Variation in STRmix™ regarding calculation of expected heights of dropped out peaks, 4 July 2016

Summary:
STRmix™ V2.3.10 and V2.4.05 include a change to calculation of the expected height of dropped out peaks at loci where all contributors have at least one dropped allele. This differs to the calculation in the v2.3 series and all versions subsequent to this up to v2.3.09 and v2.4.04 (inclusive). The effect on likelihood ratios (LRs) is in a conservative direction. Our opinion is that the number of profiles affected within a laboratory is likely to be low. Below we provide specific information about the calculation and highlight situations where it has an effect on the LR.

Specific mechanism:
STRmix™ was summing the template amounts proposed for each contributor with a dropped allele (a -1 or Q allele), so that parameter T (template, unit RFU) within the mass parameters (DART) is the sum of each individual contributor's T. For example, if at one iteration:
- contributor 1 has T = 100 and -1,8 genotype;
- contributor 2 has T = 200 and -1,-1 genotype; and
- contributor 3 has T = 150 and -1,11 genotype;

The total allelic product (unit RFU) for contributor 1's 8 allele will use T = 100 but the -1 will use T = 450 (the sum of the three contributors' Ts); TAP for contributor 2's two -1 alleles will use T= 450; and TAP for contributor 3's 11 allele will use T = 150 but the -1 will use T = 450. In each case, all four -1 alleles are given the exact same RFU.

The effect of the above is that genotype sets that contain multiple dropped alleles are being selected by the Metropolis-Hastings acceptance/rejection algorithm less than they should. In turn this means those genotype sets are assigned lower weights than they should be.

Effect on the LR calculation:
The only profiles affected are those that contain multiple low level (non-assumed) contributors, where multiple genotype sets with dropped alleles for both contributors are being considered.
When the above conditions are met (multiple contributors with dropped alleles at the same loci), STRmix™ versions affected will produce LRs that are lower or unchanged (within the normal variations resulting from MCMC run to run variability) compared to unaffected versions. The variation is acting conservatively on the LR. The effect is more pronounced for proposition sets containing a difference of more than one unknown between H_p and H_d.

This observation is demonstrated visually in Figure 1 for v2.3 (left pane) and v2.4 (right pane). Figure 1 shows the comparison of LRs between v2.3.09 and v2.4.04 and revised versions of STRmix™ for 552 and 579 interpretations, respectively. The profiles include two, three and four person mixtures. Propositions include the consideration of both one and all known contributors as sources of DNA under the prosecution proposition. In addition, for some interpretations an individual was assumed under both the prosecution and defence propositions (conditioned).
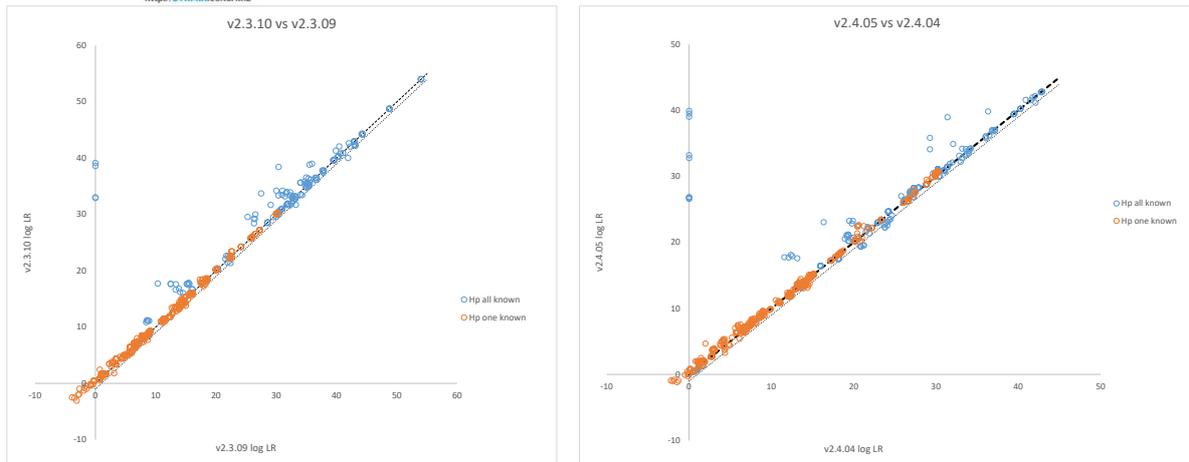
Figure 1: Example of magnitude of effect on size of LR, for two, three and four person mixtures considering different propositions

The plots in Figure 1 show a very close alignment of LRs produced by the two versions. Data points above the dotted line at $x=y$ show that there was an underestimate of the LR using the previous version. The blue data points are for propositions considering all known contributors under the prosecution position and all unknown under the defence proposition. The orange data points are considering only one known under the prosecution proposition. The lower dashed line at $x=y$ indicates one order of magnitude difference in the log(LR) between the different versions. This is the maximum expected variation in LR due to MCMC variation between repeat interpretations of the same profile.

The points at LR = 0 for the affected versions are due to genotype sets assigning lower weights than expected. This was seen at only one locus within each of these profiles, triggering a diagnostic for further review.