

This PowerPoint and opinion expressed during the presentations are solely those of the presenter. They are not the opinions of the United States Department of Defense, Department of Army, United States Criminal Investigation Division Command, or the United States Criminal Investigation Laboratory. The opinions and presentation should not be misrepresented or misused as such in any way.

This PowerPoint is the original work product of Dr. Timothy Kalafut and Mr. Thomas Overson, United States Army Criminal Investigation Laboratory (USACIL), Forensic Biologist. This work is being used for educational purposes. Its contents may be reproduced and used for educational purposes only with attribution to the authors and USACIL. Further use or distribution is prohibited by Title 17 United States Code Section 107.

Mr. Tom Overson and the Serology and DNA Branch, United States Army Criminal Investigation Laboratory (USACIL) created and developed the software and analytical applications contained in the presentation. They may not be reproduced. Reproduction or usage without the permission of the USACIL for any purpose may result in the user's assumption of any and all risk, consequence and liability for their actions.

DNA_DataAnalysis

- Developed by Tom Overson at USACIL with input from USACIL DNA Examiners
- Excel VBA Application
- Total Casework Data Management Tool
- (Post GeneMapper ID)

Major Features of DNA_DataAnalysis

Matching

- Within cases, between cases, to Staff Database
 Highlight Foreign Alleles
- Statistical Analysis

Single Source

- Mixed Profile (more than one possibility at a locus)

- CPI/CPE

- LR
- No manual data entry (just mouse clicks)

Major Features of DNA_DataAnalysis

- QA/QC Checks
- Examiner/Reviewer Concordance
- Identifiler, Profiler Plus/COfiler, Yfiler, PowerPlex 16
- CODIS Features
- Mixture Deconvolution

Benefits of Using DNA_DataAnalysis

- Significant time savings
 - Simple case can go from GMID table to write up in 5 minutes (record of alleles, matches, QA checks, stats, profile for CODIS entry)
 - Instantaneous check for Examiner/Reviewer concordance
- Less errors
 - No typos (especially for stats)
 - No transcription (don't need pen and paper)

Benefits of Using DNA_DataAnalysis

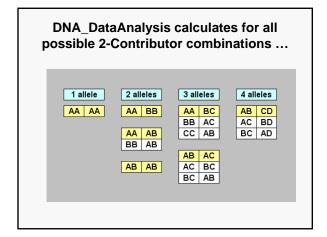
- · Record of mixture interpretation
- Can document the support of the interpretation
 - Summary of proportions and peak height ratiosGraph of contributor proportions
- Consistent math used
 - No fat fingers on the calculator
 - Same equations for every sample
 - Easy to understand and explain

Mixture Deconvolution

- · For two- and three- person mixtures
- Considers all possible combinations of alleles at all loci
- Allows for conditioning on required profiles (can set up to 6 references)
- Creates record of interpretation and rationale of examiner's decision

Mixture Deconvolution

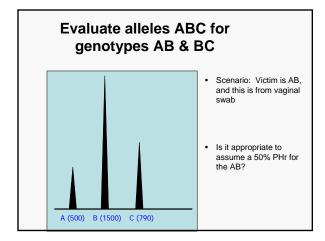
- NOT an Expert System
- A comprehensive tool that assists an expert
- Does everything you would do using pen and paper
- · Based on proportionate allele sharing

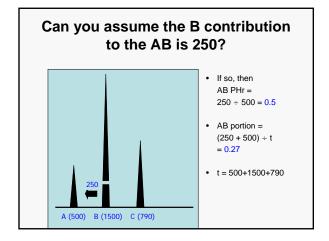




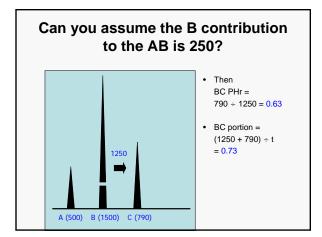
DNA_DataAnalysis calculates for all possible 2-Contributor combinations ...

- Only 7 "families" of possibilities
- Only 14 total possibilities
- Largest "family" n=3

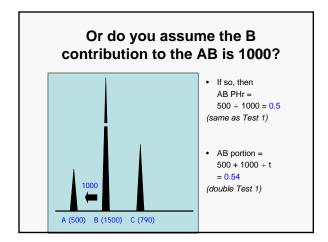


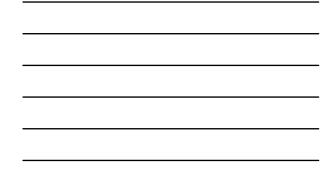


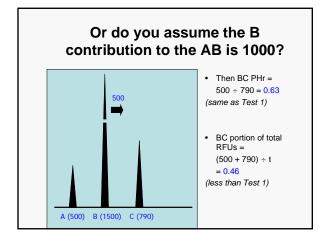












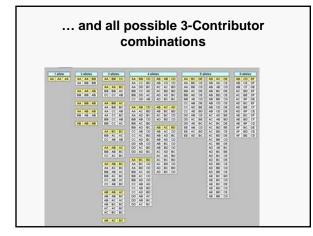


What is the rationale for choosing Test 1 ... or Test 2 ... or any other scenario?

| Test 1 | Test 2 |
|----------------------|----------------------|
| • AB PHr = 0.5 | • AB PHr = 0.5 |
| • AB p = 0.27 | • AB p = 0.54 |
| • BC PHr = 0.63 | • BC PHr = 0.63 |
| • BC p = 0.73 | • BC p = 0.46 |
| | |

The approach developed for DNA_DataAnalysis

- Calculates PHr's and p's without any arbitrary conditioning based upon a known reference or major contributor
- · Uses the same set of calculation rules for every instance
- Calculations based on 3 simple rules
- Proportionate Allele sharing
- PHr and p both important





... and all possible 3-Contributor combinations

- 23 "families" of possibilities
 3 allele pattern has 8 "families" alone
- 150 total possibilities
 5 alleles, 3 heterozygotes has 30 possibilities

3-contributor combinations

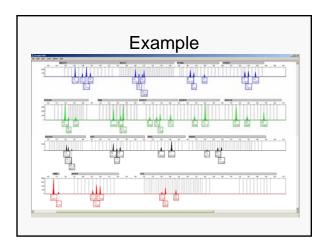
- The same rules apply
- Again, calculates for each and every combination
- Most 3-contributor patterns break down into simple 2-person patterns
 - (plus a somewhat independent 3rd person)

3-contributor combinations

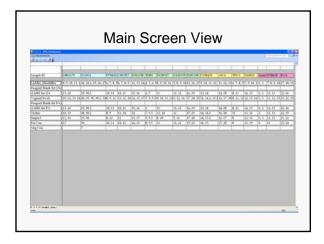
- Where 2-contributors share a type, the p is a combined proportion
- Four situations with "double sharing" are treated differently

 Cannot calculate PHr or p

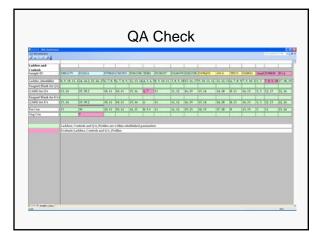
 - Valid combinations described as "not excluded" based on required PHr and mPH







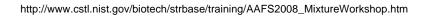


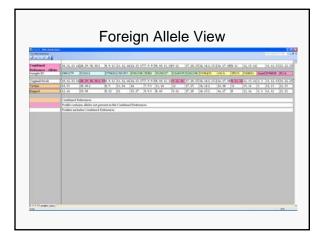


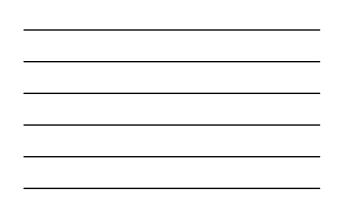


| 4.2, 15-2 (A, 17, 18 4.2 (A, 18 | T. 18(8) 11, 12 | Dimit 2 | | |
|------------------------------------|-----------------|------------|---------------|------------|
| 4.2. 15.214.17.18 4.2. [14,18 | T. 18(8) 11, 12 | DIRAL D | - | 1 |
| 4.2. 15.214.17.18 4.2. [14,18 | T. 18(8) 11, 12 | 1018011 [2 | | |
| 4.2 (14, 16 | | | Amail 1594015 | 90.4 |
| 4.2 (14, 16 | | | | 1811 11 15 |
| | | | < (0.0) | 11, 23 |
| 15.4 [16, 17] | 17. 0 | 82,34 3 | CY 10, 12 | 28,22 |
| | | | | |
| | | | | |
| | | | | |

| 12, 14 (25, 30) 1986 (179) (2006) 16, 12, 13, 14 (26, 27) 16, 15 (26, 36) 14, 14 (25, 36) 14, 14 (25, 36) 16 (26, 36) (26, 36) 16 (26, 36) (26, 36) (26, 36) | 29 30 30 1 19 30 30 1 | | | | | (in said | N 12 | 17, 39 | D196433 | 14.17 WWA | a TRUS | LL 10 | DOV DIG O | 11.23 |
|---|--------------------------|-------|-------------|--------|--|----------|----------|-----------|----------|--------------|-----------|-----------|----------------|--------|
| 19661176 DDD6 16.12.13.16(20.25 16.13 20.16 12.14 25.56 Targle Searce False | 29 30 30 1 19 30 30 1 | 10.1 | 1 10, 12, 1 | 119419 | | (in said | | | | | | | | |
| 14, 12, 13, 16, 28, 29 14, 13, 13, 29, 28, 50 12, 14, 29, 50 Tangle Searce Fals | 28 30 MI | | | | | | Ellen's | 1025133 | 11045435 | WWA. | CTPS25 | Trans. to | Annual Street | S PLAN |
| 10, 13 24, 54 12, 14 24, 54 Tangle Searce Fields | M1 | 36.9 | | | | | | | | | | | | |
| 10, 13 24, 54 12, 14 24, 54 Tangle Searce Fields | M1 | 36.9 | | | | | 147.12.1 | 4115.24.2 | | 214.17.1 | | | -N. V. 141, 12 | |
| tingle Searce False | 38 | 10.05 | | 14 | 7.83 | 31, 14 | 14 | 17, 25 | DATE | 14,18 | 11 | 15.30 | K 00.0 | 11, 23 |
| | | | 14 | 16.17 | 18.83 | 8.10 | 4.12 | 17.30 | 04.152 | 14.17 | 1 | 112, 24 | | 14.21 |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| Saught Scourse Dates | | | | | | | | | | | _ | | | |
| | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | |
| | ange sourt i | | | | Sugle-Source Follower is not actualed as the Frede | | | | | | | | | |

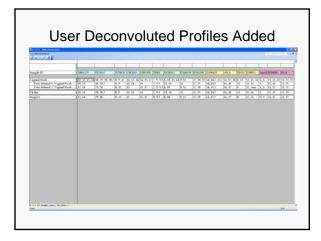


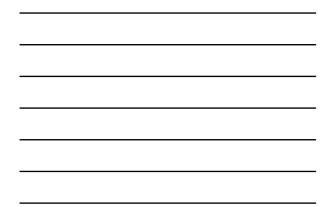




| Alleles 16, 12, 13, 14 | 10 12 13 14 |
|--|-------------|
| US EVA 2154, 783, 1374, 666 US EVA 2154, 783, 1374, 666 US EVA 2154, 7164, 143, 144, 144 Mail Frage April Mail Frage Mail Mail Frage Mail Mail Frage Mail Mail Frage Mail | |
| Refs 00 5 Refs 200 Sectors 200 | |







| | | | S | ingle | SOL | irce | State | S | | |
|---------------------|-----------------------|---------------------------|--------------|-------------------------|----------------------------|---------------------------------------|--|----------------------------|------------------|-------|
| | DHA Dataka | a tan n | | 0 | | | | | | |
| 1 DM. 5 | | | | | | | | | | |
| | 1410 | | | | | | | | | |
| Single So User d | arce atined 1: Var | ainh Samh | | | | | | | 0 | 4.01 |
| | 1 | Contraction of the second | 1 | <u>1</u> | 14.5 | ingenet soores | | | | |
| Locus | Locus Profile | Allala1 | Alle1e2 | Frequency: Unrelated | Frequency: Full ablings | Frequency: Farents and Othpring | Frequency: Hall Sibs, Uncles, Neph's | Troquency: FirstCouning | Database Fize | 1 |
| 0851179 | 10, 13 | 10 | 13 | N- 30 | | 12231110122803 | | s | 1992 - 1992 | - 122 |
| COULT 1 | Jun 10 | 0,1020 | 0,3390 | 0.069217 | 0,377625 | 0.320650 | 0.144934 | 0.107075 | | |
| | | 0.0250 | 0.2222 | 0.011120 | 0.3145/% | 0.123600 | 0.0#7355 | 0.039233 | | |
| | Marrie Contractor | 0.0904 | 0.3251 | 0.060859 | 0369030 | 6,209350 | 0.135114 | 0.097982 | | |
| 024811 | 28,30.2 | 28 | 36.2 | 0.012700 | 0.304707 | 0.102050 | 0.02223 | 0.005000 | | |
| | | 0,2151 | 0.0140 | 0.006023 | 0,306791 | 0.114550 | 0.060296 | 0.033155 | | |
| | | 0.0690 | 0.0020 | 0.004419 | 6,276354 | 0.050500 | 0.027450 | 0.015937 | | |
| DV5820 | 8,9 | 8 | . 9. | | | | | | | |
| | | 0.1624 | 0.1479 | 0.040065 | 0.33901el | 0.155200 | 0.000402 | 0.174545 | | |
| | | Caur | | 2.53908+21 | 5.71808+06 | 1.74018+11 | 2.25368+14 | 6.57148+16 | | |
| | | Flack | 1 in | 8.9423E+22 | 9.3134E+06 | 1.01058+12 | 1.64198+15 | 6.5443E+17 | | |
| | | Pasp | | 6.0577E+22 | 0.31568+06 | 1.50338+12 | 2.30618+15 | 0.0601E+17 | | |
| | | Case | | 2.5 motilion | 5.71 million | 174 billion | 225 trillion | 45 quadrillion | | |
| | | Black | 1 in | 89 sextilion | 9.31 million | 1.01 million | 1.0 guadallion | n50 quadrillion | | |
| | | Hisp | | 60 sectilion | 8.31 million | 1.58 tallion | 2.3 quadrillion | 800 quadrillion | | |
| | | FEICau | atian / Elac | k / Huparit alle | le frequencies | | | | | |
| | | | | based on databas | | | | | | |



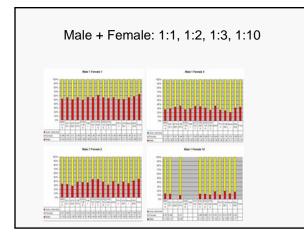
| | 1111 | xture Stats | |
|----------------------------|--|---|-------|
| Contraction | | | |
| User defined 2: Vagoal Lee | Allele CAllele 2 Allele 1 [Allele 4] | Typel Type2 Type2 Type8 Type5 Sum of | 0 4.4 |
| (8)179 [[12]16 [| 32 34 | 22 14 10 0.000 0.000 0.000 0.000 0.000 0.000 | |
| 7903 0.8.93 | 0.4291 1.1341 7 9 5.3 0.1754 0.1450 0.3054 0.4462 0.1452 0.3445 0.3059 0.1555 0.2455 1 55 | 6.300 0.300 9 9 9 9.33 6.306 6.360 6.360 6.027 6.304 0.360 6.013 6.327 6.304 6.027 6.304 0.306 6.0113 6.364 0.367 | |
| Anel K.Y | 12 0.178 0.178 0.399 X Y | 0.240 0.218 0.218 0.215 0.215 | |
| Case Flatk Nag | 1.51428 + 35 3.86478 + 35 6.57578 + 15 | [PII Caucaraa / Black / Hurpane aliele Irequencier | |
| Case art Hag | 10 quadrilion 33 quadrilion 67 quadrilion | | |



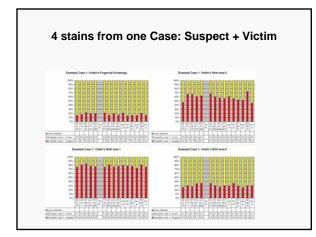
| | DHA Dataksatyris | | | | | | | | | | |
|---------------|----------------------|---------|------------------------|--------|--------|-----------|-----------|-------------|--------------|----------|--------|
| D DAM (D | and a | | | | | | | | | | |
| | ty of Inclusion | 1 | | | | | | | | | |
| Vaginal S | | _ | | | | | | | | | |
| Locus | Locus Perfile | Aliele1 | Allele 2 | | | Alleleð | | AIRIN | Allelet | 18 | [H] |
| D851179 | 10, 12, 13, 14 | 10 | 12 | 13 | 14 | - | 1 | 1 | II | | |
| | | 6,1020 | 0.5454 | | 0,2015 | - | 1 | - | | 0.3767 | 6153.0 |
| | | 0.0250 | 0.5383 | 0.2222 | 0.3333 | | 1 | 1 | | 0.5256 | 0.4744 |
| | | 0.07834 | 0.1207 | 0.3251 | 0.2463 | | | | | 0.3427 | 0.6175 |
| DU1511 | 28, 29, 30, 30.2, 33 | 20 | 29 | 30 | 30.2 | 33 | | | | | |
| | | 0.1456 | 0.5911 | | 1,0365 | 0.01229 | <u> </u> | | | 0.6030 | 8,3970 |
| | | 0,2151 | 0.1999 | 0.1798 | 0.0140 | 0.0140 | | | | 0.6257 | 0.3743 |
| | | 0.0490 | 0.2044 | | 8,0920 | 0.0123 | | | | 0.5904 | 0.4196 |
| D/5#20 | 8, 9, 12 | | | 12 | | | | | | | |
| | | 0.1626 | | 0.3404 | | | | | | 0,7968 | 6.2032 |
| | | 0.1796 | 0.1573 | 0.0905 | | | 1 | | | 0.8224 | 0,1776 |
| Caur | | 1 | 02512407 | | | ITSIC MAR | neine 7.1 | Carly J. Mu | panic allele | Francias | |
| Elleck | 11 in | 1. | 0615+09 | | | | | | , | | |
| Нир | 1 | 5. | 36258+07 | | | | | | | | |
| | 10 | | 2 miluto | | | | | | | | |
| Caue Riark | 110 | | 2 milion 80 billion | | | | | | | | |
| Нир | 6 ID 11- | | .6 million | | | | | | | | |

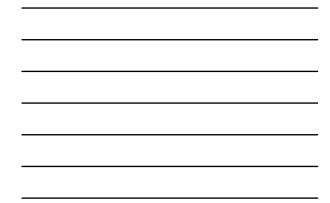


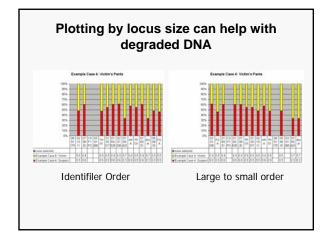
| | | R Stats | |
|-----------------------------|---|--------------------------------|--|
| - J. L. J. Disk (Databasely | | | |
| () [Mr.] windowicz | | | |
| Likelihand Lake | _ | | |
| Vagra Imal | | | |
| Lora To Lora Polle | | 170 170 1 | 0101 |
| CALIFY THE D. D. D. | 17. 12 1 17 1 14 1 | PROFILITION - PRODUCTION | and the second s |
| | 8 1520 U 1474 U 17947 G 2019 | 111 | 10747W2 |
| | <u> 1020 1207 1207 1207 1207 1207 1207 1207 1207 1207 1207 1207 1207 </u> | | 0.171219 |
| | | 0 | C. Constant of Constant |
| team 3[35,35,36,313 | 18 8 8 8 | NARABAN DESCRIPTION | T DECK T |
| | 6.3638 0.8441 0.2724 0.0860 | | D-3a-Notice |
| | 1000 0 0.200 0.000 0.000 | 1 14 K | 2134448 |
| 17444 [R.K.G | | MARKON CONTRACTOR | 120000-022 |
| | A.3408 0.1476 0.1414 | 1.56 | 71047540 |
| | 0.1798 0.1275 0.3965 | 147 | 10 34404713 30 3421925% |
| | time of total of the of | ц | - Province |
| | | п. п | |
| FGA. [21, 22, 25 | | Fi(+11.20.27) - Fi(21120.2029) | |
| | 0.1175 0.1000 0.2007 0.1170 0.2270 0.1000 | | D 1195(415 |
| | 01120 02220 01000 01300 01779 01279 | 113 | 0 296(916) |
| | | | |
| Cest | 2.0008404 | | |
| Fack Fin | 1.00000-00 | | |
| *z | | | |
| Catier Black 1 ton | 200 Million Ni quadrilion | | |
| Hark 1 to | N guadminen | | |
| | | | |



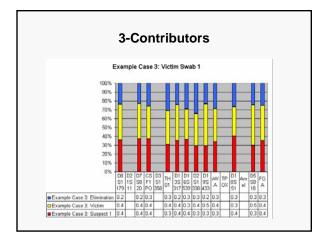


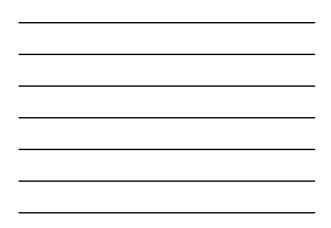


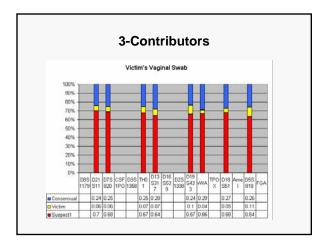


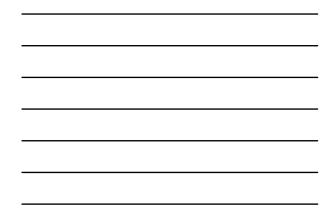






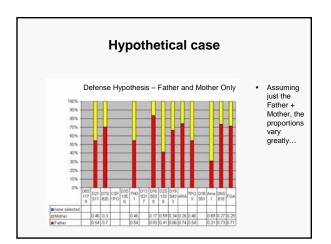


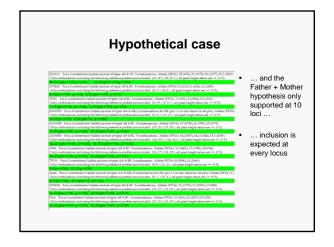


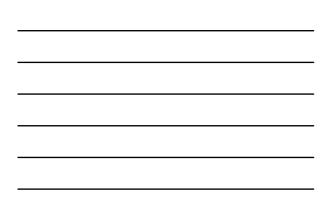


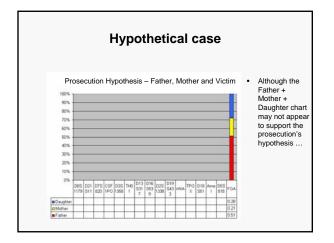
Hypothetical case

- 14 year old girl accuses Dad of raping her
- Semen stain from parent's bed
- All alleles from profiles of Dad, Mom, and Victim found in stain
- Prosecution hypothesis: the evidence is from the Father + Mother + Daughter
- Defense hypothesis: the evidence is from the Father + Mother
 - Of course the daughter's alleles or any child's are included
 - There is no reason to believe the daughter contributed to the stain

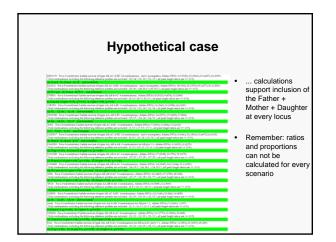


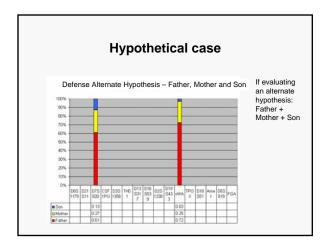




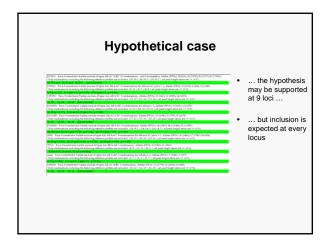














Thanks to...

- Tom Overson - USACIL (Ret)
- USACIL DNA Examiners
- John Butler, PhD
 NIST
- Rhonda Roby, MPH, MS

 NIJ Consultant

This PowerPoint and opinion expressed during the presentations are solely those of the presenter. They are not the opinions of the United States Department of Defense, Department of Army, United States Criminal Investigation Division Command, or the United States Criminal Investigation Laboratory. The opinions and presentation should not be misrepresented or misused as such in any way.

This PowerPoint is the original work product of Dr. Timothy Kalafut and Mr. Thomas Overson, United States Army Criminal Investigation Laboratory (USACIL), Forensic Biologist. This work is being used for educational purposes. Its contents may be reproduced and used for educational purposes only with attribution to the authors and USACIL. Further use or distribution is prohibited by Title 17 United States Code Section 107.

Mr. Tom Overson and the Serology and DNA Branch, United States Army Criminal Investigation Laboratory (USACIL) created and developed the software and analytical applications contained in the presentation. They may not be reproduced. Reproduction or usage without the permission of the USACIL for any purpose may result in the user's assumption of any and all risk, consequence and liability for their actions.

Example

