DEVELOPMENT PROCESS VALIDATION FOR KINSHIP ANALYSIS ALGORITHM

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Computing likelihood ratio in kinship analysis 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 forensics, missing person and paternity. The forensics community has validated stand-alone software for calculating Likelihood ratio (LR) using trios and many biologically related family members. Software such as Familias and MPKin are used regularly for such calculations. Because these implementations are standalone, transcription errors can occur on transferring data from data collection, table input and result storage, in addition it can also be time consuming.

Life Technologies (LT) has incorporated its version of a kinship algorithm, based on ES algorithm, to data collection and storage for ease of use and reliability of results, therefore avoiding human transcription errors. This presentation will encompass the steps taken by our team to validate our kinship analysis algorithm given the available methods, data and external collaborators. Building on previous literature, we have used NIST, CEPH and real data from collaborators to compare results of the kinship algorithm to those currently used in the paternity and forensics laboratories. We show that the standard calculations, including complex pedigree trees, mutations and rare alleles concur with currently used methods.

Through this work we have established the LT-kinship algorithm, a more flexible implementation with state-of-the-art models, as accurate. We have further tested the algorithm with SNP data, showing that for a small number of SNPs, the algorithm produces Likelihood ratio (LR) values, which may be a option once expert data and tables become available.