

Abstract 58

STR ANALYSIS AND DATABASE SEARCHING FOR PATERNITY, KINSHIP, MISSING PERSONS, AND MASS DISASTER APPLICATIONS WITH GENEMARKER HID

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There are many laboratories in the United States and across the world using STR genotyping techniques to identify individuals and their biological relationships; however, there are few software programs available to perform the necessary calculations. SoftGenetics' GeneMarker HID, with its new Paternity module, integrates STR analysis, relationship calculations, and database searching capabilities into one software program. GeneMarker HID applies the recommended relationship formulas from AABB's Guidance for Standards for Relationship Testing Laboratories 7th Edition ©2006 (RT Standards). The Paternity Index (PI), Posterior Probability (W), Random Men Not Excluded (RMNE), and frequency estimate calculations are used to rank individuals in a database. The person with the highest rank is the most probable match for the missing person in the family pedigree tree. In addition to simple trio relationships of mother-father-child, the situations of a motherless case, kinship, and one-step/two-step mutations can be addressed. This program will be useful for many applications including paternity and kinship relationships, missing persons, and mass disaster scenarios.