

FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

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

DATE EFFECTIVE
10/14/2016

APPROVED BY
NUCLEAR DNA TECHNICAL LEADER

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

1. Using Internet Explorer, open the US Y-STR Database Webpage at www.usystrdatabase.org. Next, click on the “Mixture Analysis Tools” tab. Once on this tab, click on the link for “California Department of Justice Y-Mix Database Filter Tool.” Click Open.
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

Microsoft Office Security Options
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.
Warning: It is not possible to determine that this content came from a trustworthy source. You should leave this content disabled unless the content provides critical functionality and you trust its source.
More information
File Path: M:\...Y_MAIN\Validations\Y STR mixture tool\Testing\CADDOJY-MixTool.xlsm
 Help protect me from unknown content (recommended)
 Enable this content
Open the Trust Center

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

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

Desired UCI 95.0%

New Variant:
Observed Alleles:

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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 101915ppm

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

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

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

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

Desired UCI: 95.0%

New Variant:

	DYS 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	YGATA 543	DYS 570	DYS 576	DYS 627	DYS 635	DYS 643	YGATA H4
Observed Alleles:	23	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	9	24	18	6	7	3	11.1	7	6	14	25	11	10	10	13	33.2	8	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	9	9	12	11	15	17	6	<8
	34	10	9	18	26	20	7	9	11	<13	8	9	<16	27	<15	12	12	12	11	24.2	10	10	13	12	16	10	9
	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	<13	10	9
	36	12	10.2	13	28	21	8	10.9	13	14	9	10.1	16.2	29	14	14	15	18	36	11	11.1	15	14	18	13	11	10

- a. 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.
- b. 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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- c. 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 101915ppm

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

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

Database: x N x/N 1 in... 95% UCI 1 in...

- African American
- Asian
- Caucasian
- Hispanic
- Native American
- Combined

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

Desired UCI: 95.0%

Y-STR Profile	D/YF	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	YGATA 549	DYS 570	DYS 578	DYS 627	DYS 635	DYS 643	HH
Allele 1	33			10																							
Allele 2	36			12																							
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																											

New Variant: (Red arrow pointing here)

Observed Alleles:

23	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
52	6	7	3	24	18	6	7	3	11.1	7	8	16	25	11	10	10	13	33.2	8	7	11	8	14.2	12	7	6	
53	<0	8	10	25	19	6	8	10	12	8	15	26	12	11	11	16	34	3	3	12	11	15	11	8	8	8	
24	10	3	11	26	30	17	3	11	13	9	9	16	27	11	13	17	34.3	10	10	13	12	16	18	9	9		
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	19	10	3	
36	12	10.2	13	26	21	9	10.2	13	14	3	10.1	16.2	23	14	14	19	36	11	11.1	15	14	19	13	11	10	0	
27	13	11	14	28.3	21.6	3	11	14	16.3	10	11	17	30	14.3	14	20	27	12	12	16	15	19.2	19	11	11	11	
31.3	13.2	16.2	16	23	22	10	11.1	15	15	11	12	17	31	15	14.1	21	31.1	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	31.2	14	14	17.3	17	19.2	21	13	13	13	
59	14.1	12	13	31	24	16	13	17	17	13	14	17.4	33	17	15	23	38	15	15	18	17.2	20	21.3	14	10	15	
23.2	16.2	12.1	32	24.3	13	13.1	16	13.1	15	14	18	15.1	34	18	15.1	24	39.2	17	16	19.2	19	20.1	22	15	14	14	
40	15	12.2	33	25	14	14	14	14	15	15.2	15	15.2	35	18	15.2	24.1	39	18	19	19	20.2	23	16	15	15	15	
41	16	13	34	26	14.1	15	15	15	15.2	15	15.4	36	19	16	25	40				19.3	20	21	24				
41.2	17	13.3	35	27	15	15	15	15	15.5	17	20	16.1	37	20	16.1	25.1	41				20	21	22	25			
42	18	13.2	36	28	16	16	16	16	16	16	16	16.2	38	21	16.2	26	42				20.3	21.3	23	26			
43	19	14	37	29	17	17	17	17	17	17	17	17	39	22	17	26.1	43				21	22	24	>26			
14.2			38	30	18	18	18	18	18	18	18	18	40	23	18	27	44				21.2	23	25	27			

Average: 220.4693878 Count: 56 Sum: 10803 75%

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4. In the center of the screen, ensure the following options are selected (see red arrows in diagram below):
 - a. Where it says: “Limit database to samples with all the loci entered above”, choose **YES**
 - b. Where it says: “Treat this profile as a single source sample”, choose **NO**
 - c. The desired Upper Confidence Interval (Desired UCI) should be set to **95%**.

The screenshot displays the CADJOY-MixTool1 software interface. The main window shows a spreadsheet with columns for various STR loci (DYS 385I, 389I, 390, 391, 392, 393, 437, 438, 439, 448, 449, 456, 458, 460, 481, 518, 533, 549, 570, 576, 627, 635, 643, YGATA 4, YGATA 8) and rows for alleles 1 through 15. A control panel is visible with options for Database Source (African American, Asian, Caucasian, Hispanic, Native American, Combined), Upper Confidence Interval (95.0%), and a 'Compare the profile to the database' button. Red arrows point to the 'Yes' option for limiting the database and the '95.0%' UCI value. A green arrow points to the 'Compare the profile to the database' button. A disclaimer box on the right states: 'This is a BETA v Filter spreadsheet. If results have been performed, there is no accuracy. Prior to case matters, use own validated independently co case basis. If assumes no associated performance responsibility steve!'

5. 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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- 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.

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

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

Database	x	N	x/N	1 in...	95% UCI	1 in...
African American	2	550	0.003636364	275	0.011402276	88
Asian	1	331	0.003021148	331	0.014251119	70
Caucasian	3	531	0.005649718	177	0.014536745	69
Hispanic	0	383	0	0	0.007791245	128
Native American	0	63	0	0	0.046438451	22
Combined	6	1,858	0.003229279	310	0.006363715	157

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

This is a BETA version. Filter spreadsheet, been performed to results, there is no accuracy. Prior to its case matters, users own validation independently confirms case basis. The assumes no responsibility for performance. I associated with steven.m

- Print the screen by selecting “Print” from the printer menu at the top of the page and selecting a printer.
- Verify on the printout that the Y-haplotype alleles were correctly entered into the website.
- 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).
- If both autosomal and Y-STRs are typed, the results are reported separately.

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