

**STRmix™ performance check: v2.3.07**

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*Introduction*

STRmix™ is an expert system that applies a fully continuous approach to DNA profile interpretation. STRmix™ v2.3.06 is currently being used in casework. New versions of the software are currently in development, and the most recent upgrade (STRmix™ v2.3.07) has recently become available. This upgrade has been described to primarily improve the performance of mixture deconvolution, especially on higher order mixtures. The release report states that ModelMaker does not need to be re-run, and that all parameters can remain the same. The summary of changes is:

- Coding change to prevent previous situation where assuming a contributor with a blank locus (even if ignored) would cause degradation to start at zero if it was set to use the smallest molecular weight allele (-1 within settings).
- Added limiting ranges for DNA amounts so that contributor n cannot have a higher template value than contributor n-1. The exception to this is assumed contributors who can take any value. As a result the non-assumed contributors now appear in template order in the STRmix™ output.
- The limit on the number of chains has been removed and the way the chains behave in the MCMC has been optimised. Each chain undertakes the full number of burn-in accepts and continues on independently to undertake an even share of the post burn-in iterations (calculated by (total accepts – burn-in accepts)/number of chains).
- Improvements to the generation of genotype arrays at the start of burn-in, resulting in improved memory use and speed.
- Improvement to the method that calculates dropout probabilities when the analytical threshold is high (removing the large penalty when the probability of the allele was greater than 8 standard deviations from the mean).
- A change to how the seed is calculated.

The testing done before the release of this software included extended output calculations, likelihood ratios (LRs) for unrelated and related hypotheses, Model Maker results and diagnostics, database and familial search results, Advanced Report plugin parsing, and run conditions (including number of chains and iterations). All tests gave the expected results.

*Purpose*

The initial validation of the STRmix software was done using v2.3.06. The purpose of this study is to test the functionality of this upgrade at SDPD and ensure that the software upgrade to STRmix™ v2.3.07 does not impact interpretation.

*Materials and Methods*

STRmix™ v2.3.07 was installed on a computer designed by Silicon Forensics with 128 GB of RAM with Intel Dual Xeon E5-2630V3, 2.5 GHz (16 cores total), running Java Version 7 Update 79. The same input files were used to test this software update as were previously used in the internal validation of v2.3.06. The contributors in these samples had varying template levels. 11 mixtures were chosen for comparison: 4 single source, 4 two-person mixtures, 2 three-person mixtures (one was also run as a conditioned mixture), 1 four-person mixture, and 1 five person mixture. The five person mixture was run on the same computer before and after the software upgrade. All other mixtures were previously run on a computer with 32 GB of RAM with Intel Core i5-4570, 3.2 GHz, running Java Version 7 Update 79.

A database search was run after every deconvolution to get an LR for each of the contributors. The same allele frequencies, theta values and database file was used between the two versions. Because the new version of the software no longer limits the number of MCMC chains, even setting the same seed does not necessarily result in the same genotype weights. Single source samples were chosen because the genotype weights are expected to be the same between software versions, and these samples should result in identical LRs. Mixed DNA profiles should result in different, but similar LRs due to the expected variability within the MCMC.

In this performance check, several variables were compared between the two software versions: Run time of 4 and 5 person mixtures, contributor proportions, and LRs of all contributors to the mixtures. A comparison of running 4 chains vs 8 chains was also done using v2.3.07 of the software.

## Results

### Contributor Proportion and LRs

The single source samples resulted in genotype weights of 1 for the first three samples listed in Table 1. The LRs were identical between the two software versions. The weights for sample 161 did vary slightly because of the stochastic nature of the sample and the possibility of dropout. When the LR is extended to additional decimal points, the two versions differ slightly. This is to be expected when the weights are different, and the weights are slightly different because of the nature of the MCMC. Ultimately, the interpretation of the sample is not different, and the discrimination of the known contributor is still at a magnitude well above any inclusionary threshold.

Single Source samples		
Sample ID	LR v06	LR v07
RK	1.20E+28	1.20E+28
52	1.61E+34	1.61E+34
61	5.63E+31	5.63E+31
161	4.31E+32	4.31E+32

Table 1. Single source deconvolution

The known two person mixture results are presented in Table 2. As the release notes suggested there was some variability in the MCMC. These mixtures were run three separate times with the same seed number. Despite a slight variation in contributor proportion, genotype weights, and LRs, the magnitude of difference between the results is very small. All known contributors were included with LRs at least in the quadrillions, and all known non-contributors were excluded.



Two person mixtures						
Sample ID	Contributor ID	v06 proportion	v07 proportion	LR v06	LR v07	LR v07 (4 chains)
Mix 2-6	156	82	81	1.20E+28	1.20E+28	1.20E+28
	150	18	19	7.09E+29	7.25E+29	7.25E+29
Mix 2-18	156	50	53	1.51E+16	2.73E+16	2.02E+16
	150	50	47	9.91E+17	1.79E+18	1.32E+18
Mix 2-38	62	55	56	1.93E+26	2.93E+24	4.30E+24
	31	45	44	2.30E+26	3.39E+24	4.88E+24
Mix 2-42	62	8	8	5.32E+24	4.93E+24	5.55E+24
	31	92	92	1.99E+33	1.99E+33	1.99E+33

Table 2. Two person mixture deconvolution results

Three, four and five person mixtures were also compared using the two different versions of STRmix. Like the two person mixtures, there were differences in the percent contribution. None of these differences affected relative contribution of one contributor to another, however (i.e. the person contributing the most DNA in one version was still contributing the most DNA in the upgraded version). The LRs also had a very similar magnitude of discrimination. The biggest difference between the two different versions of the software was seen in the minor contributor of mixture 3-52. This contributor had 6 alleles dropping out, and the LR was in the billions with v2.3.06

Three, four, and five person mixtures					
Sample ID	Contributor ID	v06 proportion	v07 proportion	LR v06	LR v07
Mix 3-20	61	41	44	4.14E+21	1.93E+22
	30	19	20	2.29E+27	1.19E+26
	69	40	35	8.09E+16	3.69E+16
Mix 3-52	56	58	50	1.09E+20	5.03E+19
	39	23	36	1.12E+13	6.16E+12
	81	19	15	4.78E+10	2.61E+13
Mix 3-52 assume 39	56	49	47	5.05E+30	2.07E+30
	39	38	39	1.28E+28	1.28E+28
	81	15	13	2.03E+15	2.24E+15
Mix 4-35	103	52	50	1.42E+12	6.00E+12
	16	17	22	2.90E+23	3.11E+23
	36	17	17	8.92E+12	5.26E+13
	147	15	12	8.91E+07	1.84E+09
Mix 5-3	17	66	64	3.07E+27	2.91E+27
	71	9	13	5.24E+06	1.70E+06
	150	9	10	3.31E+10	7.75E+10
	79	8	8	6.62E+09	2.03E+10
	137	8	6	4.22E+06	9.53E+06

Table 3. Three, four and five person mixture deconvolution results

and in the trillions with v2.3.07. Either way, this contributor would be strongly included with the SDPD current interpretation guidelines. When this same mixture was conditioned on the ~40% contributor, the results became even more consistent between the two versions.

### Run time

The 4 person mixture took 3 hours, 30 minutes to run on v2.3.06, and 2 hours, 55 minutes to run on v2.3.07. This could be a combination of software version, computer processing speed and number of chains, but ultimately, it is a decrease in processing speed.

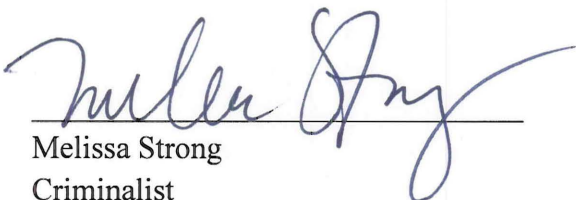
The 5 person mixture took 36 hours to run on v2.3.06 and 17 hours to run on v2.3.07. This mixture was run on the same computer, so it demonstrates how an upgrade to the software can improve run time.

### *Conclusions*

Results obtained with the two different versions of STRmix were comparable. STRmix™ v2.3.07 did not require any user parameters to be recalculated. The low level and mixed DNA samples resulted in different but similar contributor proportions and LR. The deconvolution time for the higher order mixtures decreased. Ultimately, the interpretation of each of these samples wouldn't change by using the v2.3.07 of the software.

### *References*

1. STRmix™ v2.3.07 Release and Testing Report 23 October 2015
2. STRmix™ v2.3 Users Manual October 2015



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