

FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

Usage of the “Y-Mix Database Filter”

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Usage of the “Y-Mix Database Filter”

1 Procedure

1.1 Open the [Y mixture database](#) filter

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

The screenshot displays the Microsoft Excel application window titled "CADOY-MixTool1 - Microsoft Excel". The ribbon includes Home, Insert, Page Layout, Formulas, Data, Review, and View. A Security Warning bar at the top indicates "Macros have been disabled." A dialog box titled "Microsoft Office Security Options" is open, showing a "Security Alert - Macro" warning. The warning text states: "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." The file path is listed as "M:\...Y_MAIN\Validations\Y STR mixture tool\Testing\CADOY-MixTool.xlsm". There are two radio buttons: "Help protect me from unknown content (recommended)" and "Enable this content". The "Enable this content" option is selected. The background spreadsheet shows a "Y-STR Profile" section with columns for markers like DYS 387S1, 19, 385, 388I, 388II, 390, 391, 392, 393, 437, 438, 439, 446, 445, 456, 458, 460, 461, 518, 533, 549, 570, 576, 627, 636, 643, and YGATA 14. Below this is a "Database Source" section with the URL "www.usstrdatabase.org" and "Release 4.1 (Sept. 20, 2015)". Further down is the "Upper Confidence Interval" section, mentioning "Clopper and Pearson approach (Biometrika 1934)". At the bottom, there is a "New Variant:" section and a table of "Observed Alleles" with numerical data for each marker.

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1.3 Using drop-down menu, enter all of the alleles of the single source, deconvoluted donor, or 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 10/15/15pm

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

Desired UCI: **95.0%**

New Variant:	DYS 387	DYS 391	DYS 393	DYS 395	DYS 399	DYS 406	DYS 413	DYS 426	DYS 437	DYS 438	DYS 439	DYS 448	DYS 449	DYS 456	DYS 458	DYS 460	DYS 481	DYS 518	DYS 533	DYS 543	YGATA 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	24	0	0	3	0	33	7	0	0	14	0	0	0
	32	6	7	9	24	18	6	7	3	11	7	8	14	25	11	10	10	13	33.2	8	7	11	8	14.2	12	7
	33	<10	6	10	25	19	6	4	10	12	8	15	26	12	11	11	16	34	9	3	12	11	15	17	8	8
	34	10	8	11	26	20	11	3	11	13	8	9	16	27	13	12	12	11	24.2	10	10	13	12	16	15	9
	35	11	10	12	27	20.1	7	10	12	13	8.2	10	16	20	13	13	13	16	35	10.1	11	14	13	17	13	9
	36	12	10.2	13	26	21	6	10.2	13	14	9	10.1	16.2	23	14	14	19	36	11	11.1	15	14	18	13	11	10

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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- 1.4 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”:
 - 1.4.2.1 For a single source sample or deconvoluted donor profile: choose **YES**
 - 1.4.2.2 For a mixed profile: 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**

Y-Mix Database Filter 3.1
BETA 041017sp.m

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

Upper Confidence Interval:
Clopper 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? **Yes**

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

Desired UCI Use (x+1) / (N+1)? **95.0%**

Use (x+1) / (N+1)? **No**

Di
This is a BETA version Filter spreadsheet. It has not been performed to results, there is no accuracy. Prior to its use, users must perform their own validation independently on a case basis. The author assumes no responsibility for associated with performance. I am responsible for steven.m

New Variant:	D/YF 38751	D/Y5 19	D/Y5 385	D/Y5 389I	D/Y5 389II	D/Y5 390	D/Y5 391	D/Y5 392	D/Y5 393	D/Y5 437	D/Y5 438	D/Y5 439	D/Y5 448	D/Y5 449	D/Y5 456	D/Y5 458	D/Y5 460	D/Y5 481	D/Y5 518	D/Y5 533	D/Y5 549	D/Y5 570	D/Y5 576	D/Y5 627	D/Y5 635	D/Y5 643	YGATA H4
Observed Alleles:	23	0	0	0	0	0	0	0	0	0	0	0	0	0	24	0	0	3	0	33	7	<7	0	0	14	0	0
	32	6	7	9	24	16	6	7	9	11	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	6	15	26	12	11	11	16	24	9	9	12	11	15	17	8	<8
	34	10	9	11	26	20	<7	9	11	<13	6	9	<16	27	<13	12	12	17	34.2	10	10	13	12	16	16	9	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	<19	10	9
	36	12	10.2	13	28	21	8	10.2	13	14	9	10.1	16.2	23	14	<14		19	36	11	11.1	15	14	18	13	11	10
	37	13	11	14	28.3	21.1	9	11	14	14.3	10	11	<17	30	14.3	14		20	37	12	12	16	15	19.2	<20	11	11
	37.2	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		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

- 1.5 Click on the macro button “Compare the profile to the database.” (see green arrow below). This will filter the database, leaving only those haplotype(s) 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 04/07/17pm

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? Yes No

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

- 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 truncate 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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