Statement relating to STRmix™ miscodes, Updated Thursday, 19 January 2023

Two miscodes were present in STRmix™ versions up to but not including version 2.0.6.

The first miscode affected the *LR* in an exceptionally minor way in versions prior to 1.08. It was detected by a third party laboratory repeating calculations by hand. It did not result in the need to reissue any statements.

The second miscode was discovered after it was brought to the attention of Forensic Science South Australia by Queensland Health in December 2014. Within a week, a fix was issued, all customers were advised and the new version provided to them. Our view is that there are factual errors in the article published in relation to this[1].

The STRmix™ developers determined that this miscode would affect the results of an interpretation very rarely and that the effect on the likelihood ratio would be about one order of magnitude in either direction. In order for the miscode to have an effect we need a known (assumed contributor), a person of interest (POI) and at least one unknown under Hp. For this reason the miscode only affected mixtures assigned as originating from three or four individuals. Within affected profiles one unknown must be able to possess the same profile as the assumed individual and the person being compared cannot be excluded at any locus. This combination can occur when more than the minimum number of contributors is interpreted to explain the profile (note this is even when the minimum is improbable but possible). Occurrences we know include:

1. Overestimation of the number of contributors without indication (see [1] for an investigation and discussion into the effects of such a policy). This has subsequently been confirmed as the cause of the elevated number of observations within the Queensland Health laboratory[2]
2. Addition of contributor on the basis of sub-analytical threshold information but with all the above threshold peaks explainable by the known and POI (see [2] for investigation into the occurrence, effect and handling of such data)
3. Addition of a contributor on the basis on allelic peak imbalances, but not peak count and with all the above threshold peaks explainable by the known and POI
4. When all indications of one contributor can be described by artefacts such as stutter or drop-in and with all the remaining above threshold peaks explainable by the known and POI (see [1] and [3]).

This combination was considered very unlikely to happen. The occurrence of the miscode firing is related to the operator/laboratory/software grouping and is therefore difficult to estimate a theoretical rate of occurrence. We are guided by the combination of relatively rare factors required for the miscode to fire and the low rate of observations of such occurrences in our assessment that the miscode was unlikely to occur. The STRmix™ testers could reproduce the effect by overestimating the number of contributors.

Forensic Science South Australia (FSSA) identified 15 calculations out of approximately 17,000 that had the conditions required for the miscode to occur and that on recalculation the

[1] http://www.couriermail.com.au/news/queensland/queensland-authorities-confirm-miscode-affects-dna-evidence-in-criminal-cases/news-story/833c580d3f1c59039efd1a2ef55af92b

[2] https://www.health.qld.gov.au/__data/assets/pdf_file/0036/1196685/final-report-coi-dna-testing-qld-dec-2022.pdf. Refer paragraph 302.

LR moved in favour of the defendant. Of the 15, all but one LR was within an order of magnitude. For reasons of transparency FSSA reissued five statements containing six LRs. These six analyses showed small or moderate changes (only one calculation was greater than one order of magnitude) in favour of the defendant[3].

The Institute of Environmental Science and Research Limited (ESR) identified seven out of approximately 3700 profiles that warranted further review. In five of the seven, the LR decreased one order of magnitude. In the remaining two cases, the strength of the evidence within the verbal scale moved downwards one level. These results were examined in the wider context of the case and the decision reached in both cases was that there was no significant impact on the strength of the evidence (in one the LR had not been reported). No statements were reissued.

We have no evidence of false positives or retrials initiated by these miscodes in any Australasian jurisdictions.

Summary

We recognise that these miscodes may give rise to concerns about the reliability of STRmix™. As with any software product, we do not claim that the code is error free. It has however been significantly checked by multiple parties, both developers and users. This tends to mean that if there are any remaining errors they are very small and in parts of the code that activate rarely. This on-going user validation process is possible because of the transparency of our formulations and the multiple diagnostic indicators available with the output. We can assure the reader that in the hands of a fully trained user, following the instructions and training provided by the developer (including reviewing the diagnostic indicators for each run), STRmix™ is a consistently reliable tool for DNA profile interpretation.

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Log(LR) pre 2.0.6	Log(LR) 2.0.6
-1.0	-1.1
0.3	0.0
1.0	0.8
1.4	1.2
7.1	5.7
10.2	9.3

These numbers are the lower 99% bound of the HPD. A Monte Carlo process is used to make this bound. It has an inherent variability. At least some of the difference is attributable to this factor. The differences observed in the FSSA cases is close to or slightly larger (the lower two) than our normal variation. This variation is largely encompassed by the lower bound and other conservancies built in to the STRmix package.

References

1. Bright, J.-A., J.M. Curran, and J.S. Buckleton, The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation. Forensic Science International: Genetics, 2014. 12: p. 208-214.
2. Taylor, D., J. Buckleton, and J.-A. Bright, Does the use of probabilistic genotyping change the way we should view sub-threshold data? Australian Journal of Forensic Sciences, 2015: p. DOI:10.1080/00450618.2015.1122082.
3. Bright, J.-A., et al., Searching mixed DNA profiles directly against profile databases. Forensic Science International: Genetics, 2014. 9: p. 102-110.