

FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

Usage of the “California Department of Justice (Cal DOJ) Y-Mixture Analysis Software”

Status: Published

Document ID: 5787

DATE EFFECTIVE
03/19/2018

APPROVED BY
Nuclear DNA Technical Leader

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Usage of the “California Department of Justice (Cal DOJ) Y-Mixture Analysis Software”

1 Procedure

1.1 Open the [Cal DOJ Y mixture tool file](#)

1.2 Excel window will open. Enable the content by choosing Options → Enable this content → OK

Y-Mix Database Filter 3.0.1
BETA 10/15/15pm

Security Alert - Macro

Macro
Macros have been disabled. Macros might contain viruses or other security hazards. Do not enable this content unless you trust the source of this file.

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File Path: M:\..._Y_MAIN\Validations\Y STR mixture tool\Testing\CADDOJ-Y-MixTool.xlsm

Help protect me from unknown content (recommended)

Enable this content

95% UCI 1 in...

Desired UCI 95.0%

This is a BETA version of the Y-Mix Database Filter spreadsheet. It has not been performed to an accuracy standard. Prior to its use in a case, users should independently confirm the accuracy of the results on a case-by-case basis. The author assumes no responsibility for the performance of the software. User responsibility for the results is assumed by the user.

Y-STR Profile	DYS 38751	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 480	DYS 481	DYS 516	DYS 533	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA 14	
Allele 1																												
Allele 2																												
Allele 3																												
Allele 4																												
Allele 5																												
Allele 6																												
Allele 7																												
Allele 8																												
Allele 9																												
Allele 10																												
Allele 11																												
Allele 12																												
Allele 13																												
Allele 14																												
Allele 15																												

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1.3 Using drop-down menu, enter all of the alleles of the mixture into the loci columns within the “Profile” worksheet.

Note: The order of loci in the Y-STR Mixture Tool is different from the Y-STR kit order. Please carefully enter these loci as they cannot be copied and pasted.

Y-Mix Database Filter 3.0.1
BETA 101915spm

Database Source:
www.usvstrdatabase.org
Release 4.1 (Sept. 20, 2015)

Upper Confidence Interval:
Clopper and Pearson approach (Biometrika 1934)

Database Selection:
 African American
 Asian
 Caucasian
 Hispanic
 Native American
 Combined

Limit database to samples with all the loci entered above? **Yes**
 Treat this profile as a single source sample? **No**

Desired UCI: **95.0%**

Y-STR Profile	DYF 387S1	DYS 19	DYS 385	DYS 388I	DYS 389I	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
Allele 1	33			10																							
Allele 2	36			12																							

New Variant:

DYS 387S1	DYS 19	DYS 385	DYS 388I	DYS 389I	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
23	6	0	0	0	0	0	0	0	0	0	0	0	24	0	0	3	0	33	7	17	0	0	14	0	0	0

Observed Alleles:

DYS 387S1	DYS 19	DYS 385	DYS 388I	DYS 389I	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
32	6	7	9	24	18	18	6	3	11.5	7	8	14	25	11	10	10	10	33.2	8	7	11	9	14.2	12	7	6
33	10	9	10	25	19	6	8	30	12	10	6	15	26	12	11	11	16	34	9	9	12	11	15	17	0	10

Clear New Variants:

DYS 387S1	DYS 19	DYS 385	DYS 388I	DYS 389I	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
35	11	10	12	27	20.1	7	10	12	13	8.2	10	16	28	13	13	13	16	35	10.1	11	14	13	17	19	3	0
36	10	10.2	13	26	21	8	10.2	13	14	9	10.1	16.2	23	14	14	18	26	11	11.1	15	14	16	19	11	10	0

- 1.3.1 Null allele: A sample believed to contain a legitimate null allele due to mutation will be represented by a “0” allele at that locus. To include haplotypes with “0” alleles, you must manually enter “0” as an allele at that locus.
- 1.3.2 Drop Out: If drop out is suspected at any locus in the profile (i.e., there are visible peaks below analytical threshold that are unambiguously attributable to a contributor), the locus should be left blank.

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1.3.3 If an allele in the evidence profile is not present in the list below the table, enter it as a “New Variant” prior to entering it into the table (see red arrow below or the Instructions tab).

Y-Mix Database Filter 3.0.1
BETA 10/15/2015

Database Source: www.usystrdatabase.org
Release 4.1 (Sept 20, 2015)

Upper Confidence Interval:
Clopper and Pearson approach
(Biometrika 1934)

Database: African American, Caucasian, Hispanic, Native American, Combined

Limit database to samples with all the loci entered above? Yes No
Treat this profile as a single source sample? Yes No

Desired UCI: 95.0%

Profile

Observed Alleles:

Allele	DyF	DyS	DyS385	DyS389I	DyS390	DyS391	DyS392	DyS393	DyS437	DyS438	DyS439	DyS448	DyS449	DyS456	DyS458	DyS460	DyS481	DyS518	DyS533	DyS543	DyS570	DyS578	DyS627	DyS635	DyS643	YGATA	HH	
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	24	6	0	0	0	0	33	7	<7	0	0	14	0	0
32	5	7	3	24	18	<6	7	3	11.1	7	<8	14	25	11	30	10	13	33.2	8	7	11	8	14.2	12	7	6		
33	<10	9	10	25	19	6	9	10	12	<8	9	15	26	12	11	11	16	34	9	3	12	11	15	17	9	<8		
34	10	9	11	26	20	<7	3	11	<13	8	3	<16	27	<13	12	12	17	34.2	10	13	12	16	18	3	8			
35	11	10	12	27	20.1	7	10	12	13	8.2	10	16	28	13	13	13	18	35	10.1	11	14	13	17	<13	10	3		
36	12	10.2	13	28	21	9	10.2	13	14	9	10.1	16.2	29	14	<14	19	26	11	11.1	15	14	18	13	11	10			
37	13	11	14	28.3	21.1	3	11	14	14.3	10	11	<17	30	14.3	14	20	37	12	12	16	15	19.2	<20	11.1	11			
37.3	13.2	11.2	15	29	22	10	11.1	15	15	11	12	17	31	15	14.1	21	37.1	13	13	17	16	19	20	12	12			
38	14	11.3	16	30	23	11	12	16	16	12	13	17.2	32	16	14.2	22	37.2	14	14	17.3	17	19.2	21	13	13			
39	14.1	12	17	31	24	12	13	17	17	13	14	17.4	33	17	15	23	38	15	15	18	17.2	20	21.3	14	13			
39.2	14.2	12.1	18	32	24.3	13	13.1	18	>13	15	18	34	18	15.1	24	38.2	17	16	18.2	18	20.1	22	15	14				
40	15	12.2	19	33	25	14	14	19	14	>15	19.2	35	19	15.2	24.1	39	19	19	20.2	20	20.2	23	16	15				
41	16	13	20	34	26	14.1	15	20	15	16.4	19	36	19	16	25	40	20	18.3	20	21	24	24	17	14				
41.2	17	13.1	21	35	27	15	15	21	16	17.2	15	37	20	16.1	25.1	41	21	20	21	22	25	25	18	14				
42	18	13.2	22	36	28	16	16	22	17	18.4	16	38	21	16.2	26	42	22	20.3	21.3	23	26	26	19	14				
43	19	14	23	37	29	17	17	23	18	19.2	17	39	22	17	26.1	43	23	21	22	24	28	27	20	14				
43.2	19.2	14.2	24	38	30	18	18	24	19	20.4	18	40	23	18	27	44	24	21.2	23	25	27	27	21	14				

Average: 220.4693878 Count: 56 Sum: 10803 75%

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1.4 In the center of the screen, ensure the following options are selected (see red arrows in diagram below):

1.4.1 Where it says: "Limit database to samples with all the loci entered above", choose **YES**

1.4.2 Where it says: "Treat this profile as a single source sample", choose **NO**

1.4.3 The desired Upper Confidence Interval (Desired UCI) should be set to **95%**.

1.4.4 Where it says: Use $(x+1) / (N+1)$, choose **NO**

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Y-Mix Database Filter 3.1
BETA 041017spm

Database Source: www.usystrdatabase.org
Release 4.2 (Feb. 18, 2017)

Upper Confidence Interval:
Clopper and Pearson approach
(Biometrika 1934)

Compare the profile to the database.

View the filtered list.

Print.

Database: African American, Asian, Caucasian, Hispanic, Native American, Combined

Limit database to samples with all the loci entered above? **Yes** **No**

Treat this profile as a single source sample? **Yes** **No**

Desired UCI Use (x+1)/(N+1)? **95.0%** **No**

New Variant:
Observed Alleles:

	DYF 387S1	DYS 19	DYS 385	DYS 389I	DYS 389II	DYS 390	DYS 391	DYS 392	DYS 393	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	DYS 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
32	6	7	3	24	16	<6	7	3	11.1	7	<8	14	25	11	10	10	13	33.2	6	7	11	8	14.2	12	7	6	
33	<10	8	10	25	19	6	8	10	12	<8	8	15	26	12	11	11	16	34	3	3	12	11	15	17	8	<8	
34	10	3	11	26	20	<7	3	11	<13	6	3	<16	27	<13	12	12	17	34.2	10	10	13	12	16	16	3	6	
35	11	10	12	21	20.1	7	10	12	13	8.2	10	16	28	13	13	13	18	35	10.1	11	14	13	17	<19	10	3	
36	12	10.2	13	28	21	8	10.2	13	14	3	10.1	16.2	23	14	<14	13	36	11	11.1	15	14	18	13	11	10		
37	13	11	14	28.3	21.1	3	11	14	14.3	10	11	<17	30	14.3	14	20	37	12	12	16	15	18.2	<20	11.1	11		
37.3	13.2	11.2	15	23	22	10	11.1	15	15	11	12	17	31	15	14.1	21	37.1	13	13	17	16	19	20	12	12		
38	14	11.5	16	30	23	11	12	16	16	12	13	17.2	32	16	14.2	22	37.2	14	14	17.3	17	19.2	21	13	13		
39	14.1	12		31	24	12	13	17	17	13	14	17.4	33	17	15	23	38	15	15	18	17.2	20	21.3	14	>13		

- Click on the macro button “Compare the profile to the database.” (see green arrow below). This will filter the database, leaving only those haplotypes that would be included as possible contributors to your evidence.

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1.6 Summary of results. The website reports the number of times the haplotype was observed in the database (x), the database size (N), sample frequencies (x/N), and the upper bound of the 95% confidence interval (UCIs). See screenshot below.

Y-Mix Database Filter 3.1
BETA 041017spm

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American	0	560	0		0.005335239	187
Asian	0	332	0		0.008982702	111
Caucasian	0	576	0		0.005187423	193
Hispanic	0	387	0		0.007711027	130
Native American	0	239	0		0.012456216	80
Combined	0	2,094	0		0.001429604	699

Limit database to samples with all the loci entered above?
Treat this profile as a single source sample? Desired UCI **95.0%**

- 1.7 Print the screen by selecting “Print” from the printer menu at the top of the page and selecting a printer.
- 1.8 Verify on the printout that the Y-haplotype alleles were correctly entered into the website.
- 1.9 Report the 95% upper-bound confidence statistic from the African American, Asian, Caucasian, and Hispanic ethnic groups, and round down to three significant figures (the “1 in...” column furthest to the right).
- 1.10 If both autosomal and Y-STRs are typed, the results are reported separately.

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