Popstats Unplugged

14th International Symposium on Human Identification

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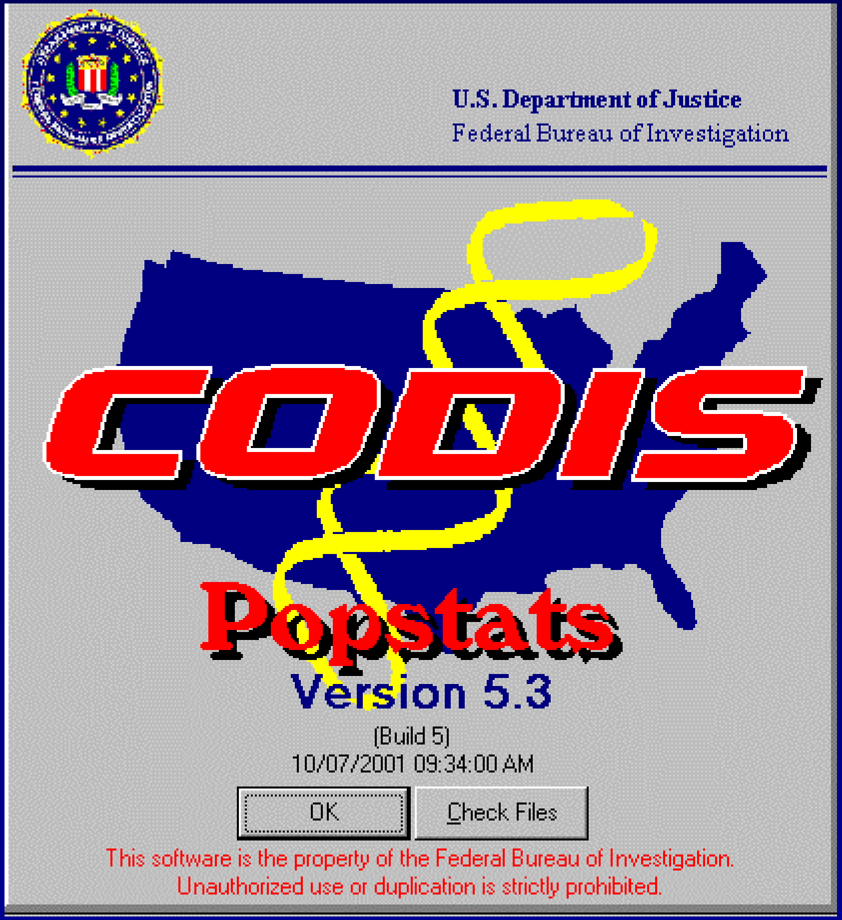
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Popstats
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Calculation of Mixture Statistics using PopStats

What are we asking Popstats to provide us??

What do we have to do before we use Popstats ??

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

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

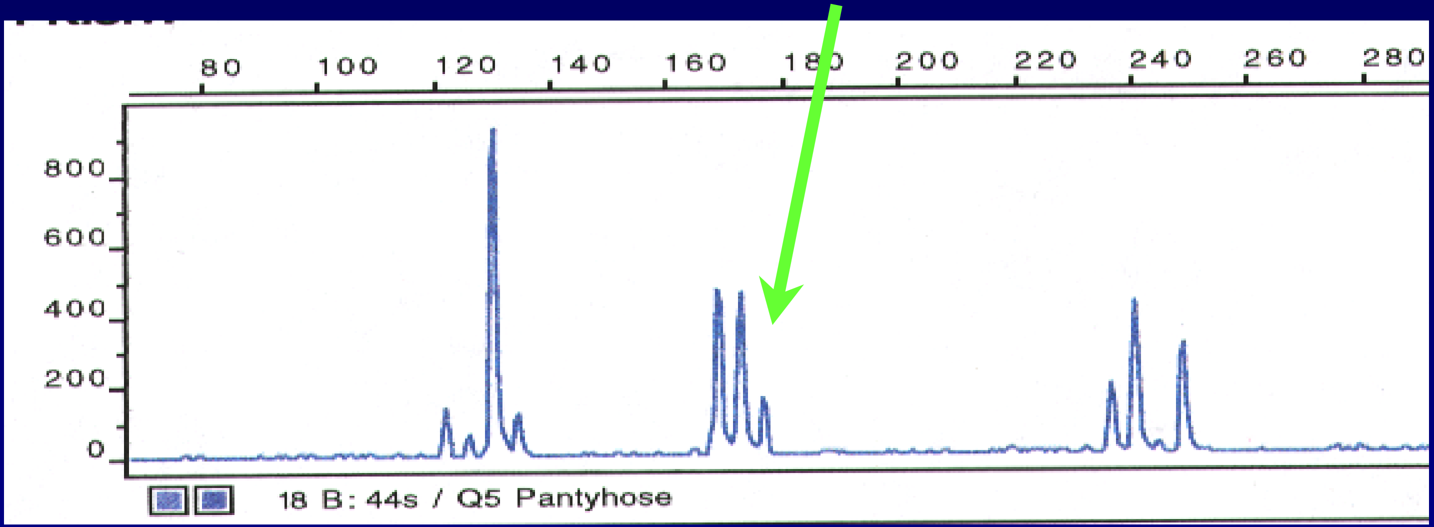
Exclusion Probability

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.

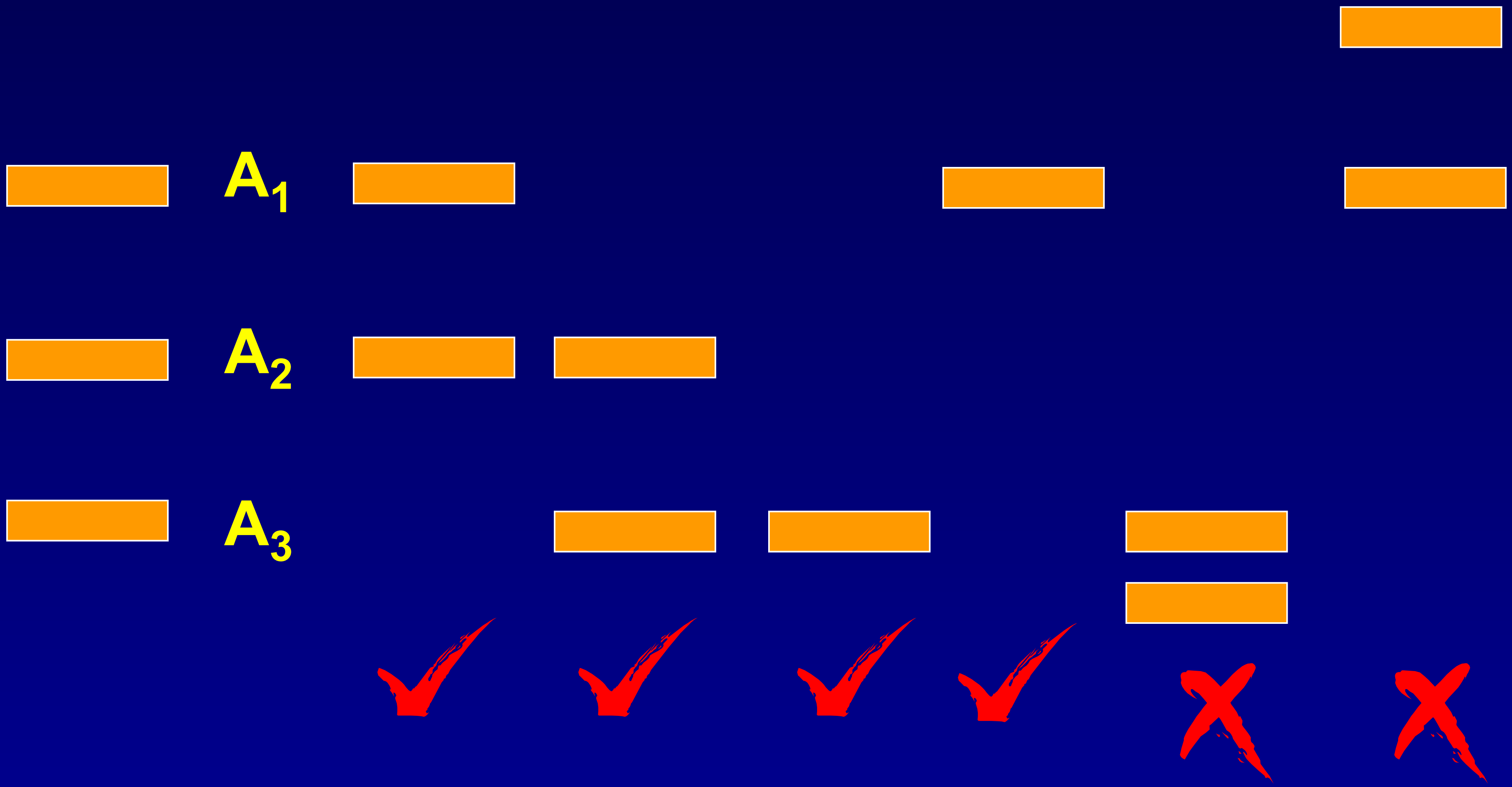
We have the following data:

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



A_1

A_2

A_3

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 $= 1 - (0.1 + 0.2 + 0.3)^2$

$= 0.64$, 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 $\theta = 0.03$?

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

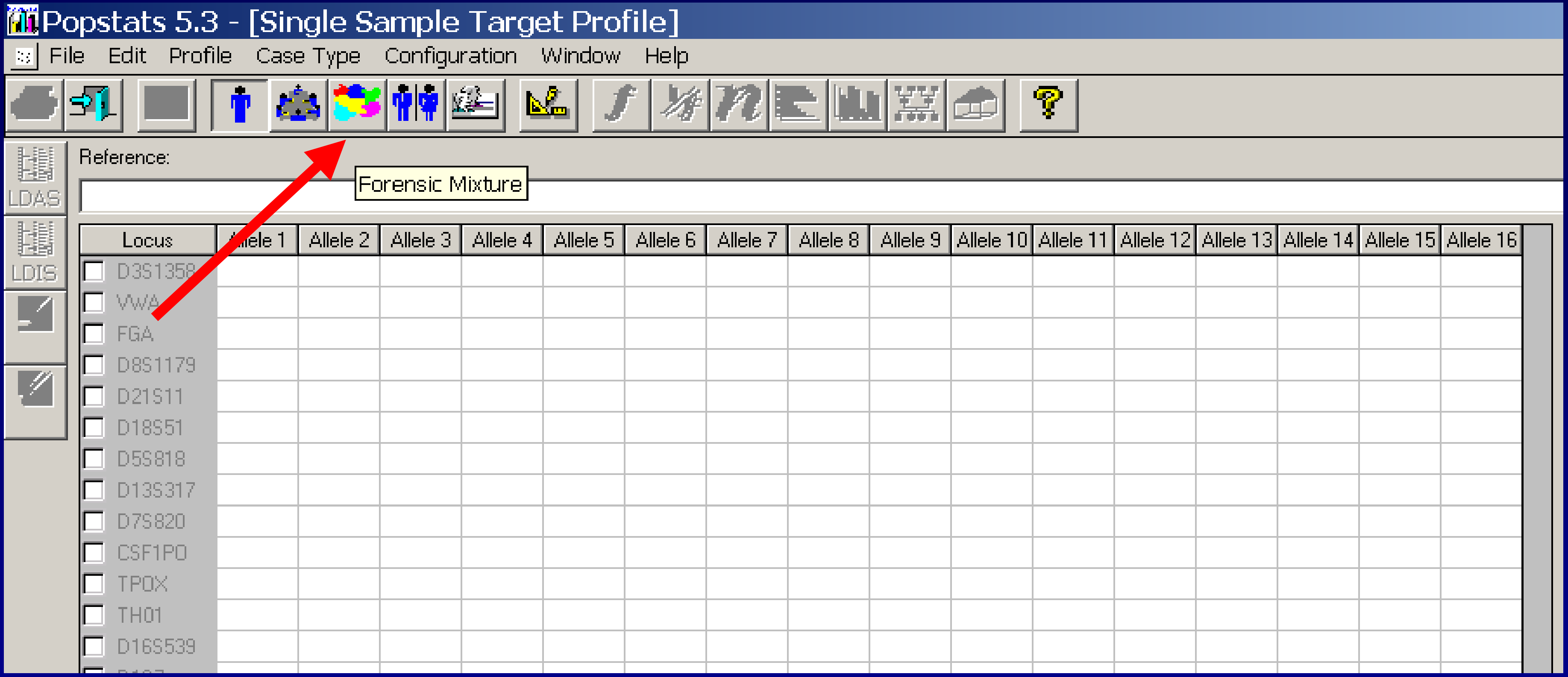
$$p = 0.6$$

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

$$= 0.6328$$

Approximately 1% change in PE

How does PopStats handle this calculation?

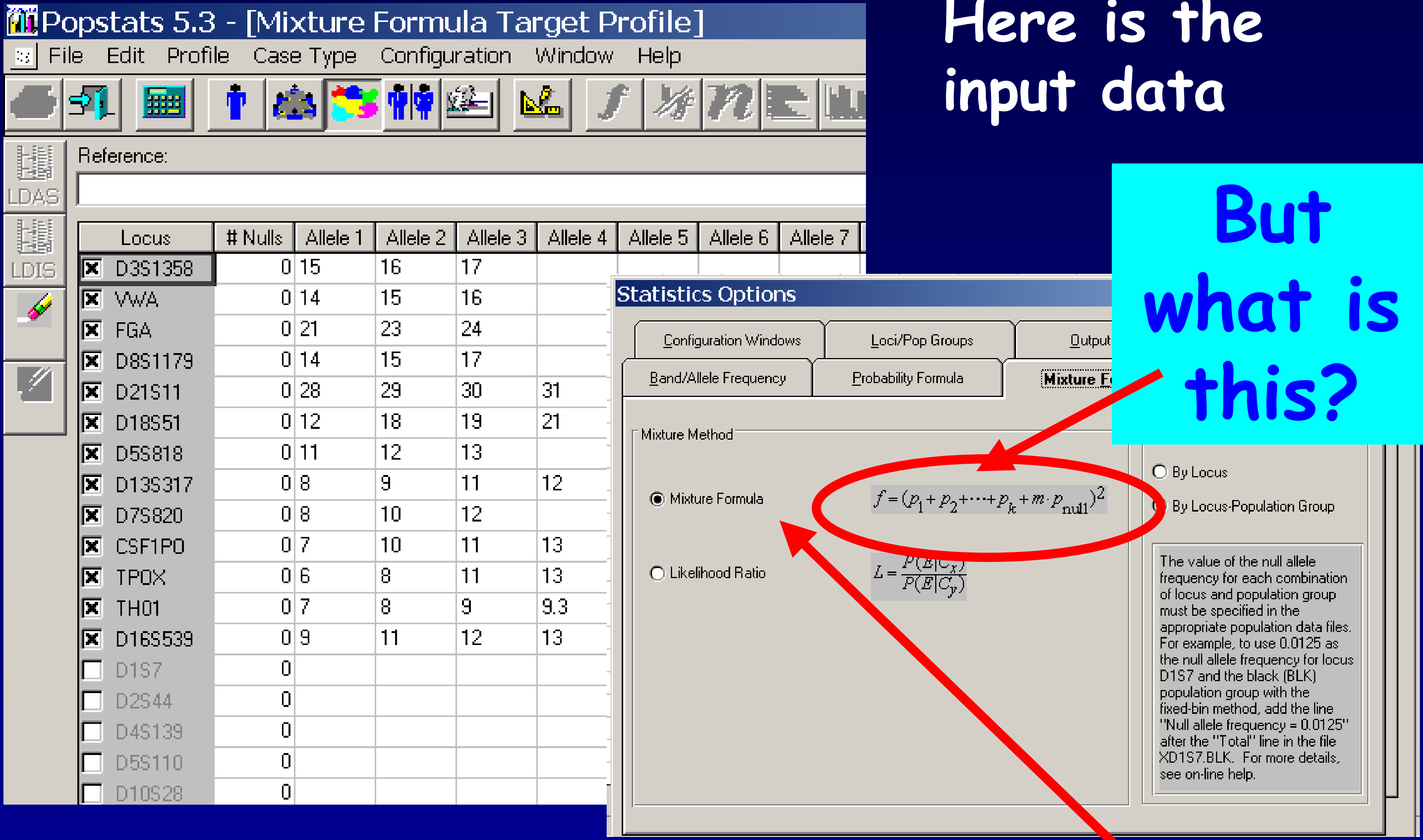


Lets work with this dataset:

Locus	Alleles	Locus	Alleles
D3S1358	15, 16, 17	D7S820	8, 10, 12
TH01	7, 8, 9 9.3	D16S539	9, 11, 12, 13
D21S11	28, 29, 30, 31	CSF1PO	7, 10, 11, 12
D18S51	12, 18, 19, 21	vWA	14, 15, 16
D5S818	11, 12, 13	D8S1179	14, 15, 17
D13S317	8, 9, 11,12	TPOX	6, 8,11, 13
		FGA	21, 23, 24

Note: we are not saying anything about the potential contributors, number of contributors or case scenario!

Here is the input data



Locus	# Nulls	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	0	15	16	17				
☒ VWA	0	14	15	16				
☒ FGA	0	21	23	24				
☒ D8S1179	0	14	15	17				
☒ D21S11	0	28	29	30	31			
☒ D18S51	0	12	18	19	21			
☒ D5S818	0	11	12	13				
☒ D13S317	0	8	9	11	12			
☒ D7S820	0	8	10	12				
☒ CSF1PO	0	7	10	11	13			
☒ TPOX	0	6	8	11	13			
☒ TH01	0	7	8	9	9.3			
☒ D16S539	0	9	11	12	13			
☐ D1S7	0							
☐ D2S44	0							
☐ D4S139	0							
☐ D5S110	0							
☐ D10S28	0							

Mixture Method

● Mixture Formula $f=(p_1+p_2+\cdots+p_k+m\cdot p_{null})^2$

○ Likelihood Ratio $L=\dfrac{P(E|C_x)}{P(E|C_y)}$

○ By Locus

By Locus-Population Group

The value of the null allele frequency for each combination of locus and population group must be specified in the appropriate population data files. For example, to use 0.0125 as the null allele frequency for locus D1S7 and the black (BLK) population group with the fixed-bin method, add the line "Null allele frequency = 0.0125" after the "Total" line in the file XD1S7.BLK. For more details, see on-line help.

But what is this?

And we are wanting to calc Prob of Exclusion

The probability of **inclusion** is given by

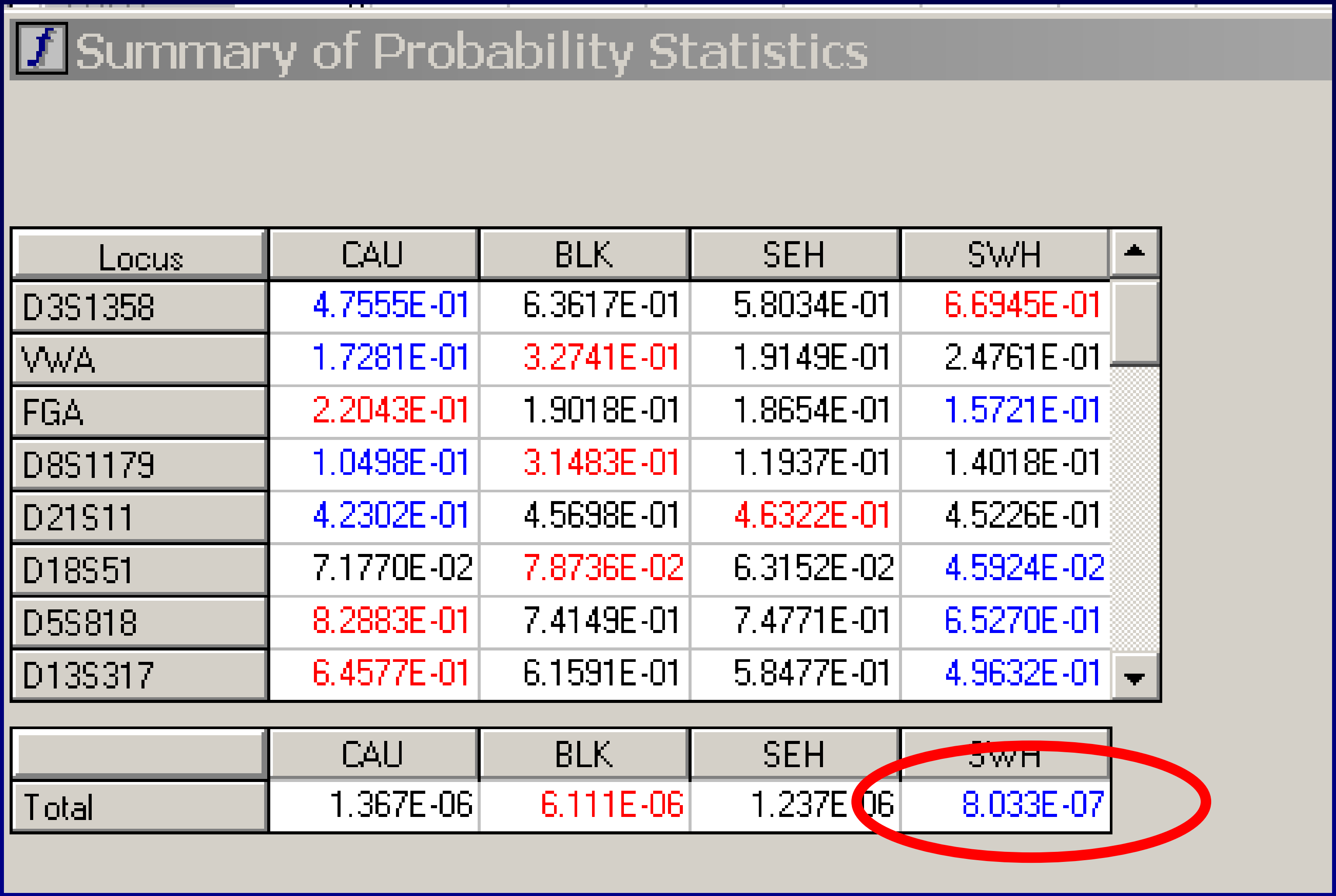
$$(p_1 + p_2 + \ldots + p_i)^2$$ **!!!!!**

It is the compliment of *Inclusion Probability* that defines the

Exclusion Probability

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

Remember this when relying on PopStats output !!!

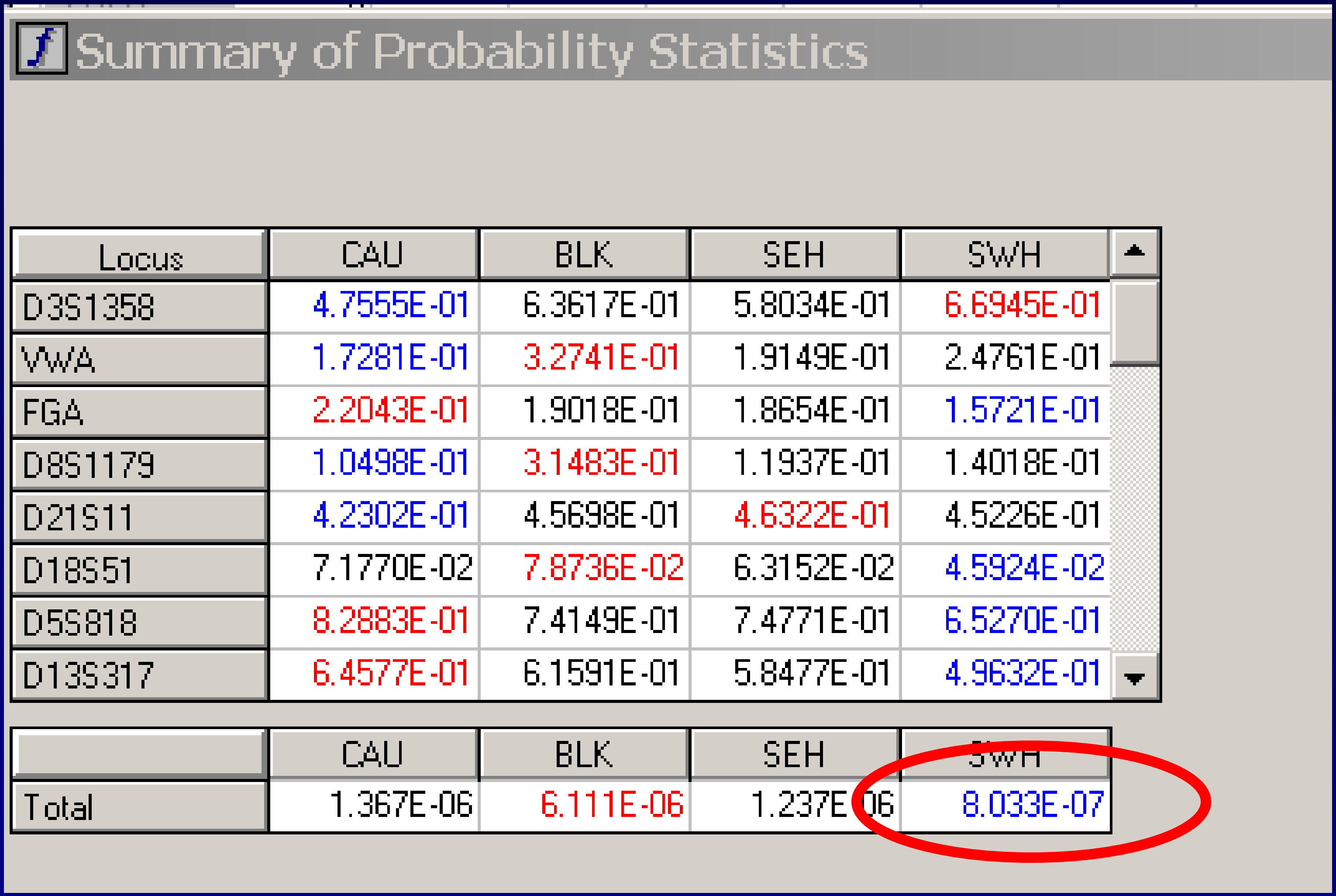


Summary of Probability Statistics

Locus	CAU	BLK	SEH	SWH
D3S1358	4.7555E-01	6.3617E-01	5.8034E-01	6.6945E-01
VWA	1.7281E-01	3.2741E-01	1.9149E-01	2.4761E-01
FGA	2.2043E-01	1.9018E-01	1.8654E-01	1.5721E-01
D8S1179	1.0498E-01	3.1483E-01	1.1937E-01	1.4018E-01
D21S11	4.2302E-01	4.5698E-01	4.6322E-01	4.5226E-01
D18S51	7.1770E-02	7.8736E-02	6.3152E-02	4.5924E-02
D5S818	8.2883E-01	7.4149E-01	7.4771E-01	6.5270E-01
D13S317	6.4577E-01	6.1591E-01	5.8477E-01	4.9632E-01

	CAU	BLK	SEH	SWH
Total	1.367E-06	6.111E-06	1.237E-06	8.033E-07

So, here's our number…what do we do with it??



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D13S317	6.4577E-01	6.1591E-01	5.8477E-01	4.9632E-01

	CAU	BLK	SEH	SWH
Total	1.367E-06	6.111E-06	1.237E-06	8.033E-07

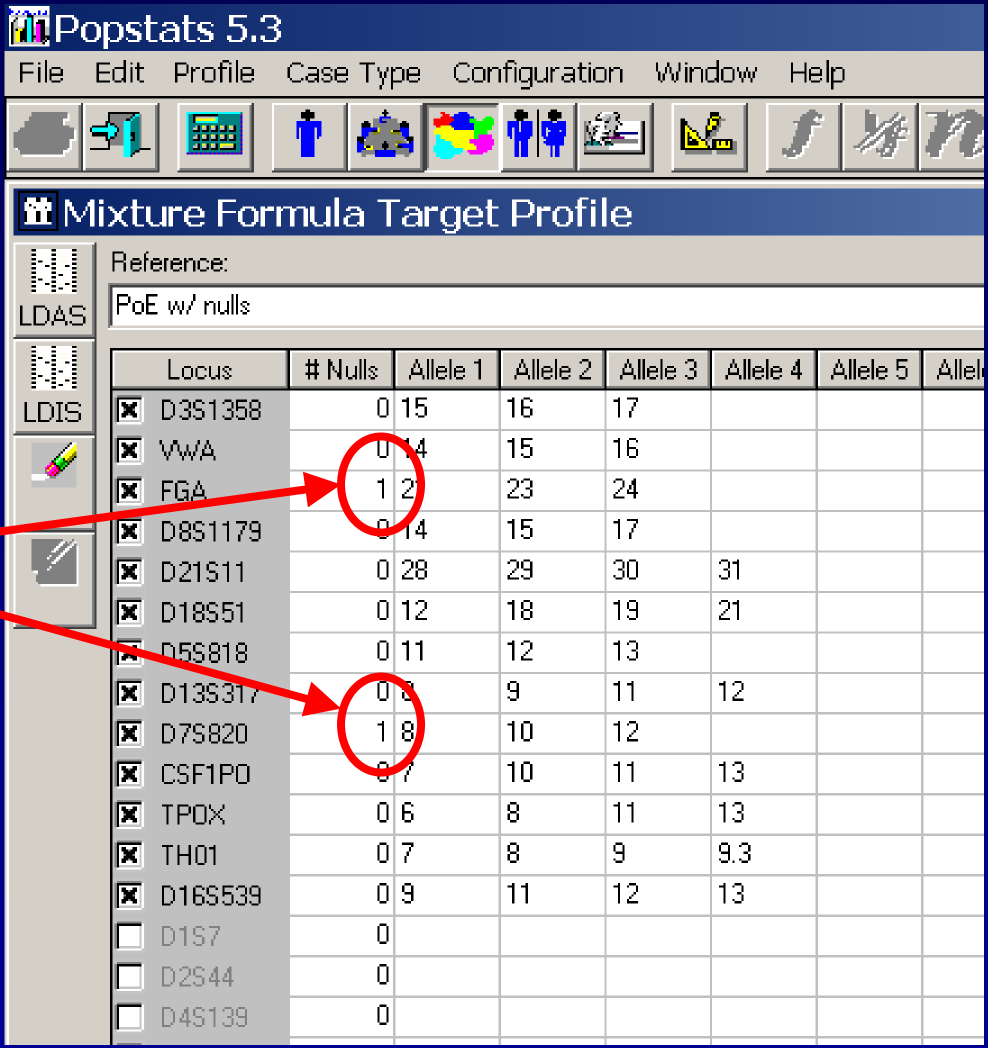
$$PE = 1 - 8.033 \times 10^{-7}$$
$$= 0.99999919 \text{ or } 99.99992\%$$

What about verbiage?

Based on the results from the thirteen DNA loci examined from the evidentiary item, 99.99992% of randomly tested persons would be excluded as potential contributors of the DNA detected in the mixed sample.

What if we have to consider some allele dropout?

Here we've added the potential for null alleles at two likely loci



Reference: PoE w/ nulls

	Locus	# Nulls	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allel
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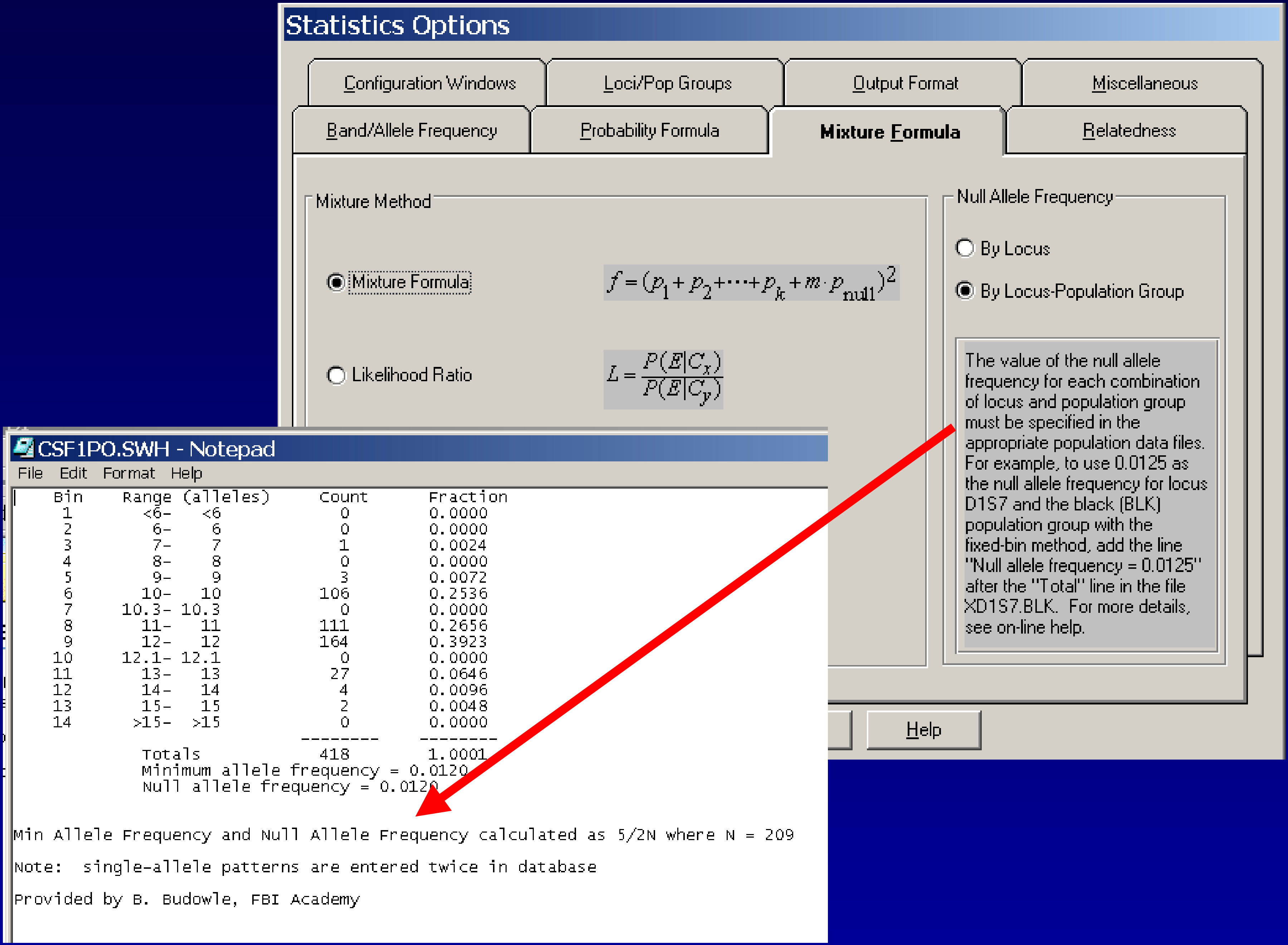
☒	TH01	0	7	8	9	9.3		
☒	D16S539	0	9	11	12	13		
☐	D1S7	0						
☐	D2S44	0						
☐	D4S139	0						

How does this effect the calculation?



Mixture Method

● Mixture Formula $f = (p_1 + p_2 + \cdots + p_k + m \cdot p_{null})^2$

○ Likelihood Ratio $L = \frac{P(E|C_x)}{P(E|C_y)}$

Null Allele Frequency

○ By Locus

● By Locus-Population Group

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```
    Bin     Range (alleles)     Count       Fraction
     1         <6-    <6          0         0.0000
     2          6-     6          0         0.0000
     3          7-     7          1         0.0024
     4          8-     8          0         0.0000
     5          9-     9          3         0.0072
     6         10-    10        106         0.2536
     7       10.3-  10.3          0         0.0000
     8         11-    11        111         0.2656
     9         12-    12        164         0.3923
    10       12.1-  12.1          0         0.0000
    11         13-    13         27         0.0646
    12         14-    14          4         0.0096
    13         15-    15          2         0.0048
    14        >15-   >15          0         0.0000
                              ---------   ---------
             Totals             418         1.0001
             Minimum allele frequency = 0.0120
             Null allele frequency = 0.0120

Min Allele Frequency and Null Allele Frequency calculated as 5/2N where N = 209

Note:  single-allele patterns are entered twice in database

Provided by B. Budowle, FBI Academy
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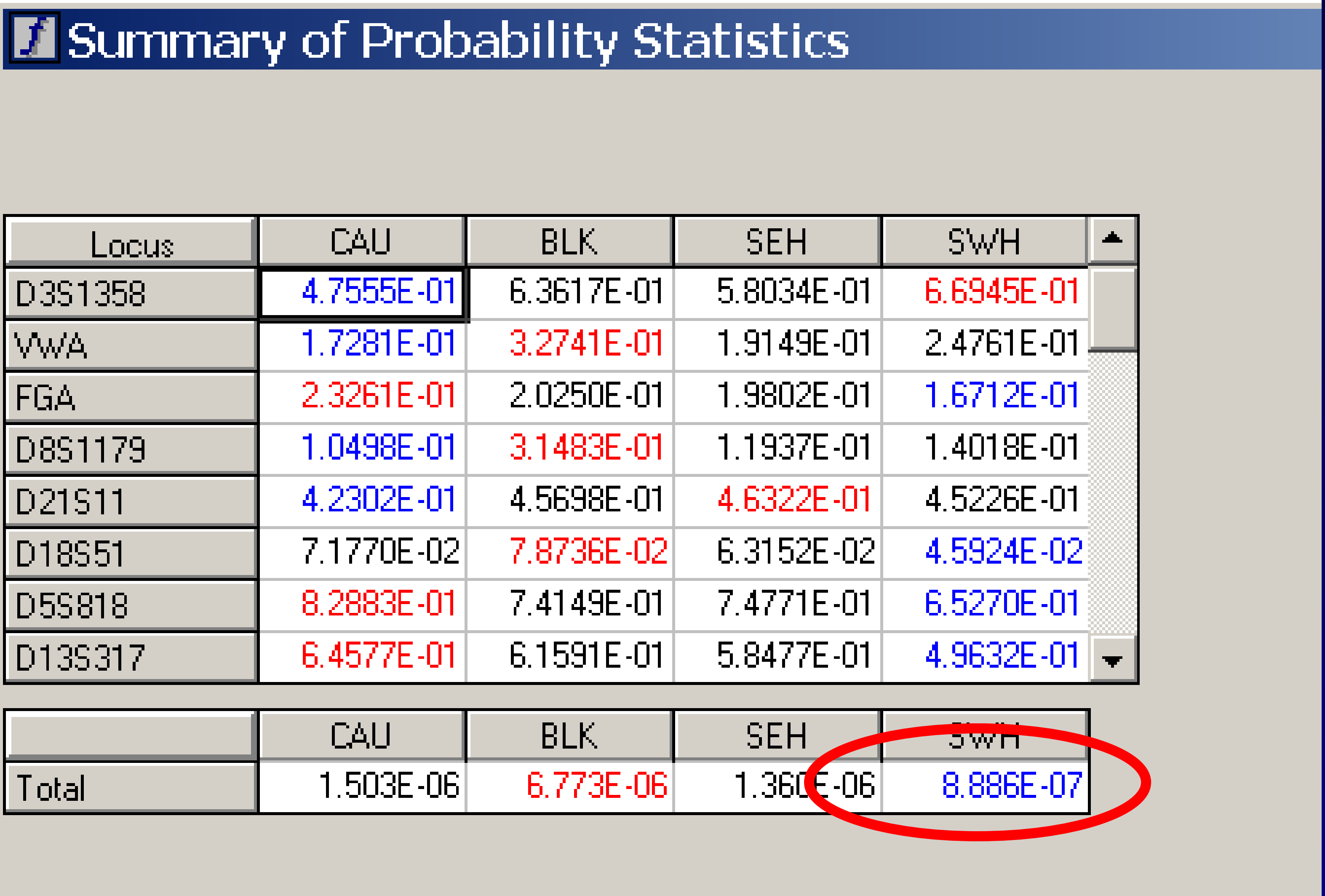

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D8S1179	1.0498E-01	3.1483E-01	1.1937E-01	1.4018E-01
D21S11	4.2302E-01	4.5698E-01	4.6322E-01	4.5226E-01
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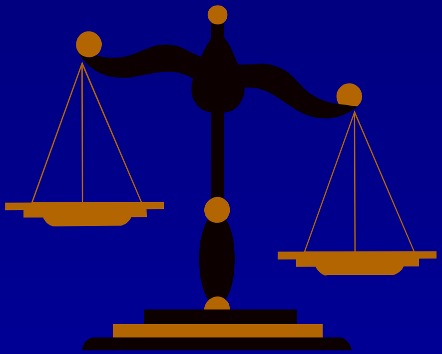
D5S818	8.2883E-01	7.4149E-01	7.4771E-01	6.5270E-01
D13S317	6.4577E-01	6.1591E-01	5.8477E-01	4.9632E-01

	CAU	BLK	SEH	SWH
Total	1.503E-06	6.773E-06	1.360E-06	8.886E-07

$$PE = 1 - 8.886 \times 10^{-7}$$
$$= 0.99999911 \text{ or } 99.99991\%$$

Mixtures and Likelihood Ratios

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



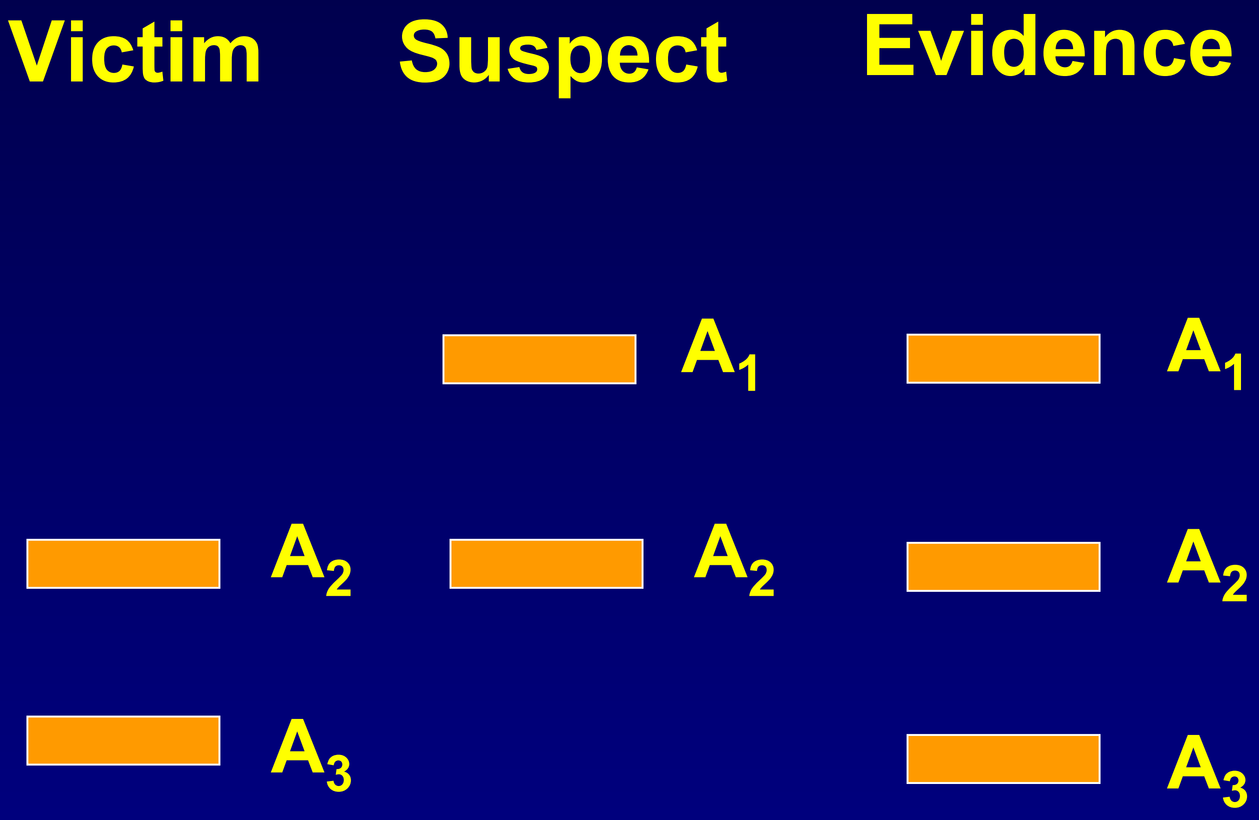
So, now we are including a statement about the circumstances of the case as well as the actual profiles determined for the victim, suspect and evidentiary sample

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

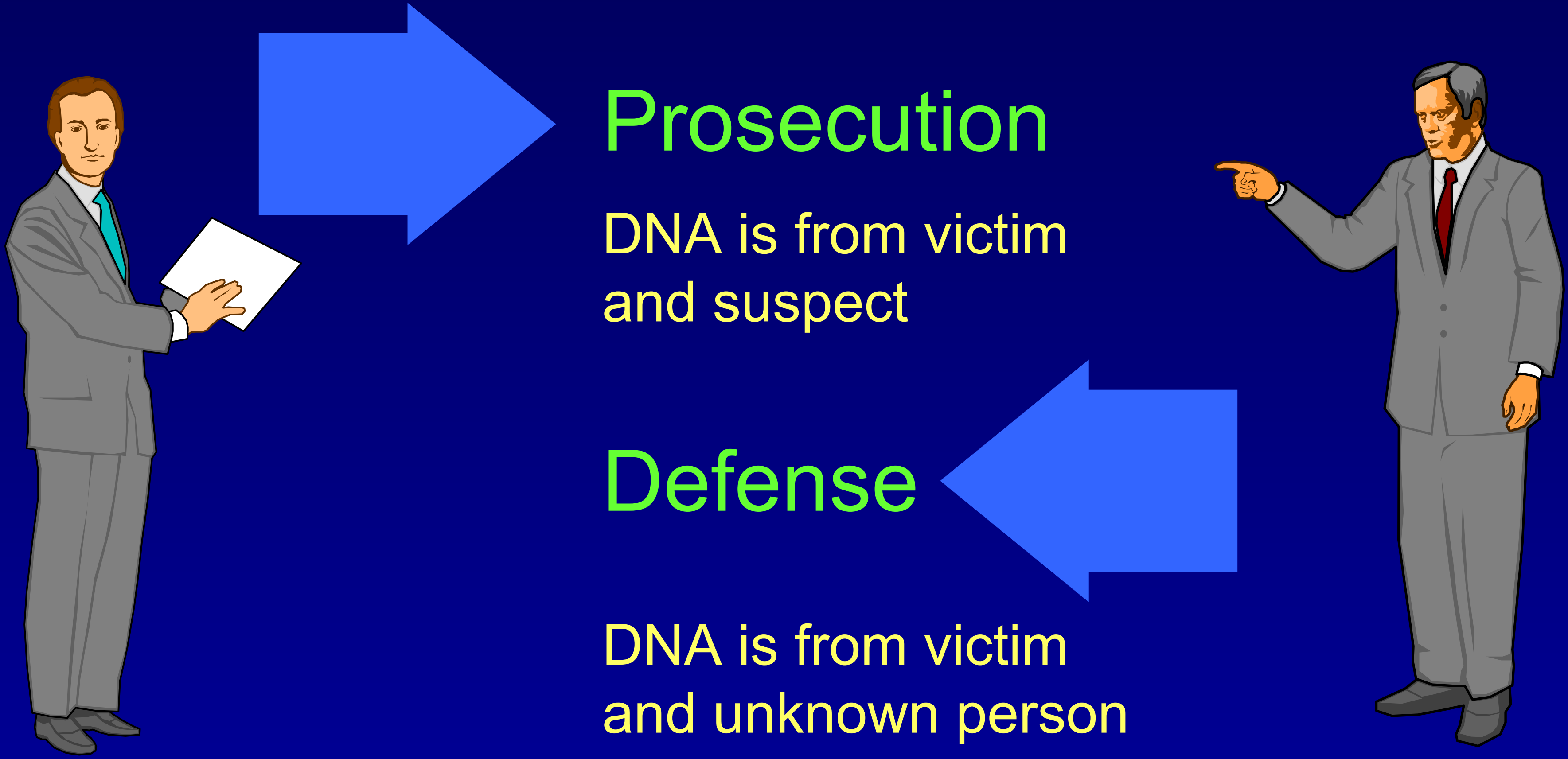
Three Allele Scenario

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:

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

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 × 0.1) × (2 × .2 × .3)
= 0.01 × 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 :

$$\Sigma p = 0.0012 + 0.0024 + \ldots + 0.0036$$

$$= \mathbf{0.0432}$$

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

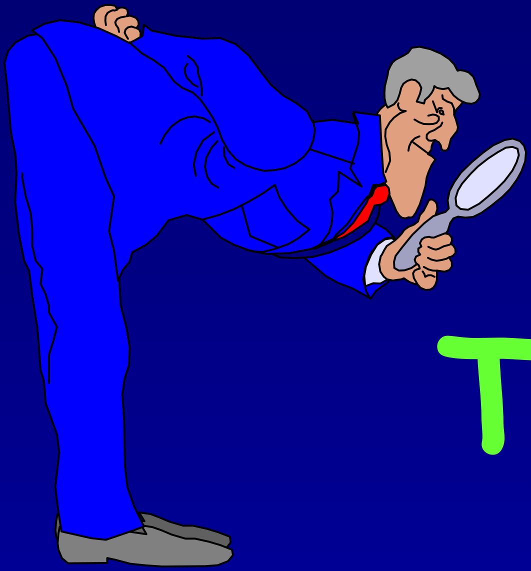
- When making statements on the statistical inferences remember that you are expressing **only the genetic data**
- You are not dealing with issues of **“chance”**
- To do so would involve Bayesian inferences which include Prior Probabilities…for which genetic data offers little assistance.

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

So, lets go back to our previous data set and see how we handle this with PopStats!

First, we need to revisit our data…

This time the genotypes of the victim and suspect are a consideration:

☛ they specify which hypotheses may be supported by the data

☛ give some indication on how many contributors to consider

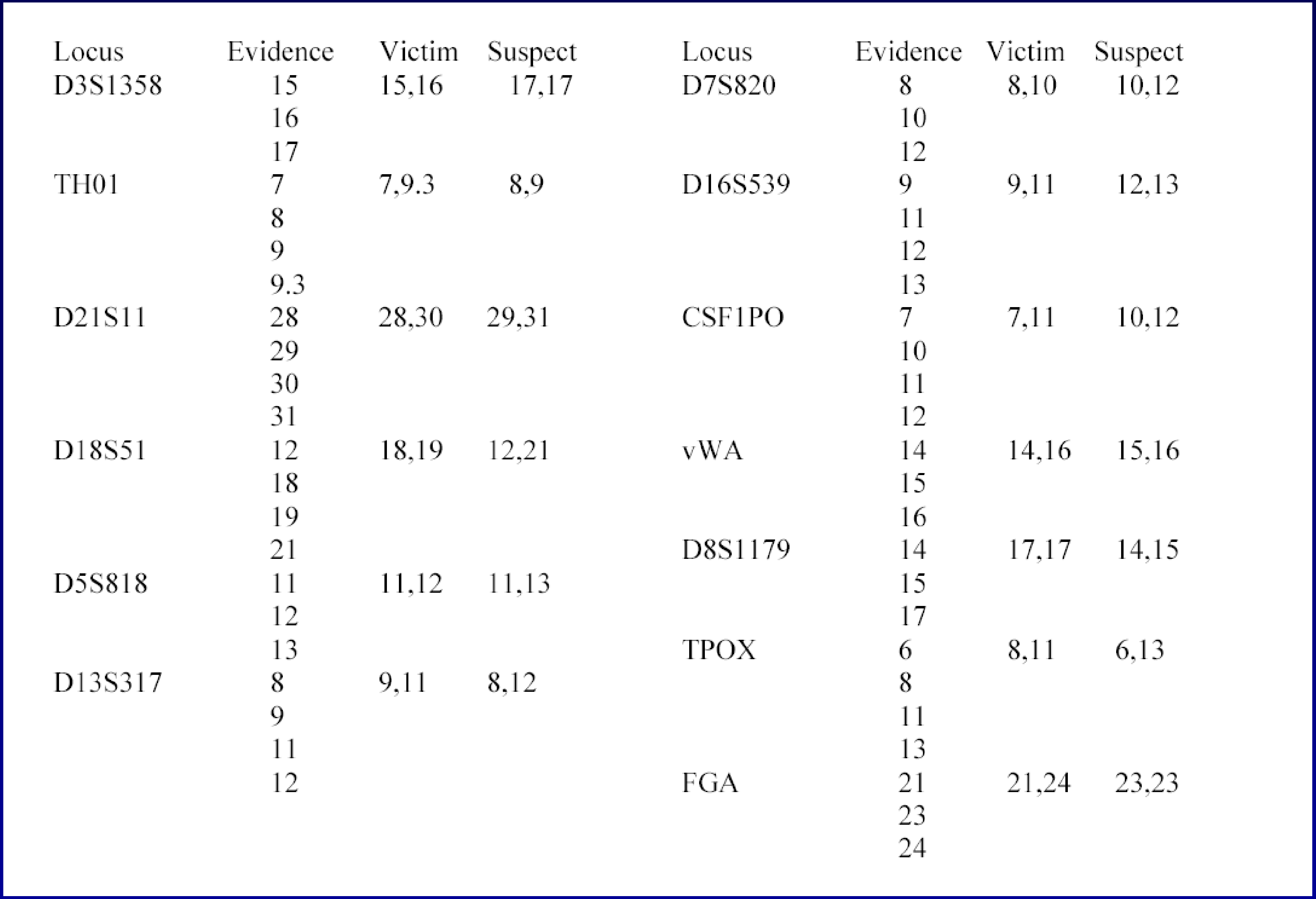
Our "Q1" data

Locus	Alleles	Locus	Alleles
D3S1358	15, 16, 17	D7S820	8, 10, 12
TH01	7, 8, 9 9.3	D16S539	9, 11, 12, 13
D21S11	28, 29, 30, 31	CSF1PO	7, 10, 11, 12
D18S51	12, 18, 19, 21	vWA	14, 15, 16
D5S818	11, 12, 13	D8S1179	14, 15, 17
D13S317	8, 9, 11,12	TPOX	6, 8,11, 13
		FGA	21, 23, 24

Now we have some specifics:

- **sexual assault case**
- **victim and suspect cannot be excluded**
- **no consentual partners**

And our "K1" and "K2" genotypes:



Locus	Evidence	Victim	Suspect
D3S1358	15 16 17	15,16	17,17
TH01	7 8 9 9.3	7,9.3	8,9
D21S11	28 29 30 31	28,30	29,31
D18S51	12 18 19 21	18,19	12,21
D5S818	11 12 13	11,12	11,13
D13S317	8 9 11 12	9,11	8,12
D7S820	8 10 12	8,10	10,12
D16S539	9 11 12 13	9,11	12,13
CSF1PO	7 10 11 12	7,11	10,12
vWA	14 15 16	14,16	15,16
D8S1179	14 15 17	17,17	14,15
TPOX	6 8 11 13	8,11	6,13
FGA	21 23 24	21,24	23,23

OK…where do we start???

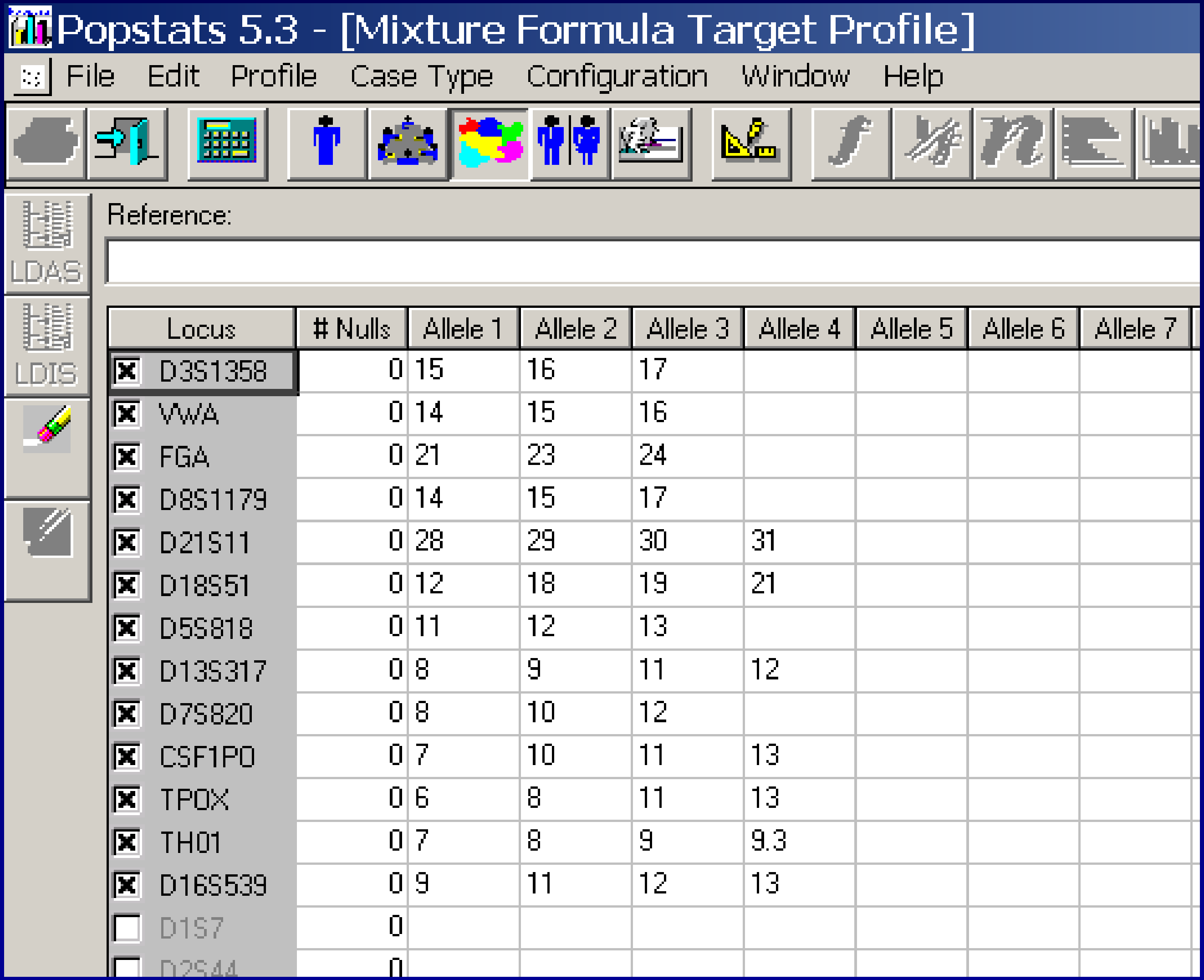
WRITE DOWN THE HYPOTHESES!!!!

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

AND

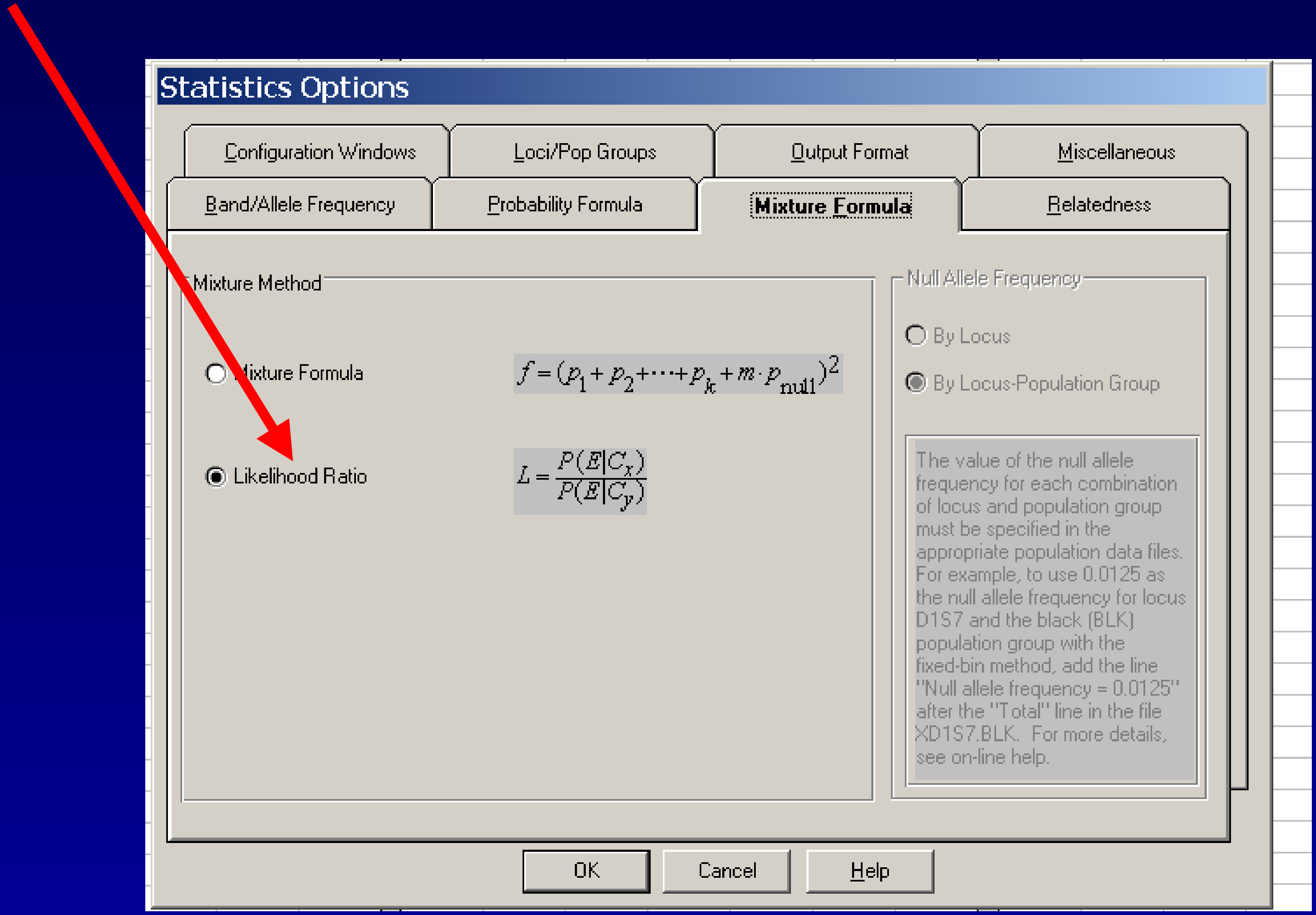
H_1: The mixture originated from the victim and an unknown person,

Our entry data from before:



Locus	# Nulls	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	0	15	16	17				
☒ VWA	0	14	15	16				
☒ FGA	0	21	23	24				
☒ D8S1179	0	14	15	17				
☒ D21S11	0	28	29	30	31			
☒ D18S51	0	12	18	19	21			
☒ D5S818	0	11	12	13				
☒ D13S317	0	8	9	11	12			
☒ D7S820	0	8	10	12				
☒ CSF1PO	0	7	10	11	13			
☒ TPOX	0	6	8	11	13			
☒ TH01	0	7	8	9	9.3			
☒ D16S539	0	9	11	12	13			
☐ D1S7	0							
☐ D2S44	0							

We can look at the same entry data using the likelihood approach



Mixture Method

○ Mixture Formula $f=(p_1+p_2+\cdots+p_k+m\cdot p_{null})^2$

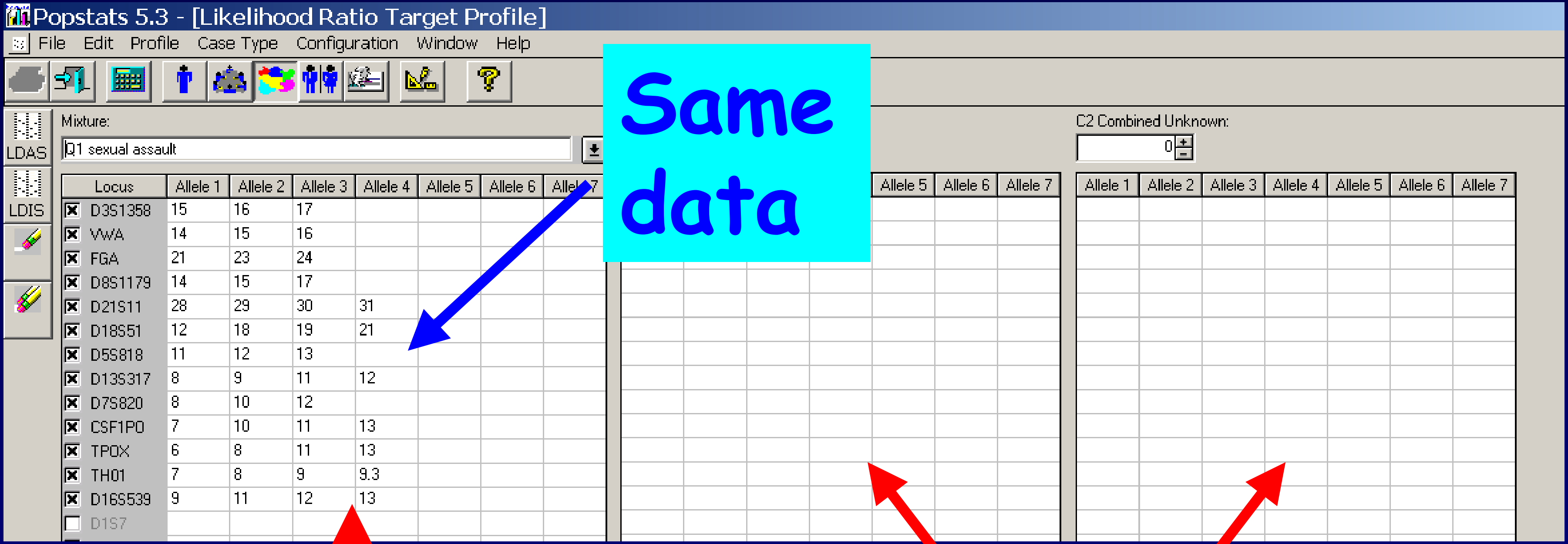
● Likelihood Ratio $L=\dfrac{P(E|C_x)}{P(E|C_y)}$

Null Allele Frequency

○ By Locus

● By Locus-Population Group

The value of the null allele frequency for each combination of locus and population group must be specified in the appropriate population data files. For example, to use 0.0125 as the null allele frequency for locus D1S7 and the black (BLK) population group with the fixed-bin method, add the line "Null allele frequency = 0.0125" after the "Total" line in the file XD1S7.BLK. For more details, see on-line help.



Mixture: Q1 sexual assault

C2 Combined Unknown: 0

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	15	16	17				
☒ VWA	14	15	16				
☒ FGA	21	23	24				
☒ D8S1179	14	15	17				
☒ D21S11	28	29	30	31			
☒ D18S51	12	18	19	21			
☒ D5S818	11	12	13				
☒ D13S317	8	9	11	12			
☒ D7S820	8	10	12				
☒ CSF1PO	7	10	11	13			
☒ TPOX	6	8	11	13			
☒ TH01	7	8	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							

Allele 5	Allele 6	Allele 7

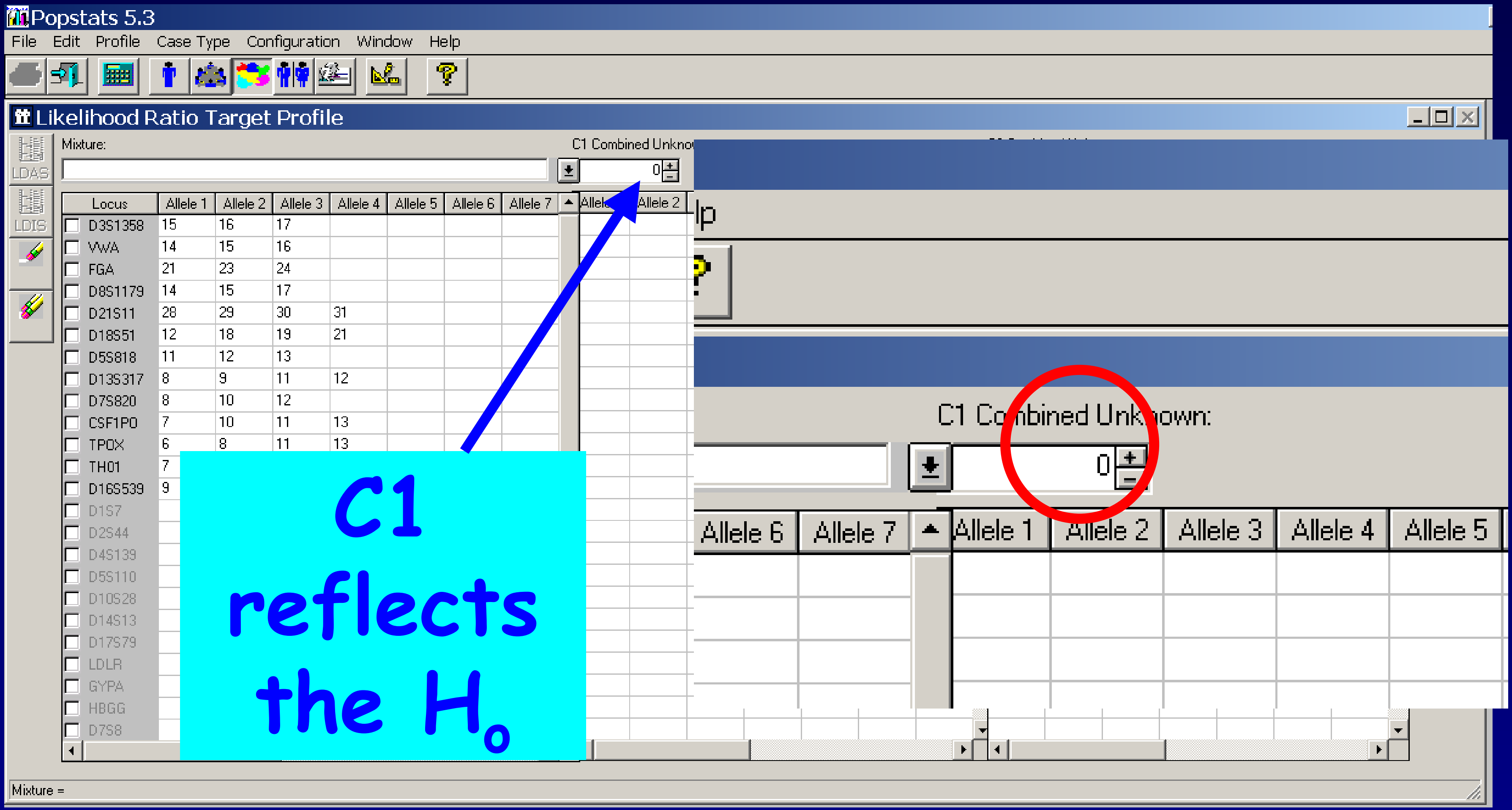
Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7

Same data

This side will autofill when changing configuration

But what about these?

How this is filled in depends on your hypotheses



Mixture:

C1 Combined Unknown: 0

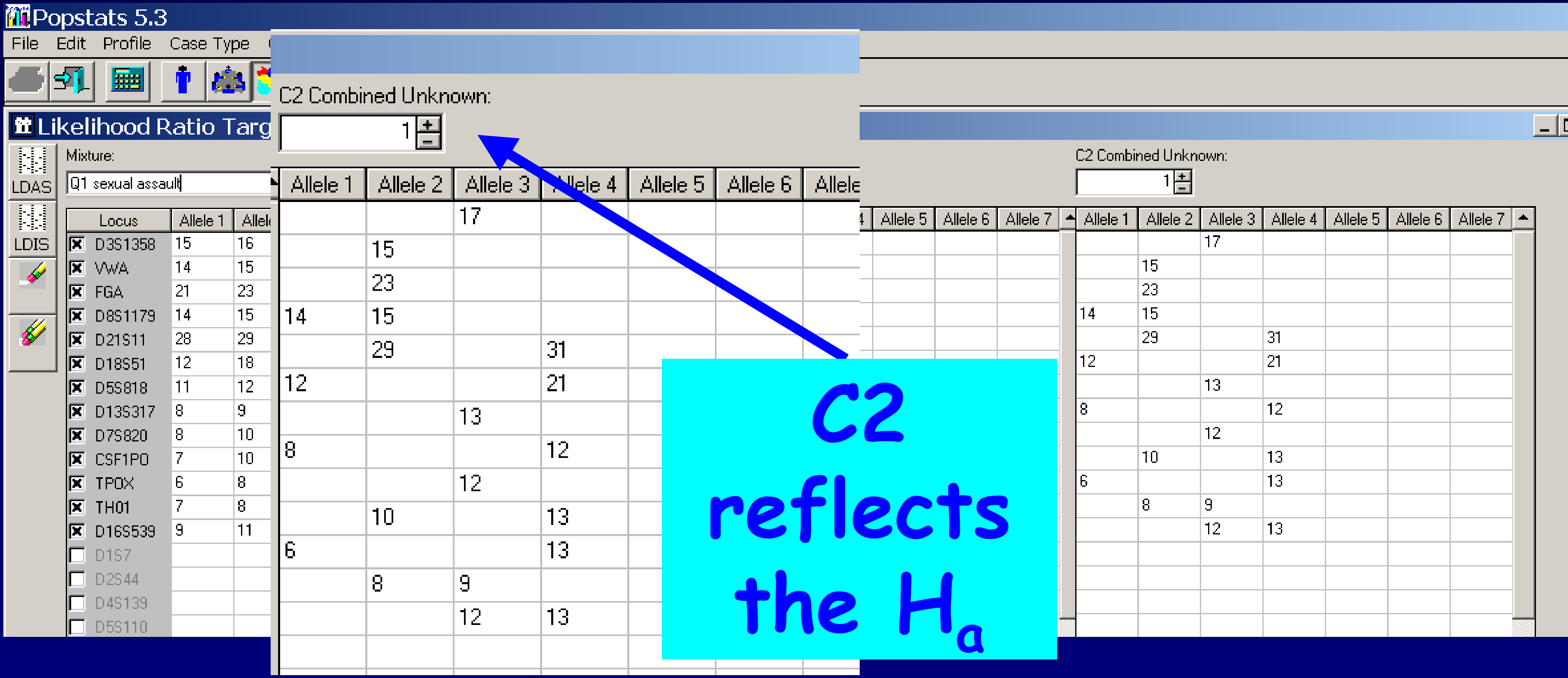
☐ Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☐ D3S1358	15	16	17				
☐ VWA	14	15	16				
☐ FGA	21	23	24				
☐ D8S1179	14	15	17				
☐ D21S11	28	29	30	31			
☐ D18S51	12	18	19	21			
☐ D5S818	11	12	13				
☐ D13S317	8	9	11	12			
☐ D7S820	8	10	12				
☐ CSF1PO	7	10	11	13			
☐ TPOX	6	8	11	13			
☐ TH01	7						
☐ D16S539	9						
☐ D1S7							
☐ D2S44							
☐ D4S139							
☐ D5S110							
☐ D10S28							
☐ D14S13							
☐ D17S79							
☐ LDLR							
☐ GYPA							
☐ HBGG							
☐ D7S8							

Mixture =

C1 reflects the H_o

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

WRITE IT DOWN!!!



Mixture: Q1 sexual assault

	Locus	Allele 1	Allel
☒	D3S1358	15	16
☒	VWA	14	15
☒	FGA	21	23
☒	D8S1179	14	15
☒	D21S11	28	29
☒	D18S51	12	18
☒	D5S818	11	12
☒	D13S317	8	9
☒	D7S820	8	10
☒	CSF1PO	7	10
☒	TPOX	6	8
☒	TH01	7	8
☒	D16S539	9	11
☐	D1S7		
☐	D2S44		
☐	D4S139		
☐	D5S110		

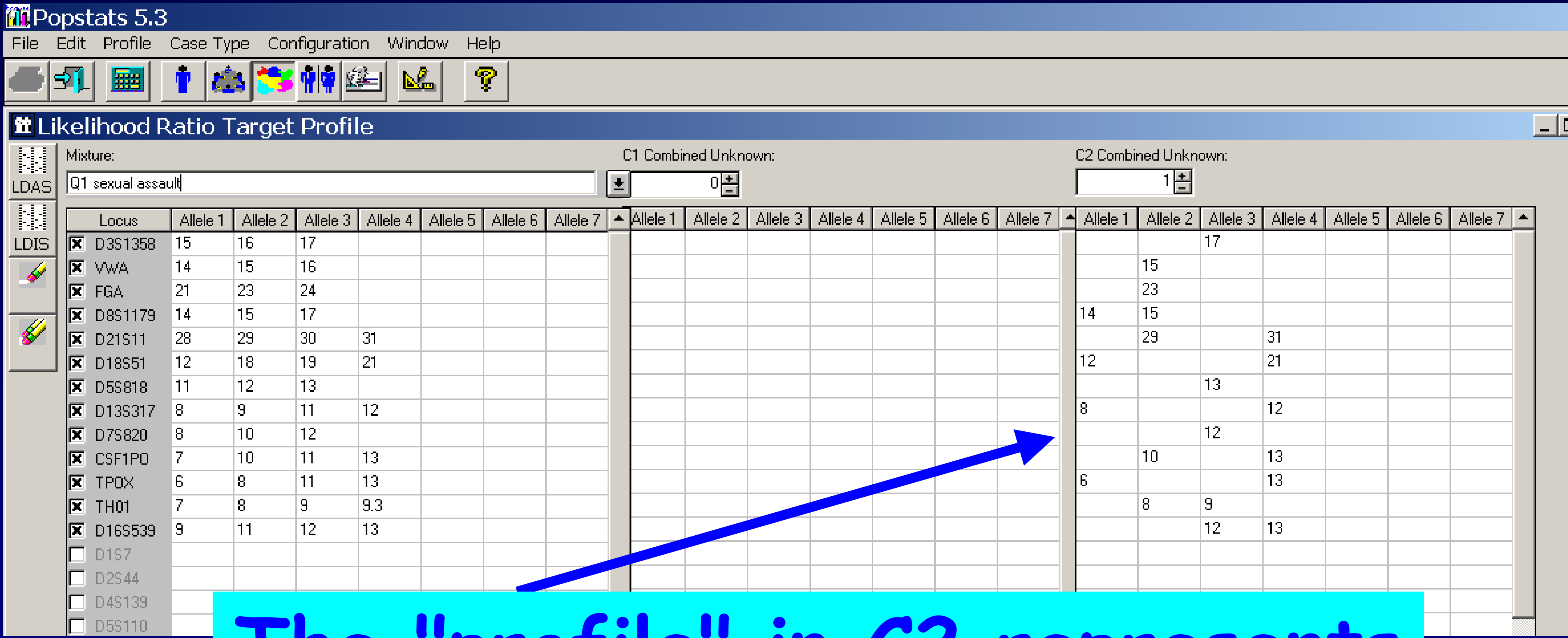
C2 Combined Unknown: 1

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
		17				
	15					
	23					
14	15					
	29		31			
12			21			
		13				
8			12			
		12				
	10		13			
6			13			
	8	9				
		12	13			

C2 reflects the H_a

H_a= The results are explained by a mixture of DNA derived from the victim and an unknown, unrelated individual

WRITE IT DOWN!!!



Likelihood Ratio Target Profile

Mixture: Q1 sexual assault

C1 Combined Unknown: 0

C2 Combined Unknown: 1

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	15	16	17				
☒ VWA	14	15	16				
☒ FGA	21	23	24				
☒ D8S1179	14	15	17				
☒ D21S11	28	29	30	31			
☒ D18S51	12	18	19	21			
☒ D5S818	11	12	13				
☒ D13S317	8	9	11	12			
☒ D7S820	8	10	12				
☒ CSF1PO	7	10	11	13			
☒ TPOX	6	8	11	13			
☒ TH01	7	8	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							
☐ D2S44							
☐ D4S139							
☐ D5S110							

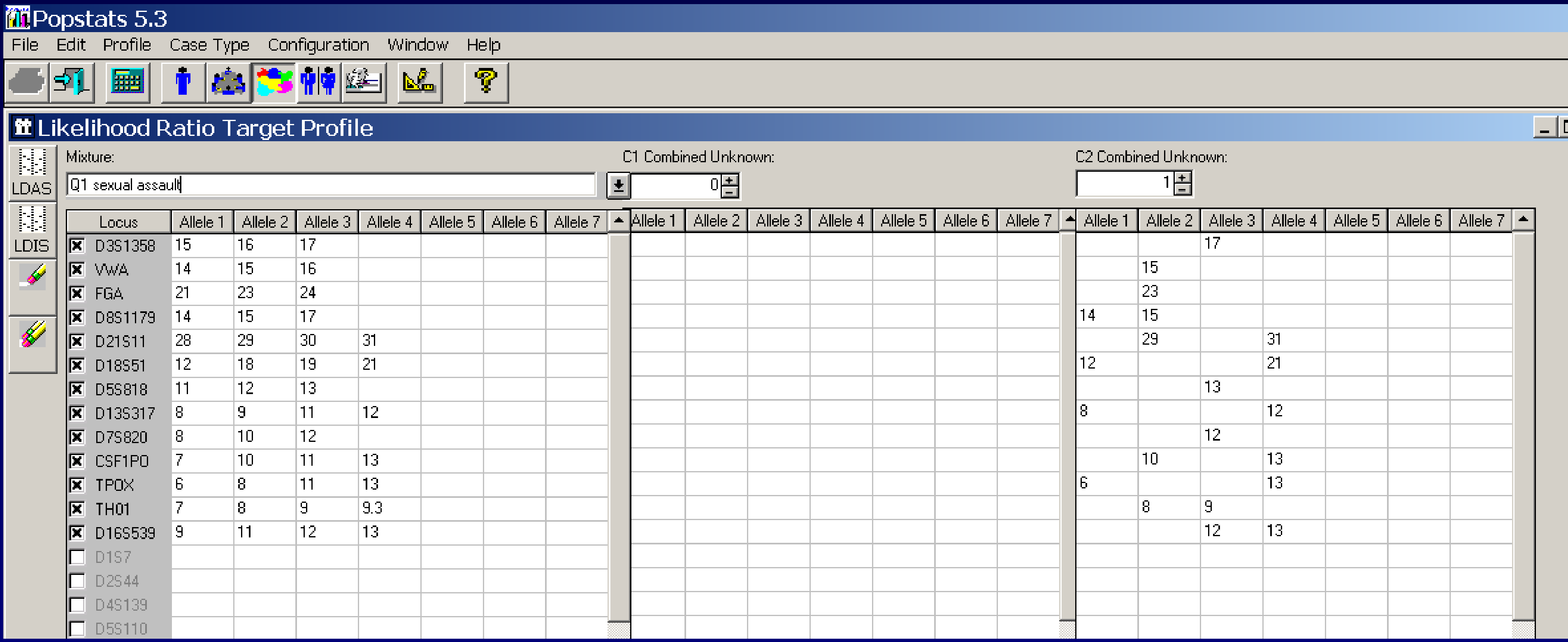
C1 Combined Unknown:

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7

C2 Combined Unknown:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358			17				
VWA		15					
FGA		23					
D8S1179	14	15					
D21S11		29		31			
D18S51	12			21			
D5S818			13				
D13S317	8			12			
D7S820			12				
CSF1PO		10		13			
TPOX	6			13			
TH01		8	9				
D16S539			12	13			

The "profile" in C2 represents all of the alleles not accounted for by the hypothesis…in this case all non-victim alleles



Mixture: Q1 sexual assault

C1 Combined Unknown: 0

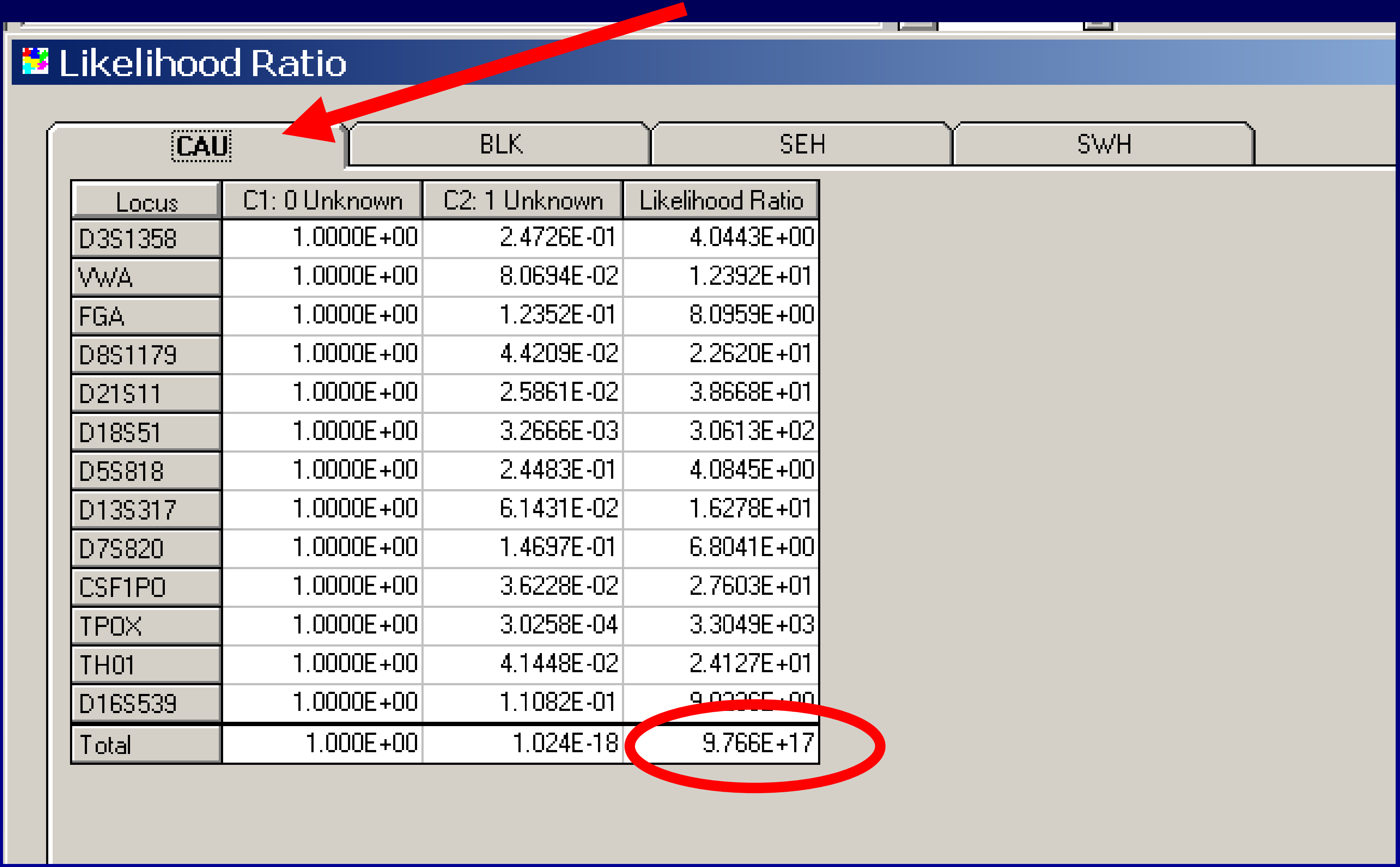
C2 Combined Unknown: 1

	Mixture							C1 Combined Unknown							C2 Combined Unknown						
Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	15	16	17														17				
☒ VWA	14	15	16													15					
☒ FGA	21	23	24													23					
☒ D8S1179	14	15	17												14	15					
☒ D21S11	28	29	30	31												29		31			
☒ D18S51	12	18	19	21											12			21			
☒ D5S818	11	12	13														13				
☒ D13S317	8	9	11	12											8			12			
☒ D7S820	8	10	12														12				
☒ CSF1PO	7	10	11	13												10		13			
☒ TPOX	6	8	11	13											6			13			
☒ TH01	7	8	9	9.3												8	9				
☒ D16S539	9	11	12	13													12	13			
☐ D1S7																					
☐ D2S44																					
☐ D4S139																					
☐ D5S110																					

Notes:

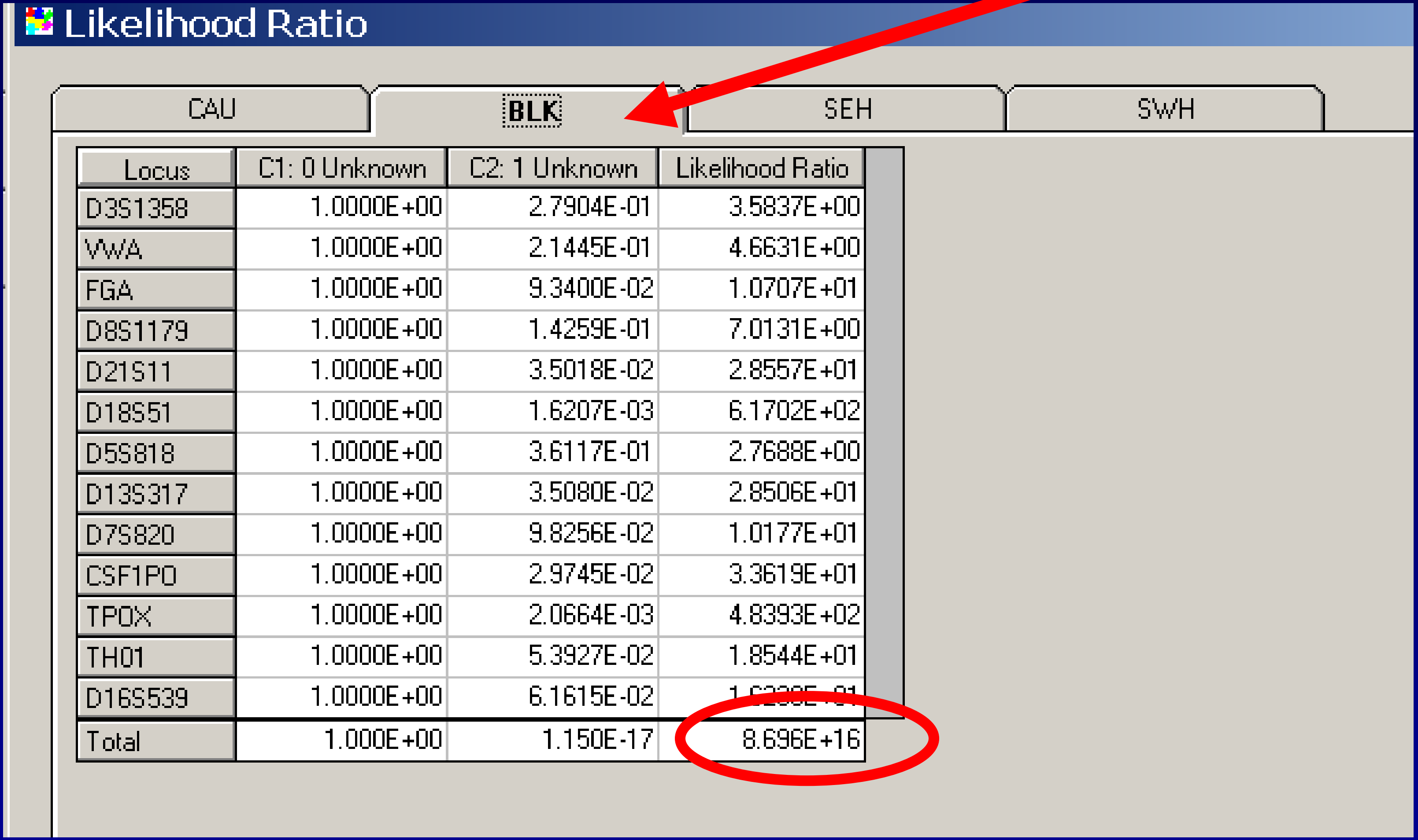
- The layout screen is position sensitive
- Drag and drop the alleles from the "Q1" to the C1 and/or C2 fields

Ok… so what do we get when we push "go"?



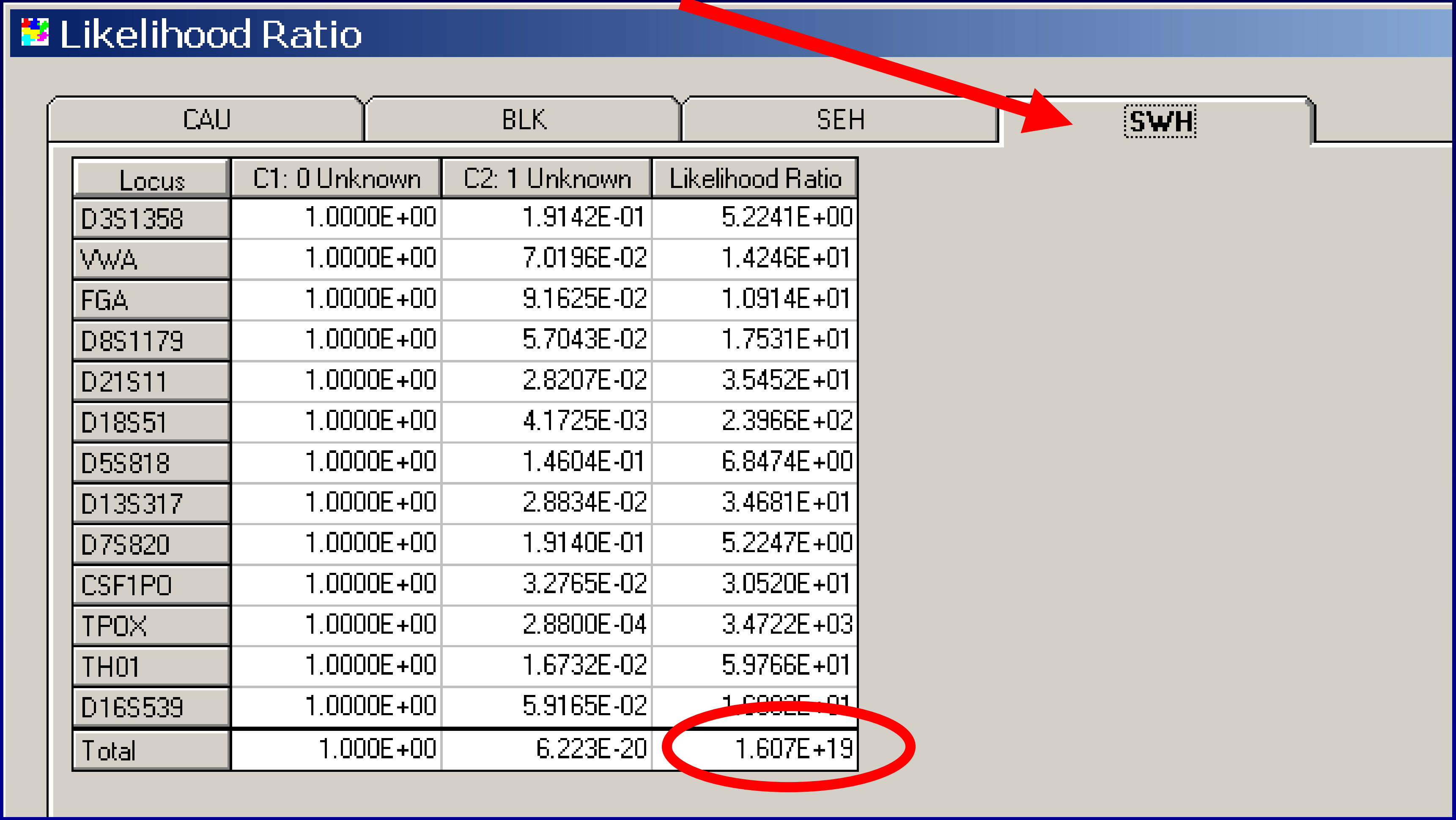
Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	2.4726E-01	4.0443E+00
VWA	1.0000E+00	8.0694E-02	1.2392E+01
FGA	1.0000E+00	1.2352E-01	8.0959E+00
D8S1179	1.0000E+00	4.4209E-02	2.2620E+01
D21S11	1.0000E+00	2.5861E-02	3.8668E+01
D18S51	1.0000E+00	3.2666E-03	3.0613E+02
D5S818	1.0000E+00	2.4483E-01	4.0845E+00
D13S317	1.0000E+00	6.1431E-02	1.6278E+01
D7S820	1.0000E+00	1.4697E-01	6.8041E+00
CSF1PO	1.0000E+00	3.6228E-02	2.7603E+01
TPOX	1.0000E+00	3.0258E-04	3.3049E+03
TH01	1.0000E+00	4.1448E-02	2.4127E+01
D16S539	1.0000E+00	1.1082E-01	9.0236E+00
Total	1.000E+00	1.024E-18	9.766E+17

Ok… so what do we get when we push "go"?



Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	2.7904E-01	3.5837E+00
VWA	1.0000E+00	2.1445E-01	4.6631E+00
FGA	1.0000E+00	9.3400E-02	1.0707E+01
D8S1179	1.0000E+00	1.4259E-01	7.0131E+00
D21S11	1.0000E+00	3.5018E-02	2.8557E+01
D18S51	1.0000E+00	1.6207E-03	6.1702E+02
D5S818	1.0000E+00	3.6117E-01	2.7688E+00
D13S317	1.0000E+00	3.5080E-02	2.8506E+01
D7S820	1.0000E+00	9.8256E-02	1.0177E+01
CSF1PO	1.0000E+00	2.9745E-02	3.3619E+01
TPOX	1.0000E+00	2.0664E-03	4.8393E+02
TH01	1.0000E+00	5.3927E-02	1.8544E+01
D16S539	1.0000E+00	6.1615E-02	1.6230E+01
Total	1.000E+00	1.150E-17	8.696E+16

Ok… so what do we get when we push "go"?



Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	1.9142E-01	5.2241E+00
VWA	1.0000E+00	7.0196E-02	1.4246E+01
FGA	1.0000E+00	9.1625E-02	1.0914E+01
D8S1179	1.0000E+00	5.7043E-02	1.7531E+01
D21S11	1.0000E+00	2.8207E-02	3.5452E+01
D18S51	1.0000E+00	4.1725E-03	2.3966E+02
D5S818	1.0000E+00	1.4604E-01	6.8474E+00
D13S317	1.0000E+00	2.8834E-02	3.4681E+01
D7S820	1.0000E+00	1.9140E-01	5.2247E+00
CSF1PO	1.0000E+00	3.2765E-02	3.0520E+01
TPOX	1.0000E+00	2.8800E-04	3.4722E+03
TH01	1.0000E+00	1.6732E-02	5.9766E+01
D16S539	1.0000E+00	5.9165E-02	1.6902E+01
Total	1.000E+00	6.223E-20	1.607E+19

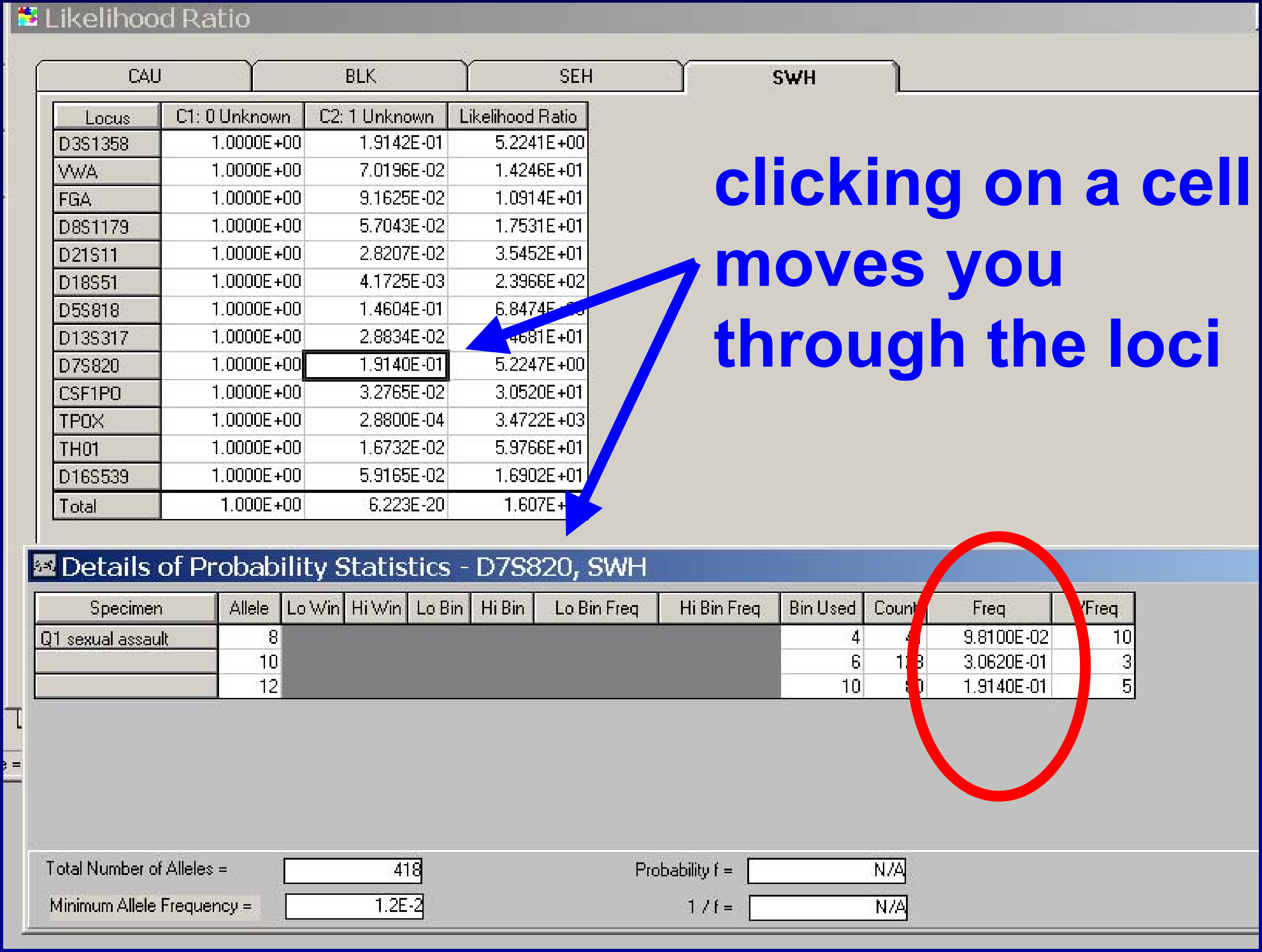
Big Number Names:

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

What about verbiage?

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

You could also look at what the allele frequencies for the target alleles are in the details screen



Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	1.9142E-01	5.2241E+00
VWA	1.0000E+00	7.0196E-02	1.4246E+01
FGA	1.0000E+00	9.1625E-02	1.0914E+01
D8S1179	1.0000E+00	5.7043E-02	1.7531E+01
D21S11	1.0000E+00	2.8207E-02	3.5452E+01
D18S51	1.0000E+00	4.1725E-03	2.3966E+02
D5S818	1.0000E+00	1.4604E-01	6.8474E[illegible]
D13S317	1.0000E+00	2.8834E-02	[illegible]4681E+01
D7S820	1.0000E+00	1.9140E-01	5.2247E+00
CSF1PO	1.0000E+00	3.2765E-02	3.0520E+01
TPOX	1.0000E+00	2.8800E-04	3.4722E+03
TH01	1.0000E+00	1.6732E-02	5.9766E+01
D16S539	1.0000E+00	5.9165E-02	1.6902E+01
Total	1.000E+00	6.223E-20	1.607E+[illegible]

clicking on a cell moves you through the loci

Details of Probability Statistics - D7S820, SWH

Specimen	Allele	Lo Win	Hi Win	Lo Bin	Hi Bin	Lo Bin Freq	Hi Bin Freq	Bin Used	Count	Freq	/Freq
Q1 sexual assault	8							4	[illegible]	9.8100E-02	10
	10							6	[illegible]	3.0620E-01	3
	12							10	[illegible]	1.9140E-01	5

Total Number of Alleles = 418

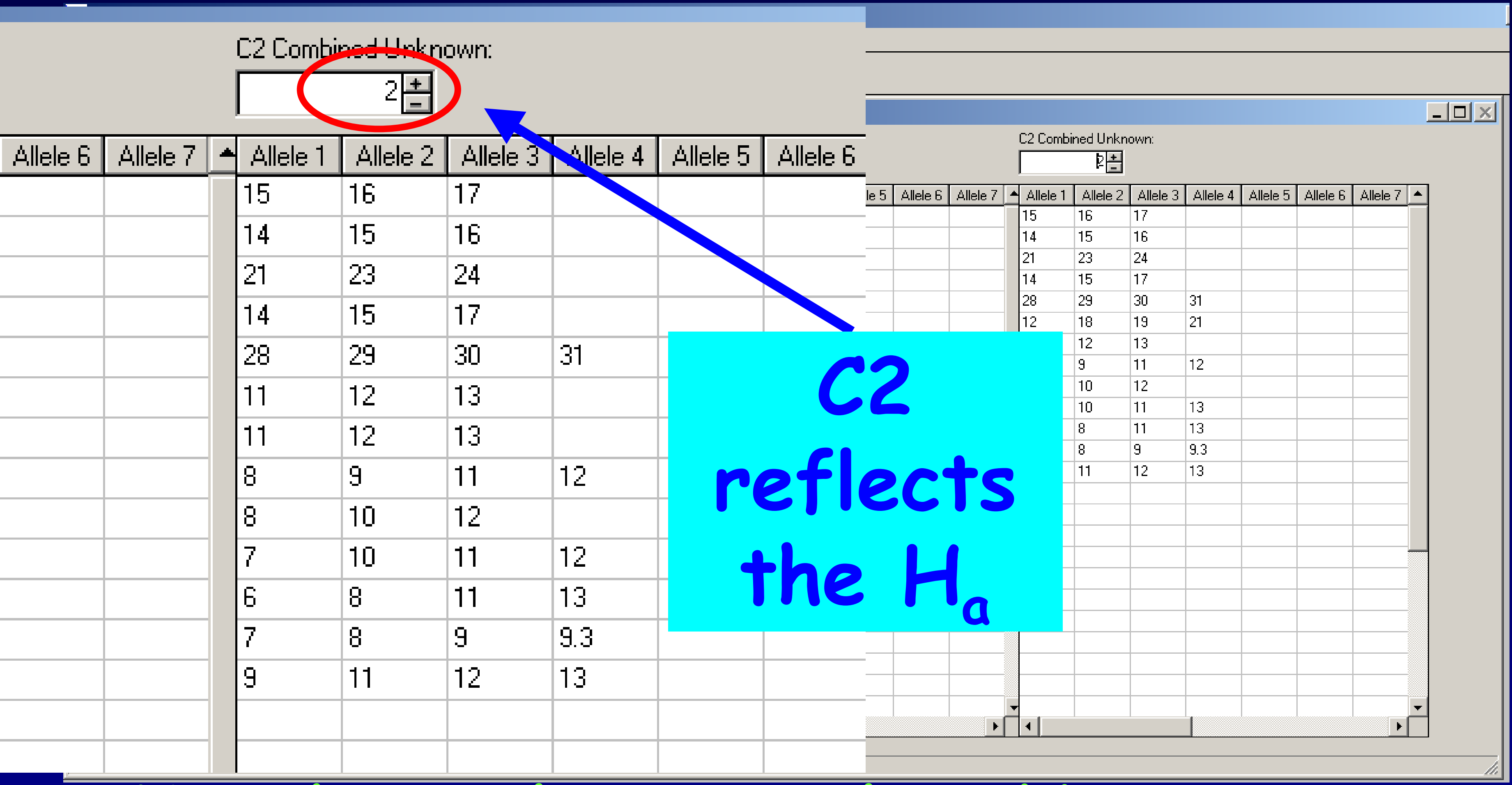
Minimum Allele Frequency = 1.2E-2

Probability f = N/A

1 / f = N/A

What if we wanted to test the other alternate hypothesis?

H_{a2}= The results are explained by a mixture of DNA derived from two unknown, unrelated individuals.



C2 Combined Unknown: 2

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6
15	16	17			
14	15	16			
21	23	24			
14	15	17			
28	29	30	31		
11	12	13			
11	12	13			
8	9	11	12		
8	10	12			
7	10	11	12		
6	8	11	13		
7	8	9	9.3		
9	11	12	13		

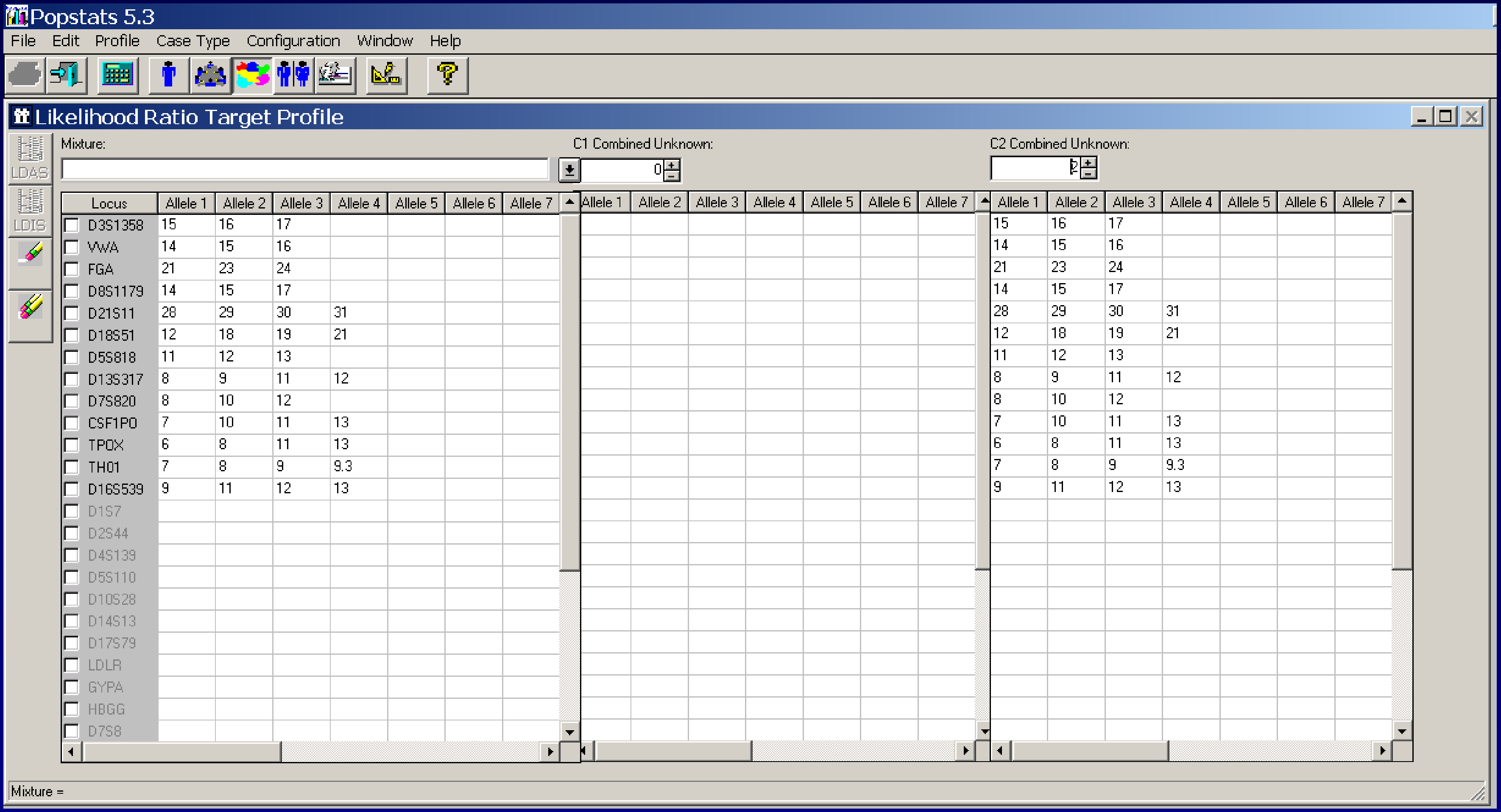
C2 Combined Unknown: 2

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
15	16	17				
14	15	16				
21	23	24				
14	15	17				
28	29	30	31			
12	18	19	21			
[illegible]	12	13				
[illegible]	9	11	12			
[illegible]	10	12				
[illegible]	10	11	13			
[illegible]	8	11	13			
[illegible]	8	9	9.3			
[illegible]	11	12	13			

C2 reflects the H_a

H_a= The results are explained by a mixture of DNA derived from two unknown, unrelated individuals

WRITE IT DOWN!!!



Mixture:

C1 Combined Unknown: 0

C2 Combined Unknown: 2

	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☐	D3S1358	15	16	17				
☐	VWA	14	15	16				
☐	FGA	21	23	24				
☐	D8S1179	14	15	17				
☐	D21S11	28	29	30	31			
☐	D18S51	12	18	19	21			
☐	D5S818	11	12	13				
☐	D13S317	8	9	11	12			
☐	D7S820	8	10	12				
☐	CSF1PO	7	10	11	13			
☐	TPOX	6	8	11	13			
☐	TH01	7	8	9	9.3			
☐	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							
☐	D5S110							
☐	D10S28							
☐	D14S13							
☐	D17S79							
☐	LDLR							
☐	GYPA							
☐	HBGG							
☐	D7S8							

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
15	16	17				
14	15	16				
21	23	24				
14	15	17				
28	29	30	31			
12	18	19	21			
11	12	13				
8	9	11	12			
8	10	12				
7	10	11	13			
6	8	11	13			
7	8	9	9.3			
9	11	12	13			

Mixture =

Note: this time the C2 block contains the entire set of alleles present in the Q1 sample.

You can drag and drop the entire field

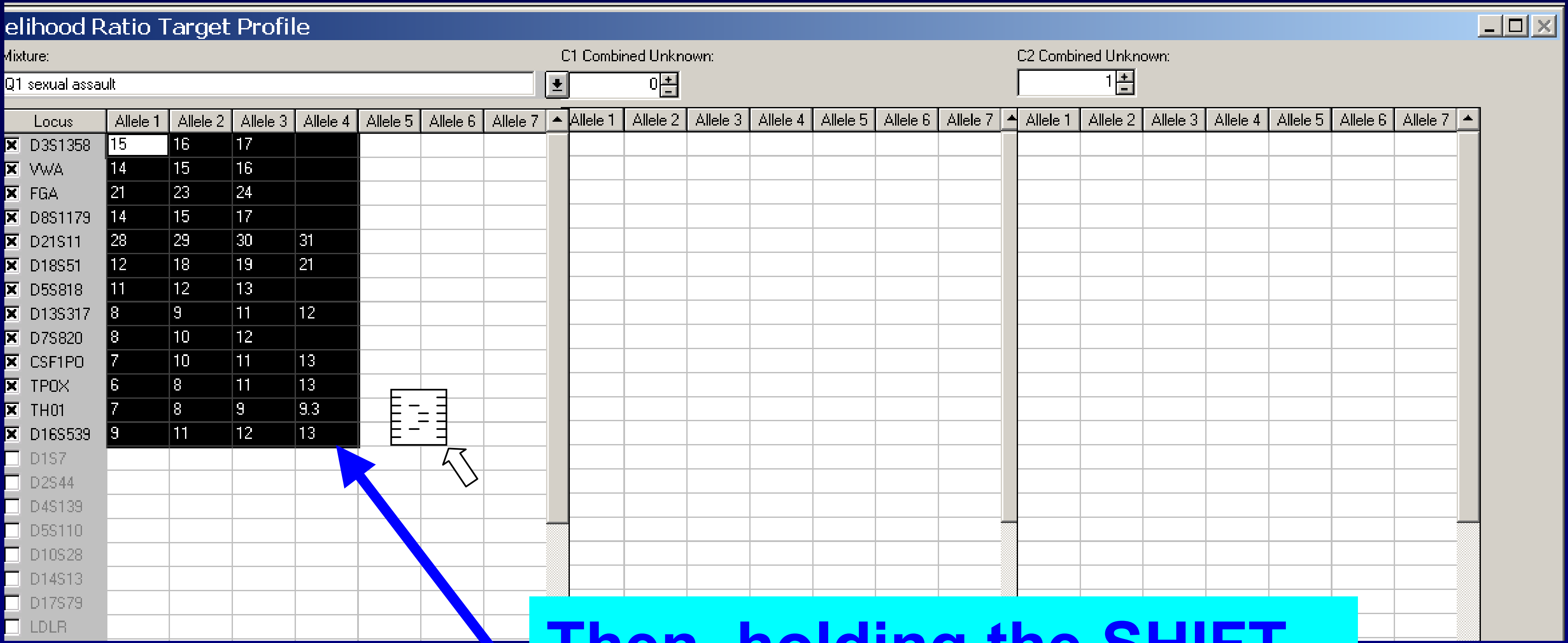
kelihood Ratio Target Profile

Mixture:

Q1 sexual assault

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6
☒ D3S1358	15	16	17			
☒ VWA	14	15	16			
☒ FGA	21	23	24			
☒ D8S1179	14	15	17			
☒ D21S11	28	29	30	31		
☒ D18S51	12	18	19	21		
☒ D5S818	11	12	13			
☒ D13S317	8	9	11	12		
☒ D7S820	8	10	12			
☒ CSF1PO	7	10	11	13		
☒ TPOX	6	8	11	13		
☒ TH01	7	8	9	9.3		
☒ D16S539	9	11	12	13		
☐ D1S7						
☐ D2S44						
☐ D4S139						
☐ D5S110						
☐ D10S28						
☐ D14S13						
☐ D17S79						
☐ LDLR						
☐ GYPA						

First click on the first cell in the field


elihood Ratio Target Profile

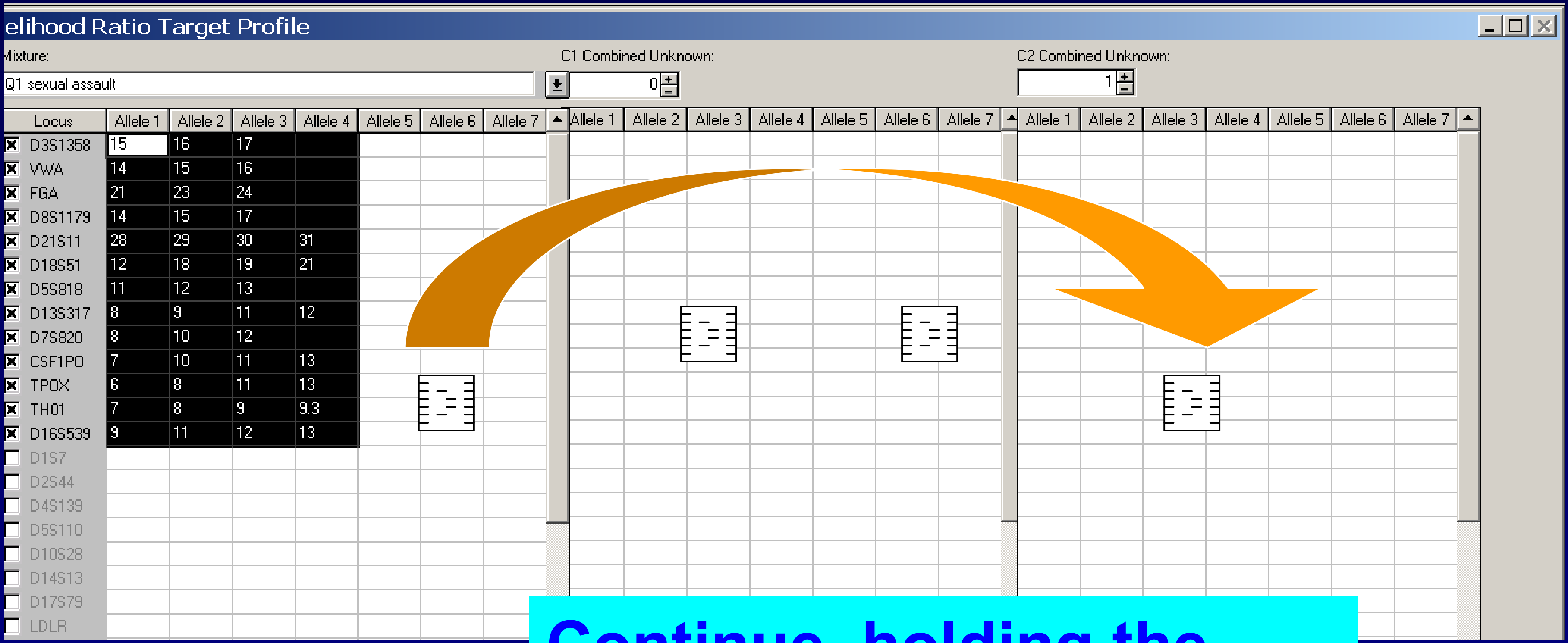
Mixture: Q1 sexual assault

C1 Combined Unknown: 0

C2 Combined Unknown: 1

	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	15	16	17				
☒	VWA	14	15	16				
☒	FGA	21	23	24				
☒	D8S1179	14	15	17				
☒	D21S11	28	29	30	31			
☒	D18S51	12	18	19	21			
☒	D5S818	11	12	13				
☒	D13S317	8	9	11	12			
☒	D7S820	8	10	12				
☒	CSF1PO	7	10	11	13			
☒	TPOX	6	8	11	13			
☒	TH01	7	8	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							
☐	D5S110							
☐	D10S28							
☐	D14S13							
☐	D17S79							
☐	LDLR							

Then, holding the SHIFT button, click on the last cell in the field



elihood Ratio Target Profile

ixture: Q1 sexual assault

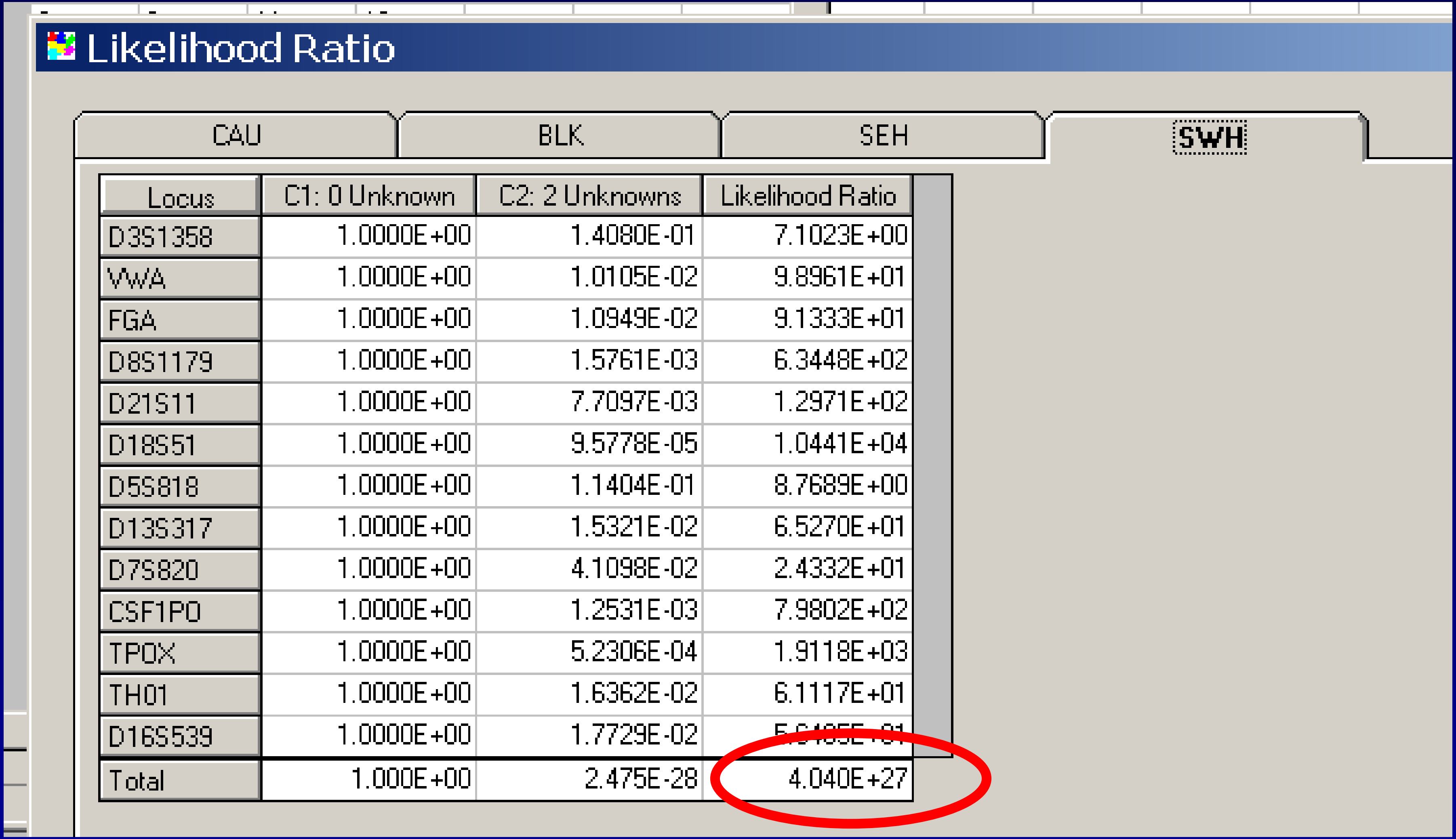
C1 Combined Unknown: 0

C2 Combined Unknown: 1

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	15	16	17				
☒ VWA	14	15	16				
☒ FGA	21	23	24				
☒ D8S1179	14	15	17				
☒ D21S11	28	29	30	31			
☒ D18S51	12	18	19	21			
☒ D5S818	11	12	13				
☒ D13S317	8	9	11	12			
☒ D7S820	8	10	12				
☒ CSF1PO	7	10	11	13			
☒ TPOX	6	8	11	13			
☒ TH01	7	8	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							
☐ D2S44							
☐ D4S139							
☐ D5S110							
☐ D10S28							
☐ D14S13							
☐ D17S79							
☐ LDLR							

Continue, holding the SHIFT button and drag and drop in appropriate field

So, what do we get?



Locus	C1: 0 Unknown	C2: 2 Unknowns	Likelihood Ratio
D3S1358	1.0000E+00	1.4080E-01	7.1023E+00
VWA	1.0000E+00	1.0105E-02	9.8961E+01
FGA	1.0000E+00	1.0949E-02	9.1333E+01
D8S1179	1.0000E+00	1.5761E-03	6.3448E+02
D21S11	1.0000E+00	7.7097E-03	1.2971E+02
D18S51	1.0000E+00	9.5778E-05	1.0441E+04
D5S818	1.0000E+00	1.1404E-01	8.7689E+00
D13S317	1.0000E+00	1.5321E-02	6.5270E+01
D7S820	1.0000E+00	4.1098E-02	2.4332E+01
CSF1PO	1.0000E+00	1.2531E-03	7.9802E+02
TPOX	1.0000E+00	5.2306E-04	1.9118E+03
TH01	1.0000E+00	1.6362E-02	6.1117E+01
D16S539	1.0000E+00	1.7729E-02	5.6405E+01
Total	1.000E+00	2.475E-28	4.040E+27

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

In this case it is even less likely

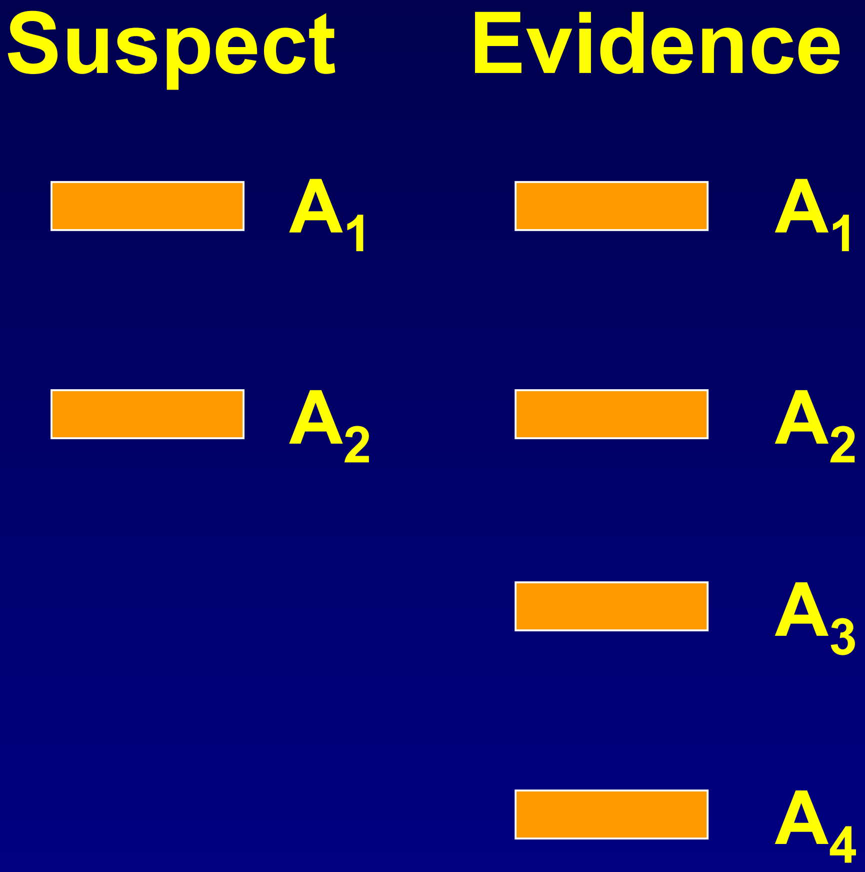
Based on the Hispanic population data available, the observed mixture profile is greater than 4 octillion times more likely to occur under the scenario that it is a mixture of DNA from the victim and the suspect, as opposed to the scenario that it originated from a mixture of DNA from two unrelated, unknown persons.

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?



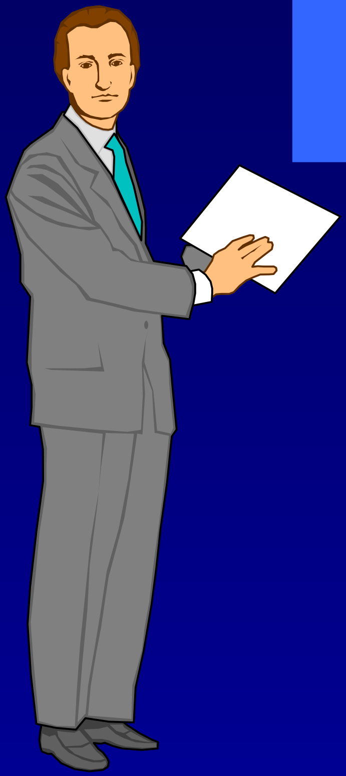
Four Allele Scenario

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

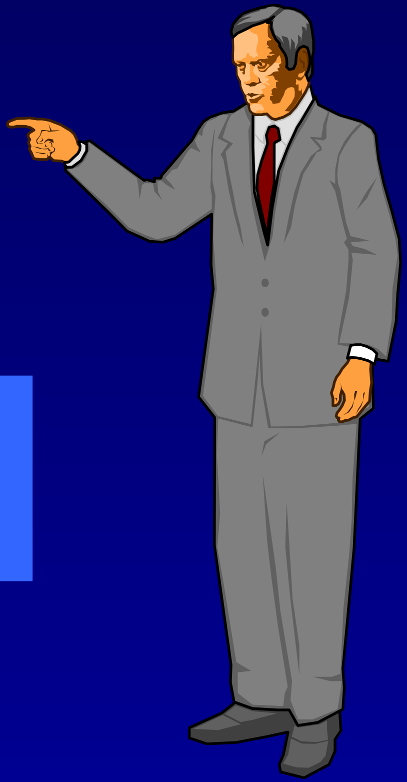


Prosecution

DNA is from suspect
and unknown

Defense

DNA is from two
unknown persons

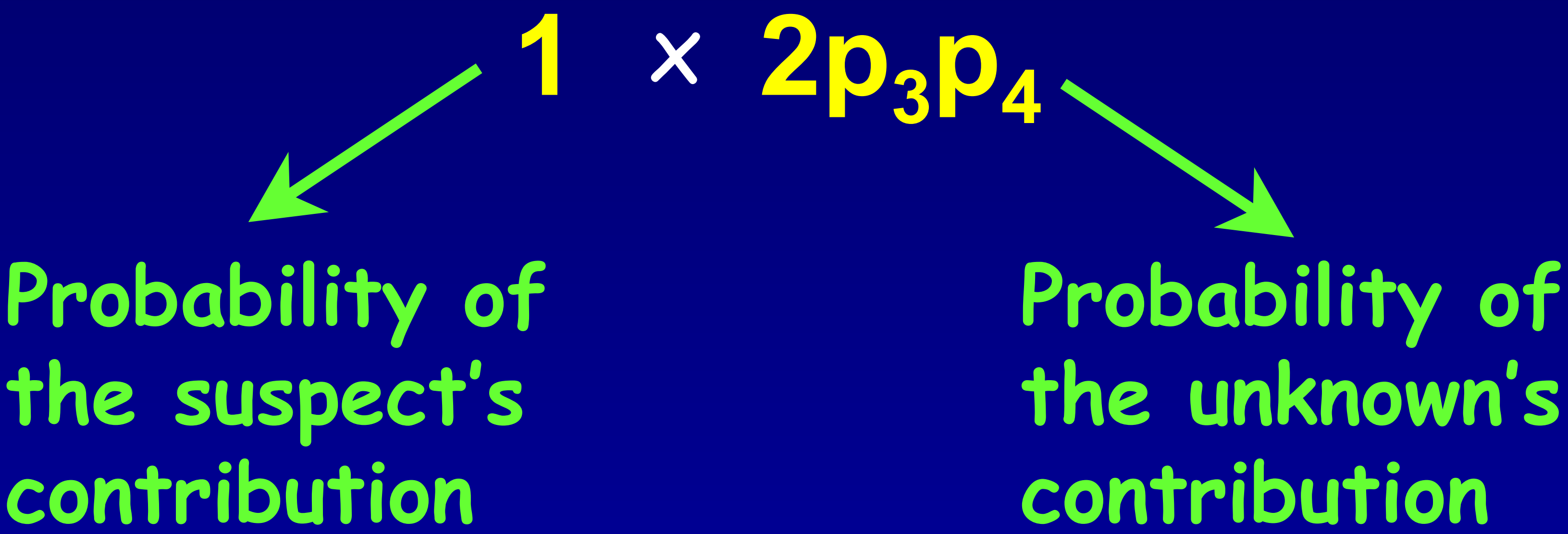


The prosecution may postulate that the suspect and and an unknown explain all alleles seen in the mixture.

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 $p_1 = 0.15$ & $p_2 = 0.2$

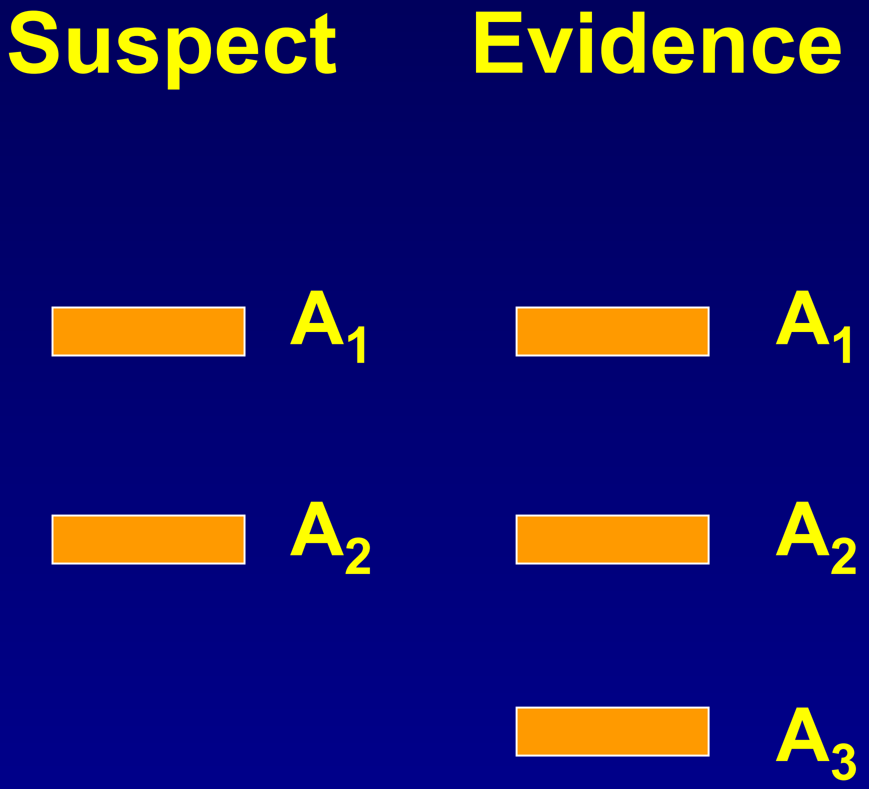
$$\frac{1}{12p_1\,p_2} = \frac{1}{12(0.15)(0.2)}$$

$$\approx \quad 3$$

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

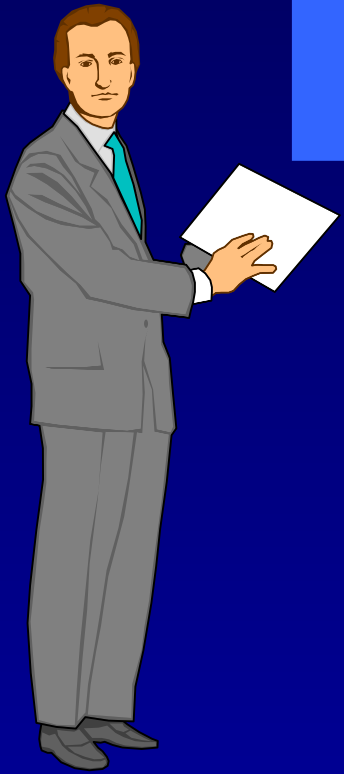
Same question as before but…

Three Alleles

Two match the suspect - A_1A_2

The unknown contributes- at least A_3

Mutually Exclusive Hypotheses

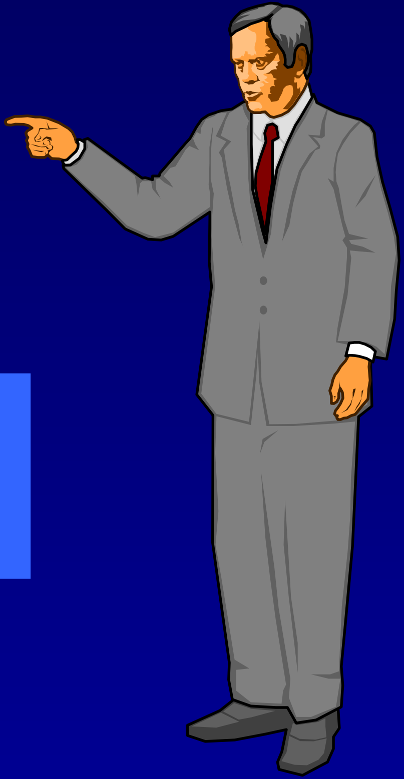


Prosecution

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 $p_3^2 \text{ x } 2p_2p_3$
A_2A_2 A_1A_3 $p_2^2 \text{ x } 2p_1 p_3$
A_3A_3 A_1A_2 $p_3^2 \text{ x } 2p_1p_2$

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

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,

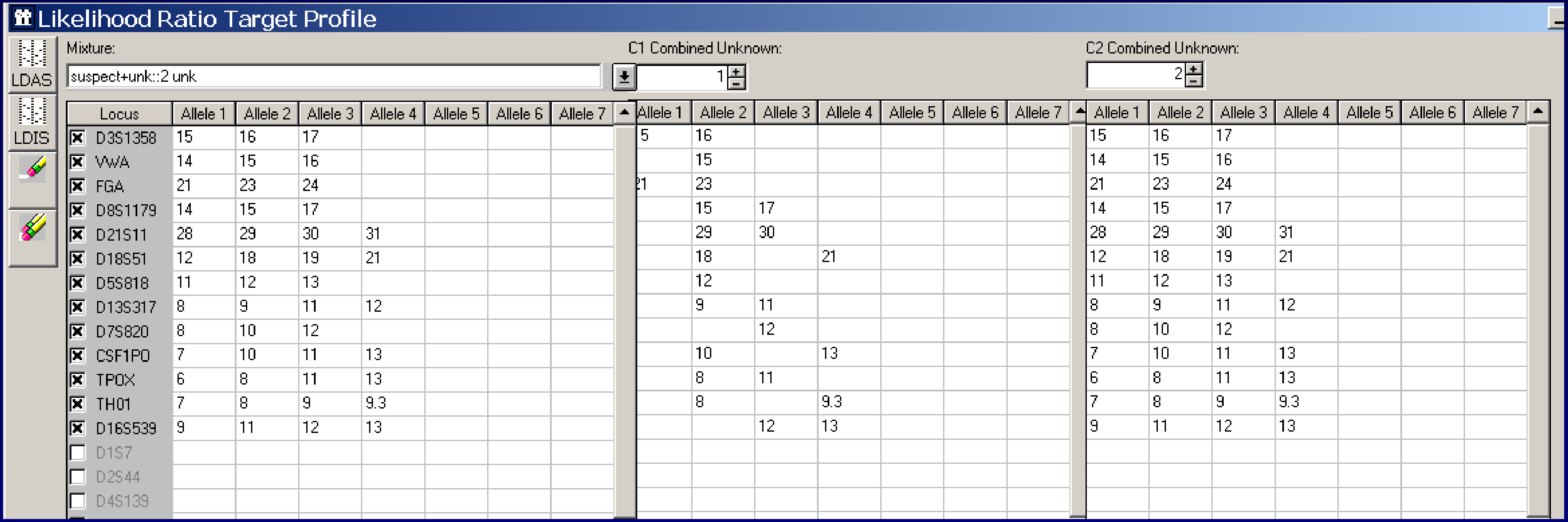
Compared with the prosecution's hypothesis (H_0), the defense scenario (H_1) is

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

So, with regard to the Defense Hypothesis 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.

Of course we can do this in PopStats as well



Mixture: suspect+unk::2 unk

C1 Combined Unknown: 1

C2 Combined Unknown: 2

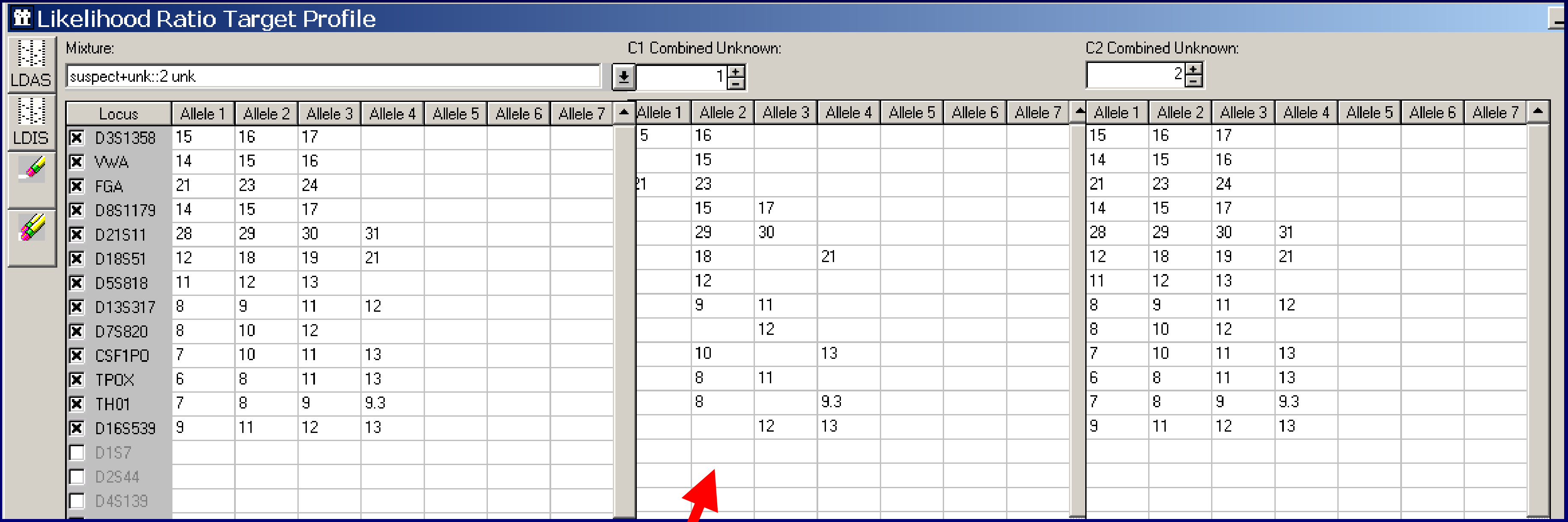
	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	15	16	17				
☒	VWA	14	15	16				
☒	FGA	21	23	24				
☒	D8S1179	14	15	17				
☒	D21S11	28	29	30	31			
☒	D18S51	12	18	19	21			
☒	D5S818	11	12	13				
☒	D13S317	8	9	11	12			
☒	D7S820	8	10	12				
☒	CSF1PO	7	10	11	13			
☒	TPOX	6	8	11	13			
☒	TH01	7	8	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
5	16					
	15					
21	23					
	15	17				
	29	30				
	18		21			
	12					
	9	11				
		12				
	10		13			
	8	11				
	8		9.3			
		12	13			

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
15	16	17				
14	15	16				
21	23	24				
14	15	17				
28	29	30	31			
12	18	19	21			
11	12	13				
8	9	11	12			
8	10	12				
7	10	11	13			
6	8	11	13			
7	8	9	9.3			
9	11	12	13			

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

Of course we can do this in PopStats as well



Likelihood Ratio Target Profile

Mixture: suspect+unk::2 unk

C1 Combined Unknown: 1

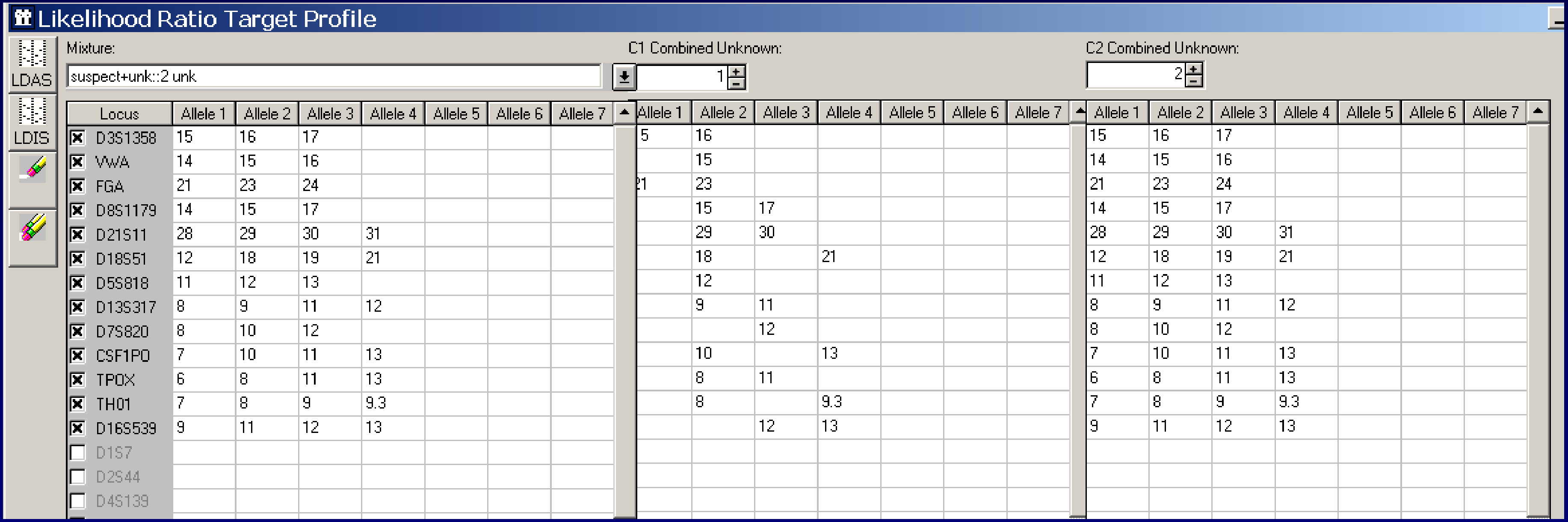
C2 Combined Unknown: 2

	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	15	16	17				
☒	VWA	14	15	16				
☒	FGA	21	23	24				
☒	D8S1179	14	15	17				
☒	D21S11	28	29	30	31			
☒	D18S51	12	18	19	21			
☒	D5S818	11	12	13				
☒	D13S317	8	9	11	12			
☒	D7S820	8	10	12				
☒	CSF1PO	7	10	11	13			
☒	TPOX	6	8	11	13			
☒	TH01	7	8	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
5	16					
	15					
21	23					
	15	17				
	29	30				
	18		21			
	12					
	9	11				
		12				
	10		13			
	8	11				
	8		9.3			
		12	13			

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
15	16	17				
14	15	16				
21	23	24				
14	15	17				
28	29	30	31			
12	18	19	21			
11	12	13				
8	9	11	12			
8	10	12				
7	10	11	13			
6	8	11	13			
7	8	9	9.3			
9	11	12	13			

C1 lists the alleles not attributable to the suspect



Likelihood Ratio Target Profile

Mixture: suspect+unk::2 unk

C1 Combined Unknown: 1

C2 Combined Unknown: 2

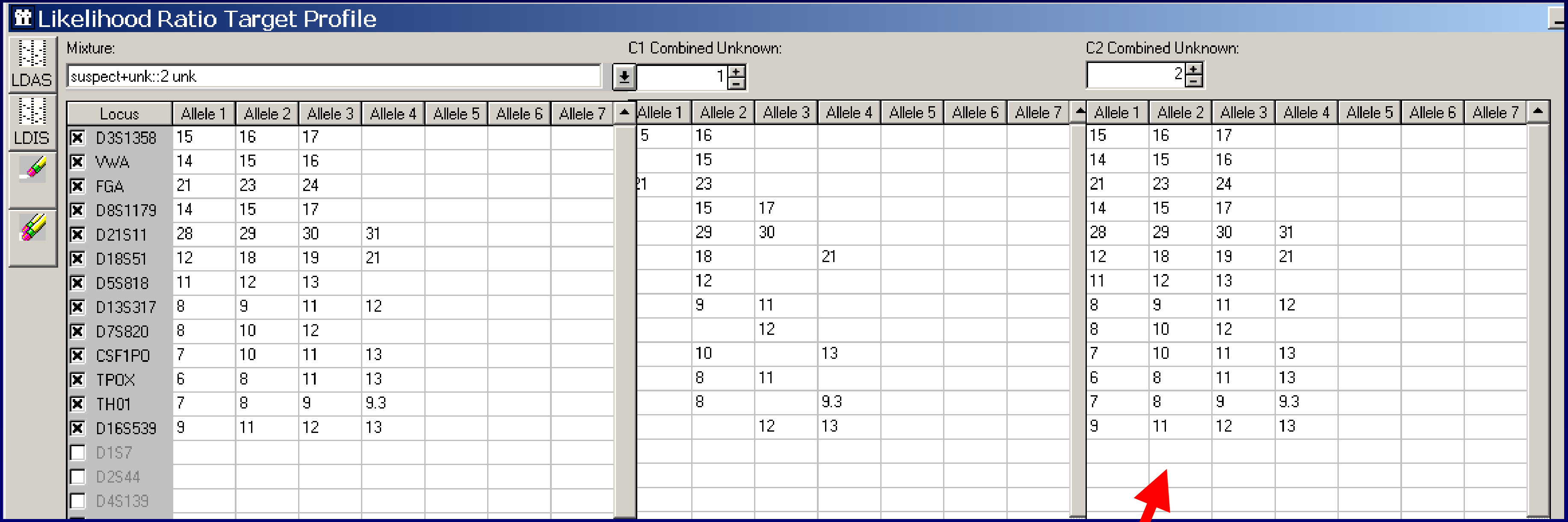
	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	15	16	17				
☒	VWA	14	15	16				
☒	FGA	21	23	24				
☒	D8S1179	14	15	17				
☒	D21S11	28	29	30	31			
☒	D18S51	12	18	19	21			
☒	D5S818	11	12	13				
☒	D13S317	8	9	11	12			
☒	D7S820	8	10	12				
☒	CSF1PO	7	10	11	13			
☒	TPOX	6	8	11	13			
☒	TH01	7	8	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
5	16					
	15					
21	23					
	15	17				
	29	30				
	18		21			
	12					
	9	11				
		12				
	10		13			
	8	11				
	8		9.3			
		12	13			

Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
15	16	17				
14	15	16				
21	23	24				
14	15	17				
28	29	30	31			
12	18	19	21			
11	12	13				
8	9	11	12			
8	10	12				
7	10	11	13			
6	8	11	13			
7	8	9	9.3			
9	11	12	13			

H_a: The mixture originated from two unknown persons

Of course we can do this in PopStats as well



Likelihood Ratio Target Profile

Mixture: suspect+unk::2 unk

C1 Combined Unknown: 1

C2 Combined Unknown: 2

Mixture:

	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	15	16	17				
☒	VWA	14	15	16				
☒	FGA	21	23	24				
☒	D8S1179	14	15	17				
☒	D21S11	28	29	30	31			
☒	D18S51	12	18	19	21			
☒	D5S818	11	12	13				
☒	D13S317	8	9	11	12			
☒	D7S820	8	10	12				
☒	CSF1PO	7	10	11	13			
☒	TPOX	6	8	11	13			
☒	TH01	7	8	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							

C1 Combined Unknown:

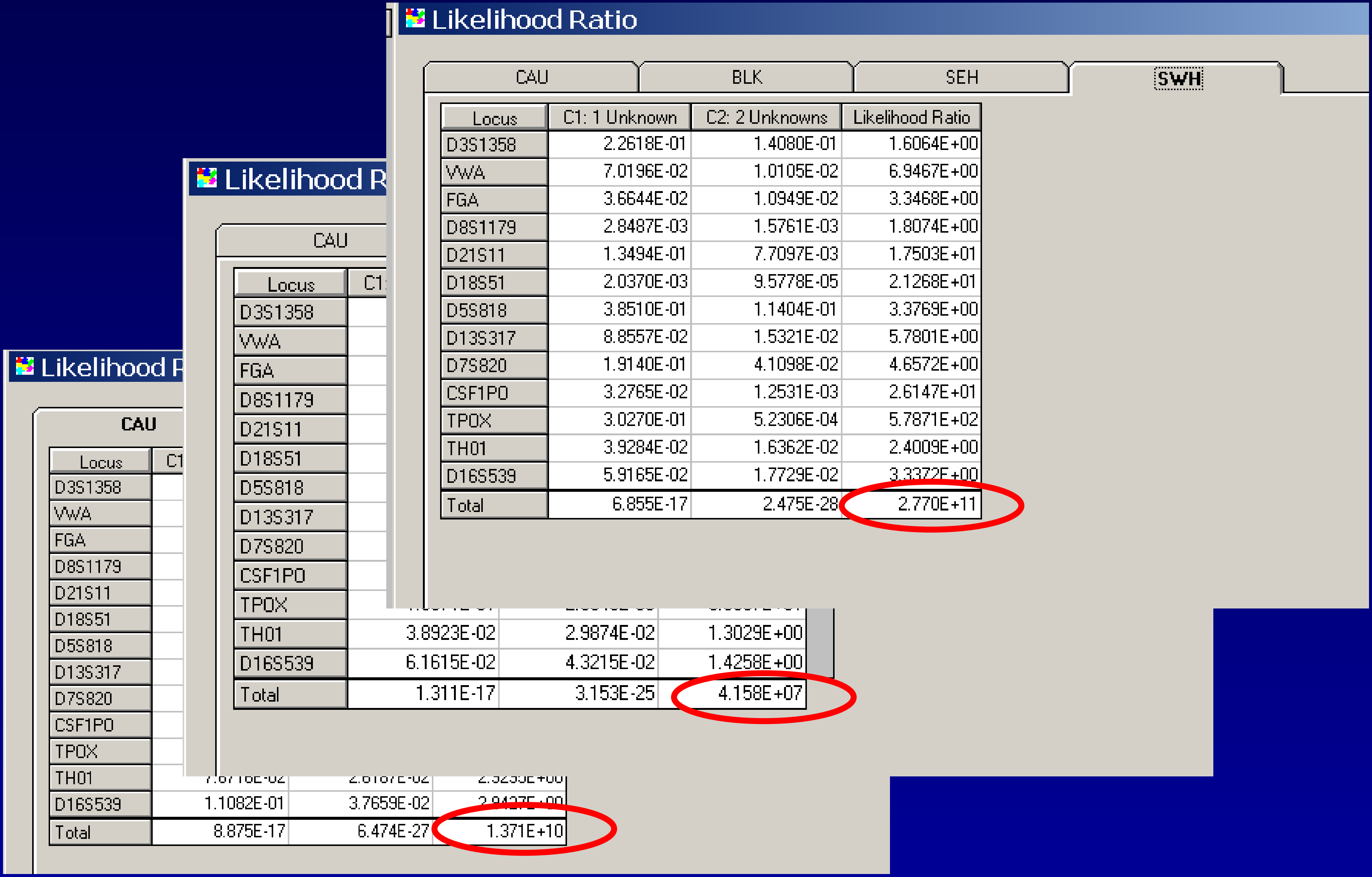
Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358	5	16					
VWA		15					
FGA	21	23					
D8S1179		15	17				
D21S11		29	30				
D18S51		18		21			
D5S818		12					
D13S317		9	11				
D7S820			12				
CSF1PO		10		13			
TPOX		8	11				
TH01		8		9.3			
D16S539			12	13			
D1S7							
D2S44							
D4S139							

C2 Combined Unknown:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358	15	16	17				
VWA	14	15	16				
FGA	21	23	24				
D8S1179	14	15	17				
D21S11	28	29	30	31			
D18S51	12	18	19	21			
D5S818	11	12	13				
D13S317	8	9	11	12			
D7S820	8	10	12				
CSF1PO	7	10	11	13			
TPOX	6	8	11	13			
TH01	7	8	9	9.3			
D16S539	9	11	12	13			
D1S7							
D2S44							
D4S139							

C2 lists all the alleles detected in the mixture and suggests 2 possible contributors

What do we get?



Locus	C1: 1 Unknown	C2: 2 Unknowns	Likelihood Ratio
D3S1358	2.2618E-01	1.4080E-01	1.6064E+00
VWA	7.0196E-02	1.0105E-02	6.9467E+00
FGA	3.6644E-02	1.0949E-02	3.3468E+00
D8S1179	2.8487E-03	1.5761E-03	1.8074E+00
D21S11	1.3494E-01	7.7097E-03	1.7503E+01
D18S51	2.0370E-03	9.5778E-05	2.1268E+01
D5S818	3.8510E-01	1.1404E-01	3.3769E+00
D13S317	8.8557E-02	1.5321E-02	5.7801E+00
D7S820	1.9140E-01	4.1098E-02	4.6572E+00
CSF1PO	3.2765E-02	1.2531E-03	2.6147E+01
TPOX	3.0270E-01	5.2306E-04	5.7871E+02
TH01	3.9284E-02	1.6362E-02	2.4009E+00
D16S539	5.9165E-02	1.7729E-02	3.3372E+00
Total	6.855E-17	2.475E-28	2.770E+11

Locus			
TH01	3.8923E-02	2.9874E-02	1.3029E+00
D16S539	6.1615E-02	4.3215E-02	1.4258E+00
Total	1.311E-17	3.153E-25	4.158E+07

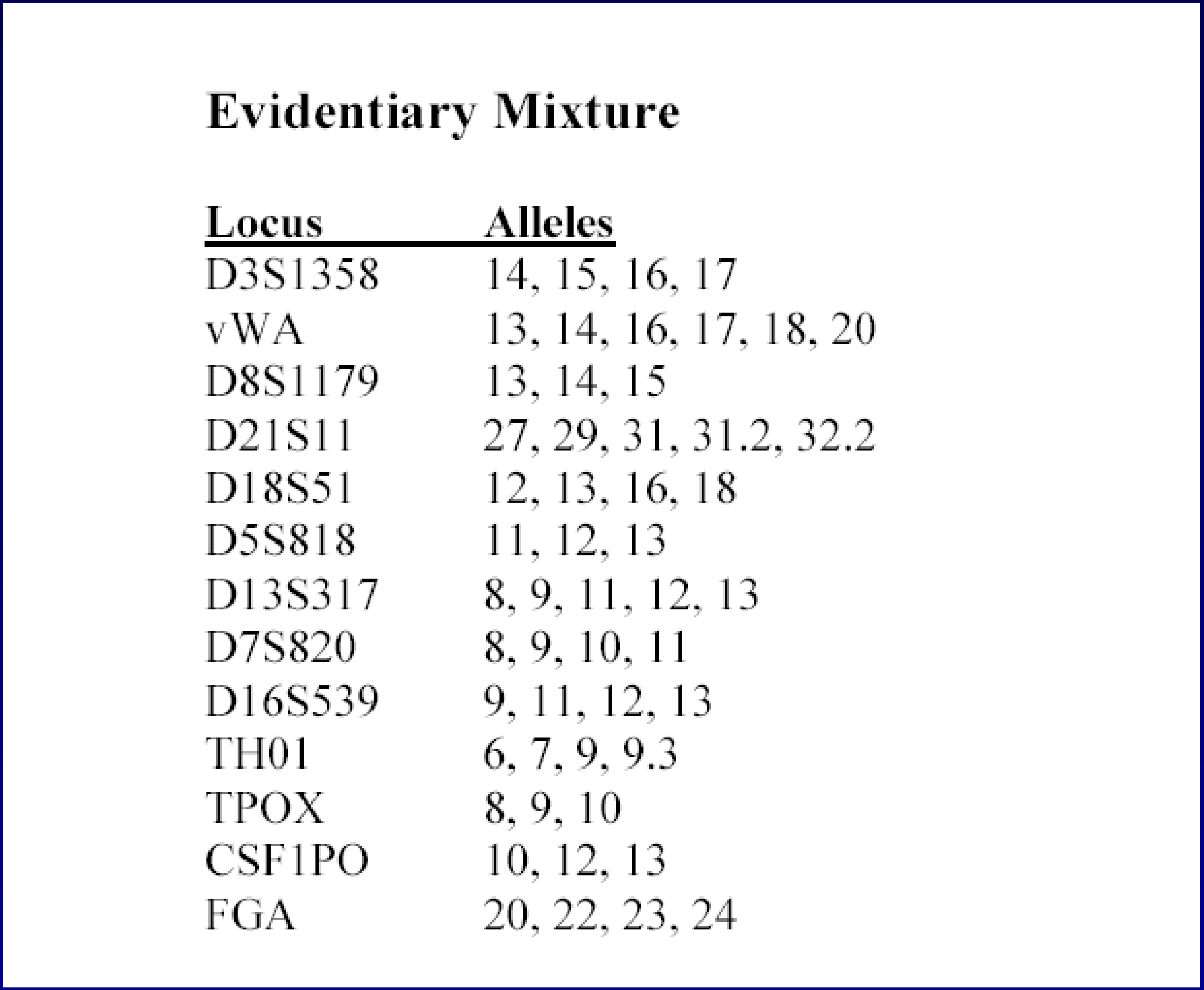
Locus			
D16S539	1.1082E-01	3.7659E-02	2.9427E+00
Total	8.875E-17	6.474E-27	1.371E+10

Now…Let's have some real fun!

Scenario:

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

Our data:

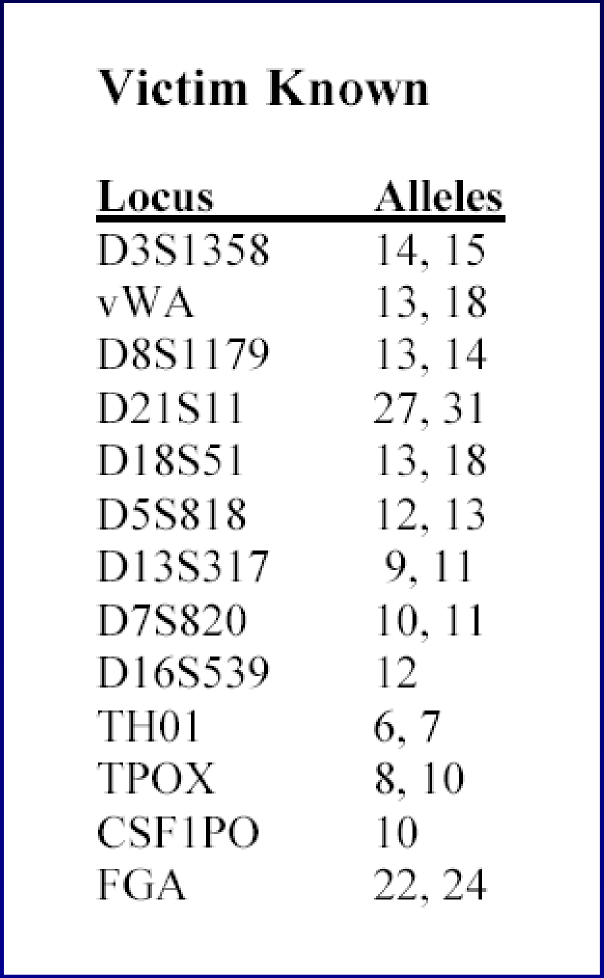


Evidentiary Mixture

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

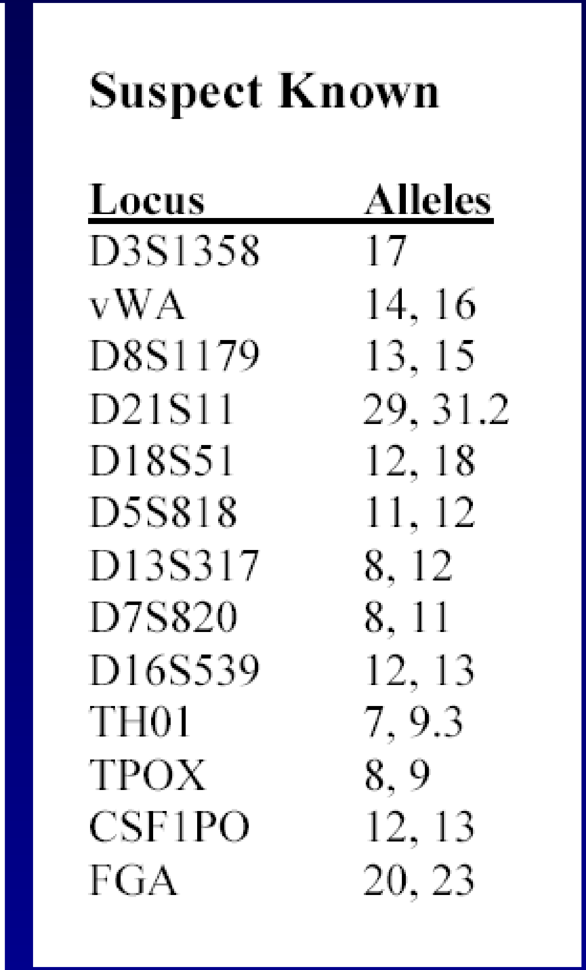
What would you suggest about this mixture??

Our Knowns:



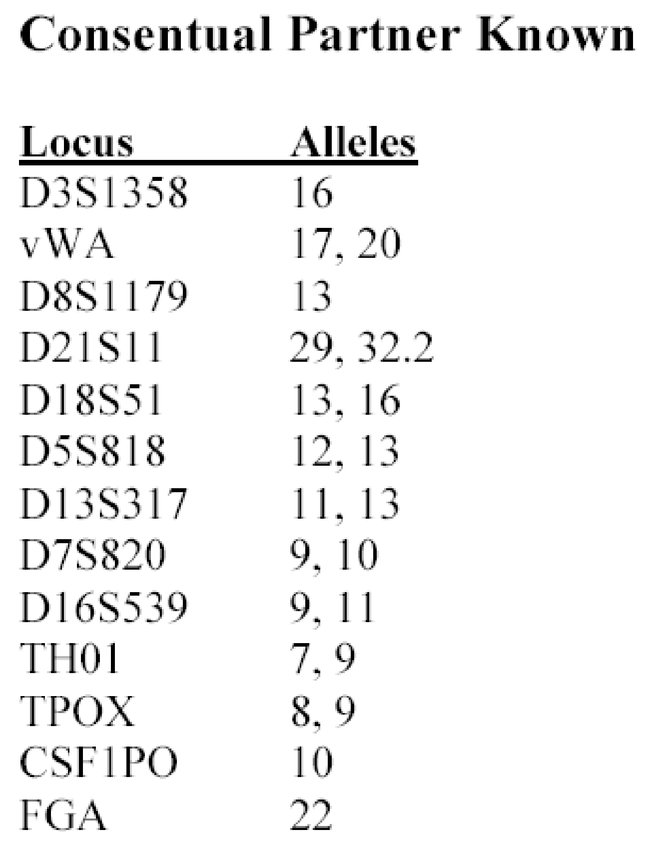
Victim Known

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

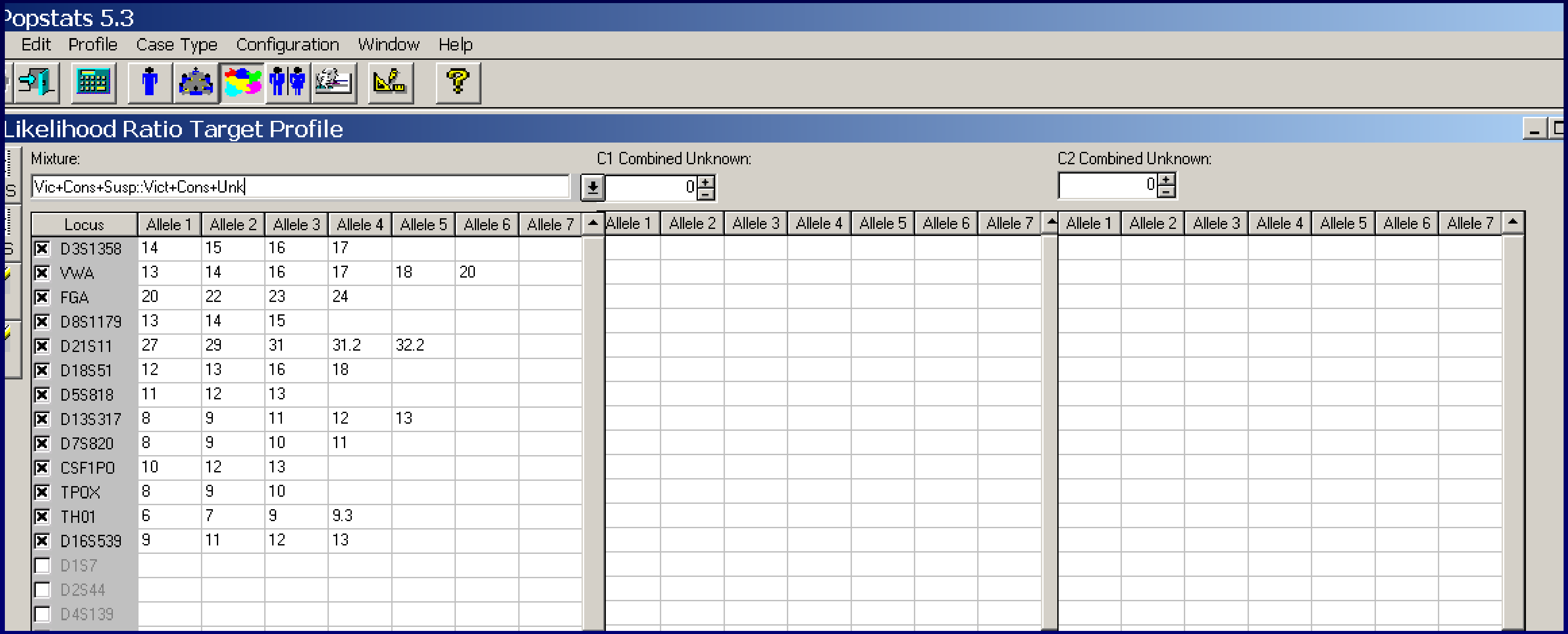
Locus	Alleles
D3S1358	17
vWA	14, 16
D8S1179	13, 15
D21S11	29, 31.2
D18S51	12, 18
D5S818	11, 12
D13S317	8, 12
D7S820	8, 11
D16S539	12, 13
TH01	7, 9.3
TPOX	8, 9
CSF1PO	12, 13
FGA	20, 23



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



Mixture: Vic+Cons+Susp::Vict+Cons+Unk

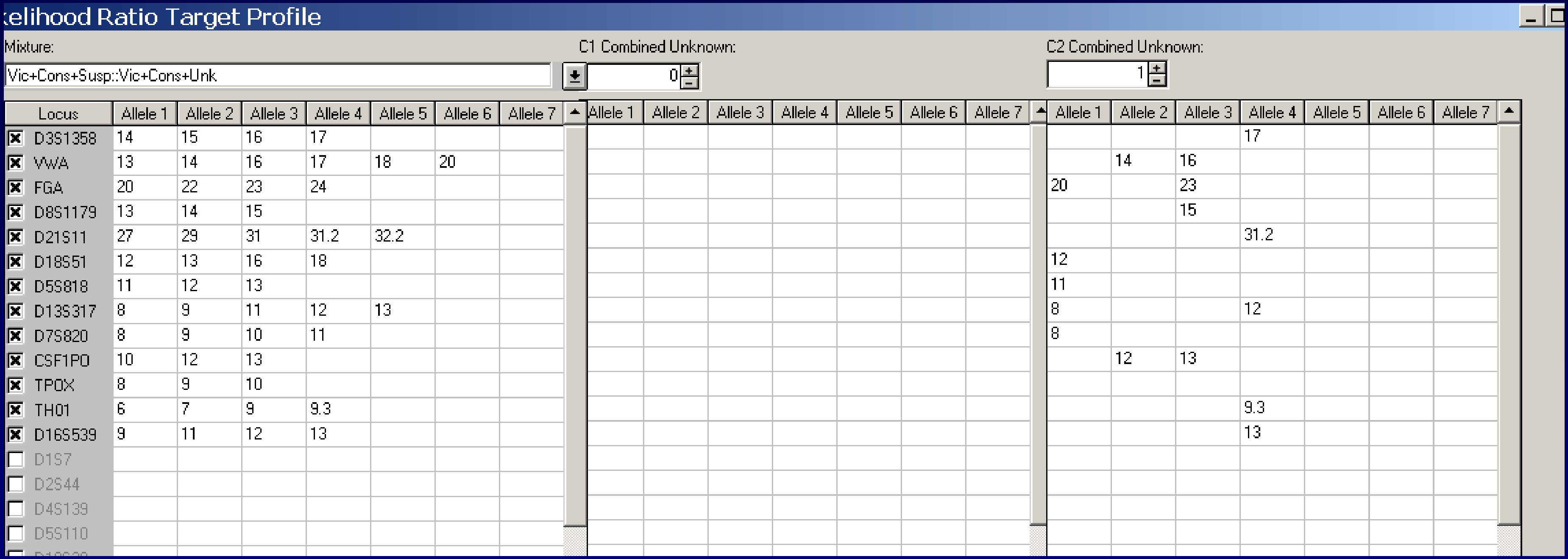
C1 Combined Unknown: 0

C2 Combined Unknown: 0

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	14	15	16	17																	
☒ VWA	13	14	16	17	18	20															
☒ FGA	20	22	23	24																	
☒ 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																	
☒ CSF1PO	10	12	13																		
☒ TPOX	8	9	10																		
☒ TH01	6	7	9	9.3																	
☒ D16S539	9	11	12	13																	
☐ D1S7																					
☐ D2S44																					
☐ D4S139																					

But before we can continue we need our Hypotheses:

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



elihood Ratio Target Profile

Mixture: Vic+Cons+Susp::Vic+Cons+Unk

C1 Combined Unknown: 0

C2 Combined Unknown: 1

Mixture:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	14	15	16	17			
☒ VWA	13	14	16	17	18	20	
☒ FGA	20	22	23	24			
☒ 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			
☒ CSF1PO	10	12	13				
☒ TPOX	8	9	10				
☒ TH01	6	7	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							
☐ D2S44							
☐ D4S139							
☐ D5S110							

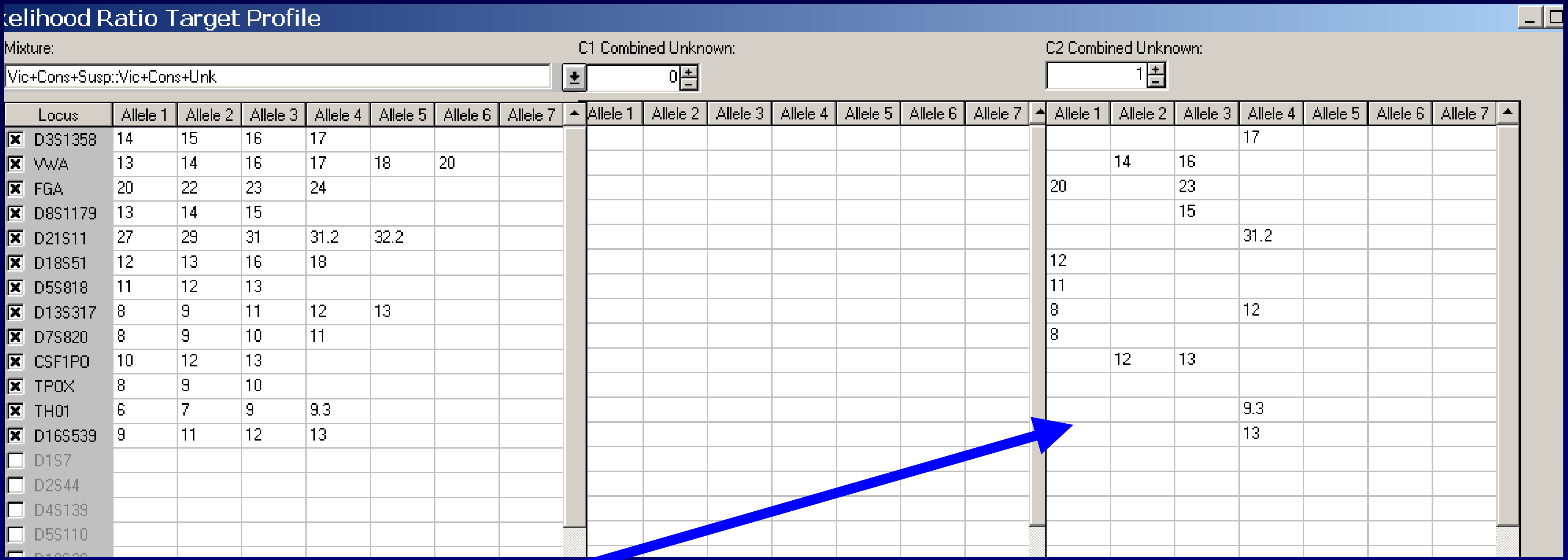
C1 Combined Unknown:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358							
VWA							
FGA							
D8S1179							
D21S11							
D18S51							
D5S818							
D13S317							
D7S820							
CSF1PO							
TPOX							
TH01							
D16S539							
D1S7							
D2S44							
D4S139							
D5S110							

C2 Combined Unknown:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358				17			
VWA		14	16				
FGA	20		23				
D8S1179			15				
D21S11				31.2			
D18S51	12						
D5S818	11						
D13S317	8			12			
D7S820	8						
CSF1PO		12	13				
TPOX							
TH01				9.3			
D16S539				13			
D1S7							
D2S44							
D4S139							
D5S110							

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



Mixture: Vic+Cons+Susp::Vic+Cons+Unk

C1 Combined Unknown: 0

C2 Combined Unknown: 1

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	14	15	16	17			
☒ VWA	13	14	16	17	18	20	
☒ FGA	20	22	23	24			
☒ 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			
☒ CSF1PO	10	12	13				
☒ TPOX	8	9	10				
☒ TH01	6	7	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							
☐ D2S44							
☐ D4S139							
☐ D5S110							

C1:

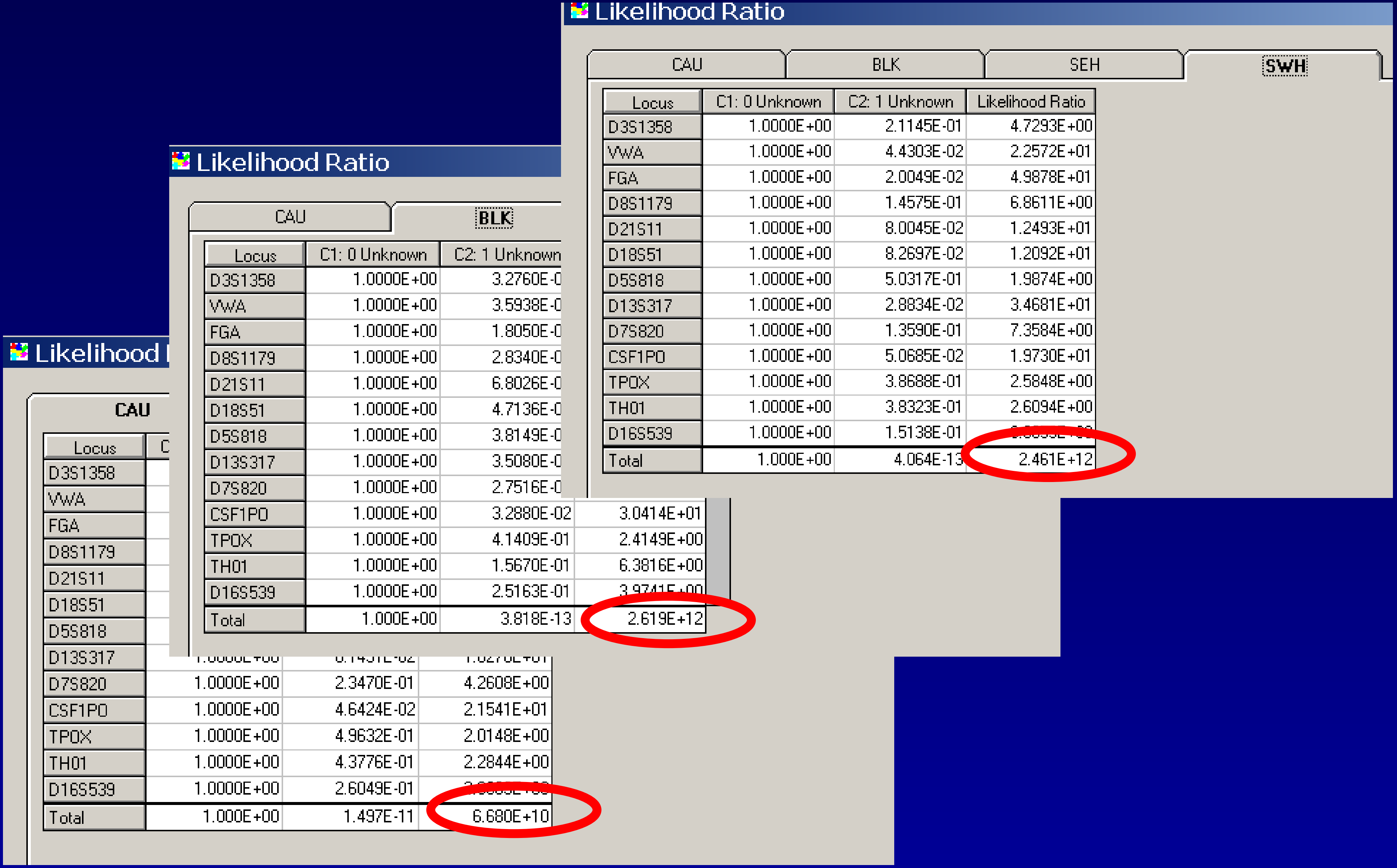
Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7

C2:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358				17			
VWA		14	16				
FGA	20		23				
D8S1179			15				
D21S11				31.2			
D18S51	12						
D5S818	11						
D13S317	8			12			
D7S820	8						
CSF1PO		12	13				
TPOX							
TH01				9.3			
D16S539				13			

The "profile" in C2 represents all of the alleles not accounted for by the hypothesis…in this case all non-victim and partner alleles

Our Results:



Likelihood I

Locus	C		
D3S1358			
VWA			
FGA			
D8S1179			
D21S11			
D18S51			
D5S818			
D13S317	[illegible]	[illegible]	[illegible]
D7S820	1.0000E+00	2.3470E-01	4.2608E+00
CSF1PO	1.0000E+00	4.6424E-02	2.1541E+01
TPOX	1.0000E+00	4.9632E-01	2.0148E+00
TH01	1.0000E+00	4.3776E-01	2.2844E+00
D16S539	1.0000E+00	2.6049E-01	[illegible]
Total	1.000E+00	1.497E-11	6.680E+10

Likelihood Ratio

Locus	C1: 0 Unknown	C2: 1 Unknown	
D3S1358	1.0000E+00	3.2760E-0	
VWA	1.0000E+00	3.5938E-0	
FGA	1.0000E+00	1.8050E-0	
D8S1179	1.0000E+00	2.8340E-0	
D21S11	1.0000E+00	6.8026E-0	
D18S51	1.0000E+00	4.7136E-0	
D5S818	1.0000E+00	3.8149E-0	
D13S317	1.0000E+00	3.5080E-0	
D7S820	1.0000E+00	2.7516E-0	
CSF1PO	1.0000E+00	3.2880E-02	3.0414E+01
TPOX	1.0000E+00	4.1409E-01	2.4149E+00
TH01	1.0000E+00	1.5670E-01	6.3816E+00
D16S539	1.0000E+00	2.5163E-01	3.9741E+00
Total	1.000E+00	3.818E-13	2.619E+12

Likelihood Ratio

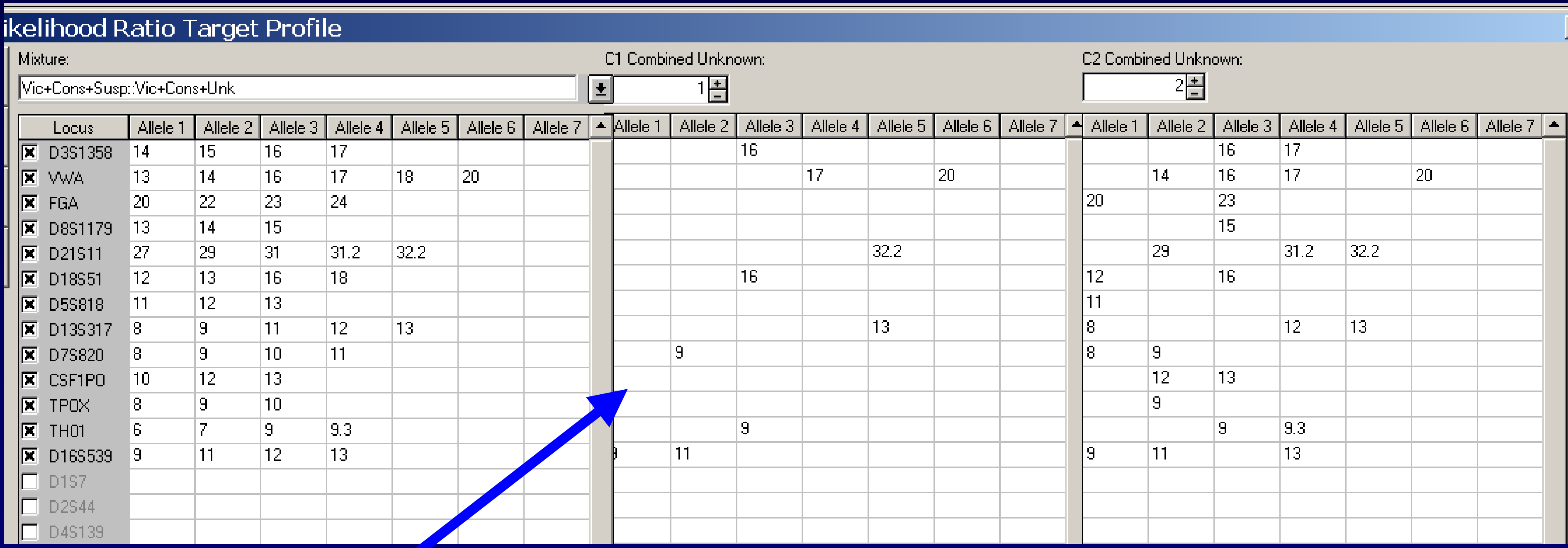
Locus	C1: 0 Unknown	C2: 1 Unknown	Likelihood Ratio
D3S1358	1.0000E+00	2.1145E-01	4.7293E+00
VWA	1.0000E+00	4.4303E-02	2.2572E+01
FGA	1.0000E+00	2.0049E-02	4.9878E+01
D8S1179	1.0000E+00	1.4575E-01	6.8611E+00
D21S11	1.0000E+00	8.0045E-02	1.2493E+01
D18S51	1.0000E+00	8.2697E-02	1.2092E+01
D5S818	1.0000E+00	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	[illegible]
Total	1.000E+00	4.064E-13	2.461E+12

What if we entertain another set of hypotheses:

H_o= The results are explained by a mixture of DNA derived from the victim, the suspect, and an unknown individual.

and

H_{a2}= The results are explained by a mixture of DNA derived from the victim and two unknown individuals.



ikelihood Ratio Target Profile

Mixture: Vic+Cons+Susp::Vic+Cons+Unk

C1 Combined Unknown: 1

C2 Combined Unknown: 2

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒ D3S1358	14	15	16	17			
☒ VWA	13	14	16	17	18	20	
☒ FGA	20	22	23	24			
☒ 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			
☒ CSF1PO	10	12	13				
☒ TPOX	8	9	10				
☒ TH01	6	7	9	9.3			
☒ D16S539	9	11	12	13			
☐ D1S7							
☐ D2S44							
☐ D4S139							

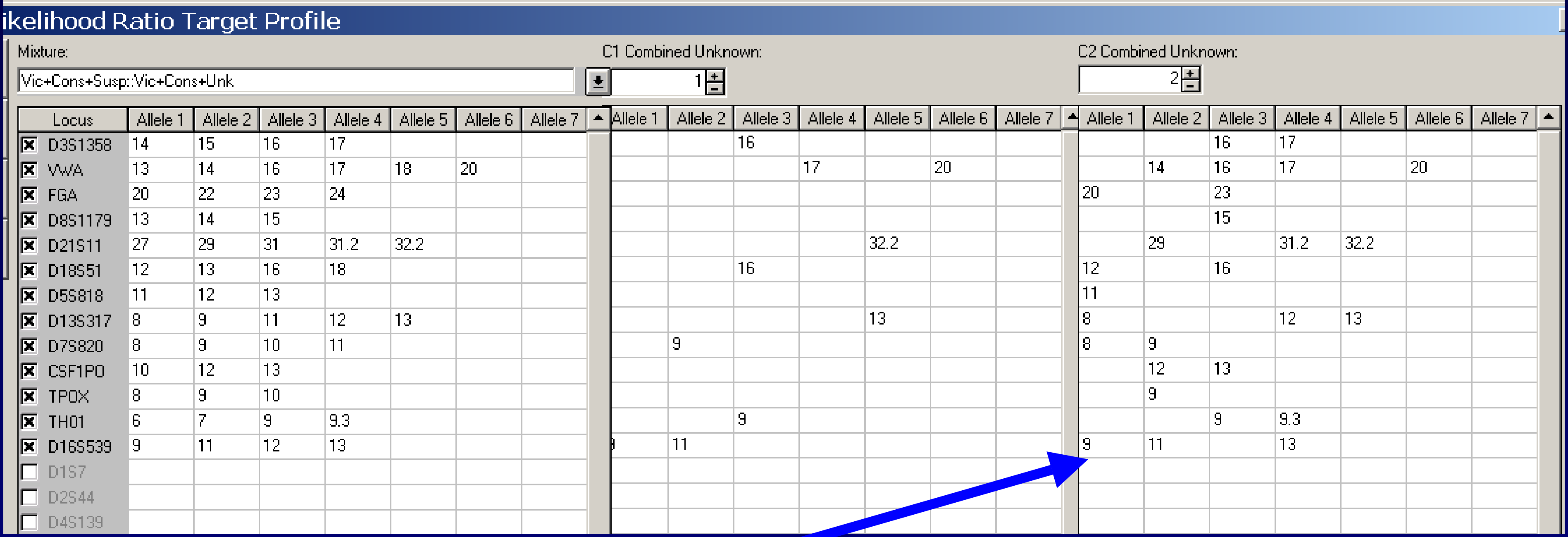
C1:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358			16				
VWA				17		20	
FGA							
D8S1179							
D21S11					32.2		
D18S51			16				
D5S818							
D13S317					13		
D7S820		9					
CSF1PO							
TPOX							
TH01			9				
D16S539	9	11					
D1S7							
D2S44							
D4S139							

C2:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358			16	17			
VWA		14	16	17		20	
FGA	20		23				
D8S1179			15				
D21S11		29		31.2	32.2		
D18S51	12		16				
D5S818	11						
D13S317	8			12	13		
D7S820	8	9					
CSF1PO		12	13				
TPOX		9					
TH01			9	9.3			
D16S539	9	11		13			
D1S7							
D2S44							
D4S139							

The "profile" in C1 represents all of the alleles not accounted for by the hypothesis…in this case all non-victim and suspect



ikelihood Ratio Target Profile

Mixture: Vic+Cons+Susp::Vic+Cons+Unk

C1 Combined Unknown: 1

C2 Combined Unknown: 2

Mixture:

	Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
☒	D3S1358	14	15	16	17			
☒	VWA	13	14	16	17	18	20	
☒	FGA	20	22	23	24			
☒	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			
☒	CSF1PO	10	12	13				
☒	TPOX	8	9	10				
☒	TH01	6	7	9	9.3			
☒	D16S539	9	11	12	13			
☐	D1S7							
☐	D2S44							
☐	D4S139							

C1 Combined Unknown:

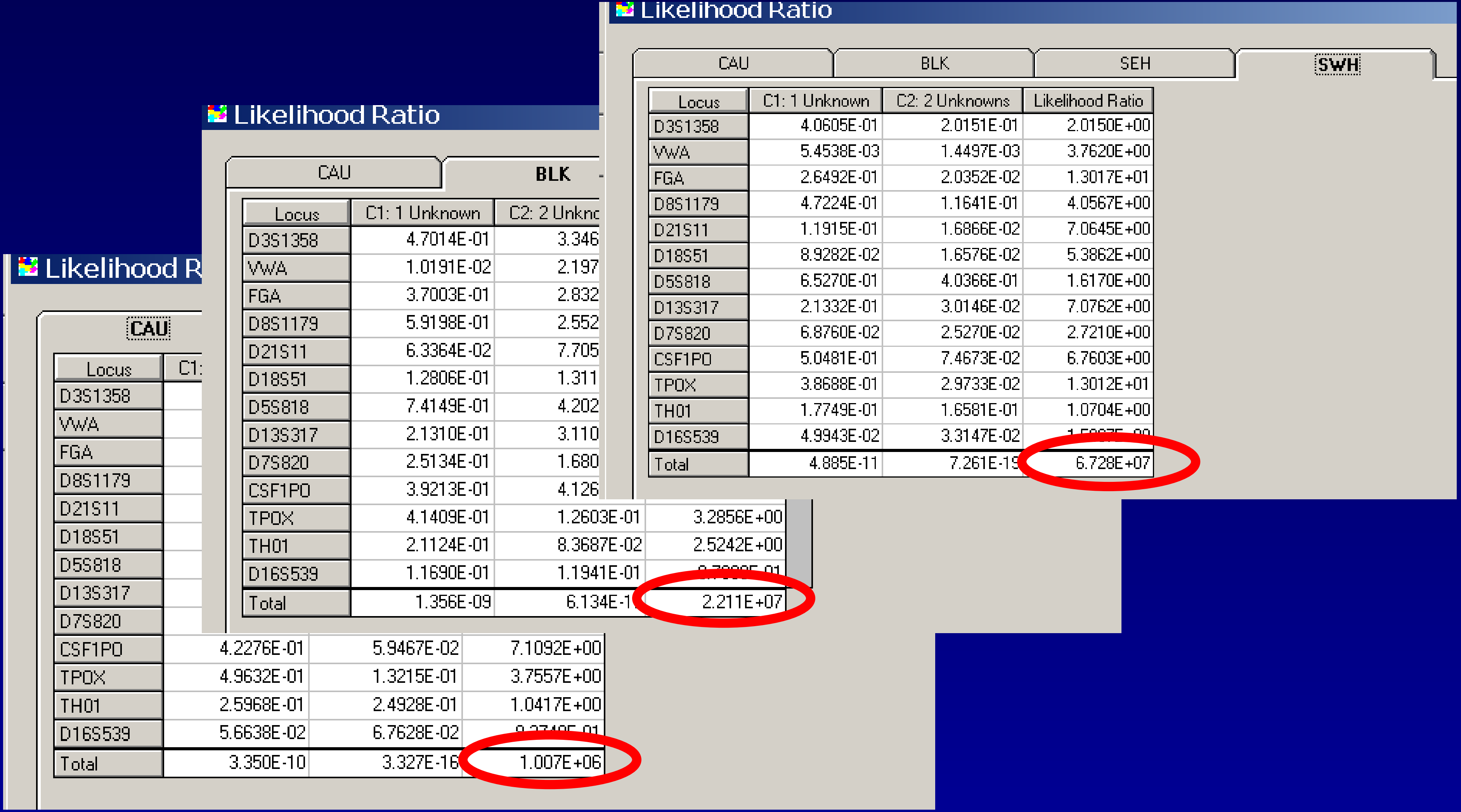
Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358			16				
VWA				17		20	
FGA							
D8S1179							
D21S11					32.2		
D18S51			16				
D5S818							
D13S317					13		
D7S820		9					
CSF1PO							
TPOX							
TH01			9				
D16S539	9	11					
D1S7							
D2S44							
D4S139							

C2 Combined Unknown:

Locus	Allele 1	Allele 2	Allele 3	Allele 4	Allele 5	Allele 6	Allele 7
D3S1358			16	17			
VWA		14	16	17		20	
FGA	20		23				
D8S1179			15				
D21S11		29		31.2	32.2		
D18S51	12		16				
D5S818	11						
D13S317	8			12	13		
D7S820	8	9					
CSF1PO		12	13				
TPOX		9					
TH01			9	9.3			
D16S539	9	11		13			
D1S7							
D2S44							
D4S139							

The "profile" in C2 represents all of the alleles not accounted for by the hypothesis…in this case all non-victim alleles

Our Results:



Likelihood R

CAU

Locus	C1:		
D3S1358			
VWA			
FGA			
D8S1179			
D21S11			
D18S51			
D5S818			
D13S317			
D7S820			
CSF1PO	4.2276E-01	5.9467E-02	7.1092E+00
TPOX	4.9632E-01	1.3215E-01	3.7557E+00
TH01	2.5968E-01	2.4928E-01	1.0417E+00
D16S539	5.6638E-02	6.7628E-02	8.3749E-01
Total	3.350E-10	3.327E-16	1.007E+06

Likelihood Ratio

CAU | **BLK**

Locus	C1: 1 Unknown	C2: 2 Unkno	
D3S1358	4.7014E-01	3.346	
VWA	1.0191E-02	2.197	
FGA	3.7003E-01	2.832	
D8S1179	5.9198E-01	2.552	
D21S11	6.3364E-02	7.705	
D18S51	1.2806E-01	1.311	
D5S818	7.4149E-01	4.202	
D13S317	2.1310E-01	3.110	
D7S820	2.5134E-01	1.680	
CSF1PO	3.9213E-01	4.126	
TPOX	4.1409E-01	1.2603E-01	3.2856E+00
TH01	2.1124E-01	8.3687E-02	2.5242E+00
D16S539	1.1690E-01	1.1941E-01	9.7898E-01
Total	1.356E-09	6.134E-1	2.211E+07

Likelihood Ratio

CAU | BLK | SEH | **SWH**

Locus	C1: 1 Unknown	C2: 2 Unknowns	Likelihood Ratio
D3S1358	4.0605E-01	2.0151E-01	2.0150E+00
VWA	5.4538E-03	1.4497E-03	3.7620E+00
FGA	2.6492E-01	2.0352E-02	1.3017E+01
D8S1179	4.7224E-01	1.1641E-01	4.0567E+00
D21S11	1.1915E-01	1.6866E-02	7.0645E+00
D18S51	8.9282E-02	1.6576E-02	5.3862E+00
D5S818	6.5270E-01	4.0366E-01	1.6170E+00
D13S317	2.1332E-01	3.0146E-02	7.0762E+00
D7S820	6.8760E-02	2.5270E-02	2.7210E+00
CSF1PO	5.0481E-01	7.4673E-02	6.7603E+00
TPOX	3.8688E-01	2.9733E-02	1.3012E+01
TH01	1.7749E-01	1.6581E-01	1.0704E+00
D16S539	4.9943E-02	3.3147E-02	1.5067E+00
Total	4.885E-11	7.261E-19	6.728E+07

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

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

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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