GeneMapper™ Software v3.6.0

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Multi-locus genetic data consists of polymorphisms found at a set of different loci. These markers vary widely in terms of their specificity, ease of amplification and their information content. However, all these features contribute to make genotyping easy to perform, cheaper and reproducible. . Some examples of genetic data can be found in human forensics, e.g. paternity testing and human identity testing, in species that are hard to get or to keep sample, for example in ruminants, such as sheep, in which the living animals are particularly difficult to raise, or as part of a biodiversity project. . In species that are not easily observed in the wild, for example in endangered species, genetic data can provide species identification through a well-defined DNA sequence search, but the identification can only be achieved once a fully sequenced reference genome is available. . In humans, genetic data can be used in forensics, where it has been used for police investigations of serious crimes such as the investigation of bomb attacks. . The gold standard of forensic DNA typing is STRs, short tandem repeats. A tandem repeat is a direct or inverted repeat sequence of a simple sequence that is repeated in a tandem fashion. STRs consist of one or more repetitions of the same simple sequence, the tandem repeat region. Multiple STRs are then found dispersed throughout the genome. . Although STRs are polymorphic, the sequence of a given STR can be identified in one individual but not in another (specific), . These markers can be used for the identification of individuals as well as the determination of relationships between individuals and the detection of criminals . There are a number of reasons for developing genotyping multiple genetic data, including human forensics, species identification and biodiversity genotyping. . Due to the polymorphism of different loci, genotyping multiple loci provides additional information about the individual, which is not provided by the analyses of single loci. . There are many different approaches to typing multiple genetic loci, e.g. multiplex PCR, short tandem repeats (STRs), single nucleotide polymorphisms (SNPs), microsatellites, mitochondrial DNA, single-nucleotide polymorphisms (SNPs), hypervariable minisatellites, or variable number of tandem repeats (VNTRs) and minisatellites (barcodes) . Multiplex PCR is used in many species that are not

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