Development Process Validation for Kinship Analysis Algorithm

Carolina Dallet, Sharada Vijaychander, Jianye Ge, Aniketan Swami, Gloria Lam, Narasimhan Rajagopalan, Allain Minn
Thermo Fisher Scientific, 180 Oyster Point Boulevard, South San Francisco, CA, USA, 94080

ABSTRACT

Our systems have developed a kinship analysis algorithm based on the ES algorithm. This presentation will encompass the steps taken by our team to validate the Life Technologies kinship analysis algorithm (LT kinship algorithm). The validation process included the following methods, data, and external sources: NIST CSPA (Comparative Statistical Performance Analysis), statistical data sets, and published literature. We implemented a 2-phase and 1 step mutation model, and tested our algorithm with various scenarios, using the LT kinship algorithm to compare our results to real data. We also compared the results of the LT kinship algorithm to other commercial software (MPKin, used extensively by the FBI) for verification and validation.

INTRODUCTION

Comparing LT to a kinship analysis algorithm is a standard method for validation purposes. It provides statistical basis for kinship analysis confidence, and offers a rigorous method for comparison. Building on extensive literature and work by the forensic community, we have chosen to use NIST CSPA, MPKin, and Liu in our software development and validation of the kinship algorithms.

METHOD

We have shown that the algorithm also works for simple and complex Family Kinship analysis. We have obtained STR and SNP genotypes from 4 related families for Life Technologies LT kinship algorithm calculations. Our aim was to compare the LT kinship for higher discriminative power. For STRs, the...