Putting it all Together: A Case Example
CE User’s Group (December 5, 2008)

• Bruce Heidebrecht organized
• Held at Maryland State Police Forensic Lab
• Presentations & discussion on 4 mixture cases
• ~60 people attended from 16 labs

• Bruce has developed several helpful tools for mixtures...
Steps in the Mixture Interpretation Process
[Adapted from Clayton et al. (1998) Forensic Sci. Int. 91:55-70]

Step 1. Identify the Presence of a Mixture

↓

Step 2. Designate Allele Peaks

↓

Step 3. Identify the Number of Potential Contributors

↓

Step 4. Estimate the Relative Ratio of the Individuals Contributing to the Mixture

↓

Step 5. Consider All Possible Genotype Combinations

↓

Step 6. Perform statistical analysis

↓

Step 7. Compare Reference/Casework Samples
Some Information

Victim’s Vaginal Swab
(sperm fraction)
ST = 150 RFUs
Determine number of contributors
2 person mixture
(no more than 4 alleles at any locus)
2 person mixture
(no more than 4 alleles at any locus)
Determine if there is a distinct major contributor
No distinct major contributor
No distinct major contributor
Determine if there are stochastic issues
Some loci have stochastic issues (obvious)
Some loci have stochastic issues (less than 150rfu)
Re-examine D8-D2 for alleles less than 150rfu
Define the mixture category

• 2 person mixture
• No distinct major contributor
• Some loci have stochastic level peaks
Schneider et al. (2009) and SWGDAM

Type A
“Indistinguishable”

Type B
“Distinguishable”

Type C
“Uninterpretable”

A statistical analysis must be performed

Category A Mixture
(with some Category C loci)

A statistical analysis should not be performed
Basic results chart
(before looking at reference standards)

<table>
<thead>
<tr>
<th>Locus</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>
<th>D2</th>
<th>D19</th>
<th>vWA</th>
<th>TPOX</th>
<th>D18</th>
<th>D5</th>
<th>FGA</th>
<th>Amelogenin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sample</td>
<td>S1179</td>
<td>S11</td>
<td>S820</td>
<td>IPO</td>
<td>S1358</td>
<td>S317</td>
<td>S539</td>
<td>S1338</td>
<td>S433</td>
<td>vWA</td>
<td>TPOX</td>
<td>S51</td>
<td>S818</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Victim’s Vaginal Swab</td>
<td>12, 13</td>
<td>28, 29</td>
<td>12, 10</td>
<td>10, 14</td>
<td>7, 6</td>
<td>--</td>
<td>12, 10, 15</td>
<td>21, 17</td>
<td>14, 13</td>
<td>15, 16</td>
<td>11</td>
<td>12, 15, 9</td>
<td>20, 23, 26</td>
<td>XY</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

-- Possible additional genetic information may be present.
Due to the sample being Category A mixture (with some Category C loci), with one “known contributor”, most likely to try

Mixture Deconvolution
Steps in the Mixture Interpretation Process
[Adapted from Clayton et al. (1998) Forensic Sci. Int. 91:55-70]

Step 1. Identify the Presence of a Mixture

Step 2. Designate Allele Peaks

Step 3. Identify the Number of Potential Contributors

Step 4. Estimate the Relative Ratio of the Individuals Contributing to the Mixture

Step 5. Consider All Possible Genotype Combinations

Step 6. Perform statistical analysis

Step 7. Compare Reference/Casework Samples
Overall profile appears to be 1:1 ratio
Imperfect PHR’s exist in Victim’s profile where 4 alleles are present in the mixture

- Since 4 alleles present in the mixture, and two match to the victim, the other two MUST be the “true attacker,” even if not perfectly balanced.
- vWA
- Evidence = 15,16,17,18
- Victim = 15,18
- “true attacker” must be 16,17 even if PHR for Victim is less than perfect (59%)
Imperfect PHR’s exist in Victim’s profile where 4 alleles are present in the mixture.

- Since 4 alleles present in the mixture, and two match to the victim, the other two MUST be the “true attacker,” even if not perfectly balanced.
- FGA
- Evidence = 19,20,23,26
- Victim = 23,26
- “true attacker” must be 19,20 even if PHR for Victim is less than perfect (55%)
Imperfect PHR’s exist in Victim’s profile where 3 alleles are present in the mixture

- Since 3 alleles present in the mixture, and two match to the victim, the other one MUST belong to the “true attacker.” This person may also share an allele with the Victim
- D18
- Evidence = 12,15,17,  
- Victim = 15,17  
- “true attacker” must have allele 12  
- “true attacker” may be 12,12 or 12,15 or 12,17 or 12,
"True attacker"
Steps in the Mixture Interpretation Process

[Adapted from Clayton et al. (1998) Forensic Sci. Int. 91:55-70]

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Step 5. Consider All Possible Genotype Combinations

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Step 7. Compare Reference/Casework Samples
Consider all possible genotypes

• “true attacker” may be 12,12 or 12,15 or 12,17 or 12,--
If “true attacker” is 12,12 that leaves 15,17 entirely as the Victim with 27%PHR (103/383)

Consider all possible genotypes

Victim
15, 17
If “true attacker” is 12, that leaves 15,17 entirely as the Victim with 27%PHR (103/383)

And unreasonable to assume dropout associated with allele 12

Consider all possible genotypes

Victim
15, 17

View all possible genotypes
Consider all possible genotypes

If “true attacker” is \(12,17\) then that splits the rfu value for allele 17, leaving the Victim with 13% PHR assuming a 1:1 ratio of contributors = \((103/2)/383\)
If "true attacker" is 12,15, then that splits the rfu value for allele 15, leaving the Victim with 54%PHR \( \frac{103}{383/2} \) and "true attacker" with 89%PHR \( \frac{383/2}{215} \).

Consider all possible genotypes.
### Example #1 (Mixture deconvolution)

<table>
<thead>
<tr>
<th>Locus</th>
<th>D8 S179</th>
<th>D21 S11</th>
<th>D7 S820</th>
<th>CSF 1PO</th>
<th>D3 S1358</th>
<th>TH01</th>
<th>D13 S317</th>
<th>D16 S539</th>
<th>D2 S1338</th>
<th>D19 S433</th>
<th>vWA</th>
<th>TPOX</th>
<th>D18 S51</th>
<th>D5 S818</th>
<th>FGA</th>
<th>Amelogenin</th>
</tr>
</thead>
<tbody>
<tr>
<td>Victim’s Vaginal Swab</td>
<td>12, 13</td>
<td>28, 29</td>
<td>9, 10</td>
<td>10, 12</td>
<td>14, 15</td>
<td>12</td>
<td>10, 12</td>
<td>10, 12</td>
<td>13, 14</td>
<td>13, 16</td>
<td>15, 8</td>
<td>12, 11</td>
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<td>19, 20, 23, 26</td>
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<td>31, 11</td>
<td>11, 13</td>
<td>10, 12</td>
<td>15, 19</td>
<td>9.3</td>
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<td>10, 13</td>
<td>17, 21</td>
<td>14, 15</td>
<td>16, 17</td>
<td>12, 15</td>
<td>9, 10</td>
<td>19, 20</td>
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<tr>
<td>Victim’s Vaginal Swab</td>
<td>12, 13</td>
<td>29</td>
<td>10, 11</td>
<td>10, 12</td>
<td>15, 19</td>
<td>9.3</td>
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<td>17, 21</td>
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<td>12, 15</td>
<td>9, 10</td>
<td>19, 20</td>
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<tr>
<td>(non-Victim contributor)</td>
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<tr>
<td>Victim</td>
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<tr>
<td>Suspect</td>
<td>12, 13</td>
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<td>10, 12</td>
<td>15, 19</td>
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<td>16, 17</td>
<td>8, 12</td>
<td>12, 15</td>
<td>9, 10</td>
<td>19, 20</td>
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</tr>
</tbody>
</table>

- Possible additional genetic information may be present.
- This DNA profile is the remaining contributor to the mixture after the contribution of the Victim has been removed.
- A complete interpretation of the results at this genetic locus was not possible due to technical limitations. No conclusion can be reached concerning this locus.
Enter deconvoluted profile into sole source calculation worksheet
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Statistical Analysis
• The MDSP uses the “unrestricted likelihood ratio”

• Allele heights for shared alleles are NOT taken into consideration using this statistical method.
Determine alleles requisite to the attacker

Victim is 12,13

No alleles are requisite to the attacker
Determine alleles requisite to the attacker

Victim is 28,31

Allele 29 is requisite to the attacker
Determine alleles requisite to the attacker

Victim is 9,13

Alleles 10,11 are requisite to the attacker
Determine alleles requisite to the attacker

Victim is 12,13
Since Victim is not fully represented, and allele 12 is below stochastic,
DROP LOCUS
Report for Likelihood Ratio
## Likelihood Ratio results chart

### EXAMPLE #1

<table>
<thead>
<tr>
<th>Locus</th>
<th>D8 S1179</th>
<th>D21 S11</th>
<th>D7 S820</th>
<th>CSF IPO</th>
<th>D3 S1358</th>
<th>TH01</th>
<th>D13 S317</th>
<th>D16 S539</th>
<th>D2 S1358</th>
<th>D19 S433</th>
<th>vWA</th>
<th>TPOX</th>
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<th>D5 S818</th>
<th>FGA</th>
<th>Amelogenin</th>
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<tbody>
<tr>
<td>Sample</td>
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</tr>
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<td>Victim's Vaginal Swab</td>
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<td>28, 29</td>
<td>9, 10</td>
<td>12, 13</td>
<td>14, 16</td>
<td>6, 7</td>
<td>12, --</td>
<td>10, 12</td>
<td>17, 13</td>
<td>15, 13</td>
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<td>12, 15</td>
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<td>19, 12</td>
<td>XY</td>
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</tr>
<tr>
<td>Victim</td>
<td>12, 13</td>
<td>28, 31</td>
<td>9, 13</td>
<td>12, 12</td>
<td>14, 7</td>
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<tr>
<td>Suspect</td>
<td>12, 13</td>
<td>29, 10</td>
<td>10, 15</td>
<td>9.3, 9</td>
<td>10, 12</td>
<td>17, 13</td>
<td>15, 15</td>
<td>8, 12</td>
<td>15, 10</td>
<td>19, 20</td>
<td>XY</td>
<td></td>
<td></td>
<td></td>
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</tr>
</tbody>
</table>

--- Possible additional genetic information may be present.
Suspect cannot be excluded from the mixture, so proceed with LR stats.
Enter alleles of the mixture into ISFG LR worksheet

Enter alleles detected, peaks "indistinguishable from stutter", and the need for stochastic interpretation:

<table>
<thead>
<tr>
<th>Locus</th>
<th>Genotype</th>
<th>Allele (a)</th>
<th>Allele (b)</th>
<th>Allele (c)</th>
<th>Allele (d)</th>
<th>dropout (F)</th>
<th>Allele (a) freq</th>
<th>Allele (b) freq</th>
<th>Allele (c) freq</th>
<th>Allele (d) freq</th>
<th>Allele (F) freq</th>
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<tr>
<td>D6S1179</td>
<td></td>
<td>12</td>
<td>13</td>
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<td></td>
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<td>#N/A</td>
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<td>D7S820</td>
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<td>11</td>
<td>13</td>
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<tr>
<td>CSF1PO</td>
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<td>#N/A</td>
<td>#N/A</td>
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<td>0.1122</td>
<td>0.2015</td>
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<td>0.2219</td>
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<tr>
<td>vWA</td>
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<td>16</td>
<td>17</td>
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<td>0.5443</td>
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<td>TPOX</td>
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<td>FGA</td>
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</tbody>
</table>
Numerator has no alleles unaccounted for by the Prosecutor's theory
Denominator has these possibilities for the "true attacker"

<table>
<thead>
<tr>
<th>Denominator:</th>
<th>Possible Unknown Contributor</th>
<th>aa</th>
<th>ab</th>
<th>ac</th>
<th>ad</th>
<th>b.b</th>
<th>b.c</th>
<th>b.d</th>
<th>c.c</th>
<th>c.d</th>
<th>d.d</th>
<th>a.F</th>
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<td>12.13</td>
<td>12.13</td>
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<td>D2S1311</td>
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<td>TH01</td>
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<td>15.19</td>
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</tbody>
</table>

| Denominator: | Genotype Frequencies of Possible Unknown Contributor | aa   | ab   | ac   | ad   | b.b  | b.c  | b.d  | c.c  | c.d  | d.d  | a.F  | b.F  | c.F  | sum of all possibilities |
|--------------|------------------------------------------------------|------|------|------|------|------|------|------|------|------|------|------|------|--------------------------|
| TH01         |                                                     | 1.381E-01 | 1.053E-01 | 6.050E-03 | 9.329E-02 |      |      |      |      |      |      |      |      | 3.665E-01                |
| D1S1307      |                                                     | 1.381E-01 | 1.053E-01 | 6.050E-03 | 9.329E-02 |      |      |      |      |      |      |      |      | 3.665E-01                |
| D1S1366      |                                                     | 1.381E-01 | 1.053E-01 | 6.050E-03 | 9.329E-02 |      |      |      |      |      |      |      |      | 3.665E-01                |
| D16S51       |                                                     | 8.027E-02 | 7.307E-02 | 2.184E-02 |      |      |      |      |      |      |      |      |      | 2.184E-02                |
| D2S3186      |                                                     | 8.027E-02 | 7.307E-02 | 2.184E-02 |      |      |      |      |      |      |      |      |      | 2.184E-02                |
| D16S51       |                                                     | 2.639E-02 | 2.902E-02 | 3.970E-02 |      |      |      |      |      |      |      |      |      | 3.408E-01                |
| D2S3186      |                                                     | 1.632E-02 | 3.970E-02 | 2.902E-02 |      |      |      |      |      |      |      |      |      | 3.408E-01                |
| FGA          |                                                     | 1.632E-02 | 3.970E-02 | 2.902E-02 |      |      |      |      |      |      |      |      |      | 3.408E-01                |

Final LR calculation
numerator / denominator
29,338,605,880,333,700
29,000,000,000,000,000
Likelihood Ratio Conclusions

DNA from two individuals was obtained from the sperm fraction of the Victim’s vaginal swab. The DNA profile present is consistent with the combined known profiles from the Victim and the Suspect.

The probability of the DNA profile at all genetic loci tested, except D13S317, is 29 Quadrillion times more likely if it originated from the Victim and the Suspect than from the Victim and an unknown individual in the Caucasian population.

The probability of the DNA profile at all genetic loci tested, except D13S317, is 330 Quadrillion times more likely if it originated from the Victim and the Suspect than from the Victim and an unknown individual in the African American population.

The genetic locus D13S317 is consistent with the Victim and the Suspect being contributors of the DNA profile obtained from this item. However, for technical considerations, this locus was not used in the above calculations.
If CPI/CPE stats used

Since statistic cannot adjust for the possibility of dropout, and does not take the number of contributors into account, any loci where alleles are below stochastic levels cannot be used in the CPI stat without modifications to the calculation.
<table>
<thead>
<tr>
<th>Can use</th>
<th>Cannot use</th>
</tr>
</thead>
<tbody>
<tr>
<td>D8</td>
<td>D7</td>
</tr>
<tr>
<td>D21</td>
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<td>TPOX</td>
<td>D5</td>
</tr>
<tr>
<td></td>
<td>FGA</td>
</tr>
</tbody>
</table>
If CPI/CPE stats used

- CPI statistics using POPSTATS
- 1 in 1,670 Caucasians included
- 99.940% Caucasians excluded
- 1 in 11,930 African Americans included
- 99.991% African Americans excluded
Acknowledgments

• Bruce Heidebrecht (Maryland State Police)

http://www.cstl.nist.gov/biotech/strbase/training.htm
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