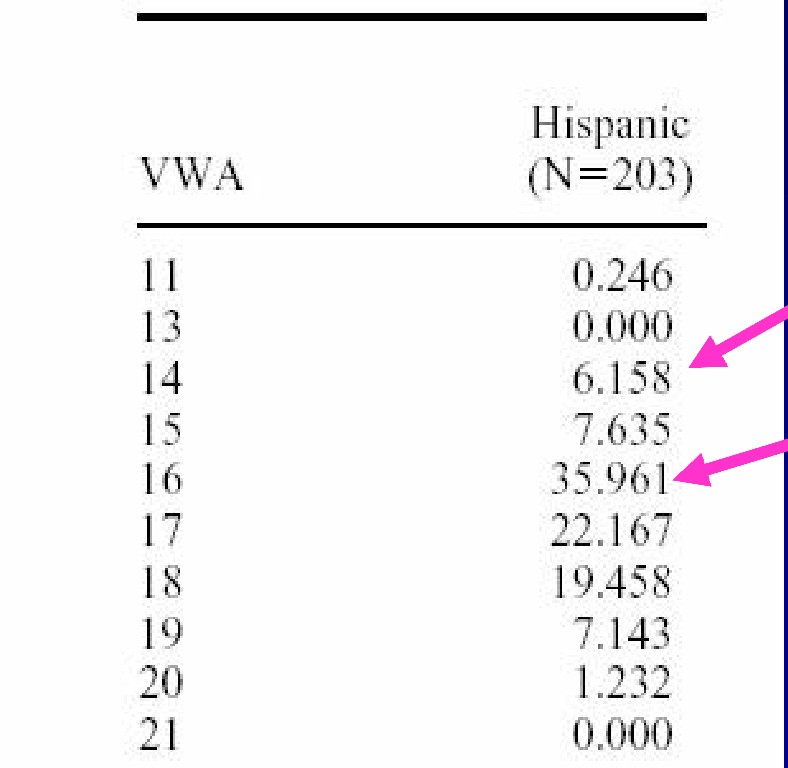
Mixture	Victim	Partner	Unknown
13,14,16,17, 18,20	13,18	17,20	14,16

Perpetrator could be:

At this locus the denominator would be:

2(14)(16)

If we used SW Hispanic allele frequencies:



VWA	Hispanic (N=203)
11	0.246
13	0.000
14	6.158
15	7.635
16	35.961
17	22.167
18	19.458
19	7.143
20	1.232
21	0.000

14 = 0.06158

16 = 0.35961

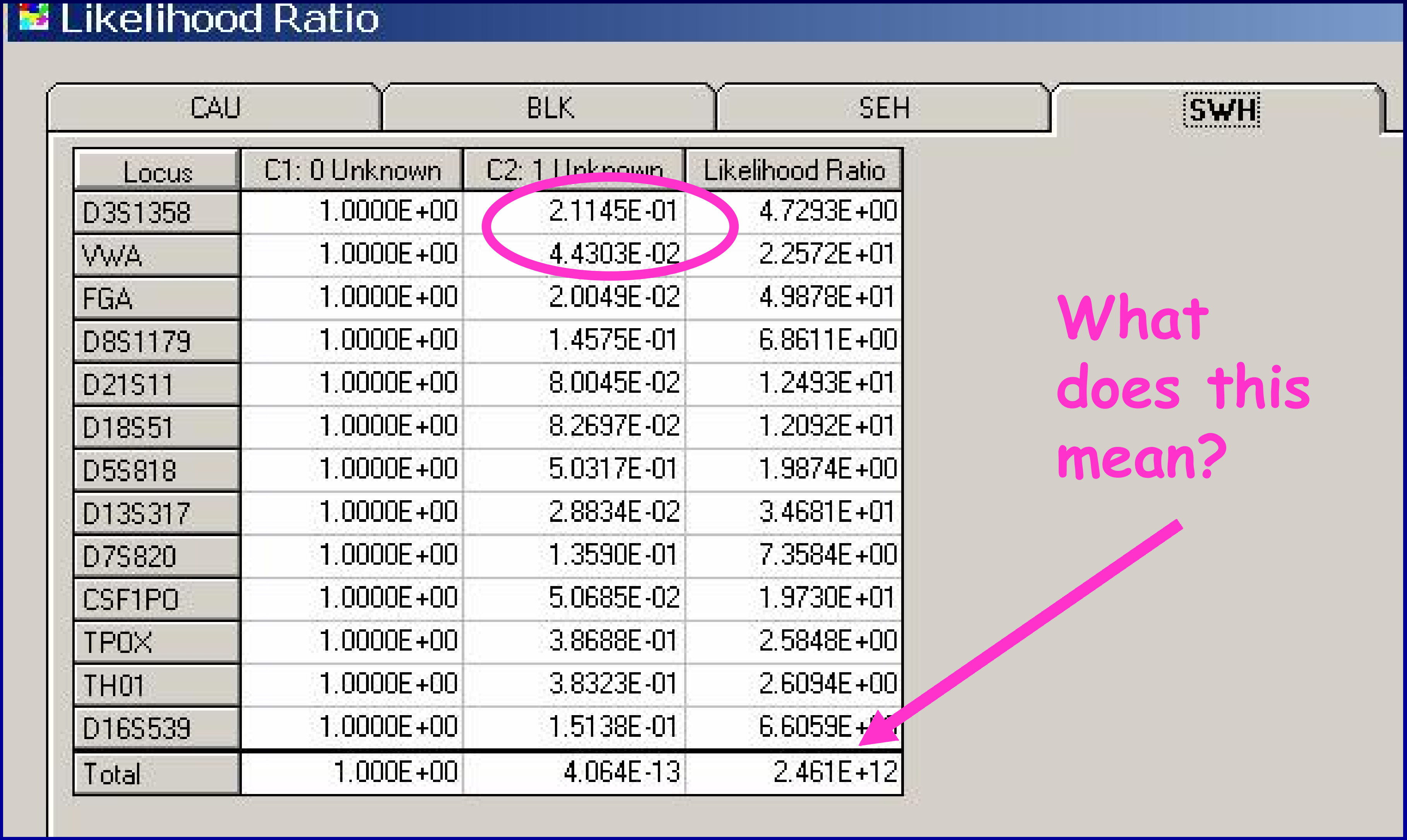
2(0.06158)(0.35961)

= 0.04429

$$LR = \frac{1}{0.04429} = 22.57$$

The observed mixture profile is approximately 22.5 times more likely to occur under the scenario that it is a mixture of DNA from the victim, her partner, and the suspect, as opposed to the scenario that it originated from a mixture of DNA from the victim, her partner, and an unrelated, unknown person.

Of course, we wouldn't want to do this by hand



Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	2.1145E-01	4.7293E+00
VWA	1.0000E+00	4.4303E-02	2.2572E+01
FGA	1.0000E+00	2.0049E-02	4.9878E+01
D8S1179	1.0000E+00	1.4575E-01	6.8611E+00
D21S11	1.0000E+00	8.0045E-02	1.2493E+01
D18S51	1.0000E+00	8.2697E-02	1.2092E+01
D5S818	1.0000E+00	5.0317E-01	1.9874E+00
D13S317	1.0000E+00	2.8834E-02	3.4681E+01
D7S820	1.0000E+00	1.3590E-01	7.3584E+00
CSF1PO	1.0000E+00	5.0685E-02	1.9730E+01
TPOX	1.0000E+00	3.8688E-01	2.5848E+00
TH01	1.0000E+00	3.8323E-01	2.6094E+00
D16S539	1.0000E+00	1.5138E-01	6.6059E+[illegible]
Total	1.000E+00	4.064E-13	2.461E+12

What does this mean?

Big Number Names:

1,000,000	million
1,000,000,000	billion
1,000,000,000,000	trillion
1×10^{15}	quadrillion
1×10^{18}	quintillion
1×10^{21}	sextillion
1×10^{24}	septillion
1×10^{27}	octillion
1×10^{30}	nonillion
1×10^{33}	decillion

The observed mixture profile is approximately 2.5 trillion times more likely to occur under the scenario that it is a mixture of DNA from the victim, her partner, and the suspect, as opposed to the scenario that it originated from a mixture of DNA from the victim, her partner, and an unrelated, unknown person.

Considerations

Mixture interpretation, and the statistical treatment of the data, is more complex than interpretation of evidence originated from a single donor. However, **with appropriate care**, the same biological and statistical principles can be used in mixture interpretation.

Considerations

Unlike interpretation of single donor profiles, the relevant questions for mixture interpretation can be varied, and a wider set of scenarios with respect to the origin of the mixture may be postulated…each hypothesis is mutually exclusive and applies a different treatment of the data

Considerations

As with the interpretation of single donor profiles, conservative approaches for calculating statistics of mixture interpretation should be made.

However, when applying the likelihood ratio approach, population substructure adjustments do not always yield conservatism.

Considerations

Subtraction of alleles found in the known samples from the mixture should be avoided in deriving statistics for mixture interpretation.

This adds to conservatism, even with the use of the simplest assumption in calculations.

Considerations

Several biological features of mixture profiles may be relatively difficult to translate in formulating statistics.

However, when they are not factors in the analysis, the derived statistics become inherently conservative.

Considerations

Most critical step of a mixture interpretation is how the statistics is verbally presented.

A LR-value, wrongly stated, may introduce the fallacy of reverse conditioning, sometimes known as the 'prosecutors fallacy'.

Had Enough???

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