EVALUATION OF THE EXACTID® V2.0 METHOD FOR ACCURATE AND RAPID TYPING OF FORENSIC 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 fast analysis times and high stringency matching with intuitive, user-friendly operations. The method achieves high specificity and sensitivity, and processes 100 MB FASTQ files for SNP panels in ~10 sec. and STR panels in ~60 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 mixtures, including mixtures of mtDNA. ExactID v2.0 is agnostic to sequencer platforms and forensic kit panels, providing laboratories independence for method development and application. It provides the user with sequence information from the regions surrounding the forensic loci proper, including a check on concordance with fragment analysis due to microvariants.