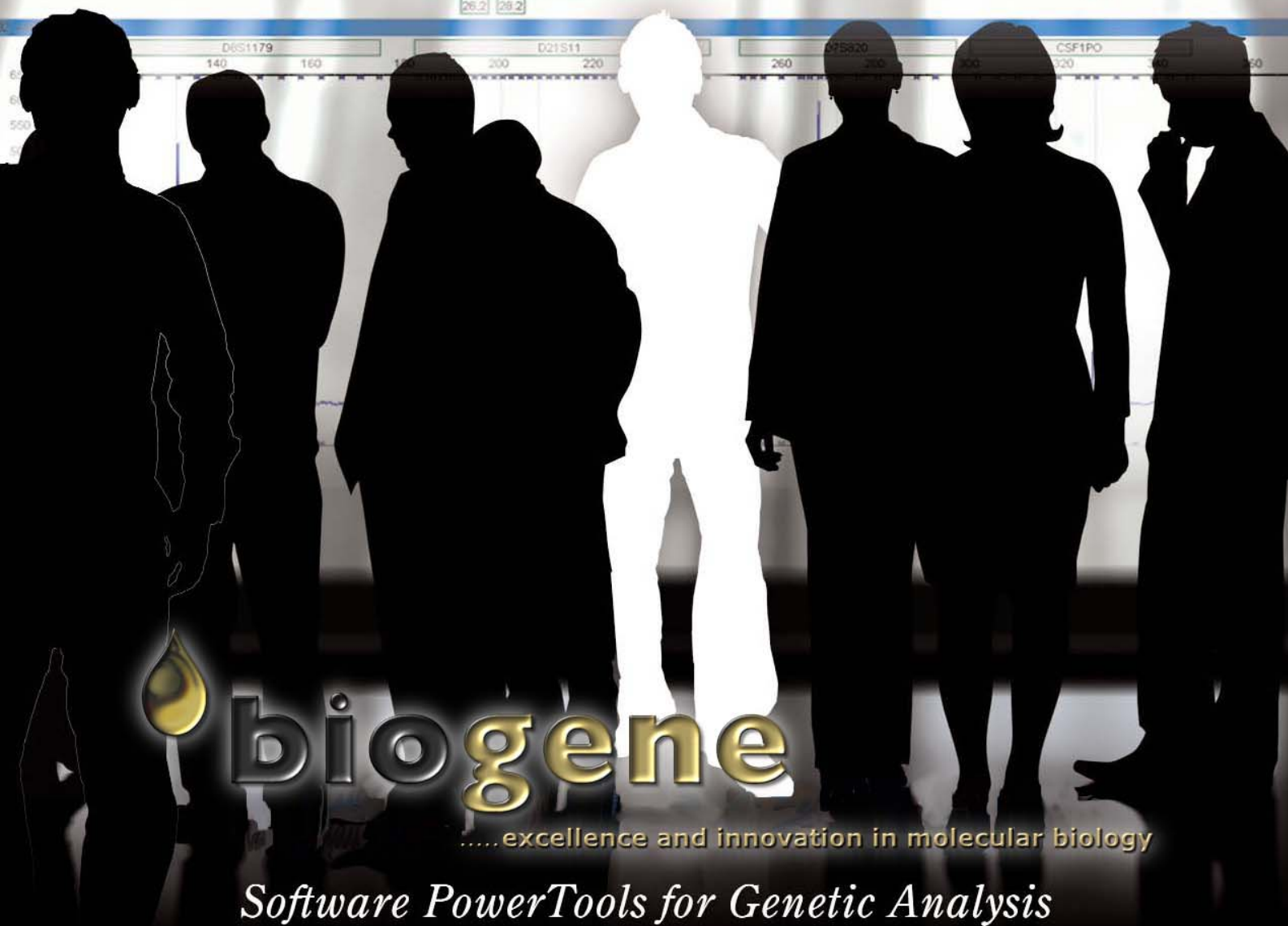
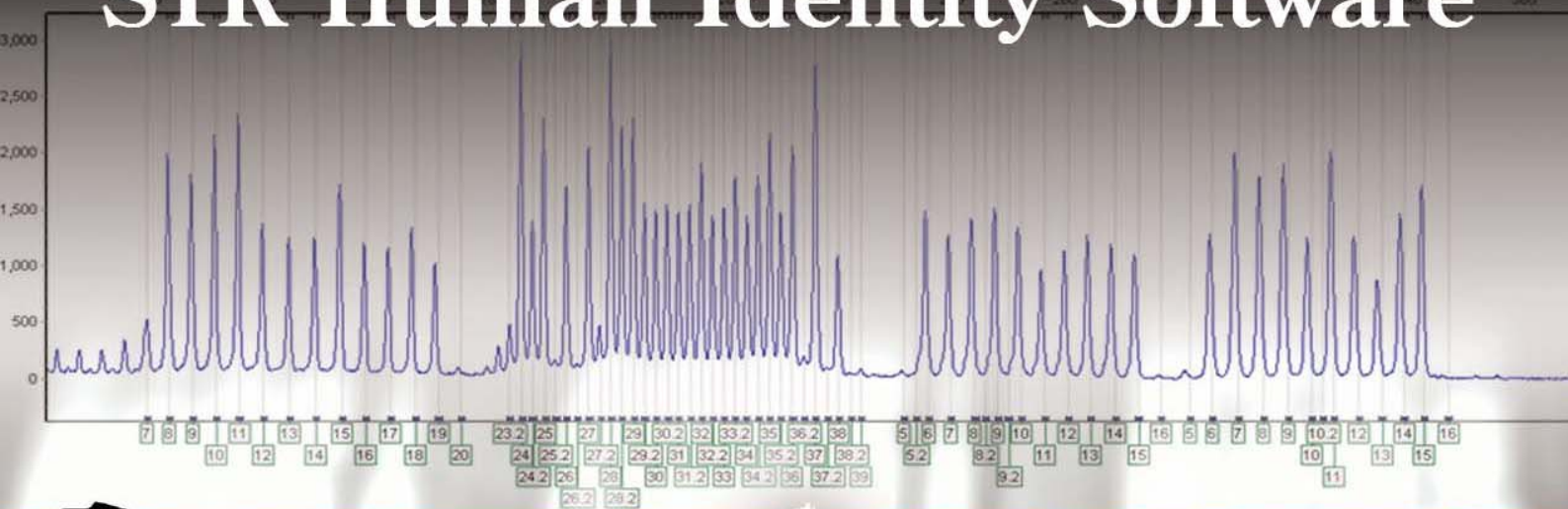


GeneMarker® HID STR Human Identity Software



GeneMarker[®] HID

STR Human Identity Software

Developed in collaboration with Mitchell Holland, Ph.D.,
Associate Director of The Pennsylvania State University's Forensic Science Program.

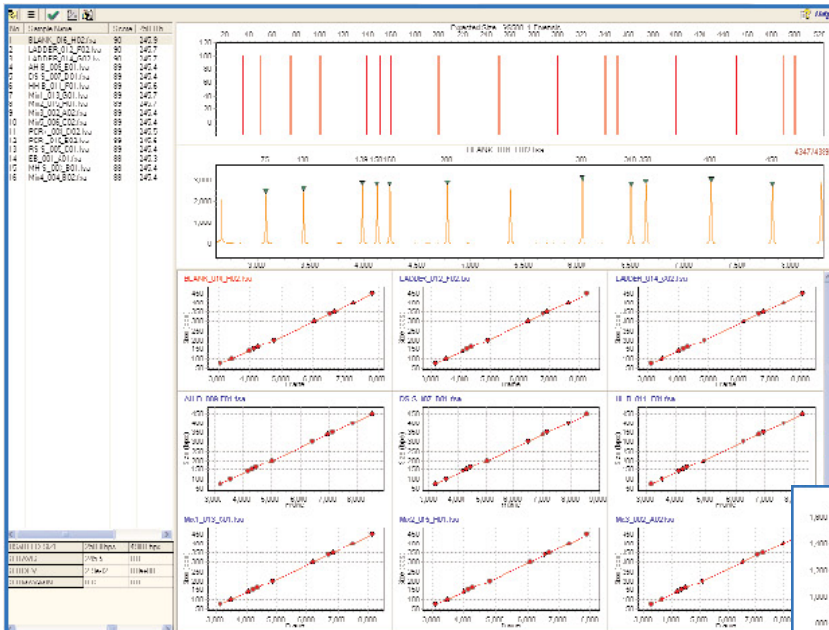
GeneMarker[®] HID is an excellent choice for forensic STR analysis. The software can be employed as a “biologist friendly” replacement for GeneScan[®]/GenoTyper[®] or an easy-to-use alternative to GeneMapper[®] ID.

GeneMarker[®] HID uses advanced Windows[®] technology that is intuitive, easy-to-learn and eliminates extraneous mouse clicks. For example, the software incorporates an automatic default to your data file folder, eliminating the frustration of sorting through several file trees.

Accurate

Advantages of GeneMarker HID are its ease-of-use, enhanced accuracy, analysis speed and robustness. GeneMarker HID employs new, unique sizing algorithms and pattern recognition technology to provide unparalleled accuracy up to 99%. Pattern recognition technology studies peak morphology automatically adjusting for instrument spikes, colour pull-up or bleed through, noisy data, saturated peaks, and stutter peaks.

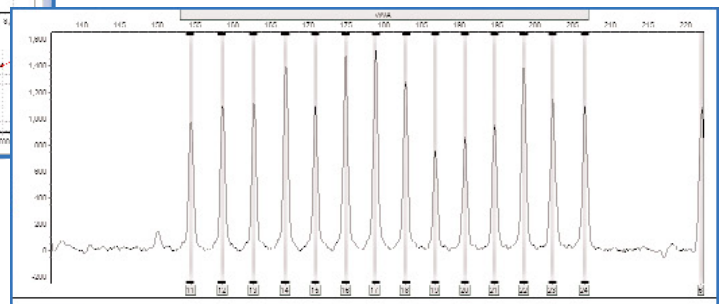
The majority of functions have been completely automated, using a “smart” software approach to eliminate the need for constant analyst intervention, and to improve analysis-to-analysis consistency.



The GeneMarker HID quality assessment tool permits quick visual inspection of sizing quality for each profile. Improperly sized lanes can be quickly marked for re-run or disabled from analysis calculations.

GeneMarker HID features:

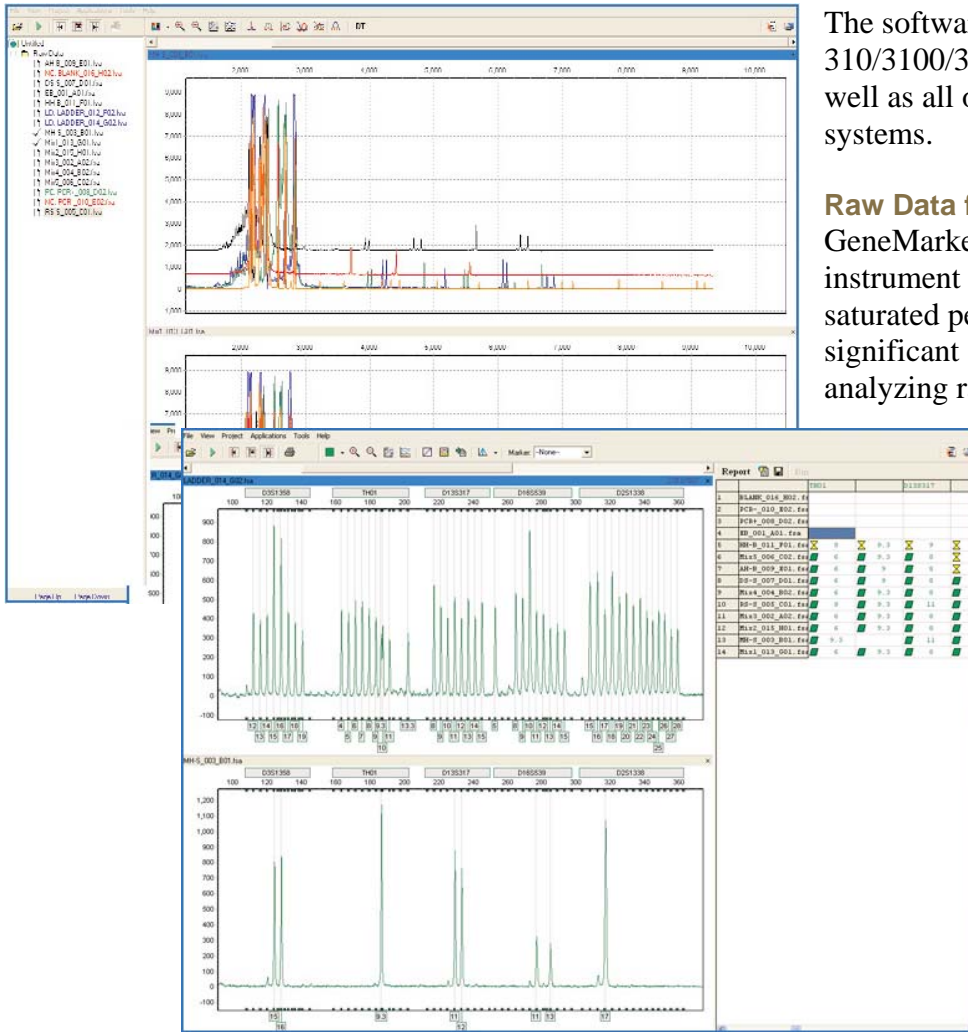
- Enhanced Accuracy
- Rapid Data Processing
- Compatibility with ABI 310/3100/3130
- Embedded ABI and Promega Kit Panels
- RFU Intensity AutoRanging
- Distinct Flag of OL Alleles
- Customizable Panels and Size Standards
- Exportable CODIS and LIMS Reports
- Bulk Printing Capabilities



GeneMarker's graphics indicate bin range by blue brackets, peak center by vertical grey bars and automatically adjust the Y-axis to match peak RFU values.

Rapid Data Processing, Instrument Correction and Compatibility

GeneMarker HID performs STR analysis in batches of up to 1,000 profiles in seconds, and is compatible with all STR Chemistries including Identifiler[®], SGM Plus[®] and PowerPlex16[®].



The software accepts output from ABI PRISM[®] 310/3100/3130 Genetic Analyzer instruments, as well as all other brands of capillary electrophoresis systems.

Raw Data from ABI Genetic Analyzer System: GeneMarker HID automatically adjusts for instrument spike, colour pullup, noisy data, saturated peaks, and stutter peaks— saving significant analysis time and cost, efficiently analyzing raw STR data within seconds. In addition,

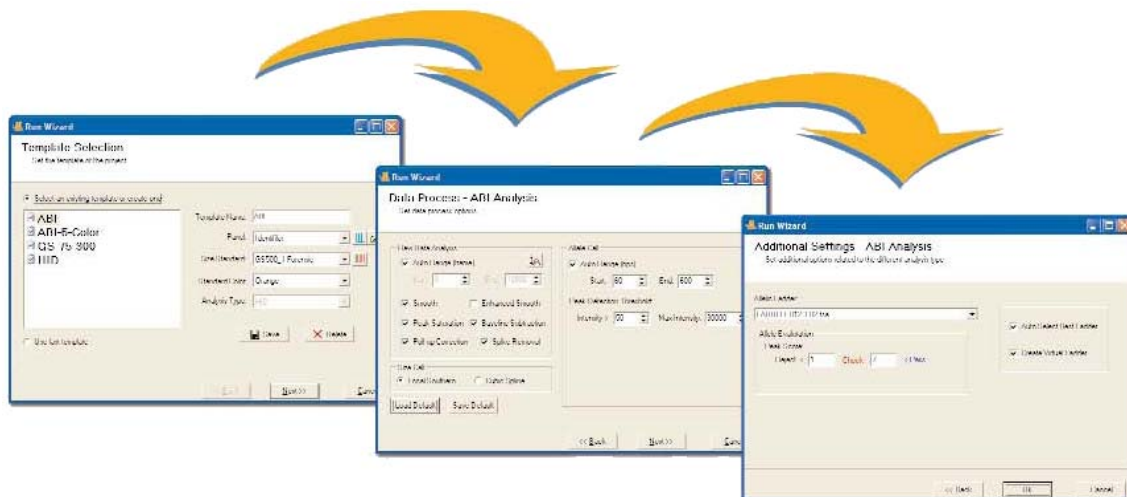
GeneMarker HID allows the user to conduct a lane-by-lane overview of unprocessed raw data, permitting a quick quality control assessment of your profiles.

Processed Profile using Identifiler chemistry:

GeneMarker HID processes up to 1,000 profiles per batch in approximately 2 minutes. Stutter filters can be adjusted by allele; software creates “phantom” bins, and provides “colour-coded” quality assessment of each profile, as indicated by yellow and green indicators in the allele report.

Simple, Easy-To-Use Operation and Analysis Parameter Setting

GeneMarker HID’s Run Wizard utilizes three simple dialogue boxes to set analysis parameters. Once optimized the parameters can be saved for future analysis, utilizing its single click, AutoRun feature.



Setting analysis parameters is accomplished through 3 easy-to-use dialogue boxes. Once parameters have been set, they can be saved for future analysis, allowing “single click” operation of the AutoRun feature.

