

THE USE OF GENEMAPPER® *ID-X* SOFTWARE V1.1 FOR THE ANALYSIS OF MIXED DNA SAMPLES

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GeneMapper® *ID-X* Software v1.1 (Applied Biosystems, Foster City, California) recently released its mixture analysis tool, which assists the forensic analyst with the analysis and interpretation of mixed DNA samples. The mixture deconvolution module of the GeneMapper® *ID-X* Software (GMID-X) evaluates two-person mixtures. GMID-X has the ability to produce best-fit major and minor profiles. The software also calculates the mixing ratio of two donors within a mixture. Using the defined Peak Height Ratio Rule and Residual Rule, a list of all possible candidate genotypes are ranked and displayed per locus. The genotype combinations are automatically sorted into either the Selected (most likely set for inclusion) or Unselected genotypes tables. These tables can be edited to filter incorrect genotype combinations. In addition, statistics such as Random Match Probability, Combined Probability of Inclusion/Exclusion, and Likelihood Ratio can be quickly generated, ranging from one (1) contributor up to three (3) or more contributors.

Cases involving sexual assault, homicide, and touch DNA often have mixtures of two or more DNA profiles, e.g. vaginal swabs, fingernail scrapings, blood stains, and swabs from door handles. The vaginal swabs and fingernail scrapings usually have the advantage of being considered intimate samples. Confidence in the resulting second contributor profile from an intimate sample is higher than if both contributors are unknown. When both contributors are unknown, deconvoluting the mixture becomes much more complex. In this study, data will be analyzed with and without a reference applied, as GMID-X allows the user to define one contributor to the mixture, e.g., a victim's profile. Additionally, low levels of input DNA from a mixture of two individuals will be explored. These low levels of DNA will exhibit stochastic effects in the amplifications resulting in allele dropout. GMID-X software considers the possibility of allele dropout by reporting an F allele. The F allele is reported for potential alleles up to 1 RFU less than the mixture analysis threshold.

The results of these studies demonstrate that the mixture deconvolution module in the GeneMapper® *ID-X* software can assist an analyst with challenging mixture casework data. The peak height ratio calculations can be time-consuming when performed by hand and introduce the risk for human error or inconsistent calculations. An advantage to this new technology is that the peak height ratios for all combinations at each locus are calculated automatically and consistently. In addition, mixing proportions for the two contributors are calculated per locus as well as over the entire sample. As a result, the forensic analyst is freed to spend less time in performing mundane calculations and more time considering the various combinations produced by the given data.

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