ABSTRACT
Computing LR by a kinship analysis algorithm for autosomal markers is straightforward and well defined. Such calculation provides a value for evidence given the prosecution versus the defense proposition. It is recommended and widely used in forensic, missing person and paternity. The forensic community has validated standalone software for calculating LR using trios and two biologically related family members. Software such as Familias[1], [2] and GeneMapper® (Life Technologies) is widely used to generate confidence values in a forensic context. In Locus Kinship application in combination to genetic algorithms, it was used in various research on kinship and forensic laboratories. We show that the standard calculations, including complex pedigree trees, mutations and null alleles can be used with current methods.

RESULTS

Figure 2. Statistical testing of LT kinship algorithm – Percent Error, in parenthesis number of tests

Table 1. Improvement over other market products

Table 2. Kinship Pedigrees.

Table 3. Kinship Input: Subset of HD Ion AmpliSeq™ Identity Panel – 43 Kari Kidd SNPs, Subset of CODIS STRs

Table 4. Input: Subset SNP Probability table

Table 5. Partial results from LT-Kinship

Figure 5. Performance of kinship algorithm for CE-STR data

INTRODUCTION
The LT-Kinship algorithm is similar to established kinship algorithms. It provides statistical basis for being referred to as a forensic kinship analysis algorithm. The LT-Kinship algorithm is known by its underlying LR (LR). Building on extensive literature and work by the forensic community, we have chosen to use Familias, MPKin and GeneMapper® as commercial software - Future Technology Inc. (FTI) for verification and validation of the kinship algorithm with STRs.

CONCLUSIONS
By testing simple trios, deficient trios (e.g. motherless) and more complex kinship relationships (5-generations of relatedness) for a wide variety of current market products using the same casework data, we have been able to demonstrate the accuracy and relative performance of the LT-Kinship algorithm. The results show that the LT-Kinship algorithm consistently produces LR that are well within the range of published literature.

REFERENCES

Databases:

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