

Dedicated to the Forensic Community...

GeneMarker® HID, NDIS approved Expert STR Human Identity System

GeneMarker® HTS, Forensic Analysis of Massively Parallel Sequencer Reads (MPS)

MaSTR™, Enlightened Probabilistic Mixture Analysis Software

Mitotyping Technologies, the Clear Choice in Forensic Mitochondrial Analysis

SoftGenetics strives to be one of your crucial suppliers of analysis software for STR Human Identification from capillary sequencers, mtDNA and STR Analysis of NGS reads, and the most advanced Probabilistic Mixture Analysis software with our Enlightened MaSTR™ program. Additionally, with our laboratory division Mitotyping Technologies, the clear choice in forensic mitochondrial DNA analysis.

Analyze mtDNA & STR/Y-STR's Simultaneously from MPS reads

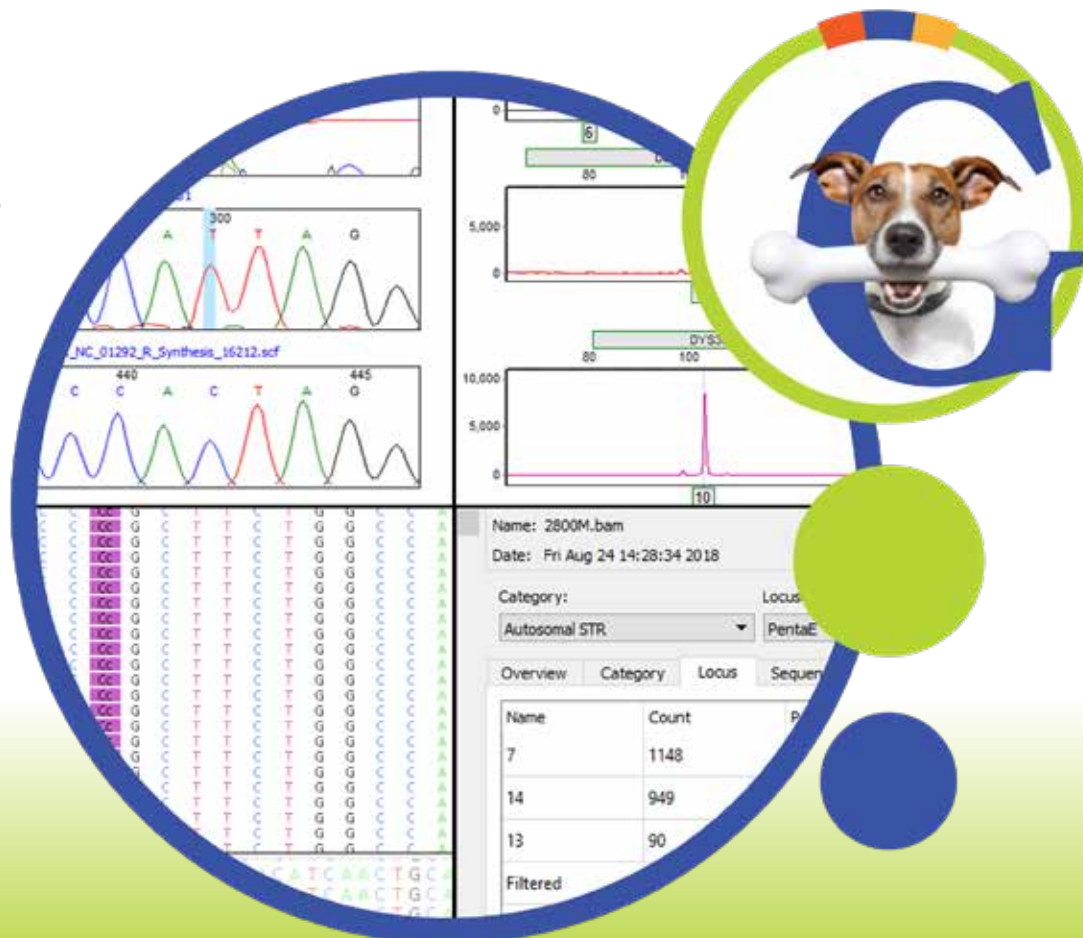
Validated Software in an Easy-To-Use Windows Interface which is compatible with Major Chemistries and Platforms. Includes Comprehensive Reporting Options, as well as full Audit Trail and Administrative /User control.

STR Analysis Features:

- Autosomal & Y-STRs
- Forensic Nomenclature
- Genotype & Iso-Aallele Reporting
- Meets the SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic Laboratories to Address Next Generation Sequencing

Simultaneous mtDNA Analysis Features:

- Whole Genome or HV1/HV2 & Control Region Analysis
- Major and Minor Variant Reporting (SNPs, Indels)
- Unique mtDNA Alignment Technologies:
 - Motif
 - Consensus
- Forensic Nomenclature
- Easily Uploads to EMPOP



MaSTR™ Enlightened Probabilistic Mixture Analysis of STR Profiles software

MaSTR software features a rapid and transparent approach to Probabilistic Mixture Analysis which utilizes your forensic acumen in an easy-to-use Windows® environment for research, validation and casework applications. Server based MaSTR software is very cost effective, includes two simultaneous user licenses, and automatic queuing of multiple analyses.

MaSTR Software features:

- **Transparency, Complete Documentation including Analysis Code to users**

MaSTR software was designed following *The Organization of Scientific Area Committees for Forensic Science (OSAC) and Scientific Working Group on DNA Analysis Methods (SWGDM)* probabilistic guidelines and published probabilistic approaches (Taylor, *et al.* and Bright *et al.*). The analysis code is available, on a confidential basis, with purchase of the software.

- **Validated**

Contact info@softgenetics.com for a copy of the validation study performed by Dr. Michael Adamowicz. Dr. Adamowicz is currently Director of the Forensic Science program at the University of Nebraska and was previously a forensic science program coordinator at the University of New Haven, Henry C. Lee College of Criminal Justice & Forensic Sciences and a member of the SWGDAM Mixture Committee developing / writing mixture analysis guidelines.

- **Lower Acquisition & Operational Costs**

Single server-based program has an exceptional capacity to meet most forensic laboratory needs. The initial license includes two concurrent users. Low cost, additional clients allows each analyst station to have access to MaSTR software.

- **Administration Tools and Modes of Operation**

MaSTR software requires the user to log in to access the software functions. This requirement allows the laboratory to password protect their individual models and mixture analysis results.

- **Flexible Capacity**

Unique System Design -- MaSTR probabilistic genotyping software makes efficient use of the lab computer resources. With Server-client based technology, processing is done on the server and multiple clients can review results and send new jobs. Each user sets up and sends analysis jobs from *existing* client computers. Expedited cases can be moved to the front of the queue by laboratory management.

- **Technology**

MaSTR software's unique, easy-to-use interface enables analysts to create and submit mixture analysis jobs in minutes. The server-client configuration provides flexibility and lowers costs by performing the analyses on a dedicated computer, freeing up the analyst's time and computer for other tasks.

- **Customizable Reporting**

Each report contains a cover page with the institution name and logo, a table of contents and the fields selected by the analyst.



Mitotyping Technologies, the **clear choice** in forensic mitochondrial analysis

We are Single-minded: Mitotyping Technologies is one of the oldest and most experienced group of scientists devoted to this forensic and anthropological DNA specialty. We have worked on criminal, civil, exoneration and federal cases in all 50 states and numerous foreign countries. We have testified over 200 times in mtDNA cases for both the prosecution and defense teams.

Ancient DNA Methodology for Highly Degraded evidence:

Mitochondrial DNA Analysis of shed hairs and hair fragments is our specialty. We have a >95% success rate developing profiles from hairs of all ages and sizes. For highly degraded samples, we offer an “ancient DNA” approach. Each sample is analyzed individually to account for its specific analytical needs.

Considerations in selecting a mtDNA Laboratory:

Is Lab fully accredited for mtDNA analysis?
(We have been since 2001)

What is their success rate?
(Ours is >95% for hair evidence, 90% overall)

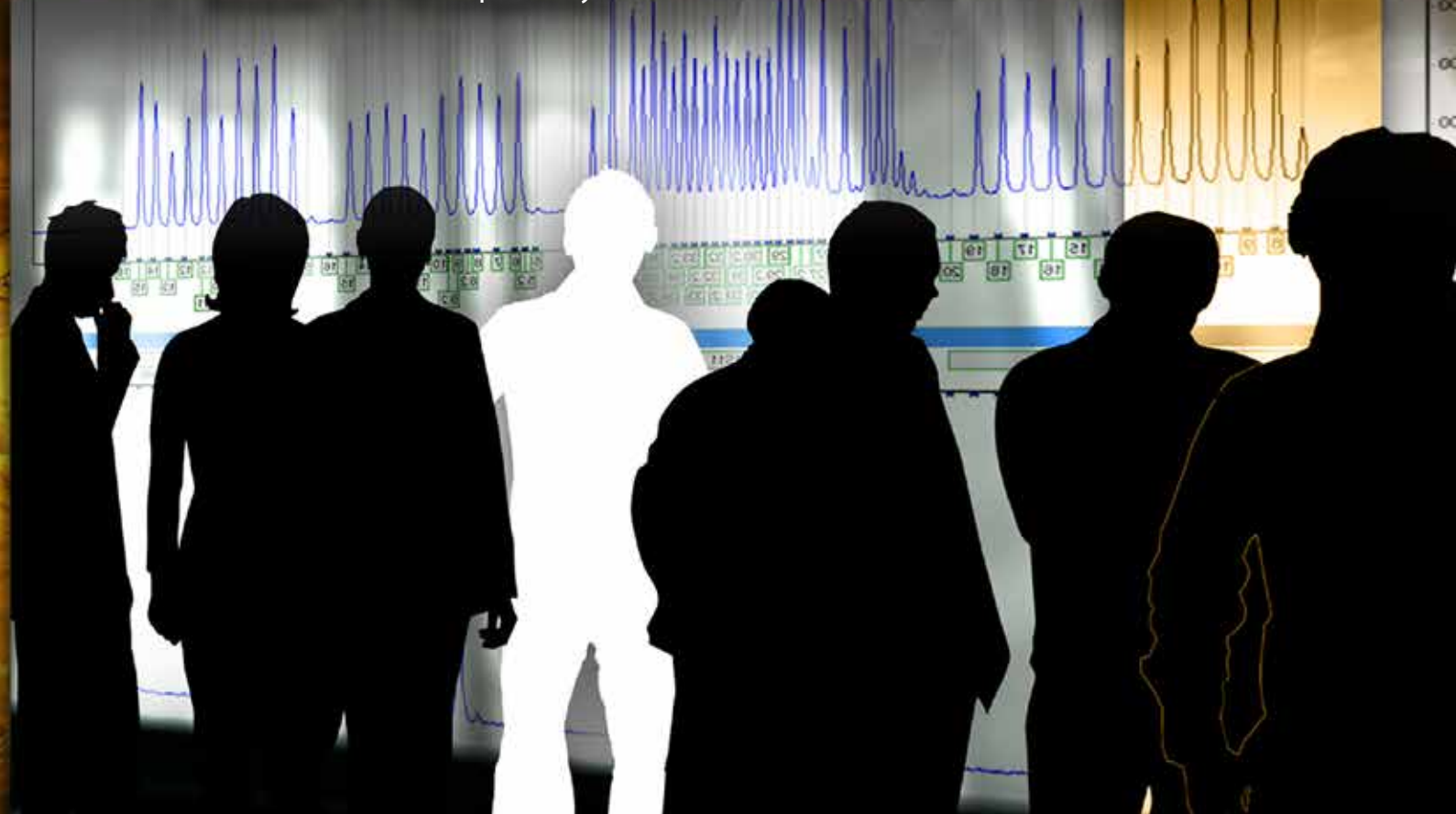
How much experience do they have?
(Our Senior Scientist has over 19 years)

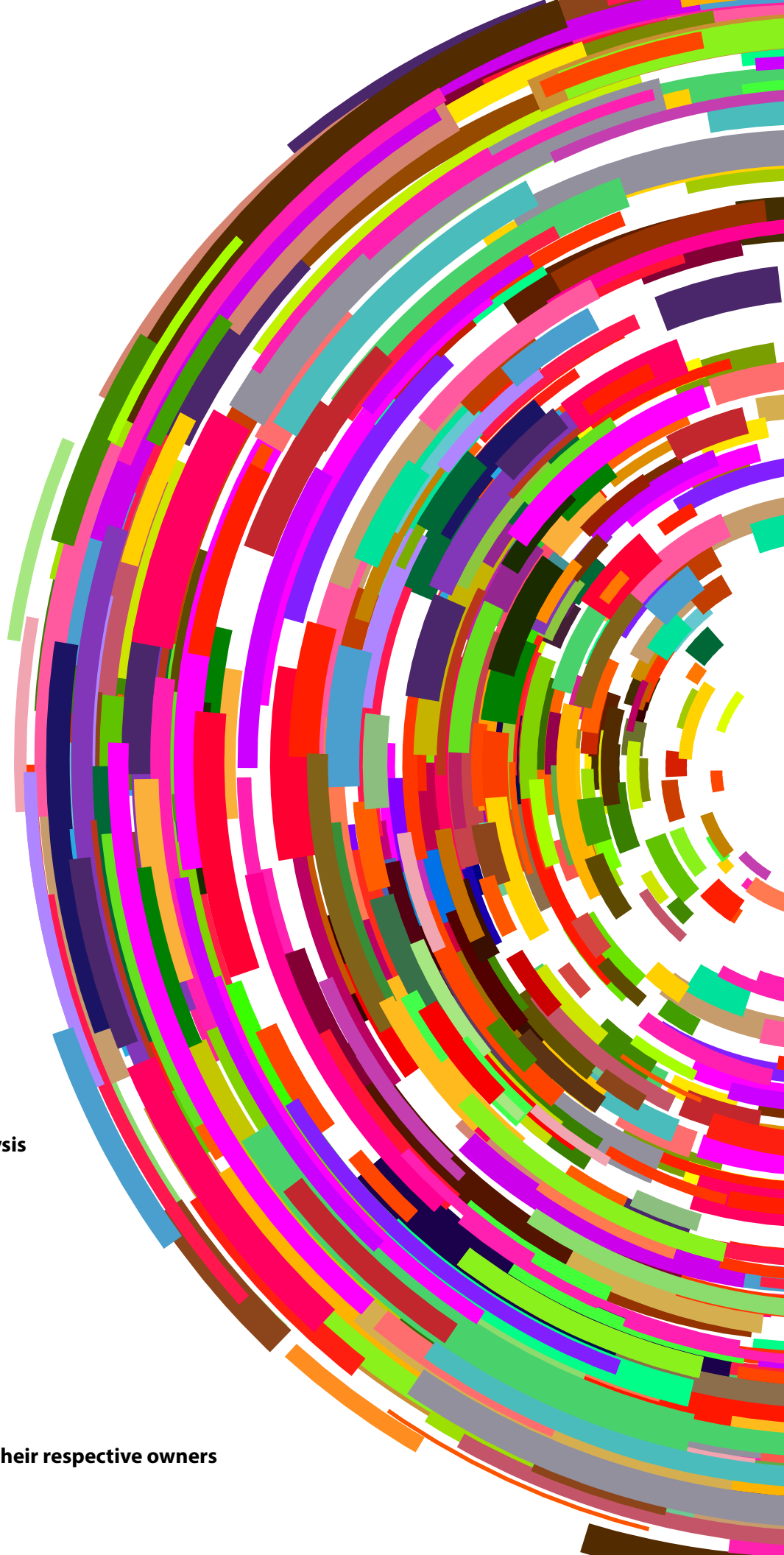
Do they batch or process evidence individually?
(Each sample is processed individually, we never batch process)

Is expedited service available?
(We will provide expedited services with the same precision and accuracy as provided with normal casework. Please contact us for more information.)



- NDIS Approved Expert System
- 4 - 6 Dye Capability
- Fast, Accurate, and User-friendly
 - Documented time savings of up to 40%
 - Up to 70% less analyst intervention
- High Capacity
- User Management with Audit Trail
- Validation Assistance - Automated Analytical Threshold Determination
 - Linked Applications
 - CODIS Reporting
 - Mixture Analysis – two-person deconvolution and likelihood ratios
- Relationship Testing /Kinship
 - Paternity (per AABB Standards)
 - Database Search Tools and Likelihood Ratio Results:
 - Missing Persons Search
 - Mass Disasters
 - State DNA Index System (SDIS) Search
 - Contamination check – percent same genotype:
 - Autosomal & Y-STR Searches
 - Sample – to – Sample in same project
 - Sample – to – database comparison
- Compatible with all Major CE and Rapid Systems
- Windows® 7 – 10 compatibility





Software *PowerTools* for Forensic Analysis

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