DNA Interpretation Workshop 2

Probabilistic Genotyping

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

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Melbourne, Australia
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NIST and NIJ Disclaimer

Funding: Interagency Agreement between the National Institute of Justice and NIST Office of Law Enforcement Standards

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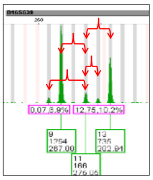
Whatever way uncertainty is approached, probability is the *only* sound way to think about it.

-Dennis Lindley

Do You Have Uncertainty in Your Data?

- **If allele dropout is a possibility** (e.g., in a partial profile), then there is uncertainty in whether or not an allele is present in the sample…and therefore what genotype combinations are possible
- **If different allele combinations are possible** in a mixture, then there is uncertainty in the genotype combinations that are possible…

Possible allele pairing with the 11

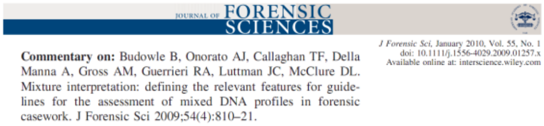


Uncertainty and Probability

- "Contrary to what many people think, **uncertainty is present throughout any scientific procedure**."
  - Dennis V. Lindley, in his foreword to Aitken & Taroni (2004) *Statistics and the Evaluation of Evidence for Forensic Scientists, Second Edition*
- "It is now recognized that **the only tool for handling uncertainty is probability**."
  - Dennis V. Lindley, in his foreword to Aitken & Taroni (2004) *Statistics and the Evaluation of Evidence for Forensic Scientists, Second Edition*

"On the Threshold of a Dilemma"

- Gill and Buckleton (2010)
- Although most labs use thresholds of some description, this philosophy has always been problematic because there is an inherent illogicality which we call the falling off the cliff effect.



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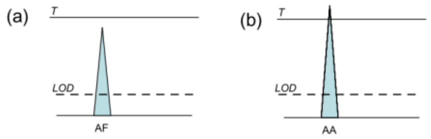
J Forensic Sci, January 2010, Vol. 55, No. 1
doi: 10.1111/j.1556-4029.2009.01257.x
Available online at: interscience.wiley.com

Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL. Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. J Forensic Sci 2009;54(4):810–21.

"Falling off the Cliff Effect"

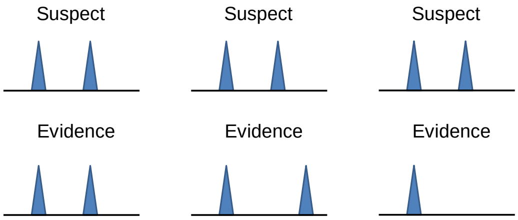
- If T = an arbitrary level (e.g., 150 rfu), an allele of 149 rfu is subject to a different set of guidelines compared with one that is 150 rfu even though they differ by just 1 rfu (Fig. 1).



Gill and Buckleton *JFS* 55: 265-268 (2010)

Gill and Buckleton *JFS* **55:** 265-268 (2010)

- "The purpose of the ISFG DNA commission document was to provide a way forward to demonstrate the use of ***probabilistic models to circumvent the requirement for a threshold*** and to safeguard the legitimate interests of defendants."



Suspect

Suspect

Suspect

Evidence

Evidence

Evidence

$$LR = \frac{1}{2pq}$$

$$LR = \frac{0}{2pq}$$

$$LR = \frac{?}{2pq}$$

"2p"

$p^2 + 2p(1 – p)$

What should we do with discordant data?

- Continue to use RMNE (CPI, CPE) (not optimal)
- Use the Binary LR with 2p (not optimal)
- Semi-continuous methods with a LR (Drop models)

Some Drop Model Examples

- LR mix (Haned and Gill)
- Balding (likeLTD - R program)
- FST (NYOCME, Mitchell *et al.*)
- Kelly *et al.* (University of Auckland, ESR)
- Lab Retriever (Lohmueller, Rudin and Inman)

Semi-continuous methods

- Use a Pr(DO) and LRs
- Speed of analysis – "relatively fast"

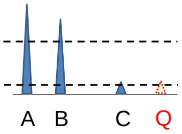
- The methods do not make full use of data - only the alleles present.

What should we do with discordant data?

- Continue to use RMNE (CPI, CPE) (not optimal)
- Use the Binary LR with 2p (not optimal)
- Semi-continuous methods with a LR (Drop models)
- Fully continuous methods with LR

Continuous Models

- Mathematical modeling of “molecular biology” of the profile (mix ratio, PHR (Hb), stutter, etc…) to find optimal genotypes, giving **WEIGHT** to the results.



Probable Genotypes

AC – 40%

BC – 25%

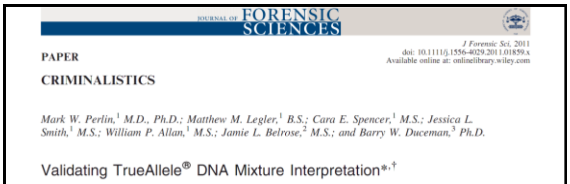
CC – 20%

CQ – 15%

Some Continuous Model Examples

- TrueAllele (Cybergenetics)
- STRmix (ESR [NZ] and Australian collaboration)
- Cowell et al. (FSI-G (2011) **5:**202-209)

Weights are determined by performing simulations of the data (Markov Chain Monte Carlo - MCMC)



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PAPER

CRIMINALISTICS

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Validating TrueAllele® DNA Mixture Interpretation*,†

- Quantitative computer interpretation using Markov Chain Monte Carlo testing
- Models peak uncertainty and infers possible genotypes
- Results are presented as a Combined LR

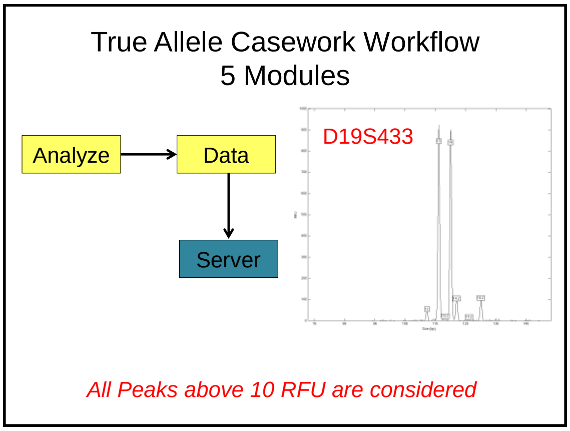
True Allele Software (Cybergenetics)

- Software runs on a Linux Server with a Mac interface.

True Allele Casework Workflow
5 Modules

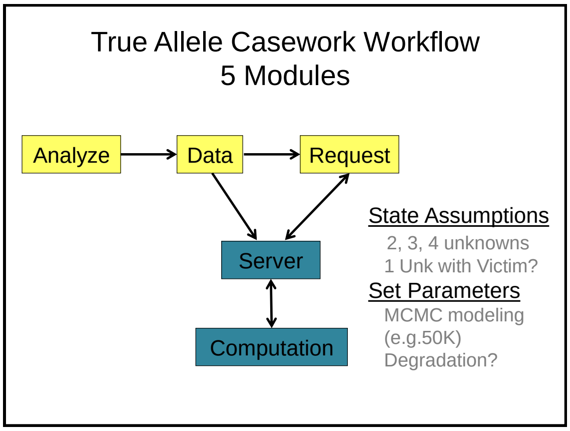
Analyze

.fsa files imported
Size Standard check
Allelic Ladder check
Alleles are called



True Allele Casework Workflow 5 Modules

All Peaks above 10 RFU are considered



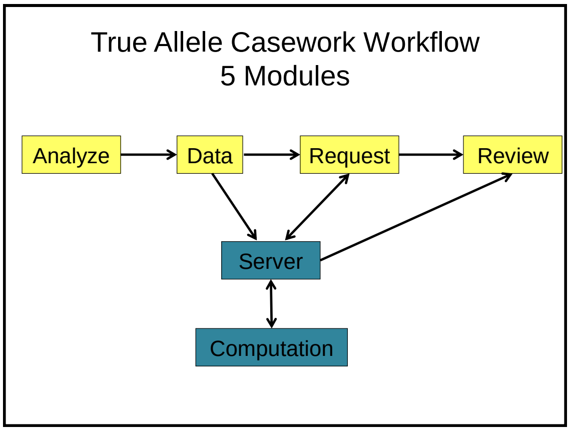
True Allele Casework Workflow 5 Modules

State Assumptions

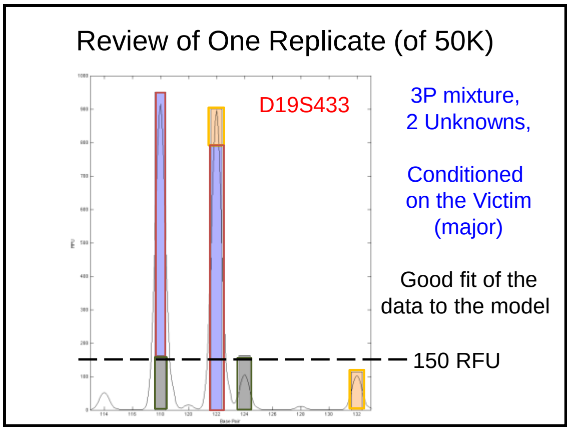
2, 3, 4 unknowns
1 Unk with Victim?

Set Parameters

MCMC modeling
(e.g.50K)
Degradation?



True Allele Casework Workflow 5 Modules

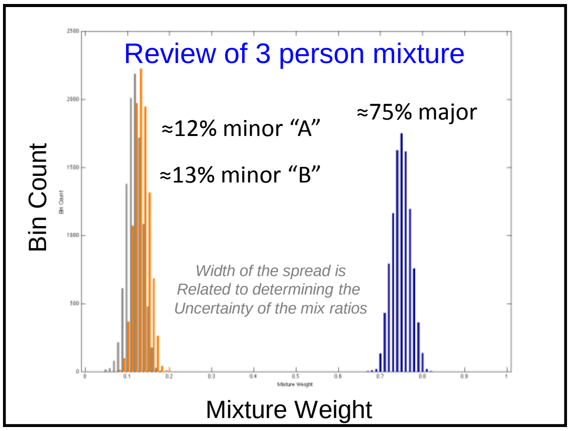


Review of One Replicate (of 50K)

3P mixture,
2 Unknowns,

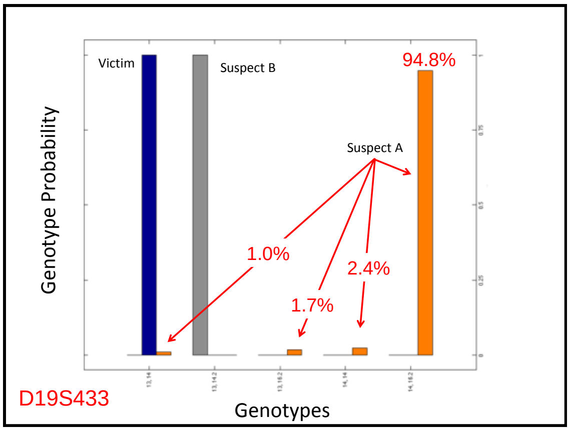
Conditioned on the Victim (major)

Good fit of the data to the model

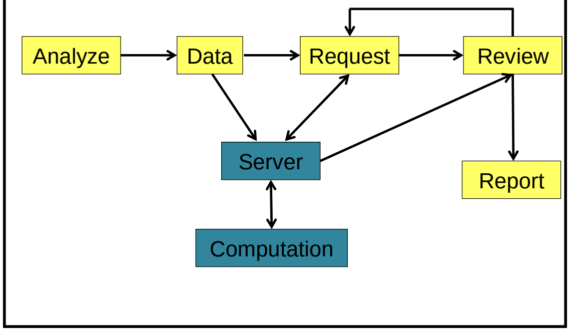


Review of 3 person mixture

Width of the spread is Related to determining the Uncertainty of the mix ratios



True Allele Casework Workflow 5 Modules



Combined LR = 5.6 Quintillion

			Genotype Probability Distribution			Weighted Likelihood		Likelihood Ratio	
	allele pair	Likelihood	Questioned	Reference	Suspect	Numerator	Denominator	LR	log(LR)
locus	x	l(x)	q(x)	r(x)	s(x)	l(x)*s(x)	l(x)*r(x)		
CSF1PO	11, 12	0.686	0.778	0.1448	1	0.68615	0.1292	5.31	0.725
D13S317	9, 12	1	1	0.0291	1	0.99952	0.02913	34.301	1.535
D16S539	9, 11	0.985	0.995	0.1238	1	0.98451	0.12188	8.036	0.905
D18S51	13, 17	0.999	1	0.0154	1	0.99915	0.01543	64.677	1.811
D19S433	14, 16.2	0.967	0.948	0.012	1	0.96715	0.01222	79.143	1.898
D21S11	28, 30	0.968	0.98	0.0872	1	0.96809	0.08648	11.194	1.049
D2S1338	23, 24	0.998	1	0.0179	1	0.99831	0.01787	55.866	1.747
D3S1358	15, 17	0.988	0.994	0.1224	1	0.98759	0.12084	8.14	0.911
D5S818	11, 11	0.451	0.394	0.0537	1	0.45103	0.07309	6.17	0.79
D7S820	11, 12	0.984	0.978	0.0356	1	0.98383	0.03617	27.198	1.435
D8S1179	13, 14	0.203	0.9	0.1293	1	0.20267	0.02993	6.771	0.831
FGA	21, 25	0.32	0.356	0.028	1	0.31986	0.01906	16.783	1.225
TH01	7, 7	0.887	0.985	0.1739	1	0.88661	0.15588	5.687	0.755
TPOX	8, 8	1	1	0.1375	1	1	0.13746	7.275	0.862
vWA	15, 20	0.998	0.996	0.0057	1	0.99808	0.00569	174.834	2.243

Results

- Results are expressed as logLR values

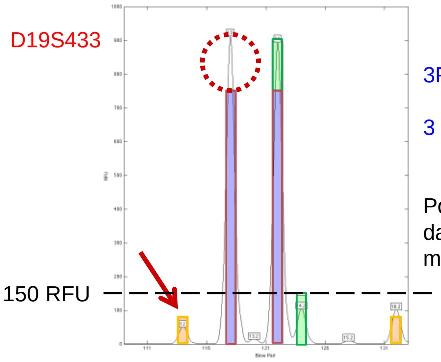
$$LR = 1,000,000 = 10^6$$

$$\log(LR) = \log 10^6$$

$$\log(LR) = 6 * \cancel{\log 10}\ (1)$$

$$\log(LR) = 6$$

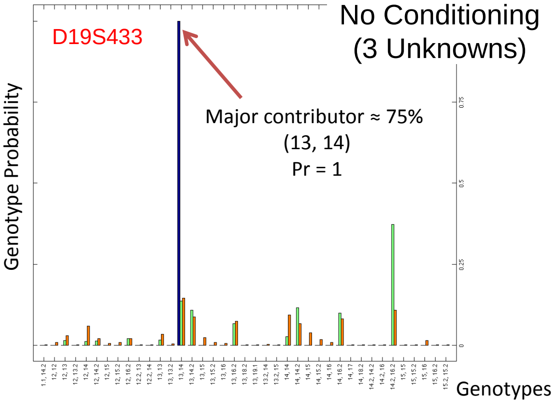
Review of One Replicate (of 50K)



3P mixture,

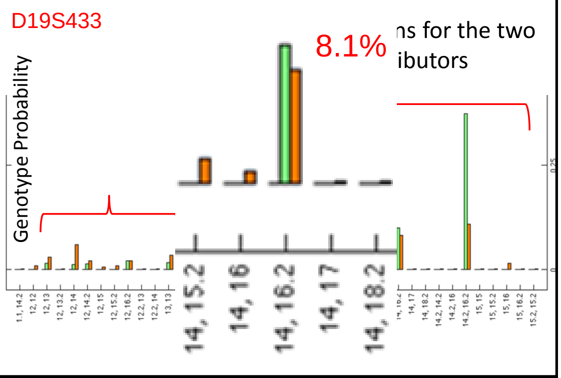
3 Unknowns

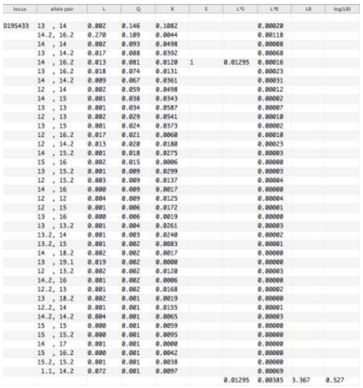
Poor fit of the data to the model



Major contributor ≈ 75%
(13, 14)
Pr = 1

No Conditioning (3 Unknowns)





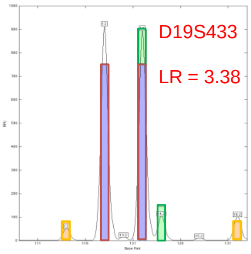
locus	allele pair	L	Q	R	S	L*S	L*R	LR	log(LR)
D19S433	13 , 14	0.002	0.146	0.1082			0.00028		
	14.2, 16.2	0.270	0.109	0.0044			0.00118		
	14 , 14	0.002	0.093	0.0498			0.00008		
	13 , 14.2	0.017	0.088	0.0392			0.00068		
	14 , 16.2	0.013	0.081	0.0128	1	0.01295	0.00016		
	13 , 16.2	0.018	0.074	0.0131			0.00023		
	14 , 14.2	0.009	0.067	0.0361			0.00031		
	12 , 14	0.002	0.059	0.0498			0.00012		
	14 , 15	0.001	0.038	0.0343			0.00002		
	13 , 13	0.001	0.034	0.0587			0.00007		
	12 , 13	0.002	0.029	0.0541			0.00018		
	13 , 15	0.001	0.024	0.0373			0.00002		
	12 , 16.2	0.017	0.021	0.0060			0.00010		
	12 , 14.2	0.013	0.020	0.0180			0.00023		
	14 , 15.2	0.001	0.018	0.0275			0.00003		
	15 , 16	0.002	0.015	0.0006			0.00000		
	13 , 15.2	0.001	0.009	0.0299			0.00003		
	12 , 15.2	0.003	0.009	0.0137			0.00004		
	14 , 16	0.000	0.009	0.0017			0.00000		
	12 , 12	0.004	0.009	0.0125			0.00004		
	12 , 15	0.001	0.006	0.0172			0.00001		
	13 , 16	0.000	0.006	0.0019			0.00000		
	13 , 13.2	0.001	0.004	0.0261			0.00003		
	13.2, 14	0.001	0.003	0.0240			0.00002		
	13.2, 15	0.001	0.002	0.0083			0.00001		
	14 , 18.2	0.002	0.002	0.0017			0.00000		
	13 , 19.1	0.019	0.002	0.0000			0.00000		
	12 , 13.2	0.002	0.002	0.0120			0.00003		
	14.2, 16	0.001	0.002	0.0006			0.00000		
	12.2, 13	0.001	0.002	0.0168			0.00002		
	13 , 18.2	0.002	0.001	0.0019			0.00000		
	12.2, 14	0.001	0.001	0.0155			0.00001		
	14.2, 14.2	0.004	0.001	0.0065			0.00003		
	15 , 15	0.000	0.001	0.0059			0.00000		
	15 , 15.2	0.000	0.001	0.0095			0.00000		
	14 , 17	0.001	0.001	0.0000			0.00000		
	15 , 16.2	0.000	0.001	0.0042			0.00000		
	15.2, 15.2	0.001	0.001	0.0038			0.00000		
	1.1, 14.2	0.072	0.001	0.0097			0.00069		
						0.01295	0.00385	3.367	0.527

Suspect "A" Genotype

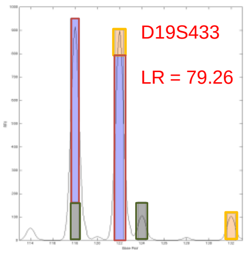
39 probable genotypes

D19S433

No Conditioning



Conditioned on Victim



Profile - Combined log(LR)
Suspect A log(LR) = 8.03
Suspect B log(LR) = 7.84

Profile - Combined log(LR)
Suspect A log(LR) = 18.72
Suspect B log(LR) = 19.45

Exploring the Capabilities

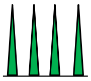
- **Degree of Allele Sharing**
- **Mixture Ratios**
- DNA Quantity

Mixture Data Set

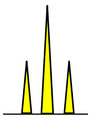
- Mixtures of pristine male and female DNA amplified at a total concentration of 1.0 ng/µL using Identifiler (standard conditions).
- Mixture ratios ranged from 90:10, 80:20, 70:30 60:40, 50:50, 40:60, 30:70, 20:80, and 10:90
- Each sample was amplified twice.

Mixture Data Set

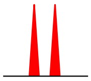
- Three different combinations:



"Low" Sharing



"Medium" Sharing

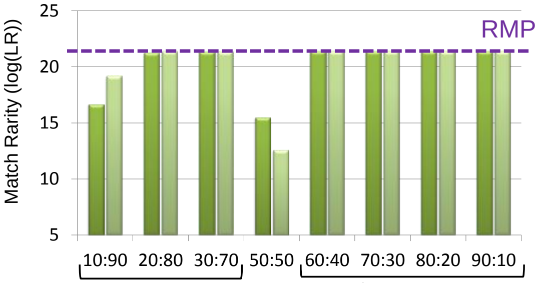


"High" Sharing

"Low" Sharing	"Medium" Sharing	"High" Sharing
4 alleles – 10 loci	4 alleles – 3 loci	4 alleles – 0 loci
3 alleles – 5 loci	3 alleles – 8 loci	3 alleles – 6 loci
2 alleles – 0 loci	2 alleles – 4 loci	2 alleles – 8 loci
1 allele – 0 loci	1 allele – 0 loci	1 allele – 1 loci

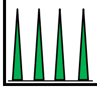
Virtual MixtureMaker - http://www.cstl.nist.gov/strbase/software.htm

Match Score in Duplicate Runs



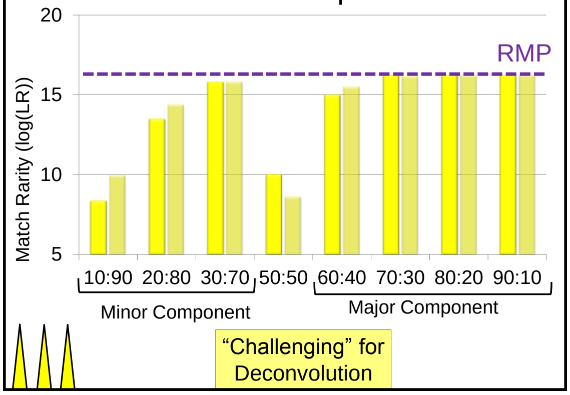
Minor Component

Major Component



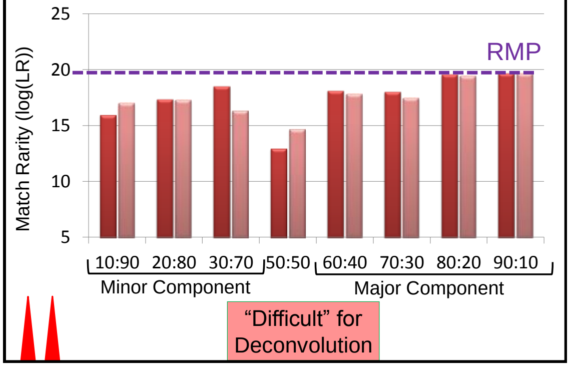
"Easy" for Deconvolution

Match Score in Duplicate Runs

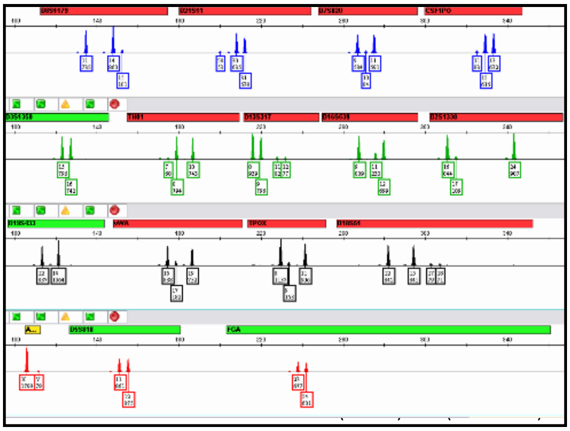


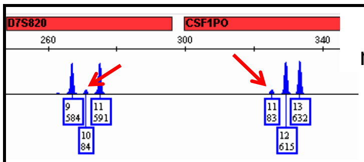
"Challenging" for Deconvolution

Match Score in Duplicate Runs

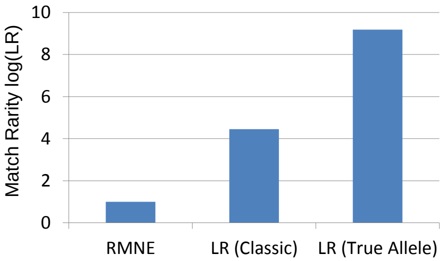


"Difficult" for Deconvolution





10:90 minor contributor

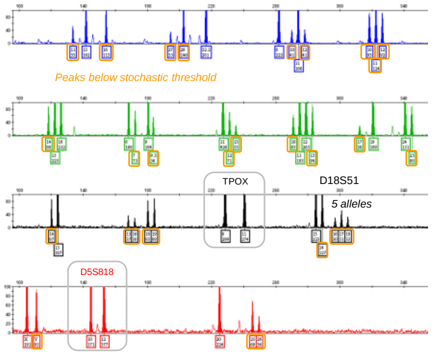


Exploring the Capabilities

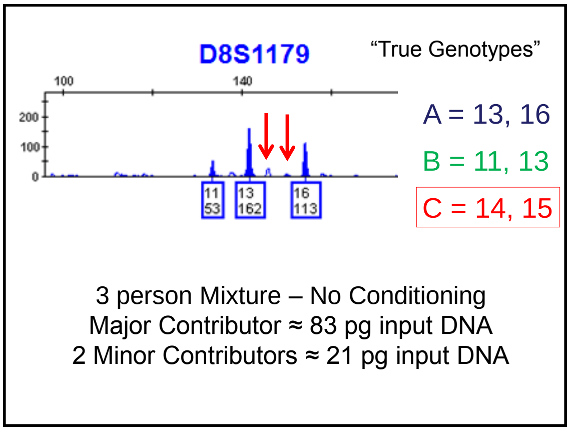
- Degree of Allele Sharing
- Mixture Ratios
- **DNA Quantity**

Identifiler
125 pg total DNA

AT = 30 RFU
ST = 150 RFU
Stutter filter off



y-axis zoom to 100 RFU



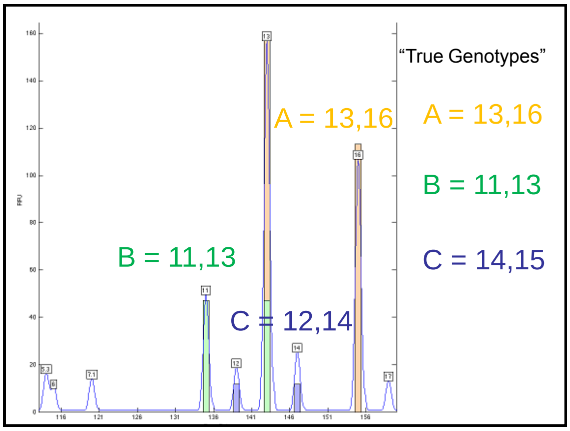
“True Genotypes”

A = 13, 16

B = 11, 13

C = 14, 15

3 person Mixture – No Conditioning
Major Contributor ≈ 83 pg input DNA
2 Minor Contributors ≈ 21 pg input DNA



“True Genotypes”

A = 13,16

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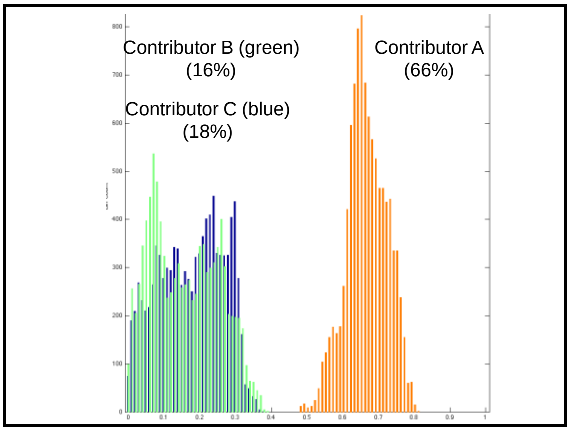
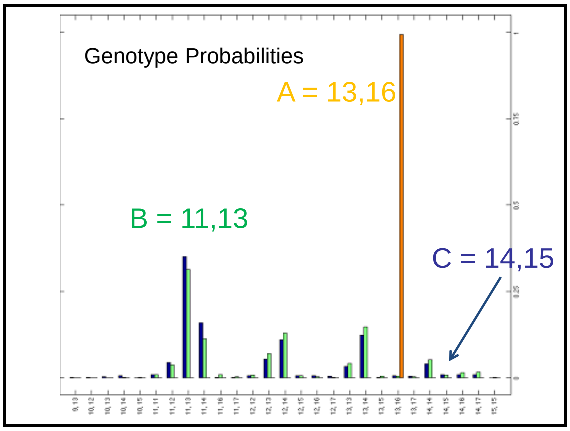


Contributor B (green)
(16%)

Contributor C (blue)
(18%)

Contributor A
(66%)

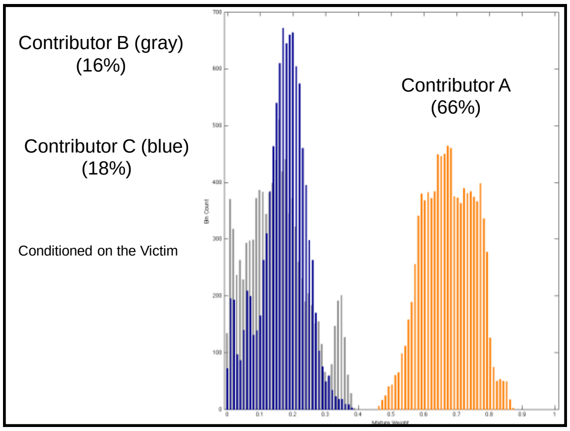


Genotype Probabilities

A = 13,16

B = 11,13

C = 14,15

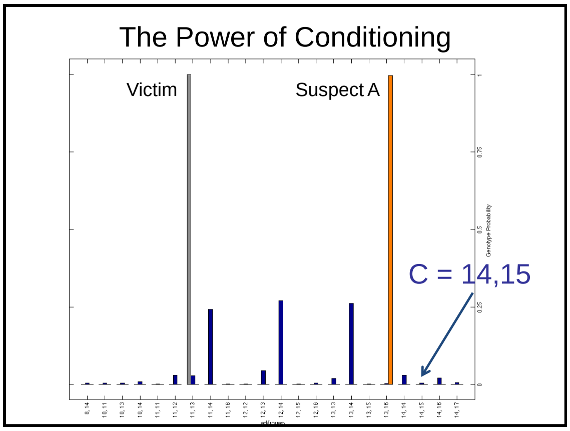


Contributor B (gray)
(16%)

Contributor C (blue)
(18%)

Conditioned on the Victim

Contributor A
(66%)



The Power of Conditioning

Victim

Suspect A

C = 14,15

The Power of Conditioning

	LR (no conditioning, 3unk)
Contributor A	1.21 Quintillion
Contributor B (victim)	1.43 Million
Contributor C	9.16 Thousand

	LR (conditioned on victim + 2unk)
Contributor A	1.32 Quintillion
Contributor B (victim)	2.19 Million
Contributor C	59.8 Thousand

↑

Ranged from 1.13 to 800K

Summary

- True Allele utilizes probabilistic genotyping and makes better use of the data than the RMNE approach.
- However, the software is computer intensive. On our 4 processor system, it can take 12-16 hours to run up to four 3-person mixture samples.

Summary

- **Allele Sharing:** Stacking of alleles due to sharing creates more uncertainty.
- **Mixture Ratio:** With "distance" between the two contributors, there is greater certainty. Generally, True Allele performs better than RMNE and the classic LR with low level contributors.

Summary

- **DNA Quantity:** Generally, with high DNA signal, replicates runs on True Allele are very reproducible.
- However, with low DNA signal, higher levels of uncertainty are observed (as expected).
- There is a need to determine an appropriate threshold for an inclusion log(LR).

STRmix

http://strmix.com/

STRmix was developed by Duncan Taylor (FSSA), Jo-Anna Bright (ESR) and John Buckleton (ESR) with oversight from a Steering Committee chaired by NIFS.

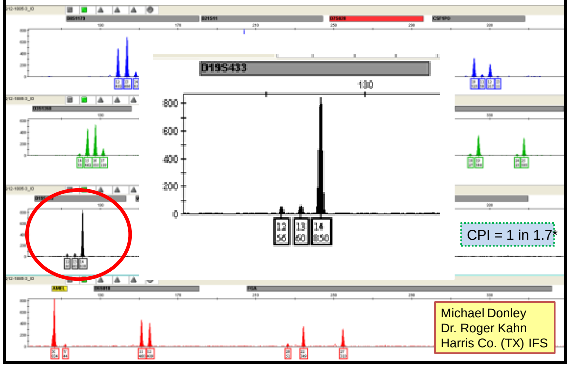
ESR

Government of South Australia
Forensic Science SA

ANZPAA

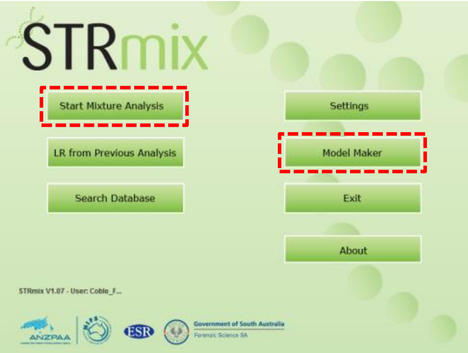
NIFS

Challenging Mixture

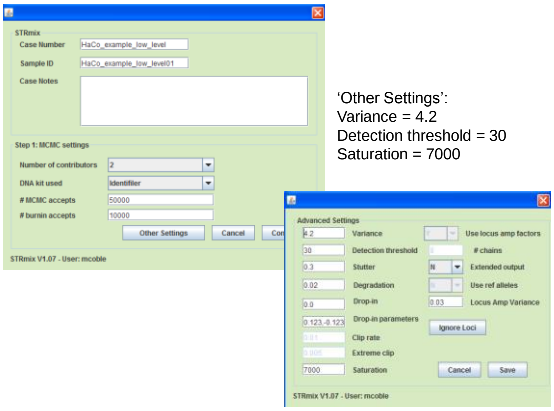


CPI = 1 in 1.7*

Michael Donley
Dr. Roger Kahn
Harris Co. (TX) IFS



STRmix V1.07 - User: Coble_F...


STRmix

Case Number: HaCo_example_low_level

Sample ID: HaCo_example_low_level01

Case Notes:

Step 1: MCMC settings

Number of contributors: 2

DNA kit used: Identifiler

MCMC accepts: 50000

burnin accepts: 10000

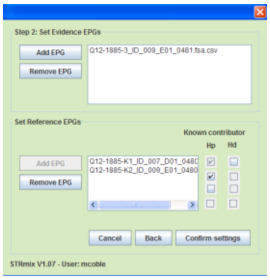
STRmix V1.07 - User: mcoble

Advanced Settings

4.2	Variance		Use locus amp factors
30	Detection threshold		# chains
0.3	Stutter	N	Extended output
0.02	Degradation		Use ref alleles
0.0	Drop-in	0.03	Locus Amp Variance
0.123,-0.123	Drop-in parameters		
0.01	Clip rate		
0.005	Extreme clip		
7000	Saturation		

STRmix V1.07 - User: mcoble

'Other Settings':
Variance = 4.2
Detection threshold = 30
Saturation = 7000


Step 2: Set Evidence EPGs

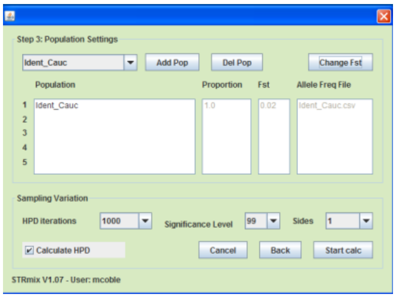
Q12-1885-3_ID_009_E01_0481.fsa.csv

Set Reference EPGs

	Known contributor Hp	Known contributor Hd
Q12-1885-K1_ID_007_D01_0480	☑	□
Q12-1885-K2_ID_009_E01_0480	☑	□
	□	□
	□	□

STRmix V1.07 - User: mcoble

Calculate the LR using hypotheses:
Hp = K1 (victim) + K2 (suspect)
Hd = 2 unknowns


Step 3: Population Settings

Ident_Cauc

	Population	Proportion	Fst	Allele Freq File
1	Ident_Cauc	1.0	0.02	Ident_Cauc.csv
2				
3				
4				
5				

Sampling Variation

HPD iterations: 1000 Significance Level: 99 Sides: 1

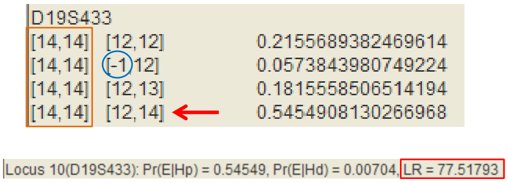
☑ Calculate HPD

STRmix V1.07 - User: mcoble

Add the population database(s)

Select 'Start calc'

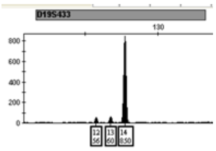
```
Mixture Proportions
Contributor 1 – 87%
Contributor 2 – 13%
```



D19S433

[14,14]	[12,12]	0.2155689382469614
[14,14]	[-1,12]	0.0573843980749224
[14,14]	[12,13]	0.1815558506514194
[14,14]	[12,14] ←	0.5454908130266968

Locus 10(D19S433): Pr(E|Hp) = 0.54549, Pr(E|Hd) = 0.00704, LR = 77.51793

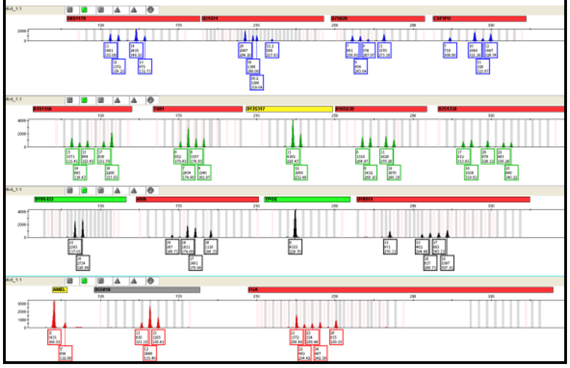


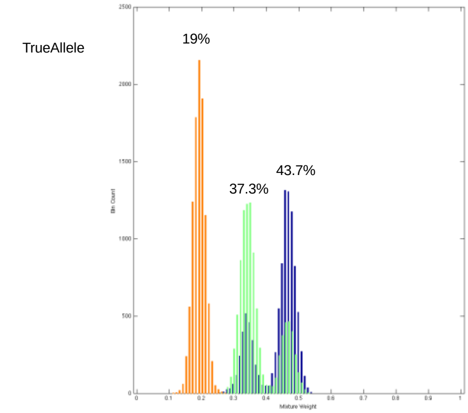
LR total = 1.73E16

Fully continuous methods

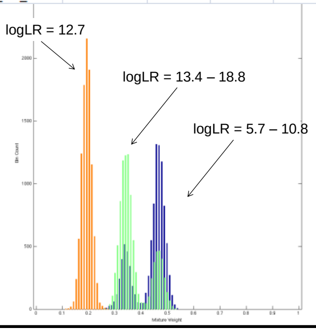
- Use a Pr(DO) and LRs
- Speed of analysis – can vary
- Attempts to use all of the data

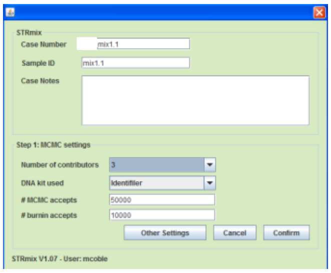
Mixture 1.1 – 3P





Evidence	Contributor	Weight	1	10	11
Mixt_1.1_3unk	1	0.4367	5.7252	18.8886	-19.1664
Mixt_1.1_3unk	2	0.3734	10.8278	13.4535	-18.1592
Mixt_1.1_3unk	3	0.19	-19.6287	-19.4984	12.7172





STRmix

Case Number: mix1.1

Sample ID: mix1.1

Case Notes:

Step 1: MCMC settings

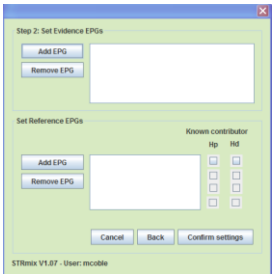
Number of contributors: 3

DNA kit used: Identifiler

MCMC accepts: 50000

burnin accepts: 10000

STRmix V1.07 - User: mcoble



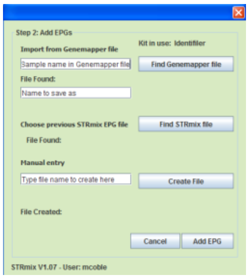
Step 2: Set Evidence EPGs

Set Reference EPGs

Known contributor

	Hp	Hd
	□	□
	□	□
	□	□
	□	□

STRmix V1.07 - User: mcoble



Step 2: Add EPGs

Kit in use: Identifiler

Import from Genemapper file

Sample name in Genemapper file

File Found:

Name to save as

Choose previous STRmix EPG file

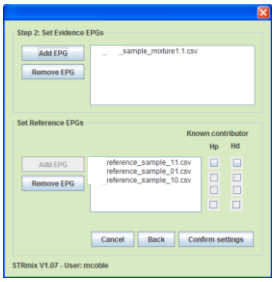
File Found:

Manual entry

Type file name to create here

File Created:

STRmix V1.07 - User: mcoble



Step 2: Set Evidence EPGs

[redacted]_sample_mixture1.1.csv

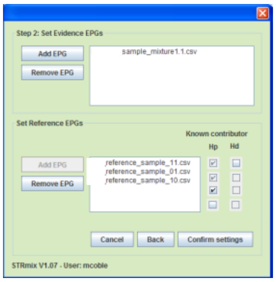
Set Reference EPGs

Known contributor

	Hp	Hd
[redacted]reference_sample_11.csv	□	□
[redacted]reference_sample_01.csv	□	□
[redacted]reference_sample_10.csv	□	□
	□	□

STRmix V1.07 - User: mcoble

H_P = Suspect 11 + Suspect 01 + Suspect 10 are in the mixture



Step 2: Set Evidence EPGs

[redacted]sample_mixture1.1.csv

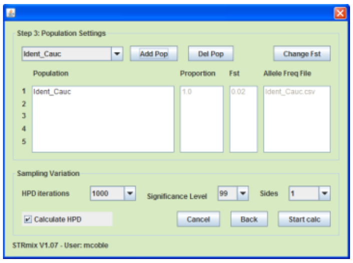
Set Reference EPGs

Known contributor

	Hp	Hd
[redacted]reference_sample_11.csv	☑	□
[redacted]reference_sample_01.csv	☑	□
[redacted]reference_sample_10.csv	☑	□
	□	□

STRmix V1.07 - User: mcoble

H_D = 3 unknown, unrelated individuals are in the mixture



Step 3: Population Settings

Ident_Cauc

	Population	Proportion	Fst	Allele Freq File
1	Ident_Cauc	1.0	0.02	Ident_Cauc.csv
2				
3				
4				
5				

Sampling Variation

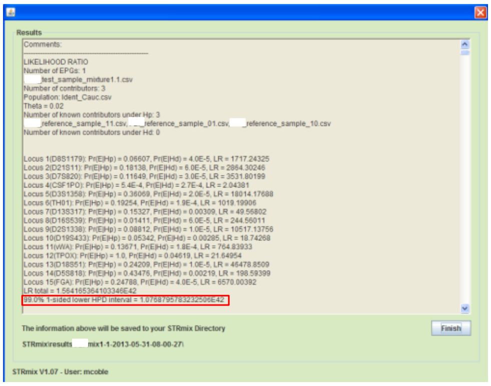
HPD iterations 1000

Significance Level 99

Sides 1

☑ Calculate HPD

STRmix V1.07 - User: mcoble



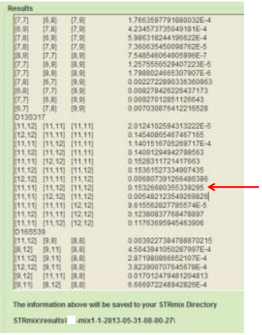
Results

```
Comments:
--------------------------------------------------
LIKELIHOOD RATIO
Number of EPGs: 1
[redacted]_test_sample_mixture1.1.csv
Number of contributors: 3
Population: Ident_Cauc.csv
Theta = 0.02
Number of known contributors under Hp: 3
[redacted]_reference_sample_11.csv, [redacted]_reference_sample_01.csv, [redacted]_reference_sample_10.csv
Number of known contributors under Hd: 0


Locus 1(D8S1179): Pr(E|Hp) = 0.06607, Pr(E|Hd) = 4.0E-5, LR = 1717.24325
Locus 2(D21S11): Pr(E|Hp) = 0.18138, Pr(E|Hd) = 6.0E-5, LR = 2864.30246
Locus 3(D7S820): Pr(E|Hp) = 0.11649, Pr(E|Hd) = 3.0E-5, LR = 3531.80199
Locus 4(CSF1PO): Pr(E|Hp) = 5.4E-4, Pr(E|Hd) = 2.7E-4, LR = 2.04381
Locus 5(D3S1358): Pr(E|Hp) = 0.36069, Pr(E|Hd) = 2.0E-5, LR = 18014.17688
Locus 6(TH01): Pr(E|Hp) = 0.19254, Pr(E|Hd) = 1.9E-4, LR = 1019.19906
Locus 7(D13S317): Pr(E|Hp) = 0.15327, Pr(E|Hd) = 0.00309, LR = 49.56802
Locus 8(D16S539): Pr(E|Hp) = 0.01411, Pr(E|Hd) = 6.0E-5, LR = 244.56011
Locus 9(D2S1338): Pr(E|Hp) = 0.08812, Pr(E|Hd) = 1.0E-5, LR = 10517.13756
Locus 10(D19S433): Pr(E|Hp) = 0.05342, Pr(E|Hd) = 0.00285, LR = 18.74268
Locus 11(vWA): Pr(E|Hp) = 0.13671, Pr(E|Hd) = 1.8E-4, LR = 764.83933
Locus 12(TPOX): Pr(E|Hp) = 1.0, Pr(E|Hd) = 0.04619, LR = 21.64954
Locus 13(D18S51): Pr(E|Hp) = 0.24209, Pr(E|Hd) = 1.0E-5, LR = 46478.8509
Locus 14(D5S818): Pr(E|Hp) = 0.43476, Pr(E|Hd) = 0.00219, LR = 198.59399
Locus 15(FGA): Pr(E|Hp) = 0.24788, Pr(E|Hd) = 4.0E-5, LR = 6570.00392
LR total = 1.564165364103346E42
99.0% 1-sided lower HPD interval = 1.0768795783232506E42
```

The information above will be saved to your STRmix Directory

STRmix\results\[redacted]mix1-1-2013-05-31-08-00-27\

STRmix V1.07 - User: mcoble



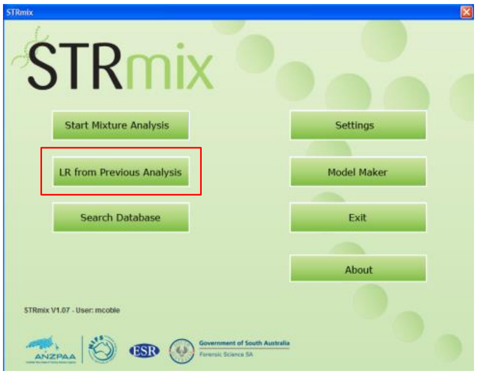
Results

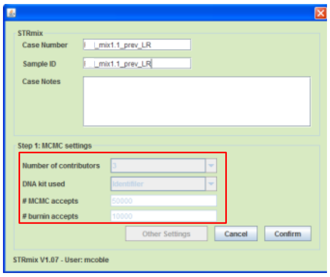
```
[7,7]   [6,8]   [7,9]      1.7663597791880032E-4
[6,9]   [7,8]   [7,9]      4.234573735049181E-4
[7,8]   [6,9]   [7,9]      5.986318244196622E-4
[7,8]   [7,9]   [7,9]      7.360635450098762E-5
[8,9]   [7,7]   [8,9]      7.548546064905996E-7
[7,7]   [6,9]   [8,9]      1.2575556529407223E-5
[7,7]   [8,9]   [8,9]      1.7988024665307907E-6
[7,8]   [6,7]   [9,9]      0.002272289033636963
[6,8]   [7,7]   [9,9]      0.008278428226437173
[7,7]   [6,8]   [9,9]      0.00927012851126643
[5,7]   [7,8]   [9,9]      0.007030876412216528
D13S317
[11,12] [11,11] [11,11]    2.0124102594313222E-5
[12,12] [11,11] [11,11]    0.14540865467467165
[11,11] [11,12] [11,11]    1.1401516705269717E-4
[11,12] [11,12] [11,11]    0.14091294942798563
[11,11] [12,12] [11,11]    0.1528311721417663
[11,12] [11,11] [11,12]    0.15361527334907435
[12,12] [11,11] [11,12]    0.006807391266486386
[11,11] [11,12] [11,12]    0.15326680355339295
[11,11] [12,12] [11,12]    0.005482123549269826
[11,11] [11,11] [12,12]    9.615562827785574E-5
[11,12] [11,11] [12,12]    0.12380837768478897
[11,11] [11,12] [12,12]    0.11763695945463906
D16S539
[11,12] [9,9]   [8,8]      0.0039227384788870215
[8,12]  [9,11]  [8,8]      4.5043941050287997E-4
[11,12] [9,11]  [8,8]      2.871980866652107E-4
[12,12] [9,11]  [8,8]      3.823900707645678E-4
[9,12]  [11,11] [8,8]      0.017012479481204813
[9,11]  [8,12]  [8,8]      5.666972248942826E-4
```

The information above will be saved to your STRmix Directory

STRmix\results\[redacted]-mix1-1-2013-05-31-08-00-27\

H_P




STRmix

Case Number: [redacted]_mix1.1_prev_LR

Sample ID: [redacted]_mix1.1_prev_LR

Case Notes:

Step 1: MCMC settings

Number of contributors: 3

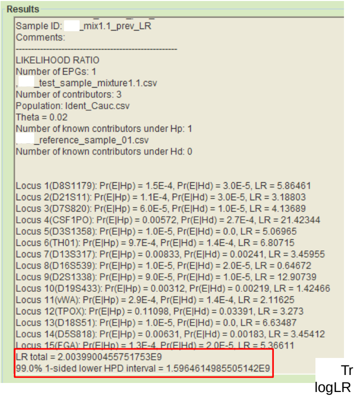
DNA kit used: Identifiler

MCMC accepts: 50000

burnin accepts: 10000

STRmix V1.07 - User: mcoble

Cannot change settings (no MCMC)

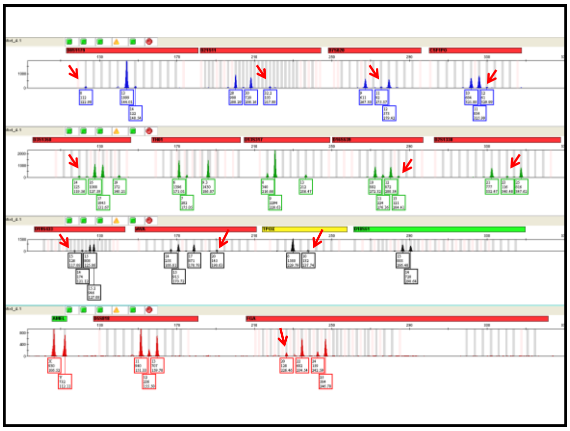

Results

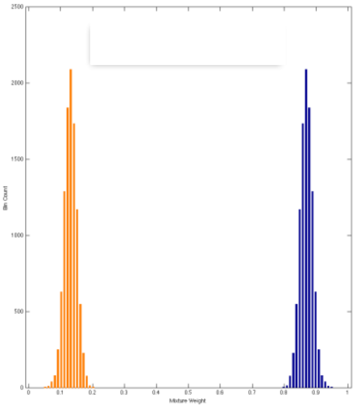
```
Sample ID: [redacted]_mix1.1_prev_LR
Comments:
----------------------------------------------------
LIKELIHOOD RATIO
Number of EPGs: 1
,[redacted]_test_sample_mixture1.1.csv
Number of contributors: 3
Population: Ident_Cauc.csv
Theta = 0.02
Number of known contributors under Hp: 1
[redacted]_reference_sample_01.csv
Number of known contributors under Hd: 0


Locus 1(D8S1179): Pr(E|Hp) = 1.5E-4, Pr(E|Hd) = 3.0E-5, LR = 5.86461
Locus 2(D21S11): Pr(E|Hp) = 1.1E-4, Pr(E|Hd) = 3.0E-5, LR = 3.18803
Locus 3(D7S820): Pr(E|Hp) = 6.0E-5, Pr(E|Hd) = 1.0E-5, LR = 4.13689
Locus 4(CSF1PO): Pr(E|Hp) = 0.00572, Pr(E|Hd) = 2.7E-4, LR = 21.42344
Locus 5(D3S1358): Pr(E|Hp) = 1.0E-5, Pr(E|Hd) = 0.0, LR = 5.06965
Locus 6(TH01): Pr(E|Hp) = 9.7E-4, Pr(E|Hd) = 1.4E-4, LR = 6.80715
Locus 7(D13S317): Pr(E|Hp) = 0.00833, Pr(E|Hd) = 0.00241, LR = 3.45955
Locus 8(D16S539): Pr(E|Hp) = 1.0E-5, Pr(E|Hd) = 2.0E-5, LR = 0.64672
Locus 9(D2S1338): Pr(E|Hp) = 9.0E-5, Pr(E|Hd) = 1.0E-5, LR = 12.90739
Locus 10(D19S433): Pr(E|Hp) = 0.00312, Pr(E|Hd) = 0.00219, LR = 1.42466
Locus 11(vWA): Pr(E|Hp) = 2.9E-4, Pr(E|Hd) = 1.4E-4, LR = 2.11625
Locus 12(TPOX): Pr(E|Hp) = 0.11098, Pr(E|Hd) = 0.03391, LR = 3.273
Locus 13(D18S51): Pr(E|Hp) = 1.0E-5, Pr(E|Hd) = 0.0, LR = 6.63487
Locus 14(D5S818): Pr(E|Hp) = 0.00631, Pr(E|Hd) = 0.00183, LR = 3.45412
Locus 15(FGA): Pr(E|Hp) = 1.3E-4, Pr(E|Hd) = 2.0E-5, LR = 5.36611
LR total = 2.0039900455751753E9
99.0% 1-sided lower HPD interval = 1.5964614985505142E9
```

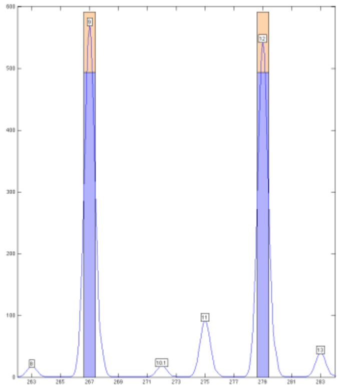
TrueAllele
logLR = 5.7 – 10.8

Two Person Mixture

4.1 – low level



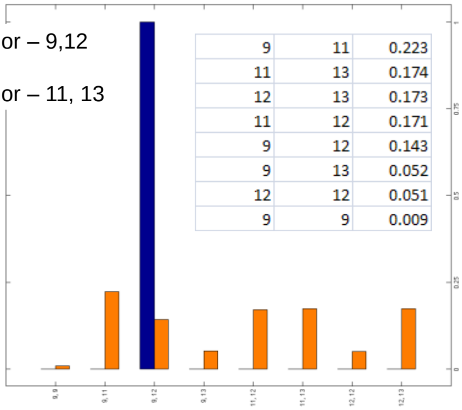




D7

Major – 9,12

Minor – 11, 13



Major – 9,12

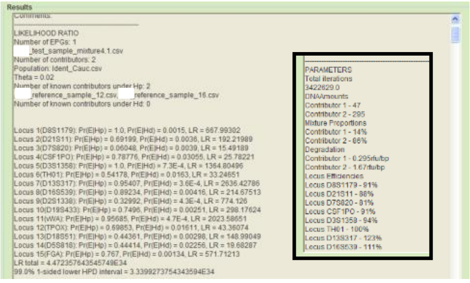
Minor – 11, 13

9	11	0.223
11	13	0.174
12	13	0.173
11	12	0.171
9	12	0.143
9	13	0.052
12	12	0.051
9	9	0.009

TrueAllele Results

Mixt_4.1_2unk	0.8709	19.5021	-26.5579
Mixt_4.1_2unk	0.1291	-24.5606	19.0005

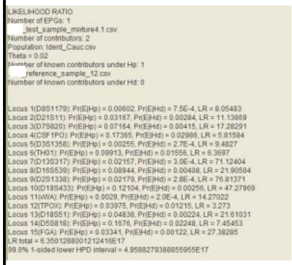
86% Major
14% Minor



```
Comments:
----------------------------------------
LIKELIHOOD RATIO
Number of EPGs: 1
[redacted]_test_sample_mixture4.1.csv
Number of contributors: 2
Population: Ident_Cauc.csv
Theta = 0.02
Number of known contributors under Hp: 2
[redacted]_reference_sample_12.csv, [redacted]_reference_sample_16.csv
Number of known contributors under Hd: 0


Locus 1(D8S1179): Pr(E|Hp) = 1.0, Pr(E|Hd) = 0.0015, LR = 667.99302
Locus 2(D21S11): Pr(E|Hp) = 0.69199, Pr(E|Hd) = 0.0036, LR = 192.21989
Locus 3(D7S820): Pr(E|Hp) = 0.06048, Pr(E|Hd) = 0.0039, LR = 15.49189
Locus 4(CSF1PO): Pr(E|Hp) = 0.78776, Pr(E|Hd) = 0.03055, LR = 25.78221
Locus 5(D3S1358): Pr(E|Hp) = 1.0, Pr(E|Hd) = 7.3E-4, LR = 1364.80496
Locus 6(TH01): Pr(E|Hp) = 0.54178, Pr(E|Hd) = 0.0163, LR = 33.24651
Locus 7(D13S317): Pr(E|Hp) = 0.95407, Pr(E|Hd) = 3.6E-4, LR = 2636.42786
Locus 8(D16S539): Pr(E|Hp) = 0.89234, Pr(E|Hd) = 0.00416, LR = 214.67513
Locus 9(D2S1338): Pr(E|Hp) = 0.32992, Pr(E|Hd) = 4.3E-4, LR = 774.126
Locus 10(D19S433): Pr(E|Hp) = 0.7496, Pr(E|Hd) = 0.00251, LR = 298.17624
Locus 11(vWA): Pr(E|Hp) = 0.95685, Pr(E|Hd) = 4.7E-4, LR = 2023.58651
Locus 12(TPOX): Pr(E|Hp) = 0.69853, Pr(E|Hd) = 0.01611, LR = 43.36074
Locus 13(D18S51): Pr(E|Hp) = 0.44361, Pr(E|Hd) = 0.00298, LR = 148.99049
Locus 14(D5S818): Pr(E|Hp) = 0.44414, Pr(E|Hd) = 0.02256, LR = 19.68287
Locus 15(FGA): Pr(E|Hp) = 0.767, Pr(E|Hd) = 0.00134, LR = 571.71213
LR total = 4.472357643545749E34
99.0% 1-sided lower HPD interval = 3.339927375434359 4E34
```

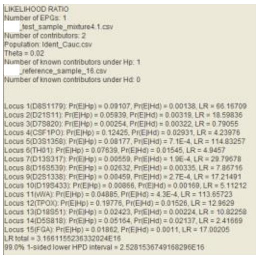
```
----------------------------------------
PARAMETERS
Total iterations
3422629.0
DNAAmounts
Contributor 1 - 47
Contributor 2 - 295
Mixture Proportions
Contributor 1 - 14%
Contributor 2 - 86%
Degradation
Contributor 1 - 0.295rfu/bp
Contributor 2 - 1.67rfu/bp
Locus Efficiencies
Locus D8S1179 - 91%
Locus D21S11 - 88%
Locus D7S820 - 81%
Locus CSF1PO - 91%
Locus D3S1358 - 94%
Locus TH01 - 100%
Locus D13S317 - 123%
Locus D16S539 - 111%
```

Ref 12 – 4.95 x 10^{17}



```
LIKELIHOOD RATIO
Number of EPGs: 1
[redacted]_test_sample_mixture4.1.csv
Number of contributors: 2
Population: Ident_Cauc.csv
Theta = 0.02
Number of known contributors under Hp: 1
[redacted]_reference_sample_12.csv
Number of known contributors under Hd: 0


Locus 1(D8S1179): Pr(E|Hp) = 0.00602, Pr(E|Hd) = 7.5E-4, LR = 8.05483
Locus 2(D21S11): Pr(E|Hp) = 0.03167, Pr(E|Hd) = 0.00284, LR = 11.13869
Locus 3(D7S820): Pr(E|Hp) = 0.07164, Pr(E|Hd) = 0.00415, LR = 17.28291
Locus 4(CSF1PO): Pr(E|Hp) = 0.17365, Pr(E|Hd) = 0.02986, LR = 5.81584
Locus 5(D3S1358): Pr(E|Hp) = 0.00255, Pr(E|Hd) = 2.7E-4, LR = 9.4827
Locus 6(TH01): Pr(E|Hp) = 0.09913, Pr(E|Hd) = 0.01556, LR = 6.3697
Locus 7(D13S317): Pr(E|Hp) = 0.02157, Pr(E|Hd) = 3.0E-4, LR = 71.12404
Locus 8(D16S539): Pr(E|Hp) = 0.08944, Pr(E|Hd) = 0.00408, LR = 21.90504
Locus 9(D2S1338): Pr(E|Hp) = 0.02179, Pr(E|Hd) = 2.8E-4, LR = 76.81371
Locus 10(D19S433): Pr(E|Hp) = 0.12104, Pr(E|Hd) = 0.00256, LR = 47.27969
Locus 11(vWA): Pr(E|Hp) = 0.0029, Pr(E|Hd) = 2.0E-4, LR = 14.27022
Locus 12(TPOX): Pr(E|Hp) = 0.03975, Pr(E|Hd) = 0.01215, LR = 3.273
Locus 13(D18S51): Pr(E|Hp) = 0.04838, Pr(E|Hd) = 0.00224, LR = 21.61031
Locus 14(D5S818): Pr(E|Hp) = 0.1676, Pr(E|Hd) = 0.02248, LR = 7.45453
Locus 15(FGA): Pr(E|Hp) = 0.03341, Pr(E|Hd) = 0.00122, LR = 27.38285
LR total = 6.350128800121241 6E17
99.0% 1-sided lower HPD interval = 4.958827938885595 5E17
```

Ref 16 – 2.52 x 10^{16}



```
LIKELIHOOD RATIO
Number of EPGs: 1
[redacted]_test_sample_mixture4.1.csv
Number of contributors: 2
Population: Ident_Cauc.csv
Theta = 0.02
Number of known contributors under Hp: 1
[redacted]_reference_sample_16.csv
Number of known contributors under Hd: 0


Locus 1(D8S1179): Pr(E|Hp) = 0.09107, Pr(E|Hd) = 0.00138, LR = 66.16709
Locus 2(D21S11): Pr(E|Hp) = 0.05939, Pr(E|Hd) = 0.00319, LR = 18.59836
Locus 3(D7S820): Pr(E|Hp) = 0.00254, Pr(E|Hd) = 0.00322, LR = 0.79055
Locus 4(CSF1PO): Pr(E|Hp) = 0.12425, Pr(E|Hd) = 0.02931, LR = 4.23976
Locus 5(D3S1358): Pr(E|Hp) = 0.08177, Pr(E|Hd) = 7.1E-4, LR = 114.83257
Locus 6(TH01): Pr(E|Hp) = 0.07639, Pr(E|Hd) = 0.01545, LR = 4.9457
Locus 7(D13S317): Pr(E|Hp) = 0.00559, Pr(E|Hd) = 1.9E-4, LR = 29.79678
Locus 8(D16S539): Pr(E|Hp) = 0.02632, Pr(E|Hd) = 0.00335, LR = 7.86716
Locus 9(D2S1338): Pr(E|Hp) = 0.00459, Pr(E|Hd) = 2.7E-4, LR = 17.21491
Locus 10(D19S433): Pr(E|Hp) = 0.00866, Pr(E|Hd) = 0.00169, LR = 5.11212
Locus 11(vWA): Pr(E|Hp) = 0.04885, Pr(E|Hd) = 4.3E-4, LR = 113.65723
Locus 12(TPOX): Pr(E|Hp) = 0.19776, Pr(E|Hd) = 0.01526, LR = 12.9629
Locus 13(D18S51): Pr(E|Hp) = 0.02423, Pr(E|Hd) = 0.00224, LR = 10.82258
Locus 14(D5S818): Pr(E|Hp) = 0.05164, Pr(E|Hd) = 0.02137, LR = 2.41669
Locus 15(FGA): Pr(E|Hp) = 0.01862, Pr(E|Hd) = 0.0011, LR = 17.00205
LR total = 3.166115523633202 4E16
99.0% 1-sided lower HPD interval = 2.528153674916829 6E16
```

Mixt_4.1_2unk	0.8709	19.5021	-26.5579
Mixt_4.1_2unk	0.1291	-24.5606	19.0005

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- Charlotte Word (Charlotte Word Consulting)