The implementation of STRmix does not invalidate previous reported results. If additional interpretation is required on samples that cannot be reanalyzed the following document will assist the analyst in the steps for additional interpretation. This guidance document must be used in conjunction with Forensic Biology procedures and controlled documents.

The analyst shall review the previous reports and supporting case notes. If the sample was previously fully interpreted and statistics were calculated, statistics will not be re-calculated without written approval from the Technical Leader. For samples where reinterpretation is the only option, the procedures that were in place at the time of the original analysis will be utilized in the re-interpretation. The procedure name and version will be documented in the case notes.

The following tasks are considered reinterpretation and require documented analyst qualification:
1. Moderate stringency matches between a candidate and target DNA profile where (1) one or both of the DNA profile(s) originate from legacy data and (2) the match involves comparisons of the original electropherograms to assess the match, and.

2. Assessment/evaluation of allele calls, genotype calls (to include potential for allelic drop-out), a change in the assumptions used, or removing alleles (or loci) from statistical estimations from legacy amplification test kit data.

An analyst will remain qualified for reinterpretation of data for 2 years after the last proficiency test of a legacy kit (or the last requalification). After the 2 year period, the analyst must go through a requalification process. This requalification process will include training and a practical component to include a competency test (e.g., evaluating previous proficiency test results and reporting). This training will be documented and a memo will be issued upon completion.

Legacy amplification kits used at the North Carolina State Crime Laboratory are PowerPlex 1.1 and 2.1, Identifiler, and Identifiler Plus. Cases worked prior to PowerPlex 1.1 will not be reinterpreted.

Best practices must be considered when legacy data is being re-visited. While an effort will be made to be consistent with the interpretation and conclusions made at the time of original analysis, profiles obtained using previous methodologies may need to be reassessed, most often to generate statistical estimates.

Generally, the conclusions drawn by the original analyst should be maintained when reassessing the case file; however, if a reference profile's status as included and/or excluded changes based upon a new review, the Technical Leader must be consulted as soon as possible. All changes made during the reassessment (alleles, loci, assumptions, etc.) will be documented within the case notes.

Random match probabilities (RMP) will be calculated if needed for these reinterpretations. RMPs will be calculated as described in the Forensic Biology procedure for ArmedXpert. For samples where CPI is previously listed in the case notes, uRMP calculations will be utilized as appropriate. The NIST database, utilizing the Caucasian, African American, and Hispanic populations will be used for the allele frequencies.

As a general rule, loci where dropout is possible must be carefully evaluated. These circumstances would include lower level profiles whether the dropout is documented in the case notes or not. A stochastic threshold was not established at the NCSCL until 2013 in conjunction with the implementation of the Identifiler Plus amplification kit.

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The information below is a summary, compiled from historical casework procedures and general section practices.

A. PowerPlex 1.1 and 2.1
   a. 2 separate amplification reactions, CODIS Core 13 loci (duplication between reactions)
   b. Poly-acrylamide gel
   c. Software – FMBio
   d. Artifact documented by hand on gel scans
   e. In use 1997-2004 (2.1 added in 2000)
   f. Amplification was performed on 1.1 first, then depending on results amplification using 2.1 may be performed.
   g. Statistics – RMP, no mixture statistics

B. Identifiler (ID)
   a. One amplification reaction, 5 dyes, Total of 15 loci
   b. Loci: D8, D21, D7, CSF, D3, TH01, D13, D16, D2, D19, vWA, TPOX, D18, D5, FGA, and Amelogenin
   c. CE: 3100
   d. Software: GeneMapper
   e. In use 2004- 2013
   f. Input target – 1ng
   g. Statistics – RMP, CPE began in 2007

C. Identifiler Plus (ID+)
   a. One amplification reaction, 5 dyes, Total of 15 loci
   b. Loci: D8, D21, D7, CSF, D3, TH01, D13, D16, D2, D19, vWA, TPOX, D18, D5, FGA, and Amelogenin
   c. CE: 3130
   d. Software: GeneMapper
   e. In use 2013-2017
   f. EZ1 investigator kits used for extraction beginning January 2013, Quantifiler Duo, Qiagility liquid handlers used for plate setups
   g. Input target – 1ng
   h. Statistics – RMP using ArmedXpert (PopStats also on-line)

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