NORTH CAROLINA STATE BUREAU OF INVESTIGATION

Likelihood Ratio for Statistical Calculations of Mixtures in PopStats

1   Once an evidentiary sample is declared to be a probative match to a reference standard, the "Random Match Probability" of this profile must be determined for the general population. This is straight forward for neat stains and mixed samples containing a predominant profile. For DNA mixtures that do not contain a predominant profile or where individuals cannot be excluded, Likelihood Ratios should be utilized for calculating population frequencies. Popstats will allow for the calculation of Likelihood Ratio Data for both single DNA profiles and those involved in mixtures.

2   Computer Procedure:

2.1   Upon entering the Popstats program, click on the *Forensic Mixture* option on the Case Type drop down menu, or click on the paint palette button at the top of the screen.

2.2   A screen similar to the one shown in Appendix 1 will appear.

2.3   The column labeled "Mixture" is the location where all of the alleles from the questioned mixture sample are to be entered.

2.4   The column labeled "C1 Combined Unknown" is the location where the unknown alleles from the questioned mixture are to be entered which don't meet the prosecutor's theory. The blank box is where the total number of unknown individuals which don't fit the prosecutor's theory is to be entered.

2.5   The column labeled "C2 Combined Unknown" is the location where the unknown alleles from the questioned mixture are to be entered which don't meet the defense's theory. The blank box is where the total number of unknown individuals which don't fit the defense's theory is to be entered.

2.6   For each locus, click and drag the appropriate bands which don't meet the theory to the respective column according to the table below:

Evidence Profile Description	C1 column	C2 column
4 bands - V1, V2, S1, S2	0 unknowns, leave blank	1 unknown, enter S1 & S2
3 bands - V1, S1, S2	0 unknowns, leave blank	1 unknown, enter S1 & S2
3 bands - V1, V2, S1	0 unknowns, leave blank	1 unknown, enter S1
2 bands - V & S share both	0 unknowns, leave blank	1 unknown, leave blank
2 bands - V1, V2, S1 share one	0 unknowns, leave blank	1 unknown, leave blank
1 band - V & S share one	0 unknowns, leave blank	1 unknown, leave blank
2 bands - S1, S2, V1 share one	0 unknowns, leave blank	1 unknown, enter S2
2 bands - V1, S2 share none	0 unknowns, leave blank	1 unknown, enter S2
4 bands - S1, S2, U1, U2	1 unknown, enter U1& U2	2 unknowns, enter S1, S2, U1& U2
3 bands - S1, S2, U1, U2	1 unknown, enter U1	2 unknowns, enter S1, S2, U1& U2

V= victim   S=Suspect   U= Unknown

2.7   If allele dropout occurs at any locus for any reason (allele dropout, degradation, etc.), exclude the alleles for that locus by clicking off the "X" in the box next to the locus' name.

2.8   If the mixture contains bands from an unknown contributor, do not use the Popstats program for the likelihood ratio calculation.

Revision History		
Effective Date	Revision Number	Reason
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APPROVAL SIGNATURES	Date
Author/Title (Print)	
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Appendix 1

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