Likelihood Ratios for Mixtures: Semi-continuous Approach

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Acknowledgement
I thank Michael Coble, Bruce Weir and John Buckleton for their helpful discussions.

Disclaimer
Points of view in this presentation are mine and do not necessarily represent the official position or policies of the National Institute of Standards and Technology.
Overview of different approaches

<table>
<thead>
<tr>
<th>Models:</th>
<th>Takes into account:</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>presence/absence of alleles</td>
</tr>
<tr>
<td>CPI</td>
<td>X</td>
</tr>
<tr>
<td>mRMP</td>
<td>X</td>
</tr>
<tr>
<td>LR (binary)</td>
<td>X</td>
</tr>
<tr>
<td>LR (semi-continuous)</td>
<td>X</td>
</tr>
<tr>
<td>LR (fully continuous)</td>
<td>X</td>
</tr>
</tbody>
</table>

Binary LR

\[ G_{POI} = \{13,16\} \]

numerator of LR: \( 1 \times 2p_{14}p_{15} \)
Binary LR

\[ G_{POI} = \{13, 16\} \]

denominator of LR (unrestricted): \(12p_{13}p_{14}p_{15}(p_{13} + p_{14} + p_{15}) + 24p_{13}p_{14}p_{15}p_Q\)

denominator of LR (restricted): \(2p_{14}p_{15}p_{13}(p_{13} + 2p_{14} + 2p_{15} + 2p_Q)\)

Binary LR

unrestricted:
\[ LR = \frac{1 \times 2p_{14}p_{15}}{12p_{13}p_{14}p_{15}(p_{13} + p_{14} + p_{15}) + 24p_{13}p_{14}p_{15}p_Q} \]

restricted:
\[ LR = \frac{1 \times 2p_{14}p_{15}}{2p_{14}p_{15}p_{13}(p_{13} + 2p_{14} + 2p_{15} + 2p_Q)} \]
**Binary LR**

Unrestricted:

\[
LR = \frac{1 \times 2p_{14}p_{15}}{12p_{13}p_{14}p_{15}(p_{13} + p_{14} + p_{15}) + 24p_{13}p_{14}p_{15}p_Q}
\]

Restricted:

\[
LR = \frac{1 \times 2p_{14}p_{15}}{2p_{14}p_{15}p_{13}(p_{13} + 2p_{14} + 2p_{15} + 2p_Q)}
\]

\[
G_{POI} = \{13, 13\}
\]
Binary LR

unrestricted:
\[
LR = \frac{1 \times 2p_{14}p_{15}}{12p_{13}p_{14}p_{15}(p_{13} + p_{14} + p_{15}) + 24p_{13}p_{14}p_{15}p_Q}
\]

restricted:
\[
LR = \frac{1 \times 2p_{14}p_{15}}{2p_{14}p_{15}p_{13}(p_{13} + 2p_{14} + 2p_{15} + 2p_Q)}
\]

\[G_{POI} = \{12,13\}\]
Binary LR

Shouldn’t there be a difference in the value of the evidence for each of these POIs depending on how probable allele drop-out is?

Likelihood Ratio

\[
\frac{\Pr(E|H_p, I)}{\Pr(E|H_d, I)}
\]

\(E\): DNA typing results

\(G_{CS}\): crime stain
\(G_K\): known contributors
\(G_V\): victim or complainant
\(G_{POI}\): person of interest
**Likelihood Ratio**

\[ LR = \frac{\Pr(E|H_p, I)}{\Pr(E|H_d, I)} = \frac{\Pr(G_{CS}, G_K|H_p, I)}{\Pr(G_{CS}, G_K|H_d, I)} = \frac{\Pr(G_{CS}|G_K, H_p, I)}{\Pr(G_{CS}|G_K, H_d, I)} \times \frac{\Pr(G_K|H_p, I)}{\Pr(G_K|H_d, I)} = \frac{\Pr(G_{CS}|G_K, H_p, I)}{\Pr(G_{CS}|G_K, H_d, I)} \times \frac{\Pr(G_K|I)}{\Pr(G_K|I)} = \frac{\Pr(G_{CS}|G_K, H_p)}{\Pr(G_{CS}|G_K, H_d)} \times \frac{1}{1} \]

- The genotypes of the POI and victim/complainant do not depend on \( H_p \) being true or \( H_d \) being true.

---

**Likelihood Ratio**

The probability of obtaining these DNA typing results for the crime stain given the genotype of the POI (and victim/complainant) and that the POI is a contributor.

\[ LR = \frac{\Pr(G_{CS}|G_K, H_p)}{\Pr(G_{CS}|G_K, H_d)} \]

The probability of obtaining these DNA typing results for the crime stain given the genotype of the POI (and victim/complainant) and that the POI is not a contributor.

Note that the background information \( I \) has been omitted in the above equation to focus your attention on \( G_{CS}, G_K, H_p \) and \( H_d \).
The probability of $G_{CS}$ depends on the genotypes considered for the contributors.

**Genotype set $S$**

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
<th>$w$</th>
<th>$match\ prob_{major}$</th>
<th>$match\ prob_{minor}$</th>
</tr>
</thead>
<tbody>
<tr>
<td>$S_1$</td>
<td>14,15</td>
<td>12,13</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>$S_2$</td>
<td>14,15</td>
<td>13,13</td>
<td>1</td>
<td>$2p_{13}p_{15}$</td>
</tr>
<tr>
<td>$S_3$</td>
<td>14,15</td>
<td>13,14</td>
<td>1</td>
<td>$p_{13}^2$</td>
</tr>
<tr>
<td>$S_4$</td>
<td>14,15</td>
<td>13,15</td>
<td>1</td>
<td>$2p_{13}p_{14}$</td>
</tr>
<tr>
<td>$S_5$</td>
<td>14,15</td>
<td>13,16</td>
<td>1</td>
<td>$2p_{13}p_{15}$</td>
</tr>
<tr>
<td>$S_6$</td>
<td>14,15</td>
<td>13,17</td>
<td>1</td>
<td>$2p_{13}p_{16}$</td>
</tr>
</tbody>
</table>
Likelihood Ratio

\[ LR = \frac{Pr(G_{CS}|G_K, H_p)}{Pr(G_{CS}|G_K, H_d)} \]

\[ = \frac{Pr(G_{CS}|S_1)Pr(S_1|G_K, H_p) + Pr(G_{CS}|S_2)Pr(S_2|G_K, H_p) + \cdots + Pr(G_{CS}|S_6)Pr(S_6|G_K, H_p)}{Pr(G_{CS}|S_1)Pr(S_1|G_K, H_d) + Pr(G_{CS}|S_2)Pr(S_2|G_K, H_d) + \cdots + Pr(G_{CS}|S_6)Pr(S_6|G_K, H_d)} \]

\[ = \frac{\sum_{j=1}^{6} Pr(G_{CS}|S_j)Pr(S_j|G_K, H_p)}{\sum_{j=1}^{6} Pr(G_{CS}|S_j)Pr(S_j|G_K, H_d)} \]

Note that the background information \( I \) has been omitted in the above equation to focus your attention on \( S_j, G_{CS}, G_K, H_p \) and \( H_d \).

Likelihood Ratio

\[ LR = \frac{\sum_{j=1}^{m} Pr(G_{CS}|S_j)Pr(S_j|G_K, H_p, I)}{\sum_{j=1}^{m} Pr(G_{CS}|S_j)Pr(S_j|G_K, H_d, I)} \]

weights

the probability of obtaining these DNA typing results for genotype set \( S_j \)
Likelihood Ratio

\[ LR = \frac{\sum_{j=1}^{m} Pr(G_{CS} | S_j) Pr(S_j | G_K, H_p, I)}{\sum_{j=1}^{m} Pr(G_{CS} | S_j) Pr(S_j | G_K, H_d, I)} \]

**match probabilities**
the probability of genotype set \( S_j \) given that we have observed genotypes \( G_K \) and that the contributors are as specified in \( H_p \) or \( H_d \)

Likelihood Ratio: from binary to semi-continuous

\[ LR = \frac{\sum_{genotype sets | H_p} weight \times \text{genotype match prob.}}{\sum_{genotype sets | H_d} weight \times \text{genotype match prob.}} \]

**stays the same**
(Hardy-Weinberg Law, NRC II recommendation 4.1, NRC II recommendation 4.2)
Likelihood Ratio: from binary to semi-continuous

\[
LR = \frac{\sum_{\text{genotype sets}|H_p} \text{weight} \times \text{genotype match prob.}}{\sum_{\text{genotype sets}|H_d} \text{weight} \times \text{genotype match prob.}}
\]

**binary weight**: value of 0 (impossible) or 1 (possible)

**semi-continuous weight**: any value between 0 and 1, including 0 and 1, assigned using probabilities of drop-out and drop-in

---

**Semi-Continuous LR**

probability of allele drop-out

\[
Pr(\text{drop-out}) = \frac{e^{\beta_0 + \beta_1 \ln(H)}}{1 + e^{\beta_0 + \beta_1 \ln(H)}}
\]

---

Cedar Crest College
Forensic Science Training Institute
Semi-Continuous LR

**probability of allele drop-out**

heterozygote: $Pr(\text{drop} - \text{out}) = D$

$Pr(\text{not drop} - \text{out}) = 1 - D = \overline{D}$

homozygote: $Pr(\text{drop} - \text{out}) = D_2$

$Pr(\text{not drop} - \text{out}) = 1 - D_2 = \overline{D_2}$

Based on the notation in:


---

Semi-Continuous LR

Examples:

$$\{8,9\}$$

$$LR = \frac{\overline{D}^2}{\overline{D}^2 \times 2p_8 p_9} = \frac{1}{2p_8 p_9}$$

$$Pr(G_{CS} | G_K, H_p, I) = \overline{D} \overline{D} \times 1 = \overline{D}^2$$

$$Pr(G_{CS} | G_K, H_d, I) = \overline{D} \overline{D} \times 2p_8 p_9 = \overline{D}^2 \times 2p_8 p_9$$
**Semi-Continuous LR**

Examples: {8,9}

\[
Pr(G_{CS}|G_K, H_p, I) = \overline{D} \times D \times 1 = \overline{D} D
\]

\[
Pr(G_{CS}|G_K, H_d, I) = \frac{D_2}{D_2} \times p_8^2 + \overline{D} D \times 2p_8p_Q
\]

<table>
<thead>
<tr>
<th>Contributor</th>
<th>(D_2 \times p_8^2)</th>
<th>(D \times 2p_8p_Q)</th>
</tr>
</thead>
<tbody>
<tr>
<td>8,8</td>
<td></td>
<td></td>
</tr>
<tr>
<td>8,Q</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

where \(p_Q = 1 - p_8\)
Assumptions

The DNA of the crime stain is a mixture of two contributors.

We assume that the major contributor is:

<table>
<thead>
<tr>
<th>Major Contributor</th>
<th>D8</th>
<th>D21</th>
<th>D7</th>
<th>CSF</th>
<th>D3</th>
<th>TH01</th>
<th>D13</th>
<th>D16</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>14,15</td>
<td>30,32.2</td>
<td>10,12</td>
<td>10,11</td>
<td>14,18</td>
<td>7,7</td>
<td>11,12</td>
<td>10,13</td>
</tr>
</tbody>
</table>

D2  D19  vWA  TPOX  D18  D5  FGA  
22,25  12,14  15,16  8,8  16,18  12,12  23,23
Assumptions

For allelic peaks **above** the stochastic threshold: allele drop-out is impossible (i.e., \( D = 0 \) and \( D_2 = 0 \)).

For allelic peaks **below** the stochastic threshold: \( D = 0.716 \) and \( D_2 = 0.256 \) (values assigned based on a logistic regression curve and the average allelic peak height of the minor contributor).

**Person of interest (POI)**

<table>
<thead>
<tr>
<th>Allele</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>D8</td>
<td>13.16</td>
</tr>
<tr>
<td>D21</td>
<td>28.28</td>
</tr>
<tr>
<td>D7</td>
<td>8.12</td>
</tr>
<tr>
<td>CSF1PO</td>
<td>12.12</td>
</tr>
<tr>
<td>D3</td>
<td>16.16</td>
</tr>
<tr>
<td>TH01</td>
<td>7.93</td>
</tr>
<tr>
<td>D13</td>
<td>12.13</td>
</tr>
<tr>
<td>D16</td>
<td>12.13</td>
</tr>
<tr>
<td>D2</td>
<td>23.25</td>
</tr>
<tr>
<td>D19</td>
<td>13.13</td>
</tr>
<tr>
<td>vWA</td>
<td>15.19</td>
</tr>
<tr>
<td>TPOX</td>
<td>11.11</td>
</tr>
<tr>
<td>D18</td>
<td>14.20</td>
</tr>
<tr>
<td>D5</td>
<td>11.13</td>
</tr>
<tr>
<td>FGA</td>
<td>20.28</td>
</tr>
</tbody>
</table>

Boston University Mixture (http://www.bu.edu/dnamixtures/): ID_2_SCD_NG0.5_R4,1_A1_V1
What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \{14,20\}?

Numerator:

\[
Pr(16,18) \times Pr(14,20) = 2p_{16}p_{18} \times D \bar{D} \times 1 = \bar{D}^2 \times 2p_{16}p_{18}
\]
What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>16,18</td>
<td>14,20</td>
</tr>
</tbody>
</table>

\[
Pr(16,18) \times Pr(14,20) = 2p_{16}p_{18} \times D \frac{D}{2} \times 2p_{14}p_{20} = D^2 \times 4p_{14}p_{16}p_{18}p_{20}
\]

If we assuming 2 contributors, then allele drop-out is impossible. This makes the \( LR_{\text{semi-cont.}} \) equal to the \( LR_{\text{binary}} \).
The DNA typing results are 207 times more probable if the DNA came from the person of interest and an unknown contributor than if the DNA came from two unknown contributors.

\[ G_{POI} = \{14, 20\} \]

Boston University Mixture (http://www.bu.edu/dnamixtures/): ID_2_SCD_NG0.5_R4,1_A1_V1
If all the peaks are above the stochastic threshold, allele dropout is considered impossible (i.e., $D = 0$ and $D_2 = 0$).

**Numerator:**

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype $\{12,12\}$?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>10,11</td>
<td>12,12</td>
</tr>
<tr>
<td>10,11</td>
<td>10,12</td>
</tr>
<tr>
<td>10,11</td>
<td>11,12</td>
</tr>
</tbody>
</table>

$$Pr(10,11) \times Pr(12,12) = 2p_{10}p_{11} \times 1 = 2p_{10}p_{11}$$
What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?

Denominator:

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>10,11</td>
<td>12,12</td>
</tr>
<tr>
<td>10,11</td>
<td>10,12</td>
</tr>
<tr>
<td>10,11</td>
<td>11,12</td>
</tr>
</tbody>
</table>

Pr(10,11) × Pr(12,12) + Pr(10,11) × Pr(10,12) + Pr(10,11) × Pr(11,12)

= 2p_{10}p_{11} \times p_{12}^2 + 2p_{10}p_{11} \times 2p_{10}p_{12}

+ 2p_{10}p_{11} \times 2p_{11}p_{12}

= 2p_{10}p_{11}p_{12}(p_{12} + 2p_{10} + 2p_{11})
The DNA typing results are about 2 times more probable if the DNA came from the person of interest and an unknown contributor than if the DNA came from two unknown contributors.
EPG of the crime stain:

Boston University Mixture (http://www.bu.edu/dnamixtures/): ID_2_SCD_NG0.5_R4_1_A1_V1

Semi-Continuous LR

\[ G_{POI} = \{28,28\} \]

\[ D21S11 \]

\[ p_{28} = 0.159 \]
\[ p_{30} = 0.283 \]
\[ p_{32.2} = 0.090 \]

peak at 28 is below the stochastic threshold
What is the probability of obtaining these DNA typing results for the crime stain if the POI **is** a contributor and the POI has genotype \{28,28\}?

**Numerator:**

\[
Pr(30,32.2) \times Pr(28,28) = 2p_{30}p_{32.2} \times D_2 \times 1 = D_2 \times 2p_{30}p_{32.2}
\]

**Denominator:**

What is the probability of obtaining these DNA typing results for the crime stain if the POI **is not** a contributor?

\[
Pr(30,32.2) \times Pr(28,F) = 2p_{30}p_{32.2} \times \left[ D \times 2p_{28}p_Q + D \times 2p_{28}(p_{30} + p_{32.2}) + D^2 \times p_{28}^2 \right]
\]
The DNA typing results are about 9 times more probable if the DNA came from the person of interest and an unknown contributor than if the DNA came from two unknown contributors.
Person of interest (POI)

<table>
<thead>
<tr>
<th>Allele</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>D8</td>
<td>13,16</td>
</tr>
<tr>
<td>D21</td>
<td>28,28</td>
</tr>
<tr>
<td>D7</td>
<td>8,12</td>
</tr>
<tr>
<td>CSF1PO</td>
<td>12,12</td>
</tr>
<tr>
<td>D3</td>
<td>16,16</td>
</tr>
<tr>
<td>TH01</td>
<td>7,9.3</td>
</tr>
<tr>
<td>D13</td>
<td>12,13</td>
</tr>
<tr>
<td>D16</td>
<td>12,13</td>
</tr>
<tr>
<td>D2</td>
<td>23,25</td>
</tr>
<tr>
<td>D19</td>
<td>13,13</td>
</tr>
<tr>
<td>vWA</td>
<td>15,19</td>
</tr>
<tr>
<td>TPXO</td>
<td>11,11</td>
</tr>
<tr>
<td>D18</td>
<td>14,20</td>
</tr>
<tr>
<td>D5</td>
<td>11,13</td>
</tr>
<tr>
<td>FGA</td>
<td>20,28</td>
</tr>
</tbody>
</table>

EPG of the crime stain: Boston University Mixture (http://www.bu.edu/dnamixtures/): ID_2_SCD_NG0.5_R4.1_A1_V1

Semi-Continuous LR

\[
D8S1179
\]

\[
p_{13} = 0.330
\]

\[
p_{14} = 0.166
\]

\[
p_{15} = 0.104
\]

\[
G_{POI} = \{13,16\}
\]

peak at 13 is **below** the stochastic threshold
What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \{13,16\}?

**Numerator:**

\[
Pr(14,15) \times Pr(13,16) = 2p_{14}p_{15} \times \bar{D}D \times 1
\]

\[
= \bar{D}D \times 2p_{14}p_{15}
\]

What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?

**Denominator:**

\[
Pr(14,15) \times Pr(13,F) = 2p_{14}p_{15} \times [\bar{D}D \times 2p_{13}p_Q + \bar{D} \times 2p_{13}(p_{14} + p_{15}) + \bar{D}^2 \times p_{13}^2]
\]
Semi-Continuous LR

\[ D8S1179 \]

\[ p_{13} = 0.330 \]
\[ p_{14} = 0.166 \]
\[ p_{15} = 0.104 \]

\[ G_{POL} = \{13,16\} \]

\[ \text{stochastic threshold} \]

\[ 13 \quad 14 \quad 15 \]

\[ LR = \frac{\bar{D} \times 2p_{14}p_{15}}{2p_{14}p_{15} \times [\bar{D} \times 2p_{13}p_{Q} + \bar{D} \times 2p_{13}(p_{14} + p_{15}) + \bar{D}^2 \times p_{13}^2]} \]

\[ = \frac{\bar{D} \times 2p_{13}p_{Q} + \bar{D} \times 2p_{13}(p_{14} + p_{15}) + \bar{D}^2 \times p_{13}^2}{\bar{D} \times 2p_{13}p_{Q} + \bar{D} \times 2p_{13}(p_{14} + p_{15}) + \bar{D}^2 \times p_{13}^2} \]

\[ = 1.10 \]

The DNA typing results are about equally probable if the DNA came from the person of interest and an unknown contributor than if the DNA came from two unknown contributors.
EPG of the crime stain:

Boston University Mixture ([http://www.bu.edu/dnamixtures/](http://www.bu.edu/dnamixtures/)):

ID_2_SCD_NG0.5_R4.1_A1_V1

**Person of interest (POI)**

<table>
<thead>
<tr>
<th>Locus</th>
<th>Allele 1</th>
<th>Allele 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>D8</td>
<td>13,16</td>
<td></td>
</tr>
<tr>
<td>D21</td>
<td>28,28</td>
<td></td>
</tr>
<tr>
<td>D7</td>
<td>8,12</td>
<td></td>
</tr>
<tr>
<td>CSF1PO</td>
<td>12,12</td>
<td></td>
</tr>
<tr>
<td>D3</td>
<td>16,16</td>
<td></td>
</tr>
<tr>
<td>THO1</td>
<td>7,9.3</td>
<td></td>
</tr>
<tr>
<td>D13</td>
<td>12,13</td>
<td></td>
</tr>
<tr>
<td>D16</td>
<td>12,13</td>
<td></td>
</tr>
<tr>
<td>D2</td>
<td>23,25</td>
<td></td>
</tr>
<tr>
<td>D19</td>
<td>13,13</td>
<td></td>
</tr>
<tr>
<td>vWA</td>
<td>15,19</td>
<td></td>
</tr>
<tr>
<td>TPOX</td>
<td>11,11</td>
<td></td>
</tr>
<tr>
<td>D18</td>
<td>14,20</td>
<td></td>
</tr>
<tr>
<td>D5</td>
<td>11,13</td>
<td></td>
</tr>
<tr>
<td>FGA</td>
<td>20,28</td>
<td></td>
</tr>
</tbody>
</table>

**Semi-Continuous LR**

**D5S818**

\[ p_{11} = 0.356 \]
\[ p_{12} = 0.388 \]
\[ p_{13} = 0.143 \]

\[ G_{POI} = \{11,13\} \]

peaks at 11 and 13 are **below** the stochastic threshold
Semi-Continuous LR

D5S818

\[ p_{11} = 0.356 \]
\[ p_{12} = 0.388 \]
\[ p_{13} = 0.143 \]

Numerator:

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \{11,13\}?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>12,12</td>
<td>11,13</td>
</tr>
</tbody>
</table>

\[ Pr(12,12) \times Pr(11,13) = \ldots \]

What is the numerator of the likelihood ratio?

A. \( D \times p_{12}^2 \)
B. \( \overline{D}^2 \times p_{12}^2 \)
C. \( \overline{D}^2 \times p_{12}^2 \)
D. \( \overline{D}D \times p_{12}^2 \)
E. I'm lost.
Semi-Continuous LR

**D5S818**

\[ p_{11} = 0.356 \]
\[ p_{12} = 0.388 \]
\[ p_{13} = 0.143 \]

**Denominator:**

**What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?**

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
<th>( Pr(12,12) \times Pr(11,13) )</th>
</tr>
</thead>
<tbody>
<tr>
<td>12,12</td>
<td>11,13</td>
<td>( = \ldots )</td>
</tr>
</tbody>
</table>

**What is the denominator of the likelihood ratio?**

- **A.** \( p_{12}^2 \times \bar{D} \times 2p_{11}p_{13} \)
- **B.** \( p_{12}^2 \times \bar{D}_2 \times 2p_{11}p_{13} \)
- **C.** \( p_{12}^2 \times \bar{D}^2 \times 2p_{11}p_{13} \)
- **D.** \( p_{12}^2 \times \bar{D}D \times 2p_{11}p_{13} \)
- **E.** I'm lost.

**Response Counter**
What is the likelihood ratio?

A. 2.79  
B. 6.64  
C. 9.82  
D. 34.58  
E. I’m lost

Response Counter

EPG of the crime stain:

Person of interest (POI)

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>D8</td>
<td>13,16</td>
</tr>
<tr>
<td>D21</td>
<td>28,28</td>
</tr>
<tr>
<td>D7</td>
<td>8,12</td>
</tr>
<tr>
<td>CSF1PO</td>
<td>12,12</td>
</tr>
<tr>
<td>D3</td>
<td>16,16</td>
</tr>
<tr>
<td>TH01</td>
<td>7,9.3</td>
</tr>
<tr>
<td>D13</td>
<td>12,13</td>
</tr>
<tr>
<td>D16</td>
<td>12,13</td>
</tr>
<tr>
<td>D2</td>
<td>23,25</td>
</tr>
<tr>
<td>D19</td>
<td>13,13</td>
</tr>
<tr>
<td>vWA</td>
<td>15,19</td>
</tr>
<tr>
<td>TPOX</td>
<td>11,11</td>
</tr>
<tr>
<td>D18</td>
<td>14,20</td>
</tr>
<tr>
<td>D5</td>
<td>11,13</td>
</tr>
<tr>
<td>FGA</td>
<td>20,28</td>
</tr>
</tbody>
</table>

Boston University Mixture (http://www.bu.edu/dnamixtures/): ID_2_SCD_NG0.5_R4,1_A1_V1

9/26/2015
Semi-Continuous LR

**D19S433**

$p_{12} = 0.071$

$p_{13} = 0.255$

$p_{14} = 0.361$

Numerator:

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \( \{13,13\} \)?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>12,14</td>
<td>13,F</td>
</tr>
</tbody>
</table>

\[ Pr(12,14) \times Pr(13,13) = \ldots \]
What is the numerator of the likelihood ratio?

A. $\bar{D} \times 2p_{12}p_{14}$  
B. $\bar{D}_2 \times 2p_{12}p_{14}$  
C. $\bar{D}^2 \times 2p_{12}p_{14}$  
D. $\bar{D}D \times 2p_{12}p_{14}$  
E. I’m lost.

Semi-Continuous LR

D19S433

$p_{12} = 0.071$  
$p_{13} = 0.255$  
$p_{14} = 0.361$

Denominator:

What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?

<table>
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</thead>
<tbody>
<tr>
<td>12,14</td>
<td>13,F</td>
</tr>
</tbody>
</table>

$Pr(12,14) \times Pr(13, F) = \ldots$
What is the denominator of the likelihood ratio?

A. $2p_{12}p_{14} \times \overline{D}p_{13}^2$
B. $2p_{12}p_{14} \times p_{13}(p_{13} + 2p_{12} + 2p_{14})$
C. $2p_{12}p_{14} \times [\overline{D}p_{13}^2 + \overline{DD}p_{13}(p_{12} + p_{14}) + \overline{DD}p_{13}p_Q]$
D. $2p_{12}p_{14} \times [\overline{D}p_{13}^2 + \overline{DD}p_{13}p_Q]$
E. I’m lost.

What is the likelihood ratio?

A. 3.50
B. 5.19
C. 9.20
D. 15.38
E. I’m lost.
EPG of the crime stain:

Boston University Mixture ([http://www.bu.edu/dnamixtures/](http://www.bu.edu/dnamixtures/)): ID_2_SCD_NG0.5_R4.1_A1_V1

Semi-Continuous LR

TH01

\[ p_7 = 0.194 \]
\[ p_{0.3} = 0.345 \]

\( G_{\text{POI}} = \{7,9.3\} \)

peak at 9.3 is **below** the stochastic threshold
Semi-Continuous LR

TH01

TH01

\[ \text{stochastic threshold} \]

\[ \text{7} \quad \text{9.3} \]

Numerator:

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \( \{7,9.3\} \)?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>7,7</td>
<td>9.3,F</td>
</tr>
</tbody>
</table>

\[
Pr(7,7) \times Pr(7,9.3) = \ldots
\]

What is the numerator of the likelihood ratio?

A. \( \overline{D} \times p_7^2 \)
B. \( \overline{D}_2 \times p_7^2 \)
C. \( \overline{D}^2 \times p_7^2 \)
D. \( \overline{D}D \times p_7^2 \)
E. I'm lost.
Semi-Continuous LR

TH01

\[ p_7 = 0.194 \]
\[ p_{9.3} = 0.345 \]

**Denominator:**

What is the probability of obtaining these DNA typing results for the crime stain if the POI **is not** a contributor?

<table>
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<tbody>
<tr>
<td>7,7</td>
<td>9.3,F</td>
</tr>
</tbody>
</table>

\[ Pr(7,7) \times Pr(9.3,F) \]

\[ = \cdots \]

What is the denominator of the likelihood ratio?

A. \[ p_7^2 \times \left[ D_2 p_{9.3}^2 + \bar{D}2 p_{9.3}p_7 + \bar{D}D2 p_{9.3}p_Q \right] \]
B. \[ p_7^2 \times p_{9.3}(p_{9.3} + 2p_7) \]
C. \[ p_7^2 \times \left[ \bar{D}_2 p_{9.3}^2 + \bar{D}2 p_{9.3}(p_7 + p_Q) \right] \]
D. \[ p_7^2 \times \bar{D}_2 p_{9.3}^2 \]
E. I'm lost.
What is the likelihood ratio?

A. 1.48
B. 3.95
C. 11.29
D. 26.30
E. I’m lost.

Semi-Continuous LR

probability of allele drop-in

\[ Pr(\text{drop - in}) = C \]
\[ Pr(\text{not drop - in}) = 1 - C = \bar{C} \]

based on the notation in:

**Semi-Continuous LR**

**Examples:**
\{8,9\}

Assumptions: 1 contributor, maximum 1 drop-in allele per locus, and no tri-allelic contributor

**Numerator:**
\[ Pr(G_{CS}|G_K, H_p) = \overline{D} \overline{D} C p_{10} \times 1 = \overline{D}^2 C p_{10} \]

**Denominator:**
\[ Pr(G_{CS}|G_K, H_d) = \overline{D} \overline{D} C p_{10} \times 2p_8 p_9 + \overline{D} \overline{D} C p_9 \times 2p_8 p_{10} \\
+ \overline{D} \overline{D} C p_8 \times 2p_9 p_{10} \\
= \overline{D}^2 C \times 6p_8 p_9 p_{10} \]
Semi-Continuous LR

Examples: \{8,9\}

Assumptions: 1 contributor, maximum 1 drop-in allele per locus, and no tri-allelic contributor

\[
LR = \frac{\bar{D}^2 C p_{10}}{\bar{D}^2 C \times 6 p_8 p_9 p_{10}} = \frac{1}{6 p_8 p_9}
\]

Semi-Continuous LR with possibility of allele drop-in

D18S51

\begin{align*}
p_{14} & = 0.134 \\
p_{16} & = 0.147 \\
p_{18} & = 0.078 \\
p_{20} & = 0.018
\end{align*}

G_{POI} = \{14,20\}

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \{14,20\}?

<table>
<thead>
<tr>
<th>Major</th>
<th>Minor</th>
</tr>
</thead>
<tbody>
<tr>
<td>16,18</td>
<td>14,20</td>
</tr>
</tbody>
</table>

\[
Pr(16,18) \times Pr(14,20) = 2p_{16}p_{18} \times \bar{D} \bar{D} \bar{C} \times 1 = \bar{D}^2 \bar{C} \times 2p_{16}p_{18}
\]
Semi-Continuous LR with possibility of allele drop-in

Denominator:

**What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?**

<table>
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<tr>
<th>Major</th>
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<tbody>
<tr>
<td>16,18</td>
<td>14,20</td>
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<tr>
<td>16,18</td>
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<tr>
<td>16,18</td>
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<td>14,14</td>
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<td>16,18</td>
<td>14,16</td>
</tr>
<tr>
<td>16,18</td>
<td>14,Q</td>
</tr>
<tr>
<td>16,18</td>
<td>20,20</td>
</tr>
<tr>
<td>16,18</td>
<td>16,20</td>
</tr>
<tr>
<td>16,18</td>
<td>18,20</td>
</tr>
<tr>
<td>16,18</td>
<td>20,Q</td>
</tr>
</tbody>
</table>

\[ Pr(16,18) \times [Pr(14,20) + Pr(14,14) + Pr(14,16) + Pr(18,20) + Pr(20,20) + Pr(16,20) + Pr(18,18) + Pr(20,Q)] = 2p_{16}p_{18} \times [\bar{D}\bar{D}\bar{C} \times 2p_{14}p_{20} + \bar{D}_2Cp_{20} \times p_{14}^2 + \bar{D}Cp_{20} \times 2p_{14}p_{16} + \bar{D}_2Cp_{20} \times 2p_{14}p_{18} + \bar{D}DCp_{20} \times 2p_{14}p_Q + \bar{D}_2Cp_{14} \times p_{20}^2 + \bar{D}Cp_{14} \times 2p_{16}p_{20} + \bar{D}Cp_{14} \times 2p_{18}p_{20} + \bar{D}DCp_{14} \times 2p_{20}p_Q] \]

Semi-Continuous LR with possibility of allele drop-in

\[
LR = \frac{\bar{D}^2 \bar{C} \times 2p_{16}p_{18}}{2p_{16}p_{18} \times [\bar{D}^2 \bar{C} \times 2p_{14}p_{20} + \bar{D}_2Cp_{20} \times p_{14}^2 + \bar{D}Cp_{20} \times 2p_{14}(p_{16}+p_{18}) + \bar{D}DCp_{20} \times 2p_{14}p_Q + \bar{D}_2Cp_{14} \times p_{20}^2 + \bar{D}Cp_{14} \times 2p_{20}(p_{16}+p_{18}) + \bar{D}DCp_{14} \times 2p_{20}p_Q]}
\]

\[
= \frac{\bar{D}^2 \bar{C}}{\bar{D}^2 \bar{C} \times 2p_{14}p_{20} + \bar{D}_2Cp_{20} \times p_{14}^2 + \bar{D}Cp_{20} \times 2p_{14}(p_{16}+p_{18}) + \bar{D}DCp_{20} \times 2p_{14}p_Q + \bar{D}_2Cp_{14} \times p_{20}^2 + \bar{D}Cp_{14} \times 2p_{20}(p_{16}+p_{18}) + \bar{D}DCp_{14} \times 2p_{20}p_Q}
\]

\[ C = 0.01: \quad LR = 196.52 \]
\[ C = 0.05: \quad LR = 161.24 \]
Semi-Continuous LR with possibility of allele drop-in

**Numerator:**

What is the probability of obtaining these DNA typing results for the crime stain if the POI is a contributor and the POI has genotype \( \{28,28\} \)?

\[
Pr(30,32.2) \times Pr(28,28) = 2p_{30} p_{32.2} \times \overline{D}_2 \overline{C} \times 1 = \overline{D}_2 \overline{C} \times 2p_{30} p_{32.2}
\]

**Denominator:**

What is the probability of obtaining these DNA typing results for the crime stain if the POI is not a contributor?

\[
Pr(30,32.2) \times [Pr(28,28) + Pr(28,30) + Pr(28,32) + Pr(28,Q) + Pr(30,30) + Pr(30,32) + Pr(30,28) + Pr(30,Q) + Pr(32,2,Q) + Pr(Q,Q)]
\]

\[
= 2p_{30} p_{32.2} \times [\overline{D}_2 \overline{C} \times p_{28}^2 + \overline{D}\overline{C} \times 2p_{28}(p_{30} + p_{32.2}) + \overline{D}D\overline{C} \times 2p_{28}p_Q + C_{p_{28}} \times (p_{14} + p_{15})^2 + D_2 C_{p_{28}} \times 2(p_{30} + p_{32.2})p_Q + D_2 C_{p_{28}} \times p_Q^2 + D_2^2 C_{p_{28}}]
\]
Semi-Continuous LR with possibility of allele drop-in

\[
LR = \frac{D_2 \bar{C} \times 2p_{30}p_{32.2}}{2p_{30}p_{32.2} \times [D_2 \bar{C} \times \bar{p}_{28}^2 + D \bar{C} \times 2p_{28}(p_{30} + p_{32.2}) + D D \bar{C} \times 2p_{28}p_Q
+ C p_{28} \times (p_{14} + p_{15})^2 + D C p_{28} \times 2(p_{30} + p_{32.2})p_Q + D_2 C p_{28} \times p_Q^2 + D^2 C p_{28}
\times 2p_Q p_{2Q}]} \]

\[
= \frac{D_2 \bar{C}}{D_2 \bar{C} \times \bar{p}_{28}^2 + D \bar{C} \times 2p_{28}(p_{30} + p_{32.2}) + D D \bar{C} \times 2p_{28}p_Q + C p_{28}
\times (p_{14} + p_{15})^2 + D C p_{28} \times 2(p_{30} + p_{32.2})p_Q + D_2 C p_{28} \times p_Q^2 + D^2 C p_{28} \times 2p_Q p_{2Q}}
\]