



B31 A Comparison of Open-Source Software for Assessing the Weight of Evidence in Forensic DNA Profiles

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After attending this presentation, attendees will better understand how known complex mixture samples are treated by different probabilistic genotyping models as implemented in various software tools.

This presentation will impact the forensic science community by providing information concerning how different probabilistic genotyping models treat the same profile.

It has been a challenge, historically, to compare different software approaches and implementations for assessing the weight of evidence. The various approaches use different models, which make different assumptions and are implemented in different ways. This makes it difficult to compare the results between approaches. An additional quagmire is that no true answer exists, so it is not possible to compare results from any model to a static neutral standard. Furthermore, for some time, software that automatically modeled variables such as peak height and stutter was only available as expensive proprietary programs. Finally, training is key to using any of these programs in an optimal way, and the expertise to execute a variety of programs does not exist in one individual or even one group.

Recently, the number and type of open source free-of-charge software programs has expanded to include options for more sophisticated modeling of multiple parameters. Thus, it became possible to perform a reasonable comparison between different models. Part of this study was the recent opportunity to spend time at the special forensic statistics program sponsored by the Isaac Newton Institute for Mathematics at Cambridge University. This time was spent learning and organizing four different software programs for the purpose of comparison. The programs were: Lab Retriever, LRmix Studio, European Forensic Mixtures (EuroForMix) and likeLTD v. 6.1. Lab Retriever and LRmix Studio use discrete models in that the programs only consider nominal alleles, but do not automatically model other parameters, such as peak height and stutter. EuroForMix and likeLTD v. 6.1 model multiple parameters and also use an iterative process to find the best-fit answer.

Another advantage that has recently become available is a set of 164 complex mixture samples created from known contributors, each amplified five times, for a total of 820 samples. This sample set was created as part of a National Institute of Justice (NIJ) and will be made publicly available. The profiles from these mixture samples provide a rich source of material with which to perform informative comparisons between the different software programs. A subset of these samples will be compared to determine how profile complexity affects the Likelihood Ratio (LR) under different approaches. Results from these comparisons will be presented.

Open-Source, Probabilistic Genotyping, Model Comparison