EVALUATION OF THE ExactID ANALYZE™ METHOD FOR ACCURATE AND RAPID TYPING OF SNP AND STR LOCI FROM SEQUENCING DATA

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The advent of affordable sequencing has launched the field of forensic genomics, which promises to greatly expand the range and informativeness of forensic genetic profiling. However, the data generated by sequencing methods is different in form and content from that generated in current fragment analysis methods, thereby requiring new data analysis tools. ExactID-based non-alignment signal processing achieves high stringency, fast analysis times and simple operation. The method achieves high specificity and sensitivity, processes 1 GB FASTQ files for SNP panels in ~15 sec. and STR panels in ~120 sec. Non-alignment signal processing achieves high stringency, and only two parameters are involved: one for analytical threshold (AT) and one for read abundance ratio (RAR). We illustrate how to format sequencing data to achieve a true S/N-based AT, and how to exploit sequence information when analyzing either SNP or STR panels for mixtures.