Investigation into the effect on the *LR* due to miscode present in STRmix™ V2.3.07

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Background

STRmix™ V2.3.07 implemented a change whereby non-assumed contributors were ordered within the report from highest to lowest template. To achieve this, contributors were free to walk to any position during burn-in but were then ordered and constrained prior to commencement of the post burn-in MCMC. After ordering, unlikely genotype sets were removed during the post burn-in cull (a feature that was introduced at the beginning of the V2.3 series). However, this process was being carried out using unordered degradation values, causing the genotype sets passed through to the post burn-in MCMC to be sub-optimal. The flow-on effects were occasional failed diagnostics and more diffuse weights for genotype combinations. Users were informed of this miscode in the STRmix™ V2.3.08 *Release and Testing Report* issued on 9 February 2016, and via an email Technical Update.

Testing

Testing was performed to examine the magnitude of the effect on the *LR* due to the miscode. Thirty mixed profiles from the PROVEDIt dataset[1] (GlobalFiler™, 29 PCR cycles, 15-second injection time) were selected. These comprised of ten each of two-person mixtures, three-person mixtures, and four-person mixtures. The selected profiles cover a range of mixture proportions and template amounts and are expected to be representative of casework DNA profiles encountered by forensic laboratories. The profiles were analysed in FaSTR™ DNA V1.0 using an AT of 30 rfu. Peak labels for allelic peaks and back stutter artefacts were retained. Peak labels for other stutter variants were removed. Following analysis, the profiles were interpreted within STRmix™ V2.3.07 and V2.3.08. The experimentally designed number of contributors (NoC) was assumed when setting up each interpretation. All other run settings were unchanged from their default values[2].

*LR*s were assigned for the known donors and 50-*N* non-contributor profiles, where *N* is the experimentally designed NoC for the mixture. *LR*s were assigned using the Database Search function of STRmix™. The FBI extended Caucasian allele frequencies were used with θ = 0. Sub-sub-source *LR*s were recorded.

In total, 90 H_p true *LR*s and 1410 H_d true *LR*s were assigned. *LR*s assigned in V2.3.08 were compared with the corresponding *LR* from V2.3.07. These are plotted below in $\log_{10}$ form. Exclusions (*LR* = 0) are plotted as $\log_{10}LR = -40$. A dashed line at $y = x$ has been added to the plot to assist with interpretation. Data points above this line indicate that the *LR* assigned in V2.3.08 was larger than that assigned in V2.3.07. Similarly, data points below this line indicate that the V2.3.07 *LR* was larger.

[1] Alfonse, L.E., Garrett, A.D., Lun, D.S., Duffy, K.R. & Grgicak, C.M. A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt. Forensic Sci. Int. Genetics 32, 62-70.

[2] SE33 was ignored during interpretation of H02_RD14-0003-44_45_46_47-1;1;4;1-M3a-0.217GF-Q0.8_08.15sec due to an unresolved 18.1 allele identified during profile analysis.

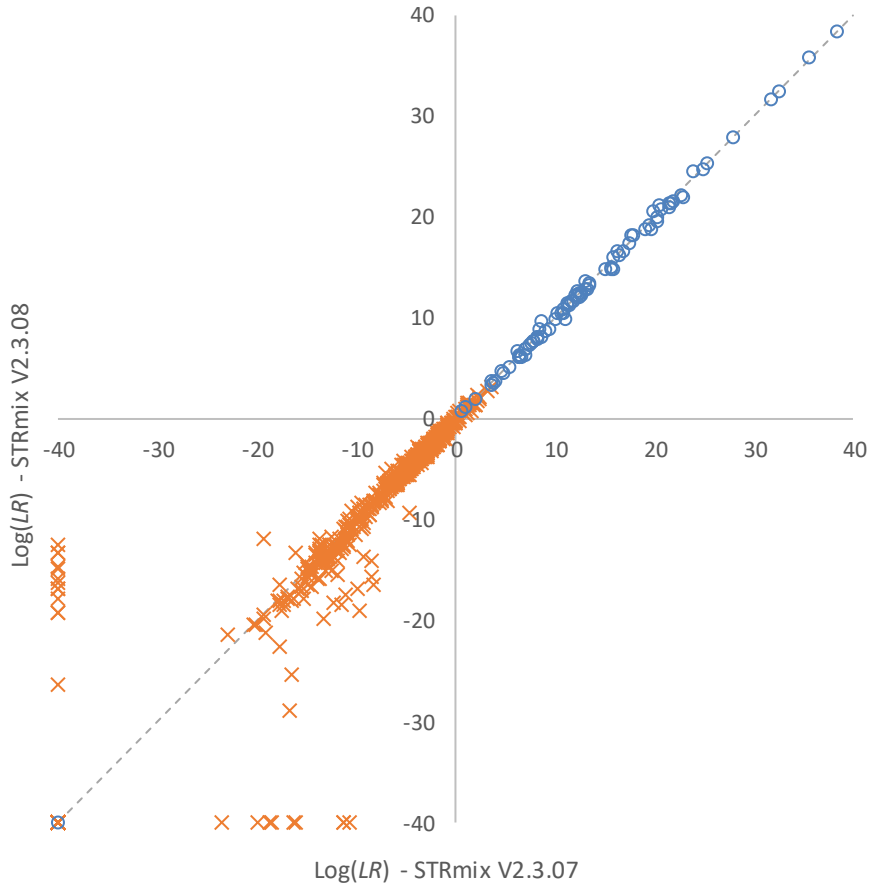

Figure 1: Comparison of log(*LR*)s assigned in STRmix™ V2.3.07 and V2.3.08. *LR*s assigned for known donors have been plotted using blue circles whilst non-contributor LRs have been plotted as orange crosses. Exclusions (*LR* = 0) have been plotted as log(*LR*) = -40.

From Figure 1 it can be seen that there was little difference in the *LR*s assigned for known donors between versions 2.3.07 and 2.3.08. Increased variability was seen for non-contributor *LR*s. This is expected and is due to low weight being assigned to genotype combinations that align with the non-contributor profile. The effect on the miscode identified in STRmix™ V2.3.07 therefore appears to be minimal. Nevertheless as previously advised, we recommend that all users should move to STRmix™ V2.5.11, V2.6.3 or V2.7.0 as soon as possible, as only limited support is available for previous versions of STRmix™. Laboratories wanting to remain using STRmix™ V2.3 series are strongly encouraged to update to STRmix™ V2.3.10 as soon as practicable.