STREAMLINED STR ANALYSIS AND RELATIONSHIP TESTING STATISTICS FOR SINGLE SOURCE (MISSING PERSONS, PATERNITY) AND MIXTURE PROFILES USING GENEMARKER® HID HUMAN IDENTITY SOFTWARE

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In addition to determining STR profiles for forensic DNA analysis, it is often necessary to search a database and perform statistical analyses to determine match likelihood or familial relationships in cases of Missing Persons, Mass Disaster, Paternity and Crime Scene DNA (mixture samples). Often, profiles are determined in one software package and exported, followed by import into a separate statistical analysis software package. GeneMarker HID human identity software contains a streamlined analysis workflow to determine STR profiles; linked to database searching, relationship testing, paternity analysis, and mixture analysis applications. Relationship testing statistics include using Identity by Descent (IBD) and classical paternity trio or motherless case paternity index calculations (following the recommendations of AABB Standards for Relationship Testing Laboratories, Appendix 8).

GeneMarker HID is an expert system, compatible with all human identification chemistries and major capillary electrophoresis file types. The results of genotyping, relationship testing and database searching for 10 single source cases amplified with PowerPlex® 16 and five different mixture samples amplified with Identifiler® and PowerPlex® 16 will be presented. Calculations performed and exported in customizable reports include: Likelihood ratios (LR), Probability of exclusion/inclusion (CPE/CPI), Random Man Not Excluded (RMNE), and Paternity Index (PI).

References:
1. Brenner, C. Symbolic kinship program, Genetics 145(1997):535-542.
2. Phillips, N., R. Roby, J. Planz, A. Eisenberg. The relationship testing application of GeneMarker HID: automated pedigree and kinship analysis with database searching capabilities. In: 19th Int. Symp. On Human Identification. 2008, Hollywood, CA.
3. Recommendations for Relationship Testing Laboratories, Appendix 8, AABB, 9th ed. 2009.
4. SWGDAM Interpretation Guidelines for Autosomal STR Typing, 2010.