THE POWER OF MASSIVELY PARALELL SEQUENCING FOR COMPLEX MIXTURE DECONVOLUTION AND OTHER FORENSIC APPLICATIONS

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With rapidly improving chemistries and decreasing cost, massively parallel Sequencing has incredible potential for forensic investigations. Sequencing Short Tandem Repeats (STRs) can overcome some of the limitations of genotyping by capillary electrophoresis and provides increased statistical significance with backwards compatibility to size based methodologies. Additionally, the information provided by sequencing can be invaluable for the deconvolution of complex DNA mixtures often obtained from forensic evidence. Under a United States Government funded effort, Bode Cellmark Forensics (Bode Cellmark) in collaboration with NexGen Forensics, LLC (NexGen) have developed a full solutions pipeline to allow for the easy data interpretation of Massively Parallel Sequencing data of forensic loci of interest, with the added functionality of deconvolution of complex DNA mixtures using commercially available and novel multiplexed chemistries. This pipeline not only includes laboratory processes, but also the development of a software algorithm and Graphical User Interface (GUI) that allows for the analysis of sequenced forensic Short Tandem Repeat (STR) markers from complex human DNA mixtures by exploiting variants found within the STR, and also from flanking regions. These sequence variants provide an advantage over traditional capillary electrophoresis technologies by adding statistical power to forensic likelihood ratios and paternity indices. Additionally, the solution provides a putative DNA profile from complex DNA mixtures to allow for easy database query and investigative lead generation.