

# DNA Mixture Analysis:

Principles and Practice of Mixture Interpretation and Statistical Analysis  
Using the SWGDAM STR Interpretation Guidelines

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# A Survey of Mixture Interpretation Software

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NIST

NIST



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# NIST Software Tools

**mixSTR** (Dave Duewer)

3	Sample		Loci								
4	Type	Description	FGA	TPOX	D8S1179	vWA	Amel	Penta E	D18S51	D21S11	TH01
5	Victim	Lane 10 Victim	19,23	8,11	10,16	16	X	7,10	14	29,30.2	8,9
6	Suspect	Lane 11 Suspect 1	19,23	8,11	10,16	16	X	7,10	14	29,30.2	8,9
7	Suspect	Lane 12 Suspect 2	19,23	8,11	15,16	15,16	X	7,10	14	29,30.2	8,9
8	Suspect	Lane 13 Suspect 3	22,26	8	13,14	14,15	X,Y	8,13	14,18	33.2,35	6,7
9	Suspect	Lane 14 Suspect 4	22,26	8,11	13,14	15,17	X,Y	8,13	16,18	33.2,35	8,9
10	Suspect	lane 15 Suspect 5	23,25	11	12,16	16	X,Y	13,20	18,22	28,30	7,9
11	Evidence	Lane 1 T-shirt-collar	19,22,26	8	11,13,14,15	14,15,16	X,Y	8,10	12,15,16,17	28,29	9,9.3
12	Evidence	Lane 2 T-shirt-side	22,24		13,14,15	14,16	X,Y	13	15,16,17	27	9,9.3
13	Evidence	Lane 3 Gun-handle	21,22,25	7,11	13,14,15,16	15,16,17,18	X,Y	8	12,15,16,21	28,29,31	7,9
14	Evidence	Lane 4 Door-Knob	22,25	7,9,11	13,14,15,16	15,16,17,18	X,Y	8,9	12,15,16,19,21	28,29,31	7,9
15	Evidence	Lane 5 West Wall	19,21,23	8,9,11	12,13,15	12,13,14,15,16	X,Y	7,10,13	12,14,16,18,19	28,29,30.2	7,8,9,9.3
16	Evidence	lane 6 east Wall	19,23	8,11	13,15,16	15,16	X,Y	7,10	14,16,18	29,30.2	8,9
17	Evidence	Lane 7 Rt Shoe	21,25	8	9,11,12	17	X,Y	5	12	32.2,33.2	6
18	Evidence	Lane 8 Rmask	19,20,22,23	8,11	12,13,14,15	17	X,Y	5,10	13,14,17,18	29,30	6,7,9
19	Evidence	Lane 9 Straw	22,26	8,11	13,14	15,17	X,Y	8,13	16,18	33.2,35	8,9
20	Control	9947A (ACP)	23,24	8	13	17,18	X	12,13	15,19	30	8,9.3
21	Control	RLT (RCP)	23,25	11	12,16	16	X,Y	13,20	18,22	28,30	7,9

# NIST Software Tools

**mixSTR** (Dave Duewer)

			lane 6 east Wall				Lane 7 Rt Shoe			
45	Locus	Lane 12 Suspect 2	Evidence	#+	#-	-Alleles	Evidence	#+	#-	-Alleles
47	FGA	19,23	19,23	2	0		21,25	0	2	21,25
48	TPOX	8,11	8,11	2	0		8	1	1	
49	D8S1179	15,16	13,15,16	2	0	13	9,11,12	0	2	9,11,12
50	vWA	15,16	15,16	2	0		17	0	2	17
51	Amel	X	X,Y	1	0	Y	X,Y	1	0	Y
52	Penta E	7,10	7,10	2	0		5	0	2	5
53	D18S51	14	14,16,18	1	0	16,18	12	0	1	12
54	D21S11	29,30.2	29,30.2	2	0		32.2,33.2	0	2	32.2,33.2
55	TH01	8,9	8,9	2	0		6	0	2	6
56	D3S1358	15,16	15,16	2	0		15,17	1	1	17
57	Penta D	13,15	13,15	2	0		10	0	2	10
58	CSF1PO	11	11,15	1	0	15	11	1	0	
59	D16S539	11	11,12	1	0	12	12,13	0	1	12,13
60	D7S820	11	10,11,12	1	0	10,12	8,10	0	1	8,10
61	D13S317	12,13	12,13	2	0		8,14	0	2	8,14
62	D5S818	12,13	11,12,13	2	0	11	11,12	1	1	11
63	# Alleles	27		27	0			5	22	
64		# Loci: In, Ex, Total		16	0	16		2	14	16
65										

# NIST Software Tools

## Virtual MixtureMaker (Dave Duewer)

Mixture females and Hispanics.xls [Compatibility Mode]

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
3	Profiles		Alleles			# Alleles / Locus														
4	#1	#2	#Sep	#Mix	Ratio	Avg	SD	#1	#2	#3	#4	#5	#6+	D8S1179	D21S11	D7S820	CSF1PO			
5	ZT80870	MT94890	63	55	0.87	3.44	0.63	0	1	7	8	0	0	11,13,14,16	28,29,30,34	8,9,10	10,11,12			
6	MT94890	ZT80870	63	55	0.87	3.44	0.63	0	1	7	8	0	0	11,13,14,16	28,29,30,34	8,9,10	10,11,12			
7	GT37869	TT51435	64	55	0.86	3.44	0.73	0	2	5	9	0	0	10,12,13	28,30,30.2,31.2	10,11	9,10,11,12			
8	TT51435	GT37869	64	55	0.86	3.44	0.73	0	2	5	9	0	0	10,12,13	28,30,30.2,31.2	10,11	9,10,11,12			
9	TT51483	TT50722	63	55	0.87	3.44	0.81	0	3	3	10	0	0	11,13,14,15	30,31	8,9,10,11	10,3,11,12,13			
10	TT50722	TT51483	63	55	0.87	3.44	0.81	0	3	3	10	0	0	11,13,14,15	30,31	8,9,10,11	10,3,11,12,13			
11	ZT80815	ZT80870	64	54	0.84	3.38	0.62	0	1	8	7	0	0	11,13,14	28,29,34	8,11,12	10,11,12,13			
12	TT51399	UT57305	63	54	0.86	3.38	0.72	0	2	6	8	0	0	11,13,14	28,29,30.2,32.2	8,11,12	10,12			
13	UT57305	TT51399	63	54	0.86	3.38	0.72	0	2	6	8	0	0	11,13,14	28,29,30.2,32.2	8,11,12	10,12			
14	ZT80869	UT57308	63	54	0.86	3.38	0.81	0	3	4	9	0	0	14,15	29,30,32.2	9,10,12	10,11,12,13			
15	UT57308	ZT80869	63	54	0.86	3.38	0.81	0	3	4	9	0	0	14,15	29,30,32.2	9,10,12	10,11,12,13			

# Match Estimator (Brian Burritt - SDPD)

## Match Estimator 3.1.1 (PP16)

Profile will hit approximately 1 in: 

Afr. Am.	Cauc.	Hisp.	Average
1.0E+00	1.0E+00	1.0E+00	1.0E+00

 13 Core Loci

Profile will hit approximately 1 in: 

1.0E+00	1.0E+00	1.0E+00	1.0E+00
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 All 15 Loci (does not reflect number of expected hits during NDIS search!)

	Afr. Am.	Cauc.	Hisp.	Average	Obligate
D3S1358	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
TH01	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D21S11	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D18S51	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
Penta E	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D5S818	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D13S317	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D7S820	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D16S539	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
CSFIPO	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
Penta D	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
VWA	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
D8S1179	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
TPOX	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00
FGA	1.0E+00	1.0E+00	1.0E+00	1.0E+00	1.0E+00

	Exact Genotypes (1 allele for homozygotes)	
D3S1358	1.0E+00	1.0E+00
TH01	1.0E+00	1.0E+00
D21S11	1.0E+00	1.0E+00
D18S51	1.0E+00	1.0E+00
Penta E	1.0E+00	1.0E+00
D5S818	1.0E+00	1.0E+00
D13S317	1.0E+00	1.0E+00
D7S820	1.0E+00	1.0E+00
D16S539	1.0E+00	1.0E+00
CSFIPO	1.0E+00	1.0E+00
Penta D	1.0E+00	1.0E+00
VWA	1.0E+00	1.0E+00
D8S1179	1.0E+00	1.0E+00
TPOX	1.0E+00	1.0E+00
FGA	1.0E+00	1.0E+00

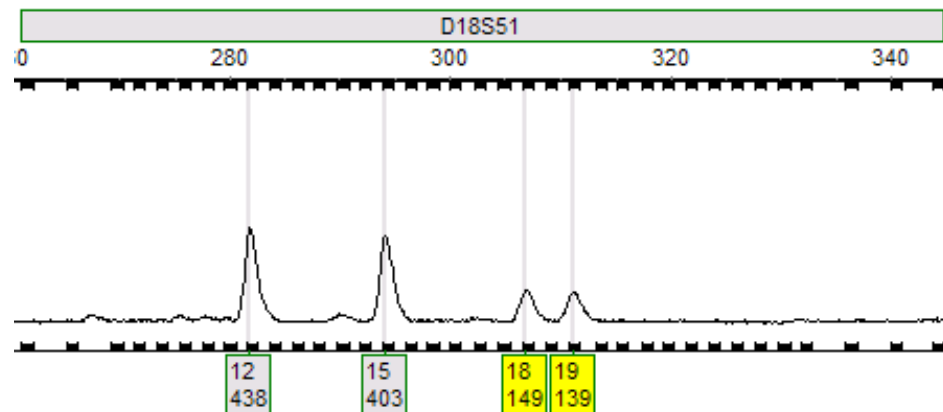
ctrl+shift+A clears all tables

For questions or comments, please contact Brian Burritt at [bburritt@pd.sandiego.gov](mailto:bburritt@pd.sandiego.gov)

[bburritt@pd.sandiego.gov](mailto:bburritt@pd.sandiego.gov)

					Obligate
D3S1358					
TH01					
D21S11					
D18S51	12				
Penta E					
D5S818					
D13S317					
D7S820					
D16S539					
CSFIPO					
Penta D					
VWA					
D8S1179					
TPOX					
FGA					

5.4



	Hispanic						
D8S1179	0	0	0	0	0	1.0	1.00
D21S11	0	0	0	0	0	1.0	1.00
D7S820	0	0	0	0	0	1.0	1.00
CSFIPO	0	0	0	0	0	1.0	1.00
D3S1358	0	0	0	0	0	1.0	1.00
TH01	0	0	0	0	0	1.0	1.00
D13S317	0	0	0	0	0	1.0	1.00
D16S539	0	0	0	0	0	1.0	1.00
Penta D	0	0	0	0	0	1.0	1.00
Penta E	0	0	0	0	0	1.0	1.00
VWA	0	0	0	0	0	1.0	1.00
TPOX	0	0	0	0	0	1.0	1.00
D18S51	0.1059	0.1379	0.0517	0.0369	0	9.1	0.11
D5S818	0	0	0	0	0	1.0	1.00
FGA	0	0	0	0	0	1.0	1.00

9.1E+00  
1.1E-01

9.1E+00  
1.1E-01

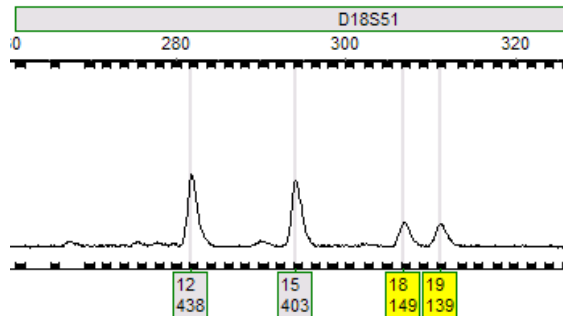




D18S51	Alleles Present	Potential Allele Drop-out	Potential Genotype Combinations													
		12		1 allele				3 alleles				4 alleles				
	15															
	18															
	19															
Possible complete loss of genotype?		N														



Random Match Probability							
US Caucasian	1	in	9.00E+00	OR	1	in	9
US African American	1	in	7.10E+00	OR	1	in	7.1
US Southwest Hispanic	1	in	1.20E+01	OR	1	in	12



			Caucasian			African American			Hispanic		
			f(Allele 1)	f(Allele 2)	RMP	f(Allele 1)	f(Allele 2)	RMP	f(Allele 1)	f(Allele 2)	RMP
12	12	AA	0			0		0.000	0		0.000
12	15	AB	0.128	0.128	0.033	0.058	0.167	0.019	0.106	0.138	0.029
12	18	AC	0.128	0.092	0.023	0.058	0.131	0.015	0.106	0.052	0.011
12	19	AD	0.128	0.036	0.009	0.058	0.078	0.009	0.106	0.037	0.008
12	X	AX	0		0.000	0		0.000	0		0.000
15	15	BB	0		0.000	0		0.000	0		0.000
15	18	BC	0.128	0.092	0.023	0.167	0.131	0.044	0.138	0.052	0.014
15	19	BD	0.128	0.036	0.009	0.167	0.078	0.026	0.138	0.037	0.010
15	X	BX	0		0.000	0		0.000	0		0.000
18	18	CC	0		0.000	0		0.000	0		0.000
18	19	CD	0.092	0.036	0.007	0.131	0.078	0.020	0.052	0.037	0.004
18	X	CX	0		0.000	0		0.000	0		0.000
<b>RMP:</b>			<b>0.104</b>			<b>0.134</b>			<b>0.076</b>		

# Deconvolutor 2.0.5

## (Bruce Heidebrecht, MDSP)

	A	B	C	D	E	F	G	H	I	J	K	LM	N	O	P/Q	R	S	T	U	V	W	X	Y	Z	AA	AB	AC
1				Mixture	RFUs		Known	Alleged	Assumed				Known's	Alleged's	Alleged	PHR		allele 1	allele 1	allele 1	allele 1	allele 2	allele 2	allele 2	allele 3	allele 3	allele 4
2	Case/item#		Profile				Contributor	Contributor	Ratio X:1				Alleles	alleles	Contributor's			allele 1	allele 2	allele 3	allele 4	allele 2	allele 3	allele 4	allele 3	allele 3	allele 4
3																											
4	D8	allele 1											-	-				n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
5		allele 2											-	-													
6		allele 3											-	-													
7		allele 4											-	-													
8																											
9	D21	allele 1											-	-				n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
10		allele 2											-	-													
11		allele 3											-	-													
12		allele 4											-	-													
13																											
14	D7	allele 1											-	-				n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
15		allele 2											-	-													
16		allele 3											-	-													
17		allele 4											-	-													
18																											
19	CSF	allele 1											-	-				n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a	n/a
20		allele 2											-	-													
21		allele 3											-	-													
22		allele 4											-	-													
23																											

locus	Percent of Alleged Contributor
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D8	n/a
D21	n/a
D7	n/a
CSF	n/a
D3	n/a
TH01	n/a
D13	n/a
D16	n/a
D2	n/a
D19	n/a
vWA	n/a
TPOX	n/a
D18	74%
D5	n/a
FGA	n/a
Amelo	n/a

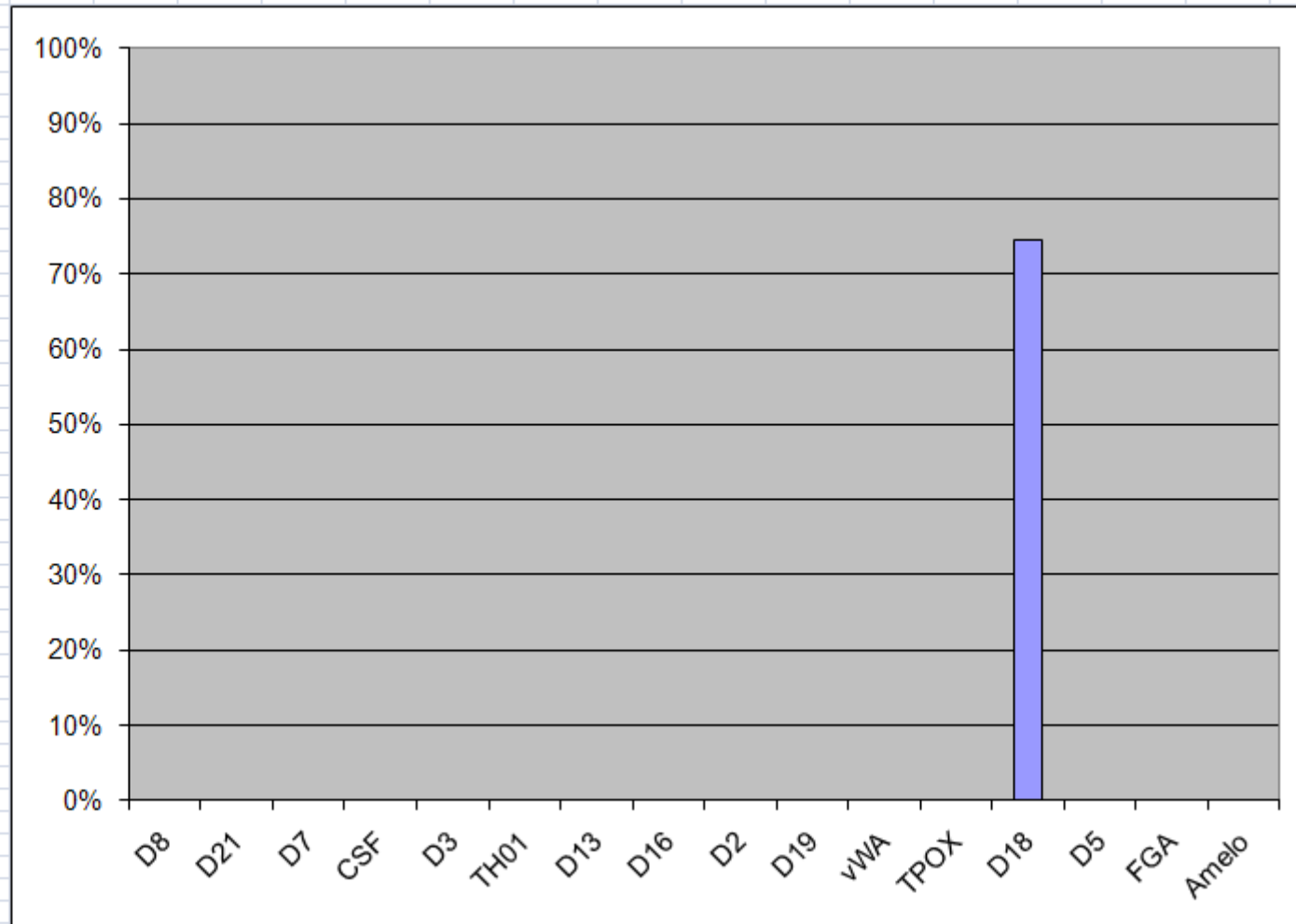
Average	74%
Std Dev	#DIV/0!

**Assumed ratio**

Known Contributor	Alleged Contributor
0.00	.1

**Calculated ratio**

Known Contributor	Alleged Contributor
0.34	.1



					4 ALLELES PRESENT							
Known contributor												
(18,19)												
					"Known" contributor				"Assumed" contributor			
					RFU if shared				RFU if shared			
					Genotype				Genotype			
					RFU's				RFU's			
					PHR				PHR			
					Contribution				Contribution			
D18	allele 1	12	438	438	(12,15)	(438,403)	92%	74%	(18,19)	(149,139)	93%	26%
	allele 2	15	403	403	(12,18)	(438,149)	34%	52%	(15,19)	(403,139)	34%	48%
	allele 3	18	149	149	(12,19)	(438,139)	32%	51%	(15,18)	(403,149)	37%	49%
	allele 4	19	139	139	(15,18)	(403,149)	37%	49%	(12,19)	(438,139)	32%	51%
					(15,19)	(403,139)	34%	48%	(12,18)	(438,149)	34%	52%
					(18,19)	(149,139)	93%	26%	(12,15)	(438,403)	92%	74%
					"Known" contributor				"Assumed" contributor			
					RFU if shared and homo				RFU if shared and homo			
	(2 allele locus ONLY)	12	438	0	438							
		15	403	0	403							
					"Known" contributor				"Assumed" contributor			
					RFU if shared and hetero				RFU if shared and hetero			
	(2 allele locus ONLY)	12	438	0	438							
		15	403	0	403							



# Automated Software for Mixture Analysis

2-Person Mixtures

# NEST – Phase II

## Evaluation of Mixture Deconvolution Tools

Phase II, the evaluation of the mixture deconvolution tools, is presently underway. DNA profiles from two contributor mixtures and other simulated mock casework scenarios have been analyzed for evaluation with these mixture deconvolution tools. Further, the Project Team will be evaluating the features and limitations of each of the software systems currently available.

## The Use of the i-STReam Mixture Deconvolution Software Tool in the FSS-i<sup>3</sup>™ Suite for the Analysis of Casework Samples

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<sup>1</sup>Marshall University Forensic Science Center, Huntington, WV 25701; <sup>2</sup>NIJ Technical Director, NEST Project, Fort Worth, TX 76107

<http://forensics.marshall.edu/NEST/PDFs-NEST/Posters/Promega%20FSSi3%20Poster10-09.pdf>

## The Use of GeneMapper® ID-X Software v1.1 for the Analysis of Mixed DNA Samples

Heather L. Harrah<sup>1\*</sup>, MS; Valerie K. Bostwick<sup>1</sup>, MSFS; Sally E. Edwards<sup>1</sup>, BS; Anthony W. Eller<sup>1</sup>, BS; Terry W. Fenger<sup>1</sup>, PhD; Rhonda K. Roby<sup>2</sup>, PhD, MPH  
<sup>1</sup>Marshall University Forensic Science Center, Huntington, WV 25701; <sup>2</sup>NIJ Technical Director, NEST Project, Fort Worth, TX 76107

<http://forensics.marshall.edu/NEST/PDFs-NEST/Posters/PromegaGMIDXPoster10-09.pdf>



<http://forensics.marshall.edu/NEST/>

# Software for Mixture Analysis



**GeneMarker**® HID





# Automated Mixture Software

## Advantages

- Can calculate parameters for mixture deconvolution: PHR, mixture ratio, etc...
- Speed of Analysis
- Statistical Analyses – RMNE, RMP, LR

## Limitations

- The ultimate decision is up to the DNA analyst.
- 3+ person mixtures are limited to RMNE (CPE) Statistics

## i-STReam Summary Sheet Export

Software Version: 5.8.3

Processor Version: 1.3.1 Rev 005

Output Created by: rickyDate: 27/07/2005 10:34:31

i-STReam File: C:\Documents and Settings\Ricky\Desktop\318 Code\i-STress Version 318 Source Code\Sys\Pendulum Input\Sample\_81.out

i-STReam Input File: C:\Documents and Settings\Ricky\Desktop\318 Code\i-STress Version 318 Source Code\Sys\Pendulum Input\Sample\_81.csv

Profile File: [None]

Gel Number	Lane Number	Barcode	Case Number	Item Number	Item and Area
-	-	-	-	-	-

Pref Amp Tolerance	Mixing Proportion Tolerance	Homozygote
60%	15%	60

Weight: Maximum	Weight: Minimum	Weight: Mean
18% 5:1	14% 6:1	16% 5:1

### Database Consolidation is on

-		Possible Contributors				Pref Amp Rule		Mix Prop Rule		-											
Locus	Allele	Area	Contributor 1	Contributor 2	Contributor 1	Contributor 2	Mix Est	RC	Contributor 1	Contributor 2	Den	Num	Comments								
D3S1358	15	5367	16	16	15	15	-	Y	-	Y	18% 5:1	Y	Include	16	16	15	15	-	-	-	
	16	24242	15	16	15	15	22%	N	100%	Y	-64% >10:1	N	-	-	-	-	-	-	-	-	-
	-	-	15	16	15	16	22%	N	22%	N	-	Y	-	-	-	-	-	-	-	-	-
	-	-	16	16	15	16	100%	Y	452%	Y	36% 2:1	N	-	-	-	-	-	-	-	-	-
	-	-	15	15	16	16	-	Y	-	Y	82% 1:5	N	-	-	-	-	-	-	-	-	-
	-	-	15	15	15	16	100%	Y	22%	N	164% <1:10	N	-	-	-	-	-	-	-	-	-
	-	-	15	16	16	16	452%	Y	100%	Y	64% 1:2	N	-	-	-	-	-	-	-	-	-
Database Consolidation for D3S1358														16	16	15	15	-	-	-	

FSS I<sup>3</sup>

Sample File : ID\_3\_EGJ\_2.0ng\_R1.1.2\_V1.1\_006\_1.fsa

Panel : Identifier\_v1X

Run Folder : Run\_HID\_2010-10-07\_17-01\_0229

Sample Name : ID\_3\_EGJ\_2.0ng\_R1.1.2\_V1.1

<< Previous Sample

Next Sample >>

CPI/CPE Statistics

Combined Probability of Inclusion/Exclusion (CPI/CPE) Statistics Summary

```

Combined Probability of Inclusion/Exclusion (CPI/CPE) for Sample ID_3_EGJ_2.0ng_R1.1.2_V1.1
Database = AB Identifier UM
Population = U.S. Hispanic
    Combined Probability of Inclusion = 3.7993E-7
                                     = 1 in 2.6 Million U.S. Hispanics
                                     = 1 in 2.6321E6

    Combined Probability of Exclusion = 99.9999% for U.S. Hispanic
    
```

CPI/CPE Statistics Details

	Database:Population	Marker	Alleles	Possible Genotype	Marker Inclusion Frequency
1	AB Identifier UM:U.S. Hispanic	D8S1179	12,13,14,15	10	0.6735
2	AB Identifier UM:U.S. Hispanic	D21S11	28,30,31	6	0.2040
3	AB Identifier UM:U.S. Hispanic	D7S820	8,10,12,F	N/A	1.0000
4	AB Identifier UM:U.S. Hispanic	CSF1PO	11,12	3	0.4616
5	AB Identifier UM:U.S. Hispanic	D3S1358	14,15,16,17,18	15	0.9657
6	AB Identifier UM:U.S. Hispanic	TH01	9,9.3	3	0.1189
7	AB Identifier UM:U.S. Hispanic	D13S317	11,12	3	0.1932
8	AB Identifier UM:U.S. Hispanic	D16S539	9,10,11,12,F	N/A	1.0000

ABI GeneMapper ID-X

Notes...

Calculate Statistics...

Export...

Mixture Analysis Parameters...

Samples Plot...

Cancel

< Back

Next >

Finish

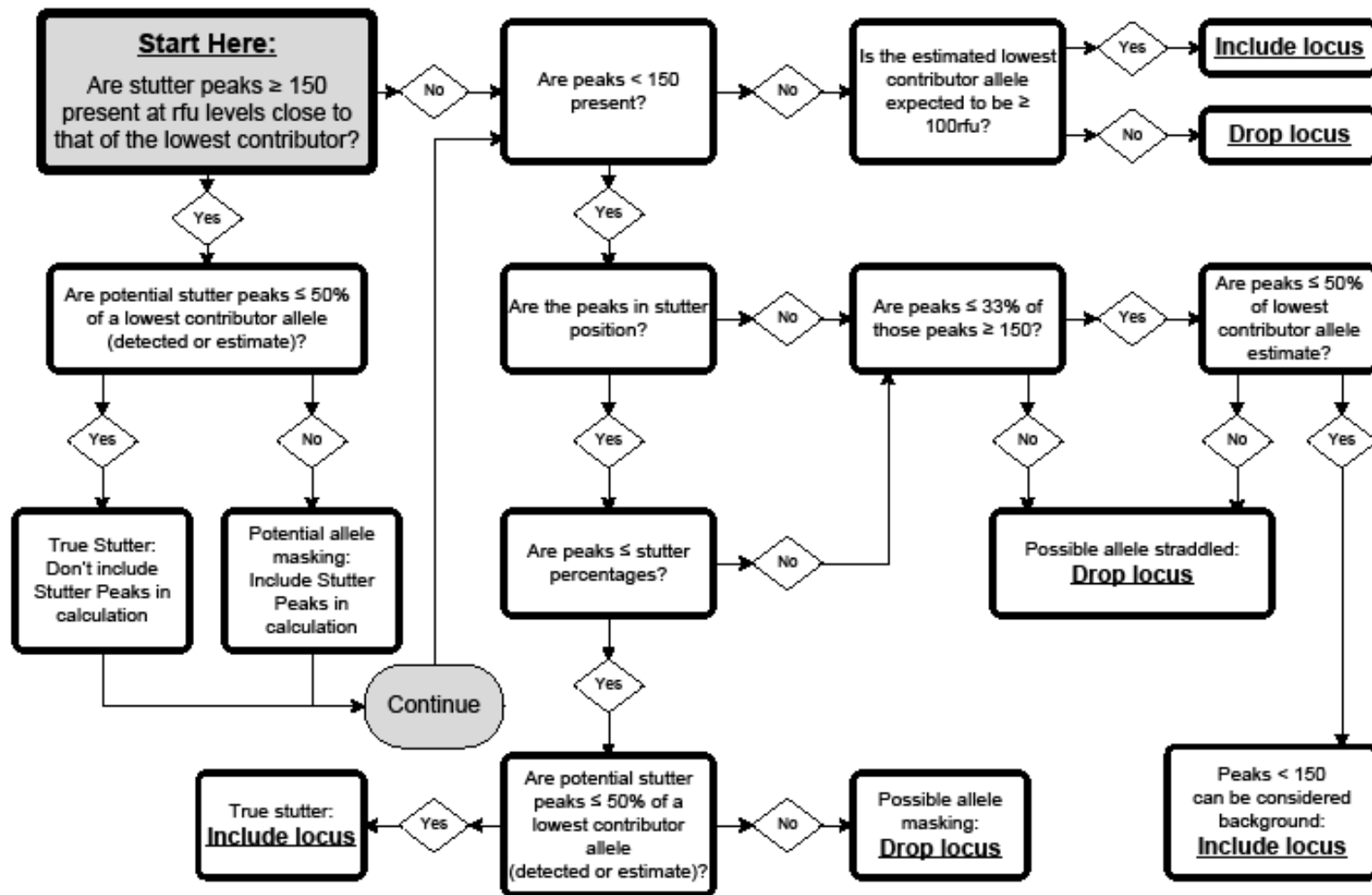


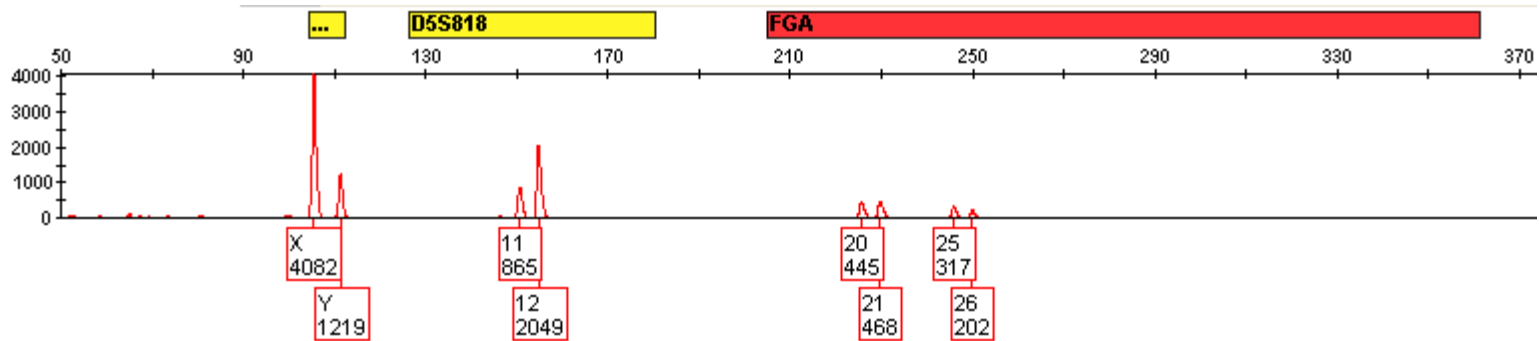
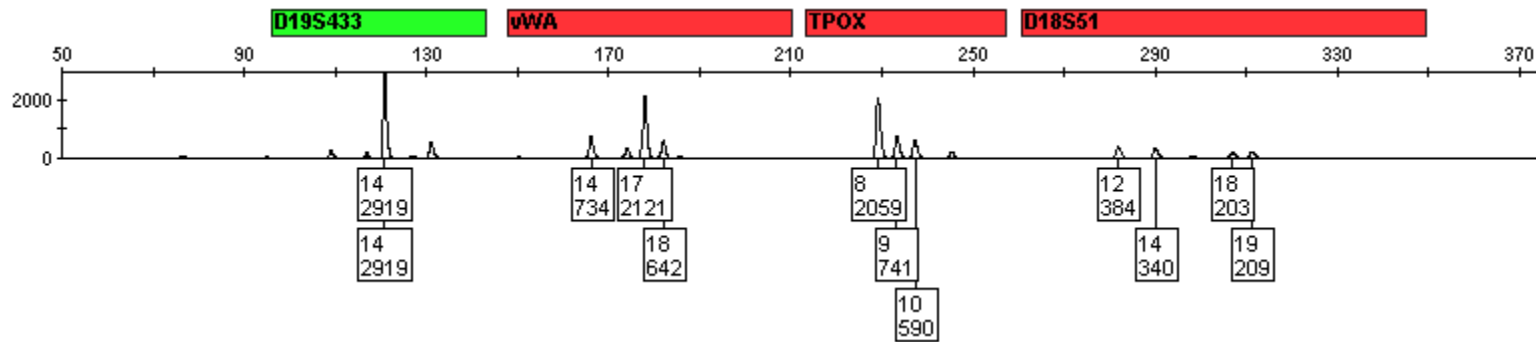
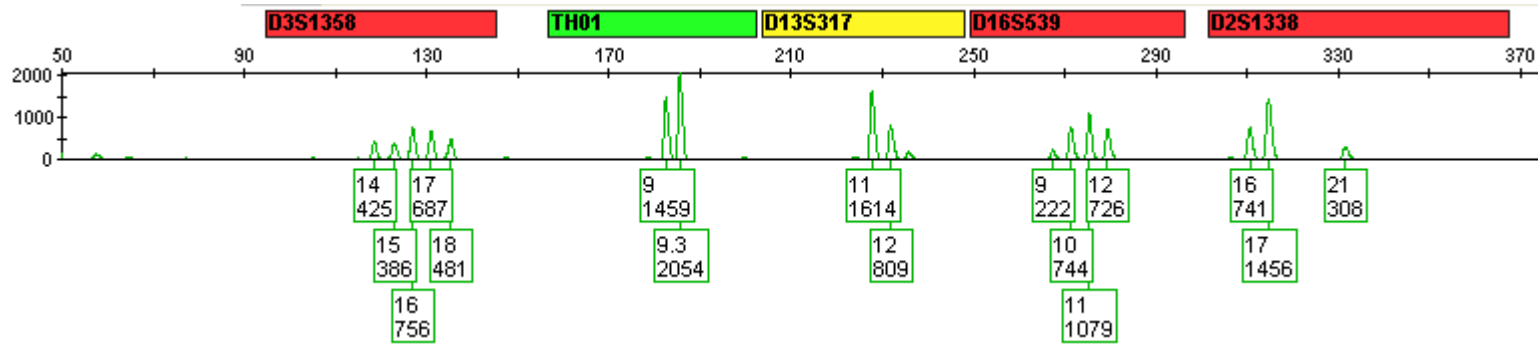
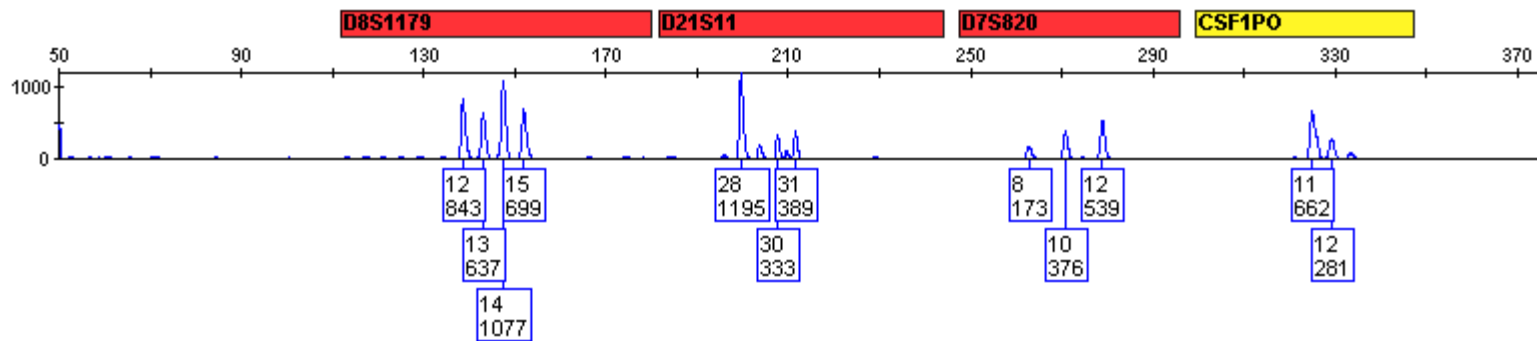


# Complex Mixtures

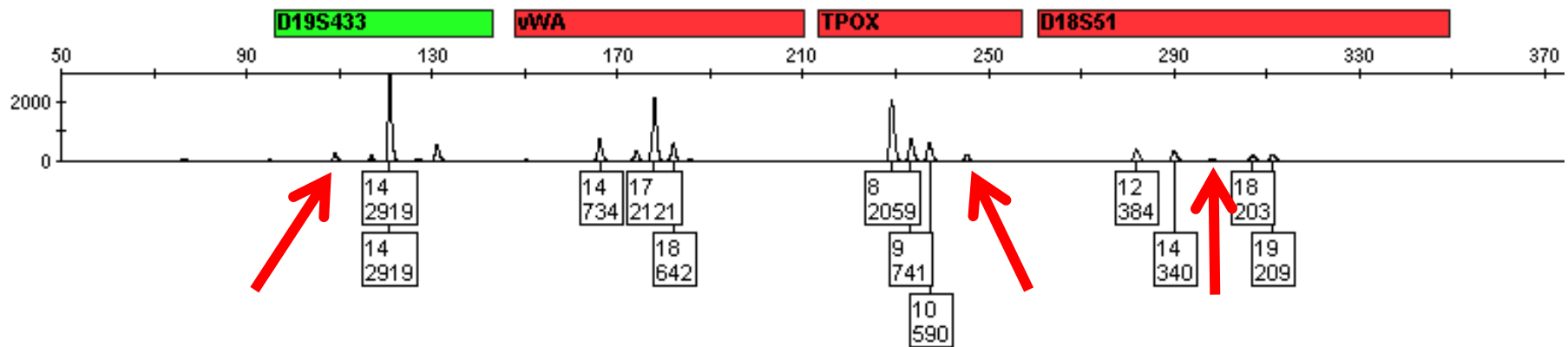
# Gary's Flowchart

The analysis of stutter is not required if one can account for all alleles of the lowest contributor (i.e. 4 peaks in a two person mix)





# Alleles below the Stochastic Threshold



4.6.3. When using CPE/CPI (with no assumptions of number of contributors) to calculate the probability that a randomly selected person would be excluded/included as a contributor to the mixture, *loci with alleles below the stochastic threshold may not be used* for statistical purposes to support an inclusion.



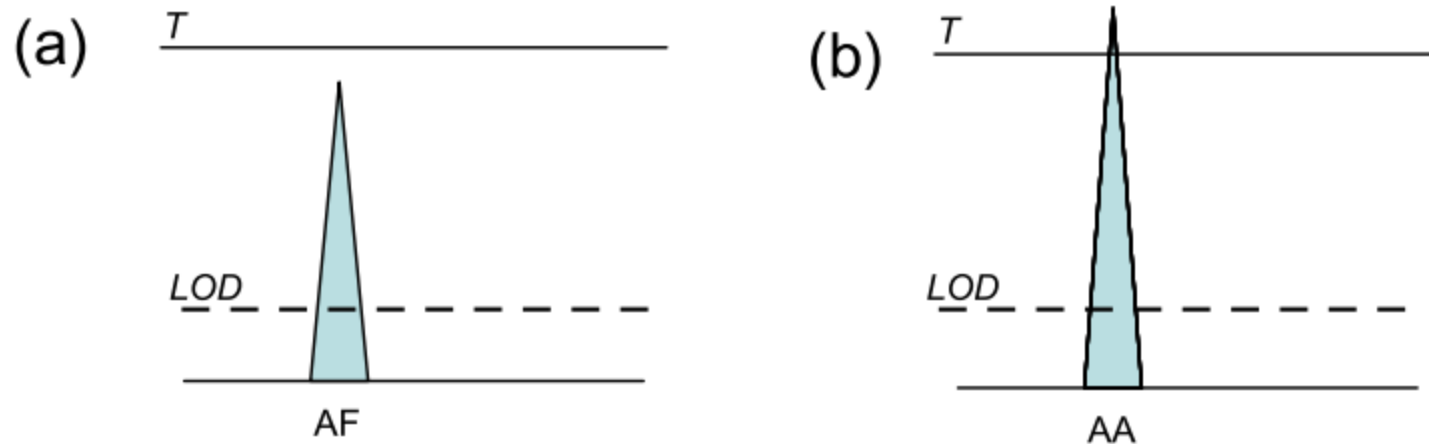
# “On the Threshold of a Dilemma”

- 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.

**Commentary on:** Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttmann 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.

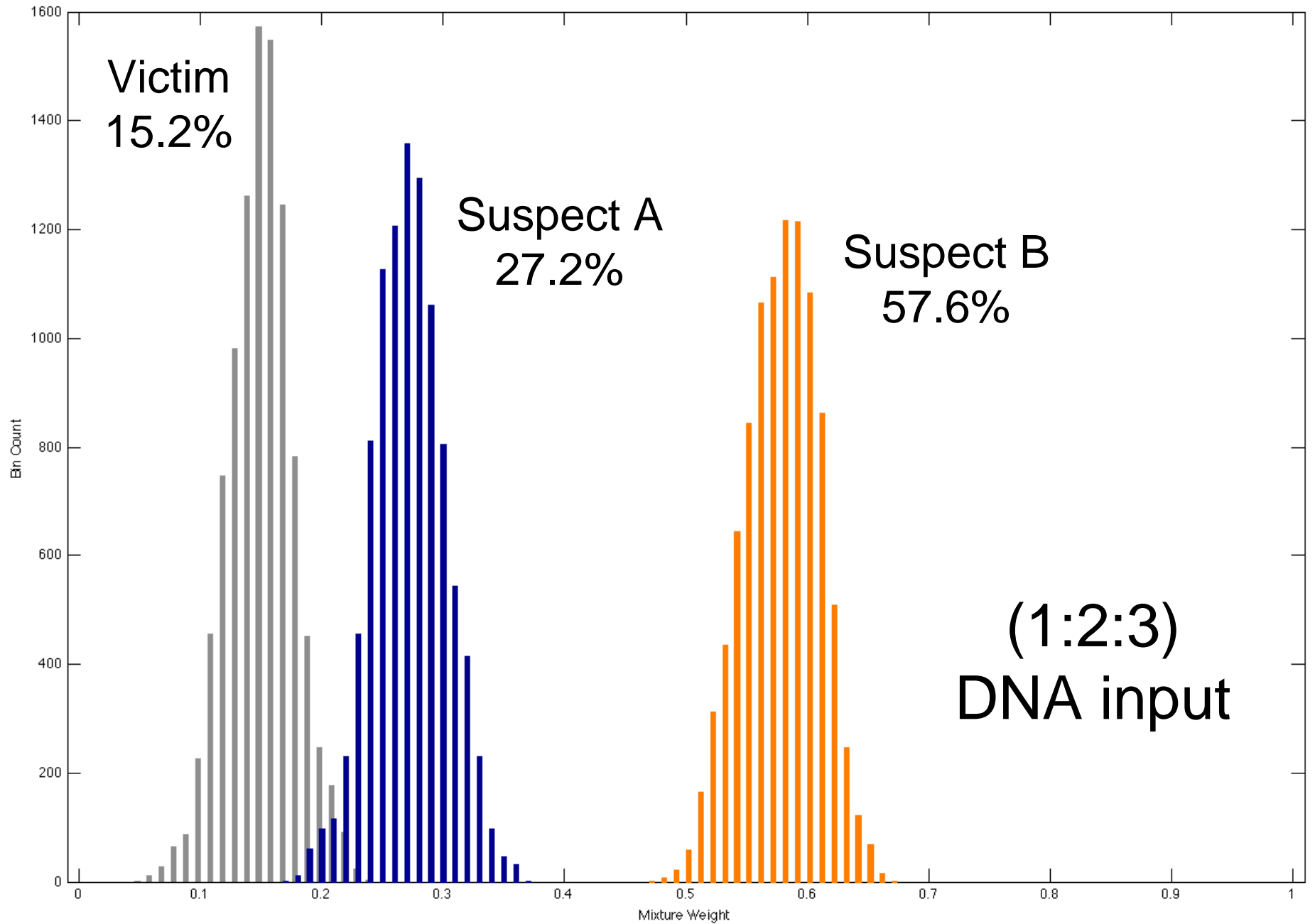
# “Falling off the Cliff Effect”

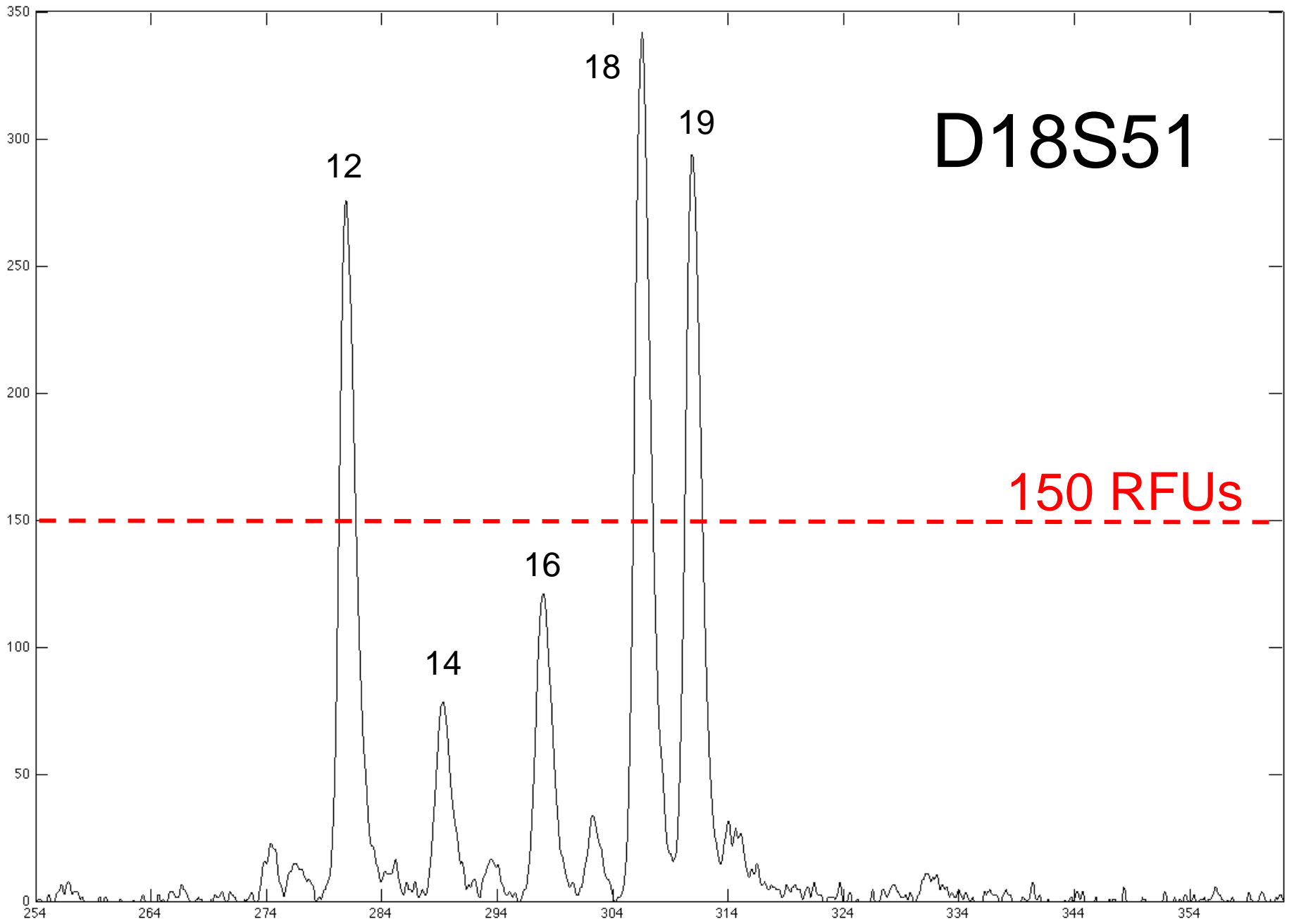
- If  $T$  = an arbitrary level (e.g., 150 rfu), an allele of 149 rfu is subject to a different set of guidelines compared with one that is 150 rfu even though they differ by just 1 rfu (Fig. 1).

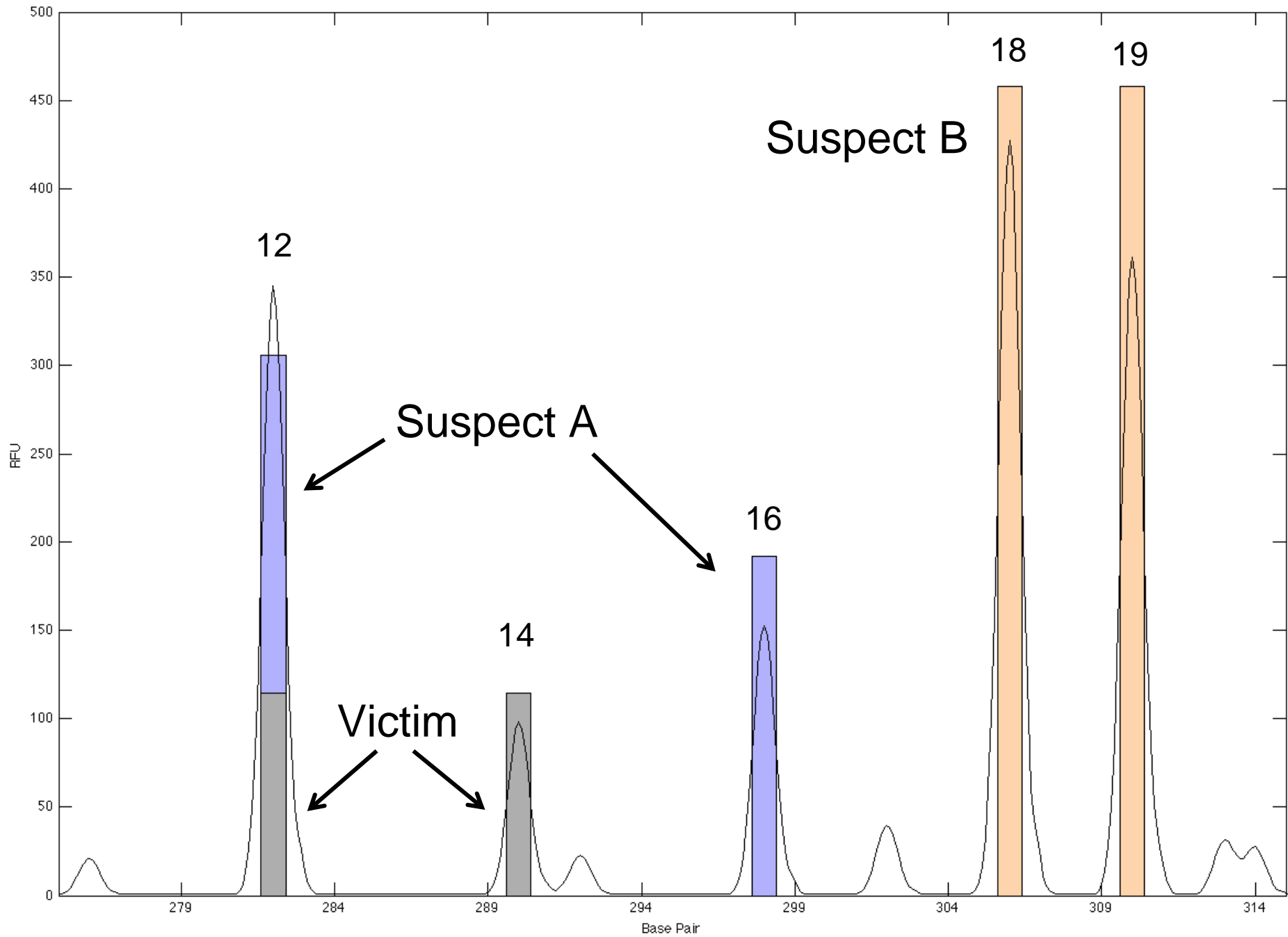


# Gill and Buckleton *JFS* 55: 265-268 (2010)

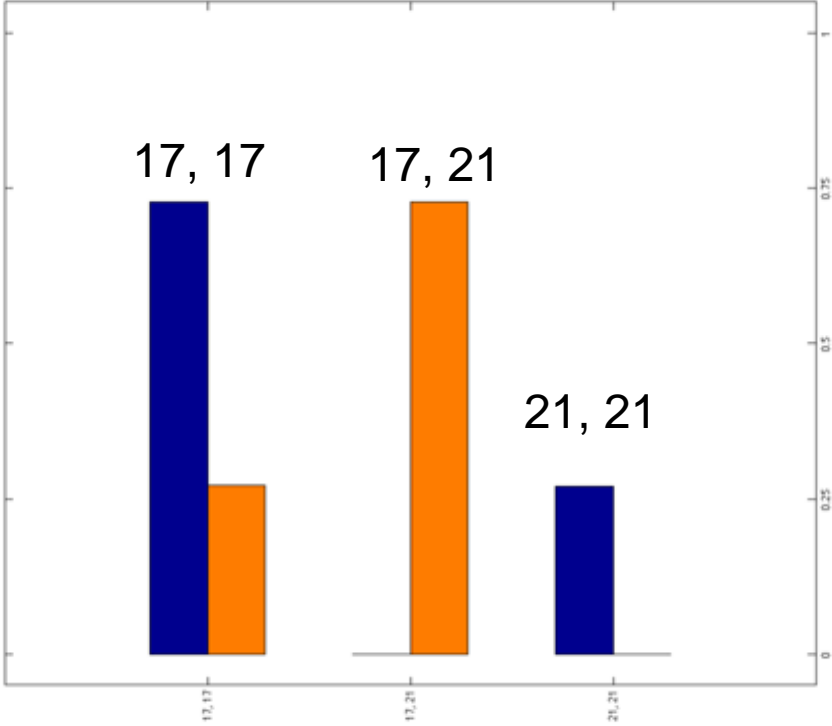
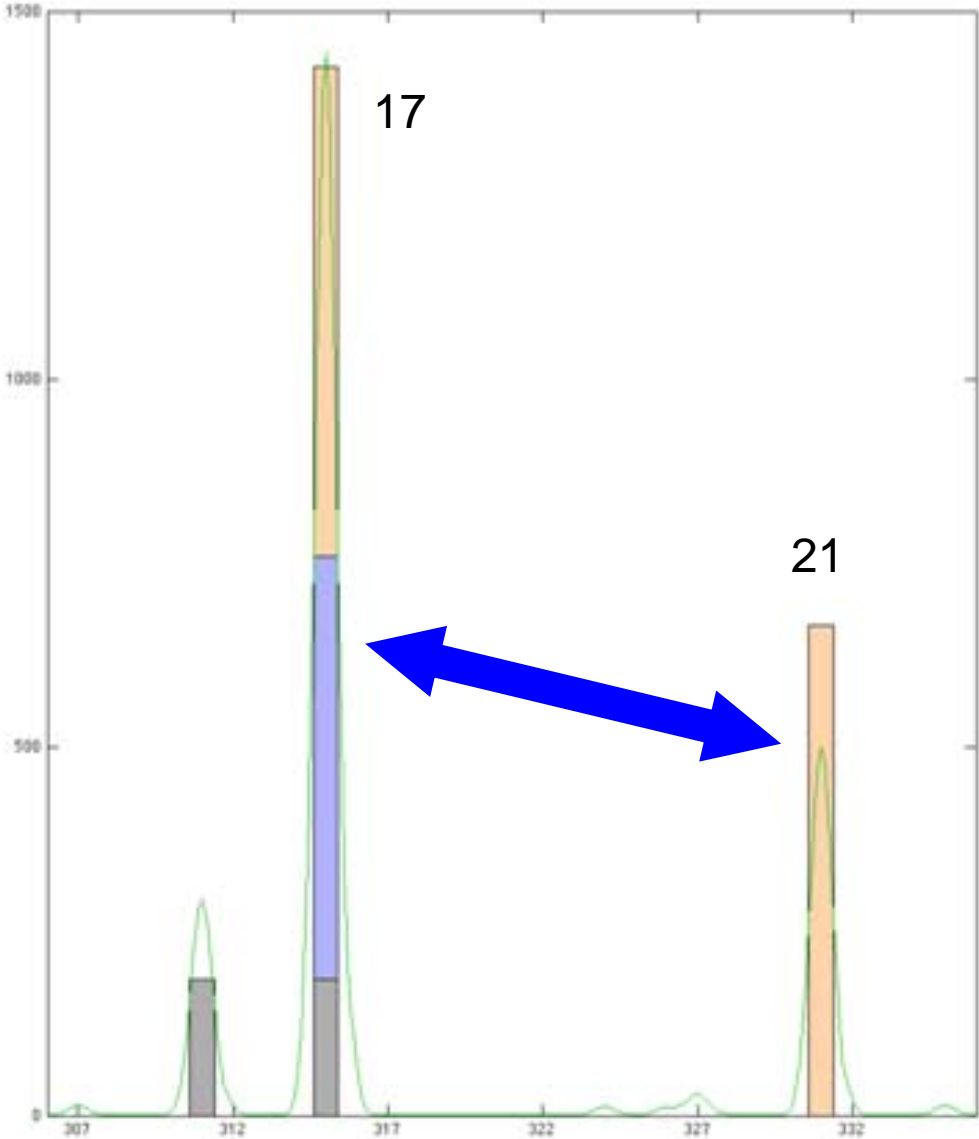
- “The purpose of the ISFG DNA commission document was to provide a way forward to demonstrate the use of ***probabilistic models to circumvent the requirement for a threshold*** and to safeguard the legitimate interests of defendants.”







# "Best Fit" of the Data



■ = Suspect A

■ = Suspect B

D2S1338

## File Signature Statement Summary Calculation

National Institute of Standards and Technology  
with victim contributor 2 vs. G  
05-Dec-2010

The LR calculation assumes two unknown contributors in the evidence with one known contributor reference relative to a US\_HIS\_NIST human population.  
The match rarity between the evidence and suspect is 34.2 quintillion.

The joint LR is approximately 34.2 quintillion.  
The log(LR) information is 19.53.

locus	allele pair	Q	R	S	LR	log(LR)
CSF1P0	11, 13	0.997	0.0340	1	29.275	1.467
D13S317	12, 13	0.998	0.0531	1	18.792	1.274
D16S539	9, 12	0.998	0.0695	1	14.348	1.157
D18S51	12, 16	0.987	0.0325	1	30.347	1.482
D19S433	11, 14	1.000	0.0107	1	93.134	1.969
D21S11	29, 30.2	1.000	0.0177	1	56.532	1.752
D2S1338	17, 17	0.728	0.0389	1	18.711	1.272
D3S1358	15, 15	0.648	0.0846	1	7.655	0.884
D5S818	12, 12	0.948	0.1226	1	7.730	0.888
D7S820	10, 10	0.822	0.0859	1	9.574	0.981
D8S1179	14, 15	1	0.0635	1	15.759	1.198
FGA	21, 21	0.890	0.0290	1	30.706	1.487
TH01	9.3, 9.3	0.635	0.0608	1	10.436	1.019
TPOX	9, 12	0.994	0.0215	1	46.240	1.665
vWA	16, 17	0.871	0.1155	1	7.541	0.877

Suspect A

LR = 34.2 Quintillion



## File Signature Statement Summary Calculation

National Institute of Standards and Technology  
with victim contributor 3 vs. E  
05-Dec-2010

The LR calculation assumes two unknown contributors in the evidence with one known contributor reference relative to a US\_HIS\_NIST human population.  
The match rarity between the evidence and suspect is 2.45 quintillion.

The joint LR is approximately 2.45 quintillion.  
The log(LR) information is 18.39.

locus	allele pair	Q	R	S	LR	log(LR)
CSF1P0	10.3, 11		0.0001	1	0.010	-2.000
D13S317	11, 11	1.000	0.0548	1	18.227	1.261
D16S539	11, 11	0.998	0.0643	1	15.505	1.190
D18S51	18, 19	0.998	0.0061	1	164.956	2.217
D19S433	14, 16.2	1	0.0214	1	46.733	1.670
D21S11	30, 31	1	0.0416	1	24.011	1.380
D2S1338	17, 21	0.728	0.0139	1	52.300	1.719
D3S1358	14, 18	0.652	0.0200	1	32.666	1.514
D5S818	12, 12	1	0.1226	1	8.157	0.912
D7S820	8, 10	0.824	0.0712	1	11.566	1.063
D8S1179	13, 15	1	0.0689	1	14.515	1.162
FGA	21, 26	0.894	0.0169	1	52.860	1.723
TH01	9, 9.3	0.635	0.0730	1	8.694	0.939
TPOX	9, 10	1	0.0058	1	173.636	2.240
vWA	14, 18	1	0.0290	1	34.459	1.537

Suspect A

LR = 2.45 Quintillion

# Summary

- Mixture Software can be useful for calculating many of the parameters of the SWGDAM guidelines for deconvolution.
- Beyond 2-person mixtures, many of the programs are limited to RMNE statistical calculations.
- These programs are more of an “expert assistant” than an “expert system”.

# Acknowledgments

- NIJ Funding to our NIST Group through NIST OLES interagency agreement 2008-DN-R-121
- **Collaborators**

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Bruce Heidebrecht (MDSP)	Brian Burritt (SDPD)
Teresa Snyder-Leiby (SoftGenetics)	

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

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