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Department of Forensic Science

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FORENSIC BIOLOGY SECTION PROCEDURES MANUAL

MODIFIED RANDOM MATCH PROBABILITY

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TABLE OF CONTENTS

1 Modified Random Match Probability

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1 Modified Random Match Probability

1.1 Background

The modified random match probability (mRMP) calculation can be applied to DNA mixtures based on an assumption of the number of contributors.

1.2 Formulas

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The formulas used in the mRMP calculation are as follows:

Heterozygote: 2pq, where p and q represent the frequencies of allele #1 and #2[1].

Homozygote: $p^2 + p(1-p)\theta$*, where p represents the frequency of the allele[1].

Heterozygote with the possibility that one allele has dropped out: $2p-p^2$, where p represents the frequency of the observed allele[1].

*Due to the conservative nature of the mRMP calculation, θ will be set to 0.

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1.3 Calculation

1.3.1 The first step in the mRMP process is to evaluate the entire profile for possible allelic drop-out, genotype drop-out, and number of contributors. Factors such as alleles at/below the LOD, alleles at/below the STH, overall RFUs and peak height ratios in addition to number of alleles at each locus should be considered when making these decisions. These determinations can be made with the aid of assumed known contributors; however, they MUST be made prior to comparing the evidence to the profile of the person of interest.

1.3.2 If there is a reasonable possibility that locus drop-out could have led to the loss of an entire genotype, then statistics should not be calculated at that locus.

1.3.3 Once the profile has been reviewed, each locus will be assessed to determine the possible genotypes which could be contributing to the mixture based on the number of contributors estimated previously.

1.3.3.1 For a mixture profile which demonstrates a lower level partial contributor whose contribution cannot be detected at most loci, deconvolution of loci at which only the higher level contributors are detected can be accomplished and the corresponding statistics reported. The loci at which the additional lower level contributor was detected will be considered inconclusive for this approach.

1.3.4 The *unrestricted* mRMP depends upon the number of estimated contributors and the number of alleles observed at a given locus without consideration of peak height differences. Peaks falling at/below the stochastic threshold for the injection time may be given an "A, any" or "A, x" genotype notation and the heterozygote drop-out formula described above is applied ($2p - p^2$).

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1.3.5 The *restricted* mRMP takes into account relative peak heights ratios (PHR) such that alleles are paired only where specific combinations of alleles are deemed possible which results in narrowing the field of possible genotype combinations contributing to the mixture. Allelic combinations not likely based on peak height ratios are not included in the calculation.

1.3.6 The use of an assumed known contributor is most commonly done with restricted mRMP calculations.

1.3.7 Discernment of major and minor contributors

1.3.7.1 If a sample appears to contain a predominance of one person's DNA, a major profile may be determined either by deducing a single source profile or allowing for genotype uncertainty. The

remaining part of the profile may be considered the minor profile with the understanding that some of the minor profile may be masked by the major profile.

1.3.7.1.1 Discernment of a single genotype for the major or minor contributor to a mixture may be limited to only some loci with the remaining loci yielding multiple potential genotypes for that contributor.[1]

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1.3.7.2 Assumed known sample profiles can assist with the major/minor deconvolution process and will be reflected in the reported assumptions.

1.3.7.3 Peak Height Ratio (PHR) expectations may be reduced due to stochastic peak height variations as a result of low-level and/or haploid template, base pair spread between sister alleles, and the additive effects of peak sharing due to an additional contributor(s) or stutter.

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1.3.7.3.1 In general, heterozygous alleles above the stochastic threshold attributed to a major contributor should meet the peak-height ratio expectations.[1]

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1.3.7.3.1.1 Remaining alleles present at a locus with a major heterozygous allele pair should not fall into PHR with the lesser allele (smaller peak) of the major heterozygous pair; otherwise, the locus may be considered inconclusive for major/minor statistical purposes.

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1.3.7.3.2 After assessing for possible drop-out, loci with a single peak which is above the stochastic threshold (STH) may be considered a major homozygous genotype. If the single peak is below the STH, the peak will calculated with the homozygous dropout formula ($2p - p^2$).

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1.3.7.3.2.1 Loci with multiple peaks in addition to a single major peak will be evaluated with consideration of reduced PHR expectations to assess whether the major genotype is likely homozygous or whether multiple potential genotypes including heterozygous combinations are possible and should be included in the calculations.

1.3.7.4 Because the evidence profile is not compared to the person of interest until after statistics have been calculated, multiple deconvolution approaches may be necessary. For example, a mixture may be deconvoluted as a major profile and as a 2-contributor profile. After comparison to the person of interest, the reported statistics for the typing results that provide the most genetic information and/or the highest discrimination potential are reported.[1]

1.3.8 Reporting results

1.3.8.1 The assumptions made in order to calculate the statistics for a profile (number of contributors, and assumed knowns) will be reported as part of the statistical statement.

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1.3.8.2 It may be necessary to report conclusions regarding the POI as a major (or minor) contributor if not addressed in a previous report.

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1.3.8.3 To report a major profile as a deduced single source, the following statement will be used:

Assuming this DNA profile is a mixture of a major contributor and minor contributor(s), the probability of randomly selecting an unrelated individual with a DNA profile matching that developed as the major contributor of the DNA mixture profile at the PowerPlex® 16 loci is…

No statistics were calculated for the minor profile of the mixture.

1.3.8.4 To report a major profile allowing for genotype uncertainty by using multiple genotypes or the dropout formula at one or more loci, the following statement will be used:

Assuming this DNA profile is a mixture of one major contributor and minor contributor(s), the probability of randomly selecting an unrelated individual who would be included as a contributor to the major profile of the DNA mixture at the PowerPlex® 16 loci is…

No statistics were calculated for the minor profile of the mixture.

1.3.8.5 To report a minor portion allowing for genotype uncertainty by using multiple genotypes or the dropout formula at one or more loci, the following statement will be used:

Assuming this DNA profile is a mixture of one major contributor and minor contributor(s), the probability of randomly selecting an unrelated individual who would be included as a contributor to the minor profile of the DNA mixture at the PowerPlex® 16 loci is approximately…

1.3.8.6 When a known sample is used during mixture deconvolution, the following statement will be used:

Assuming the minor portion of the DNA profile contained a mixture of [name] and an additional contributor, the probability of randomly selecting an unrelated individual who would be included as a contributor to the minor profile of the DNA mixture at the PowerPlex® 16 loci is approximately…

1.3.8.7 When loci have been excluded from the statistical calculation as specified in the statistical statement, the following statement may be used to reflect that additional loci were used for comparison purposes:

The remaining loci are consistent with the conclusion that [name] cannot be eliminated as a contributor to this DNA mixture profile; however, these loci did not meet the required criteria to be used in the statistical calculation.

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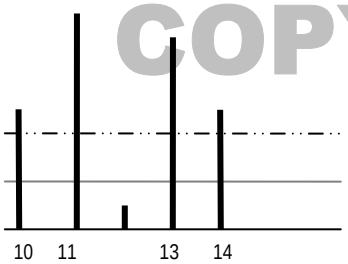
1.4 Examples

1.4.1 Assumed two person mixture as indicated below

Locus Example	Restricted based on PHR	Unrestricted	Assumed Known Contributor
	11,13 and 10,14	10,11 13,14 10,13 11,14 10,14 11,13	Assumed known is a 11,13 Statistics calculated for a 10,14 as the foreign contributor

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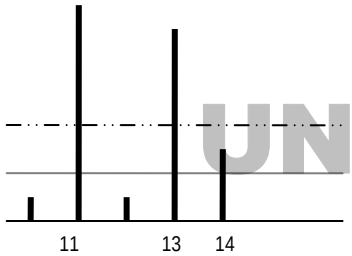
1.4.2 Assumed two person mixture as indicated below

Locus Example	Restricted based on PHR	Unrestricted	Assumed Known Contributor
	11,13 and 14,14	11,13 14,14 11,14 13,13 11,11 13,14	Assumed known is a 11, 13 Statistics calculated as a 14,14 as the foreign contributor

1.4.3 Assumed two person mixture as indicated below with possible allelic dropout

Locus Example	Restricted based on PHR	Unrestricted	Assumed Known Contributor
	11, 13 and 14, X	11,13 13,13 11,11 14, X	Assumed known is a 11,13 Statistics calculated as a 14, X as the foreign contributor

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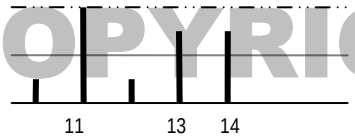
1.4.4 Assumed two person mixture as indicated below with possible allelic dropout

Locus example	Unrestricted	Assumed contributor
	11,X 13,X 14,X	Victim is an 11,11 Statistics calculated as a 13,14 as the foreign contributor

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1.5 Report Writing

The Methods statement will contain the following statements, as applicable:

- The DNA statistics calculated herein used the population allele frequencies generated by the Virginia Department of Forensic Science.
- The modified random match statistical method addressed below has been applied in accordance with the Scientific Working Group on DNA Analysis Methods (SWGDAM) 2010 Interpretation Guidelines and Departmental procedures.

The reporting statement will be as follows:

Assuming the DNA profile developed from [evidence] contained a mixture of [N] contributors, the probability of randomly selecting an unrelated individual who would be included as a contributor to the DNA mixture at the PowerPlex® 16 loci (with the exception of TPOX, D21S11, Penta D, and D13S317 loci) is approximately:

1 in 190,000 in the Caucasian population
1 in 75,000 in the Black population
1 in 270,000 in the Hispanic population

References:

1. SWGDAM (2010). SWGDAM interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories. Available at http://www.fbi.gov/about-us/lab/codis/swgdam.pdf.

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