DNA Mixture Analysis:

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

A Survey of Mixture Interpretation Software



Michael D. Coble



AAFS 2011 Workshop #17

Chicago, IL February 22, 2011



Official Disclaimer

The opinions and assertions contained herein are solely those of the author and are not to be construed as official or as views of the U.S. Department of Commerce, the U.S. Department of Justice, or the National Institute of Justice.

Commercial software, equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the U.S. Department of Commerce, the U.S. Department of Justice, or the National Institute of Justice nor does it imply that any of the software, materials, instruments or equipment identified are necessarily the best available for the purpose.

NIST Software Tools

mixSTR (Dave Duewer)

3		Sample								Loc	i
4	Туре	Description	FGA	TPOX	D8S1179	vWA	Amel	Penta E	D18S51	D21S11	TH01
5	Victim	Lane 10 Victim	19,23	8,11	10,16	16	Х	7,10	14	29,30.2	8,9
6	Suspect	Lane 11 Suspect 1	19,23	8,11	10,16	16	Х	7,10	14	29,30.2	8,9
7	Suspect	Lane 12 Suspect 2	19,23	8,11	15,16	15,16	Х	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	Х	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)

45			lane	6 ea	ast V	Vall	Lan	e 7	Rt S	hoe
46	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	Х	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	CSF1P0	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
6E										

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

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	1 17	18	19	20
3	Prof	iles		Alleles			#	Alle	les	/ Loc	cus						
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

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

Match Estimator (Brian Burritt - SDPD)

Match Estimator 3.1.1 (PP16)

Afr. Am. Cauc. Hisp. Average Profile will hit approximately 1 in: 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 All 15 Loci (does not reflect number of expected hits during NDIS search!)

			Obligate
D3S1358			
THO1			
D21S11			
D18S51			
Penta E			
D5S818			
D13S317			
D7S820			
D16S539			
CSFIPO			
Penta D			
VVA			
D8S1179			
TPOX			
FGA			

	Exact Genotypes
	(1 allele for homozygotes)
D3S1358	
THO1	
D21S11	
D18S51	
Penta E	
D5S818	
D13S317	
D7S820	
D16S539	
CSFIPO	
Penta D	
VWA	
D8S1179	
TPOX	
FGA	

ctrl+shift+A clears all tables

For questions or comments, please contact Brian Burritt at bburritt@pd.sandiego.gov

					Obligate					
D3S1358										
THO1										
D21S11										
D18S51	12					5.	4			
Penta E		<11 #	*							
D5S818		12								
D13S317		13								
D7S820		13.2								
D16S539		14.2								
CSFIPO		15	<u>×</u>							
Penta D										
VWA										
D8S1179										
TPOX							-	Hispanic		
FGA							D8S1179	0	U	
							D21511	0	0	
							CSFIPO	ŏ	ů	
							D3S1358	0	0	
							THO1	0	0	
		l	D18S51				D13S317	0	0	
)	280	3	00	320	3	40	D16S539	0	0	
							Penta D	0	0	
							Penta E	0	0	
								0	0	
							D18S51	0 1059	0 1379	0
	A	Δ					D5S818	0	0	0.
		11	<u>,</u>	L						

18 19 149 139

12 438

15 403

	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
THO1	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
VVA	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	

bburritt@pd.sandiego.gov

2 Person Mixture Interpretation Worksheet (Todd Bille, ATF)

D18S51	Allleles Present	Potential Allele Drop-out					Poten	tial Ger	notyp	oe Comt	pinations	; ;			
			1:	allele	э	1 F		3	allel	es			4 al	leles	
						1 Г							Τ		
						1 F							\top		
]			2 a	lleles	S] [
						1 [
Possible co	mplete loss	Ν				1 [
of gen	otype?														

		c	Caucasian		Afric	an Americ	an	ł	lispanic	
		f(Allele 1)	f(Allele 2)	RMP	f(Allele 1)	f(Allele 2)	RMP	f(Allele 1)	f(Allele 2)	RMP
	AA	0			0		0.000	0		0.000
	AB	0	0	0.000	0	0	0.000	0	0	0.000
	AC	0	0	0.000	0	0	0.000	0	0	0.000
	AD	0	0	0.000	0	0	0.000	0	0	0.000
Х	AX	0		0.000	0		0.000	0		0.000
	BB	0		0.000	0		0.000	0		0.000
	BC	0	0	0.000	0	0	0.000	0	0	0.000
	BD	0	0	0.000	0	0	0.000	0	0	0.000
Х	BX	0		0.000	0		0.000	0		0.000
	CC	0		0.000	0		0.000	0		0.000
	CD	0 0		0.000	0	0	0.000	0	0	0.000
Х	CX	0		0.000	0		0.000	0		0.000
	RMP:			1.000			1.000			1.000

D18S51	Allleles Present	Potential Allele Drop-out				Pote	ential Ger	notype C	Combination	s			
	12			1 al	lele		3	alleles			4 a	lleles	
	15									12	15 y	18	19
	18									12	18 <mark>y</mark>	15	19
	19									12	19 <mark>y</mark>	15	18
			F	2 all	eles								
Possible co of gene	mplete loss otype?	N									Ĭ		
						E							

			Rando	m Match Prol	bability		
US Caucasian	1	in	9.00E+00	OR	1	in	9
US African American	1	in	7.10E+00	OR	1	in	7
US Southwest Hispanic	1	in	1.20E+01	OR	1	in	1

				C	Caucasian	I	Afric	an Americ	an:	ł	lispanic	
				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
DARCEA	12	15	AB	0.128	0.128	0.033	0.058	0.167	0.019	0.106	0.138	0.029
0 280 300 320	12	18	AC	0.128	0.092	0.023	0.058	0.131	0.015	0.106	0.052	0.011
	1 2	19	AD	0.128	0.036	0.009	0.058	0.078	0.009	0.106	0.037	0.008
	12	Х	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
ΑΛΙΙ	15	19	BD	0.128	0.036	0.009	0.167	0.078	0.026	0.138	0.037	0.010
	15	Х	BX	0		0.000	0		0.000	0		0.000
		18	CC	0		0.000	0		0.000	0		0.000
12 15 18 19	18	19	CD	0.092	0.036	0.007	0.131	0.078	0.020	0.052	0.037	0.004
438 403 149 139	18	Х	CX	0		0.000	0		0.000	0		0.000
			RMP:			0.104			0.134			0.076

Deconvolutinator 2.0.5 (Bruce Heidebrecht, MDSP)

	A	В	C	D	E	F	G	н		J	K L	LM	N	0	P	Q R	S	Т	U	V	W	Х	Y	Z	AA	AB	AC
1			Mix	ture R	FUs		Known		Alleged		Assumed	ł	(nown'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/it	em#	Pro	ofile			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 4	allele 4
3										Т																	
4	D8	allele 1											-		-			n/a									
5		allele 2											-		-												
6		allele 3						1 1					-		-												
7		allele 4											-		-												
8																											
9	D21	allele 1						1 [-		-			n/a									
10		allele 2						1 [-		-												
11		allele 3											-		-												
12		allele 4						1 [-		-												
13																											
14	D7	allele 1											-		-			n/a									
15		allele 2											-		-												
16		allele 3											-		-												
17		allele 4											-		-												
18																											
19	CSF	allele 1											-		-			n/a									
20		allele 2											-		-												
21		allele 3											-		-												
22		allele 4											-		-												
23																											

locus	Percent of															
	Alleged Contributor															
	-															
D8	nła	4000/														
D21	nła	100%														
D7	nła															
CSF	nła															
D3	nła	90%														
TH01	nła	1														
D13	nła															
D16	nła	80%														
D2	nła															
D19	nfa															
vWA	nła	700/														
TPOX	nła	10%														
D18	74%															
D5	nła															
FGA	nła	60%														
Amelo	nła															
Average	74%	50%														
Std Dev	#DIV/0!															
		40%														
Assume	d ratio															
Known	Alleged															
Contribut 0.0	or <u>Contributor</u> 0 :1	30%														
Calcula	ted ratio	20%														
Known	Alleged	2070														
Contribute	or Contributor															
0.3	:4 :1	400/														
		10%														
		0%		1	1 1	I I	<u>г г</u>			-	1	т т				1
			~		4		0		6	~	~		.1	~ ~		-
			0 °	Sr)	Ó, ⁽	كخن	0° ~*	<i>b</i> , <i>V</i> ,	^^°	0 ^L	\$ ⁵	JUN LA	ot o	× v	2 40R	Amelo

						4 ALLELES	S PRESENT							
Known	contributor					4								
	(18,19)			"Known"	"Assumed"		"Known"				"Assumed"			
				contributor	contributor		contributor				contributor			
			RFU	RFU if shared	RFU if shared		Genotype	RFU's	PHR	Contribution	Genotype	RFU's	PHR	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%
				"Known"	"Assumed"		(18,19)	(149,139)	93%	26%	(12,15)	(438,403)	92%	74%
				contributor	contributor									
				RFU if shared	RFU if shared									
				and horno	and horno									
	(2 allele	12	438	0	438									
	locus ONLY)	15	403	0	403									
				"Known"	"Assumed"									
				contributor	contributor									
				RFU if shared	RFU if shared									
				and hetero	and hetero									
	(2 allele	12	438	0	438									
	locus ONLY)	15	403	0	403									

Spreadsheet #2 – Unrestricted LR

		Caucasian (FB	I)							
	Enter allele	s detected, pe	eaks "indistin	iguishable fi	om stutter",	and the need	for stochasti	c interpretati	on:	
	Genotype									
Locus	Allele (a)	Allele (b)	Allele (c)	Allele (d)	dropout (F)	Allele (a) freq	Allele (b) freq	Allele (c) freq	Allele (d) freq	Allele (F) freq
D8S1179						#N/A	#N/A	#N/A	#N/A	
D21S11						#N/A	#N/A	#N/A	#N/A	
D7S820						#N/A	#N/A	#N/A	#N/A	
CSF1P0						#N/A	#N/A	#N/A	#N/A	
D3S1358						#N/A	#N/A	#N/A	#N/A	
TH01						#N/A	#N/A	#N/A	#N/A	
D13S317						#N/A	#N/A	#N/A	#N/A	
D16S539						#N/A	#N/A	#N/A	#N/A	
D2S1338						#N/A	#N/A	#N/A	#N/A	
D19S433						#N/A	#N/A	#N/A	#N/A	
vWA						#N/A	#N/A	#N/A	#N/A	
TPOX						#N/A	#N/A	#N/A	#N/A	
D18S51	12	15	18	19		0.1276	0.1276	0.0918	0.0357	
D5S818						#N/A	#N/A	#N/A	#N/A	
FGA						#N/A	#N/A	#N/A	#N/A	

Final LR calculation numerator / denominator

6

Denominator:	Possible Ur	nknown Cont	ributor										
	a,a	a,b	a,c	a,d	b,b	b,c	b,d	C,C	c,d	d,d	a,F	b,F	c,F
D8S1179													
D21S11													
D7S820													
CSF1P0													
D3S1358													
TH01													
D13S317													
D16S539													
D2S1338													
D19S433													
vWA													
TPOX													
D18S51	12,12	12,15	12,18	12,19	15,15	15,18	15,19	18,18	18,19	19,19			
D5S818													
FGA													

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^{3TM} Suite for the Analysis of Casework Samples

Valerie K. Bostwick¹*, MSFS; Mallory K. Mest¹, BS; Cheryl A. Zakowski¹, BS; Terry W. Fenger¹, PhD; Rhonda K. Roby², PhD, MPH ¹Marshall University Forensic Science Center, Huntington, WV 25701; ²NIJ 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^{1*}, MS; Valerie K. Bostwick¹, MSFS; Sally E. Edwards¹, BS; Anthony W. Eiler¹, BS; Terry W. Fenger¹, PhD; Rhonda K. Roby², PhD, MPH ¹Marshall University Forensic Science Center, Huntington, WV 25701; ²NIJ Technical Director, NEST Project, Fort Worth, TX 76107

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

National Institute of Justice

MARSHALL UNIVERSITY



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

Software for Mixture Analysis











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: riokyDate: 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 Tolerence	Mixing Proportion Tolerence	Homozygote
60%	15%	60

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

Database Consolidation is on

	-		Po	ssible C	ontributo	ors	Pre	ef An	np Rule		Mix Prop Rul	e					-			
Locus	Allele	Area	Contrit	outor 1	Contrit	butor 2	Contributo	r 1	Contributor	2	Mi× Est		RC	Contrit	outor 1	Contrit	outor 2	Den	Num	Comments
	15	5367	16	16	15	15	•	Y		Υ	18% 5:1	Y	Include	16	16	15	15	•	•	•
	16	24242	15	16	15	15	22%	Ν	100%	Υ	-64% >10:1	Ν		-	-	-	-	•	•	
	•		15	16	15	16	22%	Ν	22%	Ν	-	Y	-	-	-	-	-	•	•	
0004050	•		16	16	15	16	100%	Y	452%	Υ	36% 2:1	Ν	-	-	-	-	-	•	•	
0351308	•	-	15	15	16	16		Y	•	Υ	82% 1:5	N	-	-	-	-	-	•	•	•
	•		15	15	15	16	100%	Y	22%	Ν	164% <1:10	Ν		-	-	-	-	•	•	
Ì	-	-	15	16	16	16	452%	Y	100%	Υ	64% 1:2	Ν	-	-	-	-	-	•	•	-
					Data	base Co	nsolidation f	or D3	3\$1358		-			16	16	15	15	•	•	-

FSS I³

http://www.promega.com/profiles/802/profilesindna_802_08.pdf

	Ranjub_2010-10-07_17-01_022	.9				I	
ample Na	me : [ID_3_EGJ_2.Ung_R1.1.2_V1.1				< Previous	s Sample	Next Sample >:
PE Statist	ics						
Comb	pined Probability of Inclusion/Exclusion ((CPI/CPE) Statistics	Summary				
Con	whined Probability of Ind	clusion/Excl	lusion (CPI/CPE)	for Sample	ID_3_EGJ_2.Ong	R1.1.2_V1	.1
Dat	abase = AB Identifiler	UM					
	Population = U.S. 1	Hispanic					
	Combined P	robability (of Inclusion = : = '	1.7993E-7	llion IIS Hier	anica	
				102.0 M	E6	Janies	
	Combined P:	robability (of Exclusion = 9	9.9999% for	U.S. Hispanic		
	Combined P:	robability (of Exclusion = 9	9.9999% for	U.S. Hispanic		
	Combined P:	robability (of Exclusion = 9	99.9999% for	U.S. Hispanic		
	Combined P:	robability (of Exclusion = 9	99.9999% for	U.S. Hispanic		
	Combined P:	robability (of Exclusion = 9	99.9999% for	U.S. Hispanic		
CPI/	Combined P: CPE Statistics Details	robability (Marker	of Exclusion = 9	99.9999% for Possible Genot	U.S. Hispanic vpe ⊆Marker Inclusion Fre	auency	
CPI/	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic	robability (Marker D851179	Alleles	99.9999% for Possible Genot 10	U.S. Hispanic ype & Marker Inclusion Fre 0.6735	quency	
CPI/ 1 2	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	Marker D851179 D21511	Alleles 12,13,14,15 28,30,31	99.9999% for Possible Genoty 10 6	U.S. Hispanic ype≰Marker Inclusion Fre 0.6735 0.2040	equency	
CPI/ 1 2 3	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	Marker D851179 D21511 D75820	Alleles 12,13,14,15 28,30,31 8,10,12,F	99.9999% for Possible Genoty 10 6 N/A	U.S. Hispanic ype≰Marker Inclusion Fre 0.6735 0.2040 1.0000	equency	
CPI/ 1 2 3 4	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	robability of Marker D851179 D21511 D75820 CSF1PO	Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12	99.9999% for Possible Genoty 10 6 N/A 3	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616	equency	
CPI/ 1 2 3 4 5	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	robability (Marker D851179 D21511 D75820 C5F1PO D351358	Alleles Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12 14,15,16,17,18	99.9999% for Possible Genoty 10 6 N/A 3 15	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616 0.9657	equency	
CPI/ 1 2 3 4 5 6	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	robability (Marker 0851179 021511 075820 CSF1PO 0351358 TH01	Alleles Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12 14,15,16,17,18 9,9.3	99.9999% for Possible Genoty 10 6 N/A 3 15 3	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616 0.9657 0.1189	equency	
CPI/ 1 2 3 4 5 6 7	Combined P: Combined P: Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	robability of Marker D851179 D21511 D21511 D75820 CSF1PO D351358 TH01 D135317	Alleles Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12 14,15,16,17,18 9,9.3 11,12	99.9999% for Possible Genoty 10 6 N/A 3 15 3 3	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616 0.9657 0.1189 0.1932	equency	
CPI/ 1 2 3 4 5 6 7 8	Combined P: Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	Marker D851179 D851179 D21511 D75820 CSF1PO D351358 TH01 D135317 D165539	of Exclusion = 9 Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12 14,15,16,17,18 9,9.3 11,12 11,12 9,10,11,12,F	99.9999% for Possible Genoty 10 6 N/A 3 15 3 3 3 N/A	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616 0.9657 0.1189 0.1932 1.0000	equency	
CPI/ 1 2 3 4 5 6 7 8	Combined P: CPE Statistics Details Database:Population AB Identifiler UM:U.S. Hispanic AB Identifiler UM:U.S. Hispanic	Marker 0 D851179 0 D21511 0 D75820 0 D351358 0 D351358 0 D135317 0 D165539 0	Alleles Alleles 12,13,14,15 28,30,31 8,10,12,F 11,12 14,15,16,17,18 9,9.3 11,12 9,10,11,12,F	99.9999% for Possible Genoty 10 6 N/A 3 15 3 3 3 3 N/A	U.S. Hispanic ype & Marker Inclusion Fre 0.6735 0.2040 1.0000 0.4616 0.9657 0.1189 0.1932 1.0000	equency	

🕌 Mixture Analysis	2															
B 3	E	Marker: All Ma	arkers	•	T											
One Contributor	No.	Marker	Major	Minor	Major Mx	Residual	Major HIM	Minor HIM		e Data Repo	ort					
Two Contributors									No.	Marker	Mixture	PI	PE	Contributor 1	Contributor 2	LR
□ I hree or more Contri									1	D8S1179	12,13,14,15	0.62298	0.37702			
ID_Ladder_014									2	D21S11	28,29,30,30.2,31	0.46046	0.53954			
ID_3_EGU_3.0n									3	D7S820	8,10,12	0.33475	0.66525			
10_0_0000_0000									4	CSF1P0	11,12,13	0.50511	0.49489			
	Mixtur	e Analysis Se	ettings						5	D3S1358	14,15,16,17,18	0.97162	0.02838) -1
									6	TH01	9,9.3	0.15716	0.84284			
	⊢ Ana	alysis			Contrib	utor Detec	tion Thresho	bld	7	D13S317	11,12,13	0.33062	0.66938			
	τU	sing						10	8	D16S539	9,10,11,12	0.59510	0.40490			
		Peak Height	C Peak A	Area	Minim	um Matche	d Markers:	12	9	D2S1338	16,17,21	0.07174	0.92826			53
					Mavin	um Unmat	ched Marker	2	10	D19S433	14,16.2	0.16000	0.84000			
		Minimum UIM:	1		PTGAIN	amonina	chea marke	13.]	11	VWA	14,16,17,18	0.54655	0.45345			
	14	Minimum mim.	1	10.000			DevideNew		12	TPOX	8,9,10,12	0.51020	0.48980			
	F	lange	Ratio (%)		Allele F	requency ·	- Population		13	D18S51	12,14,16,18,19	0.25001	0.74999			-+
	<	200	0.20		Iden	ifiler_15 U	S Hispanic	- 🕅	14	AMEL	X,Y					
		500	0.30						15	D5S818	11,12	0.49000	0.51000			
		2000	0.40		-				16	FGA	20,21,25,26	0.18675	0.81325	_		
	5	2000	0.60		ET EU	aluda LDA	(alua of O in	Cumulative I D			Cumulative:	1.07E-07	1-1.07E-07			
					I. Ex	Sique Lh V	alue or o m	Cumulative Lh		_						
					Maxim	um Numbe	r 2									
							s 1									
	Ma	ximum Residual	0.030		_ Overla	y										
	1.000		lo an	<u> </u>			o 11 r									
	V	Stutter Ratio:	JU. 15		I Sh	ow Invalid	Complination	าร								
			eitu z 100		Repor											
	1.	Drop-out miten	1910 1100			ve Parame	ters when S	Save Beport								
	_		-	_		-										
		Load	Save			<u>0</u> k		<u>C</u> ancel								
		100				29. 										

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

"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."



Cybergenetics TrueAllele







000

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
трох	9, 12	0.994	0.0215	1	46.240	1.665
v₩A	16, 17	0.871	0.1155	1	7.541	0.877

Suspect A

L	R	=	34.	2	Q	uiı	nti	lli	or)
---	---	---	-----	---	---	-----	-----	-----	----	---

000

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
трох	9, 10	1	0.0058	1	173.636	2.240
v₩A	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

Dave Duewer (NIST) Todd Bille (ATFE) Bruce Heidebrecht (MDSP) Teresa Snyder-Leiby (SoftGenetics)

Vic Meles (NicheVision) Bill Allan (CyberGenetics) Brian Burritt (SDPD)

http://www.cstl.nist.gov/biotech/strbase/training.htm michael.coble@nist.gov 301-975-4330