Change to normalisation of weights before an LR is assigned in STRmix™

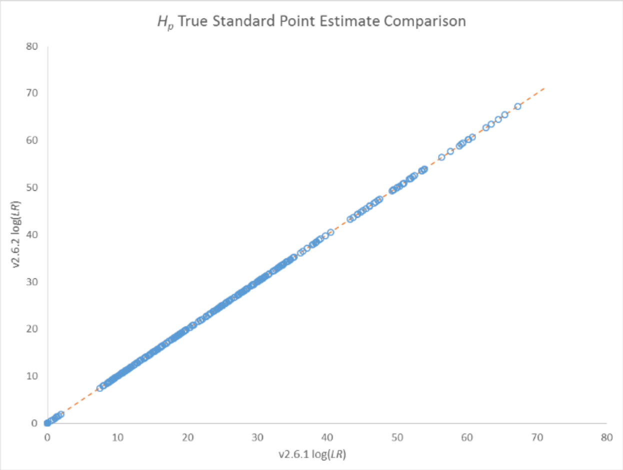
21 June 2019

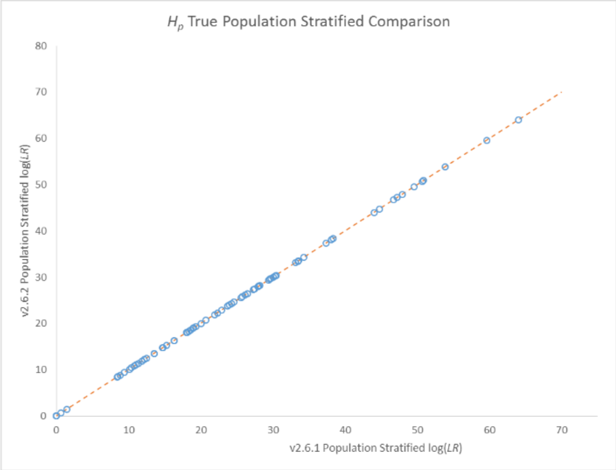
When assigning an LR, if a POI sits in a dropout position their alleles are written into a modified genotype array with corresponding weights. In v2.6.0 and v2.6.1, these weights were not being normalised before an LR is assigned. This change may result in minimal differences in a non-varNOC LR however given the precision reported in the STRmix™ pdf report these differences will be not be observed.

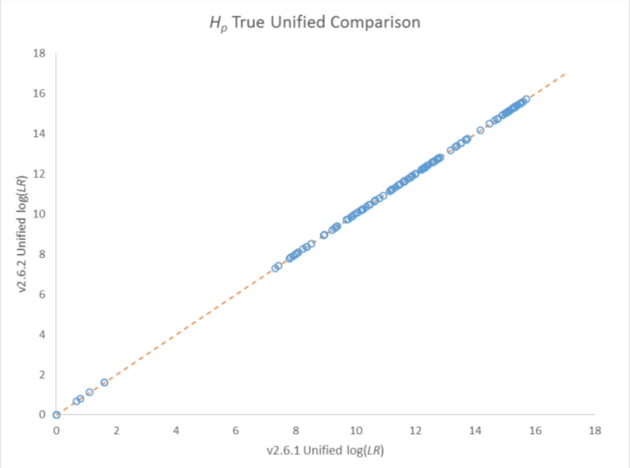
Minor differences were observed for varNOC stratified and MLE LRs (less than one order of magnitude difference). This effect was more obvious for non-contributors due to the larger N in a varNOC deconvolution having more dropout accepted and therefore larger weights in the genotype array pre-normalisation (if the POI sits in dropout positions). Normalisation has more of an effect on the larger N, which means the larger N will now have less of an effect on the stratified LR than pre-normalisation. This results in stronger exclusions of non-contributors.

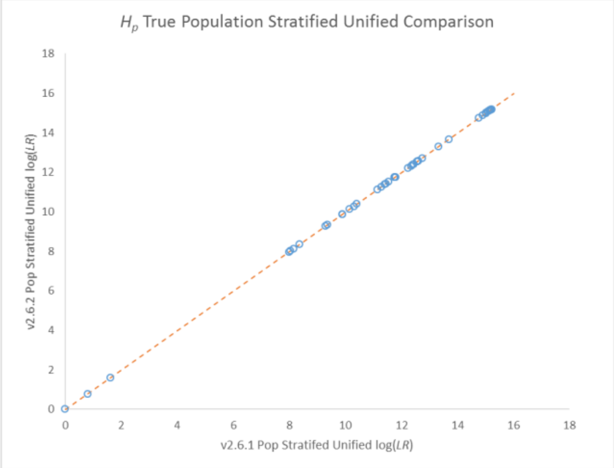
Effect on *LR*

Summary Plots – Standard *LR*s

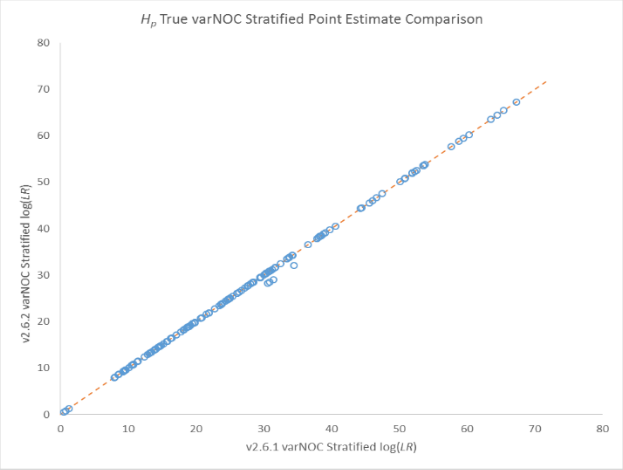








Summary Plots –varNOC *LR*s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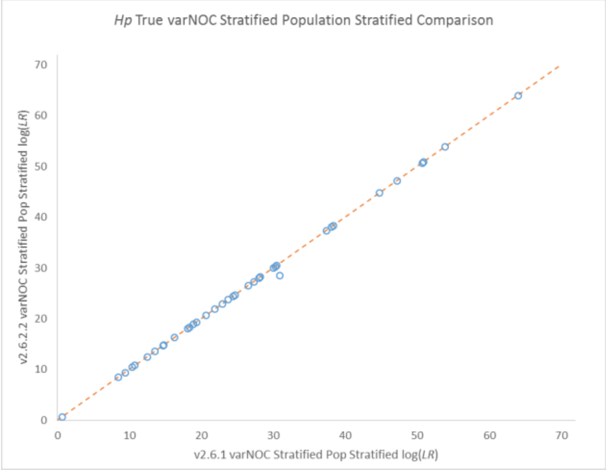
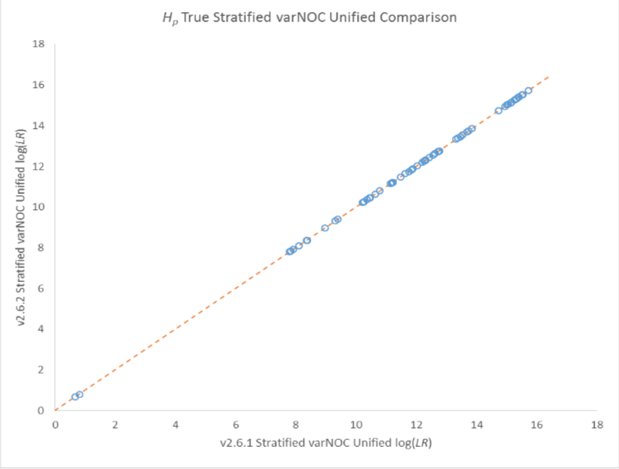

Hp True varNOC Stratified Population Stratified Comparison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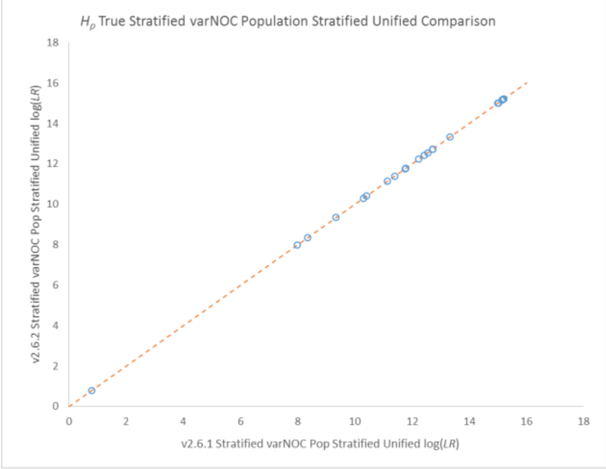
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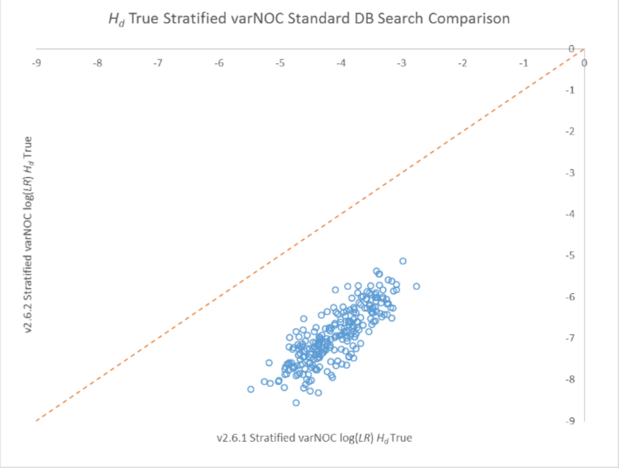
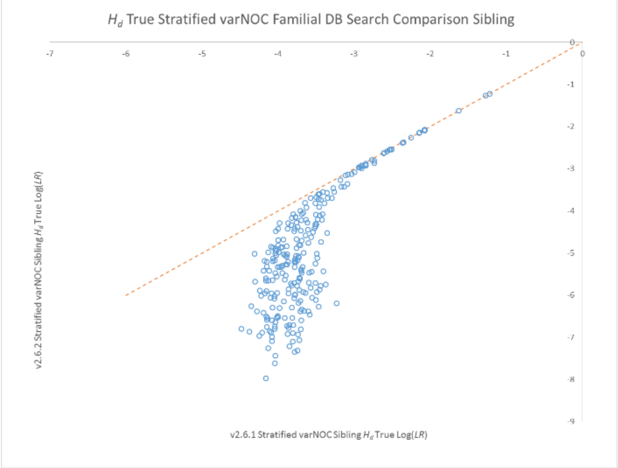

H_d True Stratified varNOC Standard DB Search Comparison


H_d True Stratified varNOC Familial DB Search Comparison Sibling