B7 Statistical Process Control in the Interpretation of DNA STR Profiles

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The goal of this presentation is to describe a data-driven method for the interpretation of low level DNA samples.

In 1992, the National Research Council recommended the use of the "ceiling principle" as a "conservative" estimate of the likelihood of a random match. This assumption was based on the limited availability of data, and by 1996 the National Research Council suggested that this "conservative" estimate was no longer necessary. Currently, many forensic DNA interpretational guidelines suggest that rfu cutoffs of 100 or 150 rfus, are a "conservative' cutoff estimate of what are callable DNA peaks. This "conservative" estimate is generally based on pre-casework validation studies of low-level DNA samples, but a continuous process may offer a better estimate.

Statistical process control offers a better and more data-driven approach for the estimation of the range of callable DNA peaks in a low level sample, rather than a pre-determined single number estimate. It is not scientifically reasonable to suggest a peak of 151 rfus is conclusively callable while a peak of 149 rfus is not without some continual basis for comparison. Statistical process control provides a reliable and accepted means of establishing an estimated range of rfu values for low-level DNA peaks, and a historical, data-driven, and continuous approach for interpreting low-level DNA peaks.

Background negative control sample data were collected, and meaningful noise levels were established. The variation ranges around the noise levels offer a degree of confidence around a recorded value, and suggest a range of values that can be used for the interpretation of 'real' low-level DNA peaks. Both positive and negative control samples were run with several sets of casework samples, and the SPC trends of data were monitored and used to adjust 'calls' for low-level samples. Thus, SPC may offer a continuous and data-driven process for the evaluation and interpretation of low-level DNA peaks.

DNA, Interpretation, Statistical Process Control

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