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Use of DBLR™ with STRmix™ – A hypothetical case example

IS THE PROFILE SUITABLE FOR INTERPRETATION? In this hypothetical example, a mixed DNA profile is obtained from swabs from the grip of a handgun located at the scene.

An apparent three-person mixture is recovered¹, and, when interpreted in STRmix™, estimated mixture proportions of 59%, 30% and 11% are obtained. The electropherogram is given in Figure 1.

In this case we are interested in the probative value of the 11% minor component of the profile. Is this component suitable for comparison to any reference profiles (standards) submitted in this case? To answer this question, we use the **Explore Deconvolution** function in DBLR™ and simulate profiles for individuals to address the following two hypotheses:

- H₁:** The DNA originated from the suspect and two unknown individuals.
- H₂:** The DNA originated from three unrelated individuals.

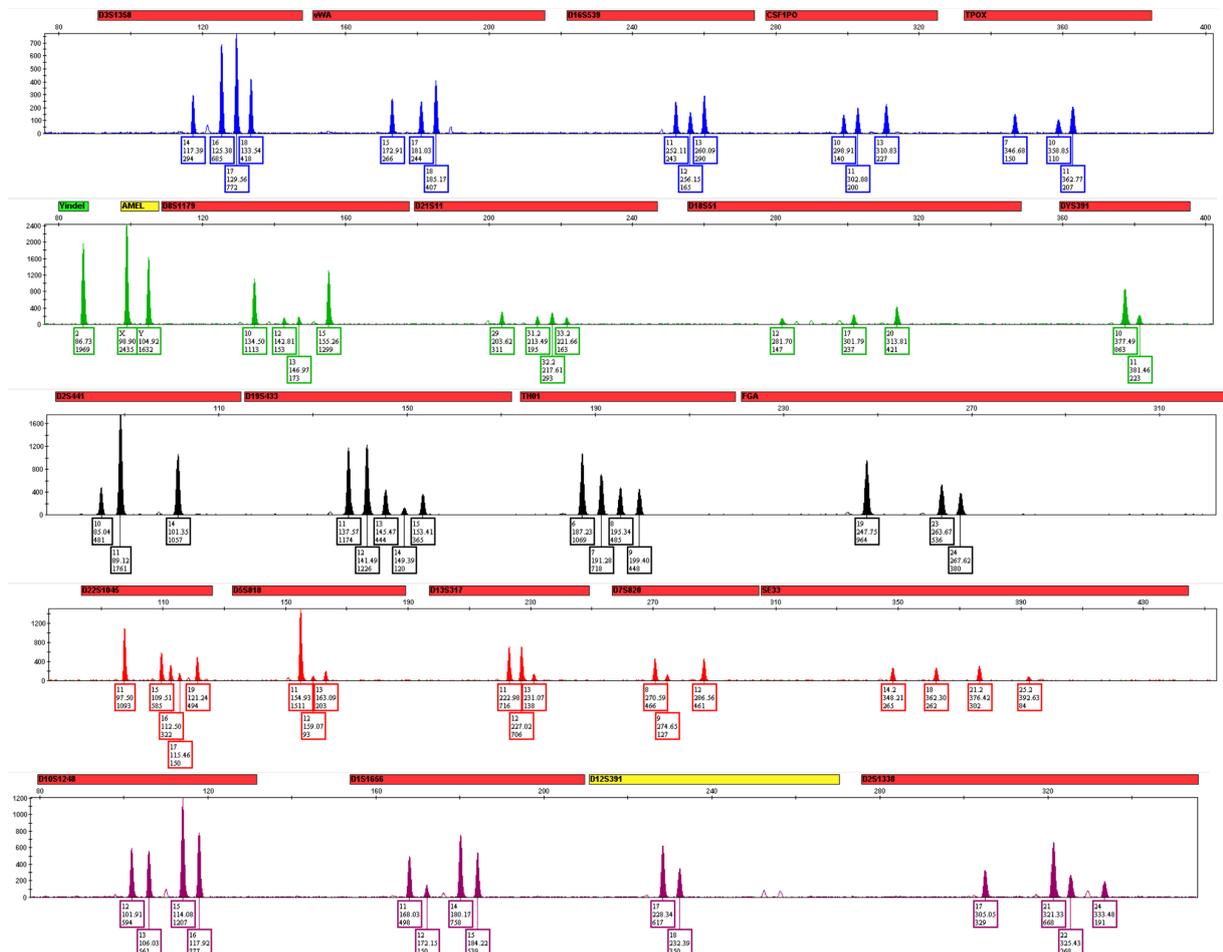
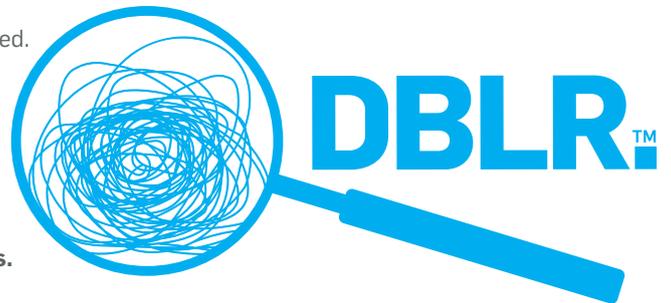


Figure 1. Apparent three-person mixture from the grip of a handgun. The average peak heights for the two smaller components are roughly 500 rfu and 200 rfu, respectively.

¹ Sample D08_RD14-0003-49_50_29-1;4;1-M2d-0.378GF-Q0.8_04.15sec.hid from mixture from the PROVEDIT data set <https://lftdi.camden.rutgers.edu/provedit/>

Genotypes are sampled considering each hypothesis and the likelihood ratios computed. The logarithm of the sampled likelihood ratios is plotted graphically in Figure 2. LRs of 0 are plotted as $\log_{10}(\text{LR})=-40$ and the black vertical line indicates $\log_{10}(\text{LR})=6$, representing a threshold of one million.

The results of the simulation testing indicate that for the 11% minor component the probability of an LR greater than one million given a true contributor is about 73%. This is indicated by 73% of the data (blue distribution) to the right of the black vertical line in Figure 2. Although the expected $\log_{10}(\text{LR})$ is about 7.5 (mode of distribution), there is considerable spread in the likelihood ratios, which reflects that there are many genotypes that could not be ruled out in the deconvolution.

The results for the simulated non-contributors (red distribution) indicate that the probability of an LR greater than one million given a non-contributor is 0. We note that we would need to sample millions of non-contributors to explore the chance of an adventitious match more thoroughly. Instead, we can use importance sampling within **DBLR™** to bias our estimate. Using importance sampling, the probability for a non-donor to exceed the threshold, is obtained as 6.44×10^{-8} (in the order of one in one hundred million).

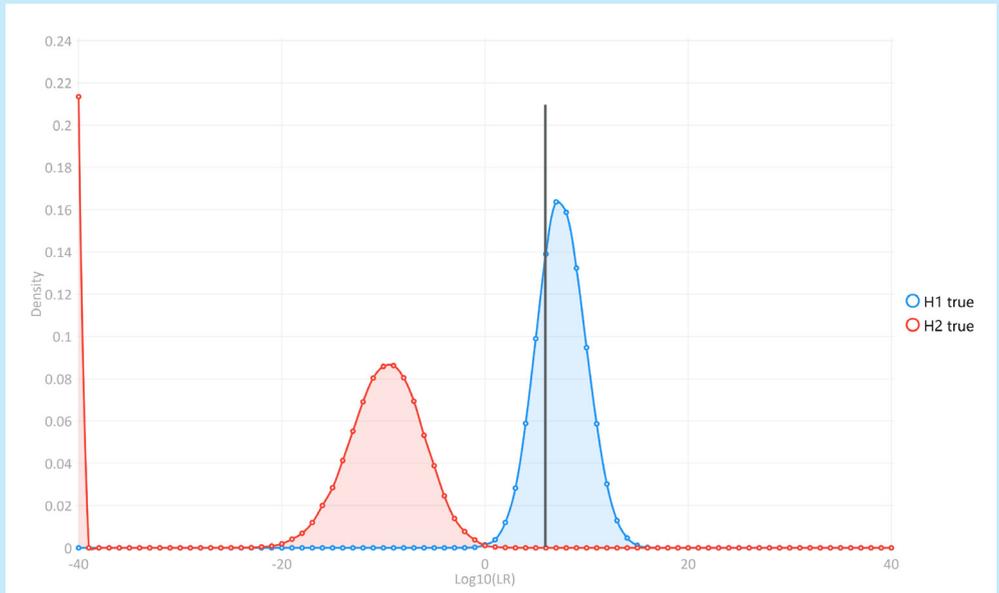


Figure 2: Simulation results for the minor component of the three-person mixture. The estimated probability for the true donor (in blue) obtaining a likelihood ratio greater than a million (indicated by the vertical line) is around 73%.

WHAT FURTHER INVESTIGATION CAN WE DO?

At the early stages of the investigation, there are no persons of interest, but we have a database containing one million individuals to which we could compare the deconvoluted profile. The third component (the 11% minor) is not suitable for upload to CODIS . . . how can we then compare our mixture to our million profile database?

In **DBLR™**, using **Database Search**, we can compare a profile or a specified component of a mixture to a large database like this in seconds. The database is not static and can be added to as needed. Profiles can also be deleted if required. In addition, profiles deconvoluted in **STRmix™** can be saved to a separate database and matches between the two can be configured.

In this case, we undertake a search of our database of one million individuals. In **DBLR™**, searches are undertaken using likelihood ratios. Component three of the mixture is compared with the database of one million individuals and a LR assigned for each contributor the following propositions:

H₁: the DNA originated from database individual and two unknown individuals,

H₂: the DNA originated from the three unrelated individuals.

The LR for one of the individuals in the database is 5.785×10^6 . None of the other individuals within the database yield a likelihood ratio above the chosen threshold of one million. This match provides very strong intelligence to the investigating agency in this case.

WHAT ABOUT EVIDENCE EVALUATION?

Finally, let's assume that a reference sample (standard) from the person of interest is submitted as part of the investigation. We can now assign a likelihood ratio using **STRmix™** to determine the strength of the association. This output can now be used for court purposes.

FOR MORE INFORMATION ABOUT STRMIX™ OR DBLR™ OR TO REQUEST A QUOTE, PLEASE CONTACT:

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