MaSTR™

Enlightened Probabilistic Mixture Analysis Software

SOFTGENETICS®

Software PowerTools for Forensic Analysis

- Transparency
- Flexible Capacity
- Admin Tools
- Technology
- Training and Support
- Validated
- Low Acquisition Cost

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Software *PowerTools* for Forensic Analysis
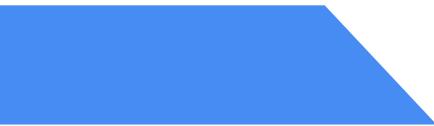
MaSTR™

Probabilistic Mixture Analysis of STR Profiles

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.

Transparency

Black Box

Gray Box

Transparent Box

MaSTR™ software provides users with:
- Complete documentation
- Analysis code

Probabilistic Software TA

Probabilistic Software SM

MaSTR Software The Clear Choice

MaSTR software was designed following *The Organization of Scientific Area Committees for Forensic Science (OSAC) and Scientific Working Group on DNA Analysis Methods (SWGDAM)* 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. SoftGenetics has a long-standing commitment to providing support to laboratories during software evaluation, validation and training to bring our software tools online in the laboratory.

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 faculty member and 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.

Contact info@softgenetics.com to arrange a trial version and introductory training for your laboratory. SoftGenetics will provide the validation data files to laboratories that wish to use it in their initial evaluation of a MaSTR software trial. Reports of additional independent evaluations from **Dr. Mitchell Holland**, Associate Professor of Biochemistry & Molecular Biology, Pennsylvania State University and **Professor Kelly Knight**, Assistant Professor Forensic Science Program, George Mason University will be available upon completion.

Low Acquisition and Running Costs

Single server-based program has an exceptional capacity to meet most forensic laboratory needs. Low cost, additional client users allows each analyst station to have access to MaSTR software. The initial license includes two concurrent users; additional low-cost licenses are available on request.

Administration Tools and Modes of Operation

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

1. **Admin**
   - Administrative tools– no data analysis
   - Assigning user name/password to individuals to log in to the software
   - Providing users with the appropriate access rights and user group access
2. **Demo/Training**
   - Guided walk-through of the software with pop-up boxes describing each step of setting up an analysis to reviewing results and saving reports
   - No password required, open access to learn MaSTR software
3. **Research/Validation**
   - Tools for validation teams to establish laboratory SOPs for casework and R&D scientists to apply their forensic expertise to advance models for complex mixture data analysis
4. **Casework**
   - Models locked in after validation

Casework and R&D

- Password protected
- User group access rights
- Flexible Reporting
- Audit Trail

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 (Figure 1). 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. The high-speed server processes data from the queued jobs submitted by client computers. The design is flexible – labs with a lower caseload may opt to install server/database and client on the same desk top computer.

1. The Database
Used to manage the job queue, store analysis results, and store important information (Panels, Models, Protocol Sets, etc).

2. The Server
Runs the analysis and communicates with the client to provide results.

3. The Client
One or more clients may connect to the server to submit jobs and review results.
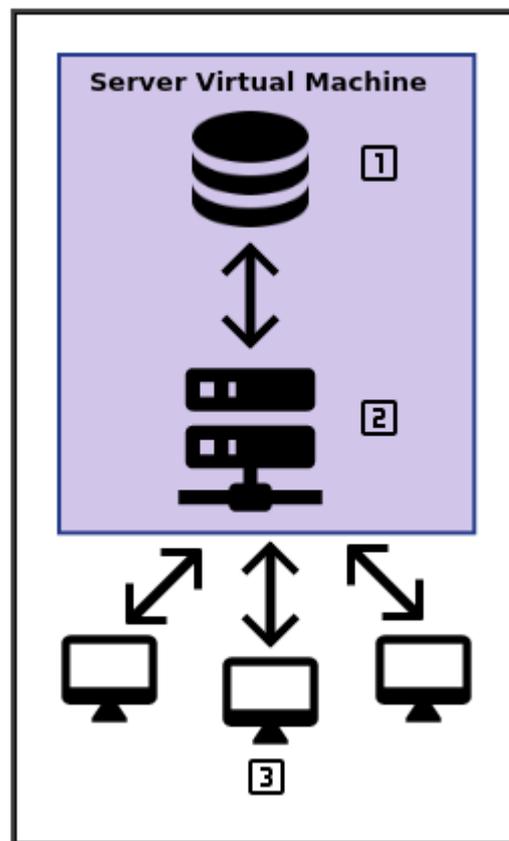

Figure 1: The software is structured into three parts, but the database (1) and server (2) are both contained within the Server virtual machine. Clients (3) are individual work stations.

High Speed with minimum computer specifications

# Contributors	Approx. mixture ratio	Run time for 2 analysis jobs (simultaneously), 4 cores	# Iterations (# of attempted steps)	# of Chains (run the sampling many times with different starting values)
2	45:55	18 min	20k	10
2	25:75	17 min	20k	10
3	30:40:30	25-26 min	30k	10
3	65:30:5	25-26 min	30k	10
4	15:25:30:30	37 min	40k	10
4	40:35:15:10	36 min	40k	10
5	50:15:15:10:10	100 min	50k	10

Table 1: Provides examples of analysis times for simple to complex mixtures; processing two jobs at a time on a server with the minimum specifications.
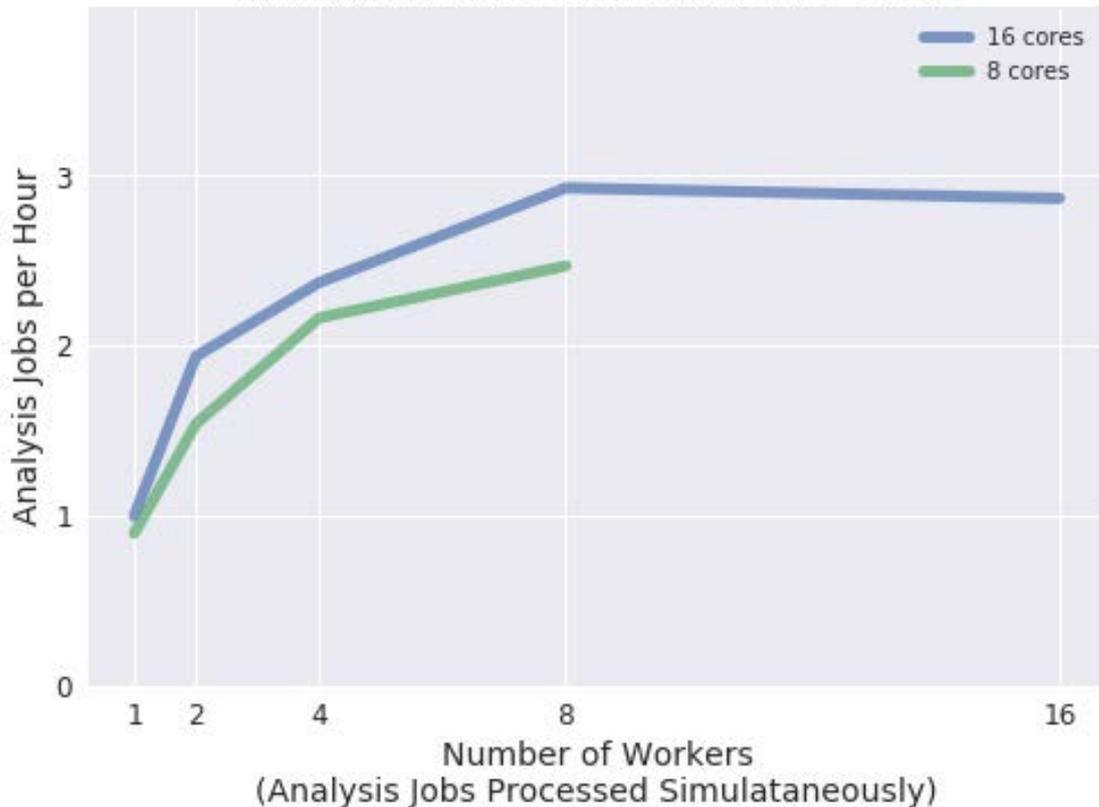
Figure 2: The capacity of MaSTR software can easily be increased with your computer hardware. The number of cores increases the capacity, not the speed.

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.

- Provides a framework for growth:
    - MaSTR software easily adapts future chemistries by importing new or updated panels (Figure 3)
    - Upgrade statistical approach without changing software version
- Utilizes the laboratory's unique data set to "train" the software (Figure 4)
- After validation, lock in models for casework

Models for the current statistical approach are preloaded in MaSTR software; statistical advances will be included with software updates. Researchers can easily experiment with new model variables and submit to the peer reviewed process for publication and advancement of forensic probabilistic analysis.

Interface

Drop-down menus enable analysts to quickly submit analysis jobs using validated protocols:

1. For Casework: Follow the lab's validated workflow. Select the appropriate protocol set, allele frequency, analysis model, co-ancestry approach and coefficient. Name the job and enter any comments. Designate the number of contributors and import a .txt file of the mixture sample allele calls and peak heights, any known contributor genotypes and genotypes to be evaluated as potential contributors to the mixture. (Figure 5)

2. For Research/Development: easily set up multiple runs to test and validate newly developed models or chemistries – no need to update the software when new chemistries are introduced. (Figure 6)

Flexibility

Easy import of new panels, allele frequencies to be used in analysis, and staff profiles to an elimination database. MaSTR software automatically checks the project's results with the database to flag potential contamination.
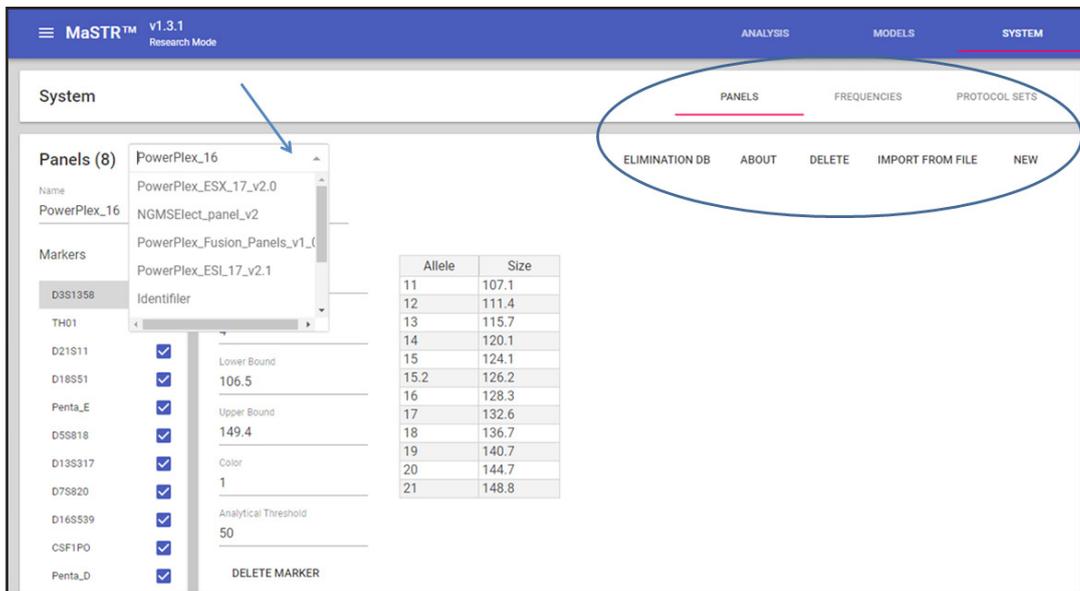

Figure 3: Simple, drop-down menus enable labs to update panels with new loci, population allele frequencies, and staff profiles to the elimination database.

Customize with a Protocol Data Set -- giving MaSTR software context to evaluate mixtures produced following the laboratory SOP
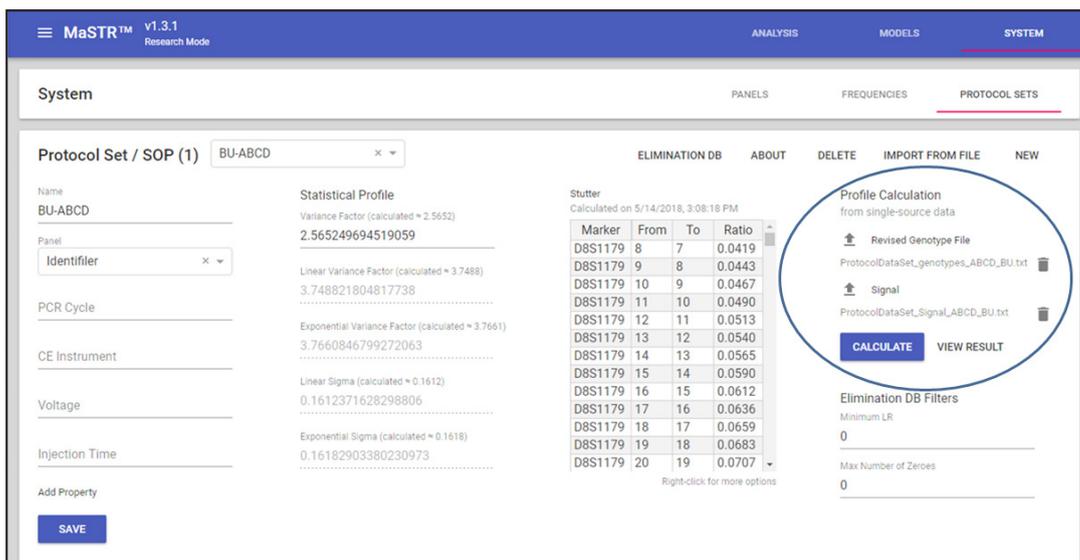
Figure 4: Protocol data sets – replicates of single source dilutions produced following lab SOP enable MaSTR software to calculate:
1. Expected peak height variation at different RFU (statistical profile).
2. Variation from typical degradation of signal due to lower amount of amplified product in higher mw loci.
3. Allelic stutter percentages.

Figure 5: *Casework analyses are easily submitted using the dropdown menu to select the validated:*

• *Protocol Set, Population Allele Frequency and Model*

• *Select the appropriate Coancestry adjustment (no adjustment to assume Hardy Weinberg equilibrium, NRCII Recommendation 4.1 or NRCII Recommendation 4.2.*

• *Enter the appropriate theta value if a coancestry adjustment is selected.*

• *Name the job and enter any comments*

• *Specify the number of contributors*

• *Select the mixture .txt file (containing all called peaks and peak heights), .txt file of person of interest genotype(s), any known contributor genotype .txt files*

Research/Development Capabilities

Figure 6: *The easy-to-use interface provides tools that allow forensic scientists to utilize their expertise without scripting. Researchers can easily experiment with new model variables and submit to the peer reviewed process for publication and advancement of forensic probabilistic analysis.*

Customized Reporting

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

PDF and Print reporting

Cover page contains:
- Laboratory Logo
- Laboratory Name
- Name of the project
- Job overview

Followed by Table of Contents

Your Logo
Your Institution's Name
Results of RapeCase_twoAccused
Generated by MaSTR™

Protocol Set	**Created By**
BU_Identifiler	researcher
Panel	**ID**
Identifiler	5b6ae2ae1d58ce001c105fdb
Frequency	**Queue Time**
Hill_et_al (2013)	8/8/2018, 12:31:42 PM
Model	**Start Time**
Standard_10k_8chains	8/8/2018, 12:31:47 PM
Coancestry Adjustment	**End Time**
NRCII Recommendation 4.1	8/8/2018, 12:48:50 PM
Coancestry Value	**Duration**
0.01	17 minutes, 3 seconds
Name	**Memory Usage**
RapeCase_twoAccused	179 MB

Comments

Contributors
2

Signal
ID_2_SAB_NG0.5_R1,1_A1_V1.txt

Reference
B_ind_genotype.txt

Known
A_ind_genotypet.txt

Alternate
C_ind_genotype.txt

Table of Contents

Efficient reporting: Include the sections of the project that are pertinent to the case. Exclude any of the support documentation that was not required for the analysis.


Flexible Technology Provides a Framework for Growth

MaSTR software provides flexible technology that allows custom modeling and development. The software provides a framework that empowers both forensic analysts and researchers. As new models are developed by researchers, the model can be tested and validated within MaSTR – when validation is completed, the model is locked in for casework. The models can be expanded; the software does not need to be updated to include improvements to the statistical analysis as the science progresses.
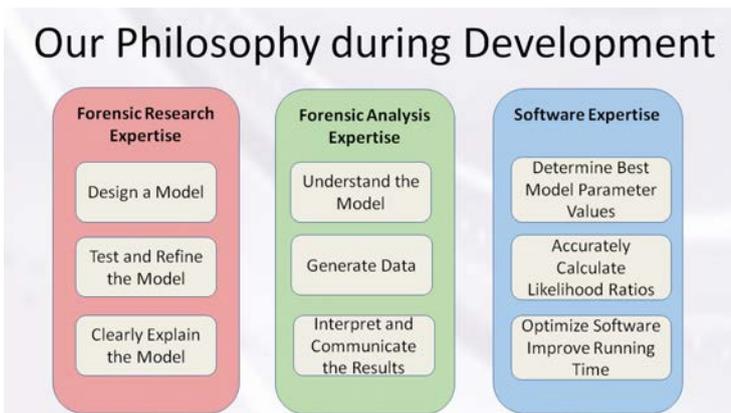
MaSTR software was developed with advances in forensic mixture analysis in mind. Validated models provide forensic analysts with powerful statistical analysis for complex mixtures. The Research and Development mode enables forensic researchers to develop more advanced models for mixture analysis (Figure 6). SoftGenetics' bioinformaticians, programmers and biologists will work with the forensic community to incorporate any future requirements and provide technical support.

REQUEST a MaSTR software time limited trial and introductory training
info@softgenetics.com

Computer Specifications

Computer Requirements - Server

- Minimum Specs (complex mixtures may not run)
    - 4-core CPU
    - 16 GB of RAM
    - Solid-State Drive (SSD) for storage
    - 64-Bit OS running Oracle VM VirtualBox with virtualization enabled
- Suggested Specs
    - 8-core CPU (or better)
    - 32 GB of RAM (or better)

Computer Requirements - Client

- Clients connect to and interact with the server on the internal network using a web-browser - either Google Chrome v56 (or higher) or Mozilla Firefox v51 (or higher)

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