

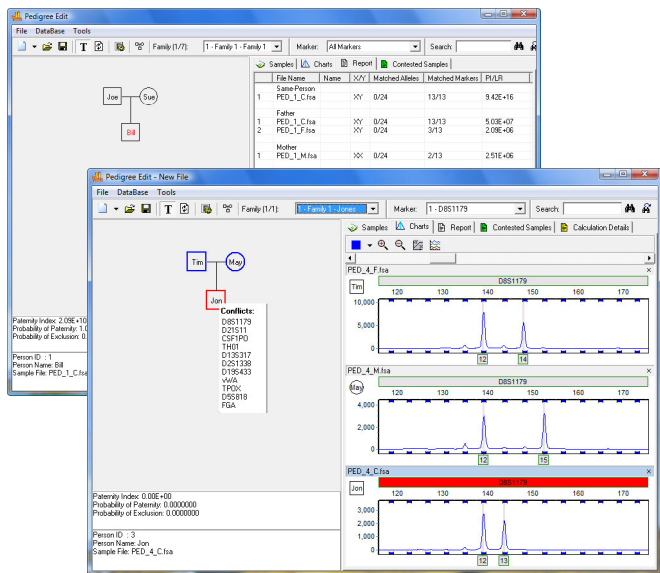
# STR Analysis and Database Searching for Paternity, Kinship, Missing Persons, and Mass Disaster Applications with GeneMarker<sup>®</sup> HID

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## Relationship Determination

A Relationship Testing module with databasing capabilities is integrated directly into the main GeneMarkerHID program. Visually create a pedigree tree or use file naming conventions to automatically generate tree diagrams for multiple families.

Use the “Find Family” and “Find Individual” functions to search the database for the missing person’s own profile, Father, Mother, Siblings, and Half-Siblings based on proven Likelihood Ratio, Paternity and Kinship Index calculations.



## References

- Butler, J. M. (2001) Forensic DNA Typing: Biology and Technology behind STR Markers. American Association of Blood Banks (2006) Guidance for Standards for Relationship Testing Laboratories.
- Brenner, C. H. (2007) DNA-View User's Manual.
- Budowle B, Shea B, Niezgoda S, Chakraborty R. CODIS STR loci data from 41 sample populations. J Forensic Sci 2001;46:453-489.

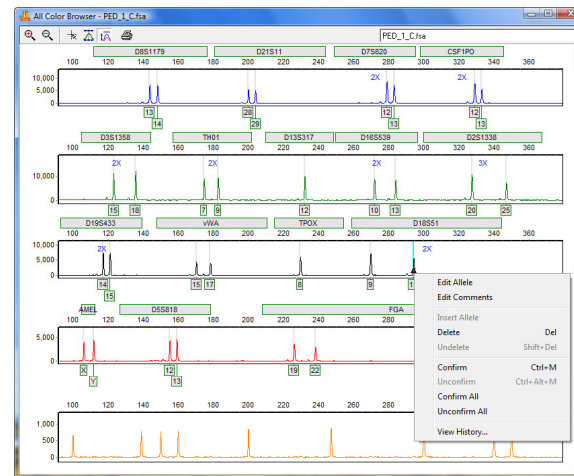
## Abstract

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' GeneMarkerHID, with its new Paternity module, integrates STR analysis, relationship calculations, and database searching capabilities into one software program.

GeneMarkerHID applies the recommended relationship formulas from AABB's Guidance for Standards for Relationship Testing Laboratories 7<sup>th</sup> 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.

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.

## Initial STR Analysis



Sizing and peak recognition performed with GeneMarkerHID's unique allele calling algorithms results in less than 1% false positive calls. Allele editing is simple with add, delete and modify options available directly in the electropherograms. Borland C++ Windows-based programming makes navigation intuitive.

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