



Transparency

Flexible Capacity

Admin Tools Admin Tools Enlightened Probabilistic Mixture Analysis Software

Training and Support

Validated

Technology

Low Acquisition Cost





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

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.

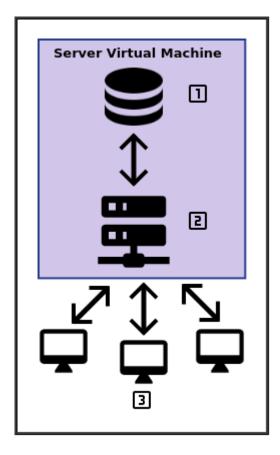
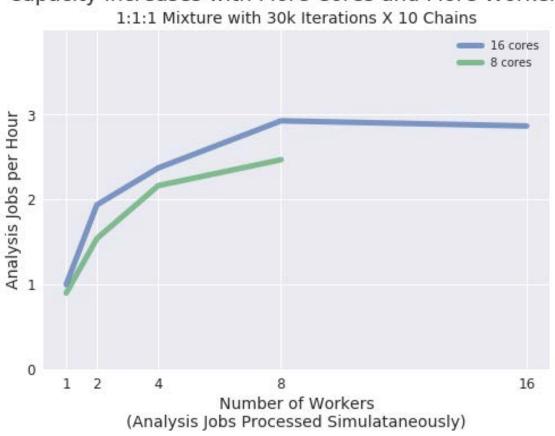


Figure 1: The software is structured into three parts, but the database (1) and server (2) are both contained within the Server virtual machine. Clients (3) are individual work stations.

High Speed with minimum computer specifications

#	Approx.	Run time for 2 # Iterations		# of Chains	
Contributors	mixture ratio	analysis jobs	(# of attempted	(run the sampling	
		(simultaneously),	steps)	many times with	
		4 cores d		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.



Capacity Increases with More Cores and More Workers

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)
- 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.

≡ MaSTR [™]	M V1.3.1 Research M	Mode				ANALYSIS	MODELS	SYSTEM
System		\mathbf{n}				PANELS	FREQUENCIES	PROTOCOL SETS
Panels (8)	PowerPlex	L16 -			ELIMINATION DE	3 ABOUT DEL	ETE IMPORT FROM F	ILE NEW
Name	PowerPlex	_ESX_17_v2.0						
PowerPlex_16	NGMSElec	ct_panel_v2						
Markers	PowerPlex	<_Fusion_Panels_v1_(
	PowerPlex	_ESI_17_v2.1	Allele	Size				
D3S1358	Identifiler		11 12	107.1 111.4				
TH01		*	13	111.4				
THUT	4	7	14	120.1				
D21S11	\checkmark	Lower Bound	15	124.1				
D18S51		106.5	15.2	126.2				
		100.0	16	128.3				
Penta_E	\sim	Upper Bound	17	132.6				
D5S818		149.4	18	136.7				
	-		19	140.7				
D13S317		Color	20	144.7				
D7S820	\checkmark		21	148.8				
D16S539		Analytical Threshold						
	_	50						
CSF1P0	\checkmark							
Penta_D		DELETE MARKER						

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

System					PANELS	FREQ	UENCIES	PROTOCOL SETS
Protocol Set / SOP (1) BU-ABCD	× *		ELIMI	ATION	DB ABOUT	DELETE	IMPORT FROM	FILE NEW
Name BU-ABCD	Statistical Profile	Stutter Calculated or	5/14/20	18, 3:08:	18 PM		le Calculation single-source data	
Panel	2.565249694519059	Marker	From	То	Ratio 🔒	+	Revised Genotype F	le
		D8S1179	-	7	0.0419			
Identifiler × 👻	Linear Variance Factor (calculated ≈ 3.7488)	D8S1179	-	8	0.0443	Protoc	colDataSet_genotype	s_ABCD_BU.txt
	3.748821804817738	D8S1179		9	0.0467	1	Signal	
PCR Cycle		D8S1179		10	0.0490	Proto	colDataSet_Signal_AE	CD PLL tyt
	Exponential Variance Factor (calculated ~ 3.7661)	D8S1179		11	0.0513	FIOLO	vibatasecoignai_Ac	BCD_BU.txt
	3.7660846799272063	D8S1179		12	0.0540	CA	LCULATE VIEW	RESULT
CE Instrument		D8S1179		13	0.0565			/
	Linear Sigma (calculated ≈ 0.1612)	D8S1179		14	0.0590			
Voltaga	0.1612371628298806	D8S1179		15	0.0612	Elimi	nation DB Filters	
Voltage		D8S1179		16	0.0636	Minim	um LR	
	Exponential Sigma (calculated ≈ 0.1618)	D8S1179		17	0.0659	0		
Injection Time	0.16182903380230973	D8S1179		18	0.0683			
	0.10102300300200370	D8S1179		19	0.0707 -	Max N	umber of Zeroes	
Add Property			R	ght-click	or more options	0		

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.

<i>Figure 5:</i> Casework analyses are easily submitted using the dropdown menu to select the validated:	New Analysis SETTINGS
	Protocol Set
	Fusion_6C × 👻
Destand Oct. Desculation Allala Francesco and Madal	Frequency
Protocol Set, Population Allele Frequency and Model	Hill_et_al 2013 × 👻
	Model
Select the appropriate Coancestry adjustment (no	Standard_70k_8chains_ex × 👻
adjustment to assume Hardy Weinberg equilibrium,	Coancestry Adjustment
NRCII Recommendation 4.1 or NRCII Recommendation 4.2.	NRCII Recommendation 4.1 -
	Adjustment Value
Enter the appropriate theta value if a coancestry	- 0.01
adjustment is selected.	Name
	Name 08172018_jobName
Name the job and enter any comments	
	Comments 5 person mixture, 1 known
Specify the number of contributors	- Number of Contributors - 5
	1 Signal
	mixture_signal_0817210918.txt
	1 Reference
· Salaat the mixture, but file (containing all colled	POI_1_08172018.txt
Select the mixture .txt file (containing all called	Reference
peaks and peak heights), .txt file of person of	POI_1_08172018.txt
interest genotype(s), any known contributor	1 Known
genotype .txt files	known_contributor_08172018.txt
	1 Alternate
	POI_2_08172018.txt
	POI_3_08172018.txt
	P0I_4_08172018.txt
	SUBMIT JOB VIEW SIGNAL
Research/Development Capabilities	

			ANALYSIS	MODELS	SYSTEM
odels (3) Marker-Contrib Adjustment × -			ABOUT	DELETE IMPORT	FROM FILE NEW
ne	Advanced Settings	Variables		Expected Height	Calculations
arker-Contrib Adjustment	Allele Step Method	Marker_Fixed_1	÷.	Multiply Contrib-M	Marker
	Subset Merge 👻	Contrib-Marker			
CMC Settings Analysis Settings	Continuous Step	Concromance		ADD	
ations Drop-In Coefficient (A) 0000 1	Metropolis +				
	Degradation	Edit Variable			
n In Preprocessing Steps	Linear 👻	Select	Contributor	× *	
0000 10000		Fixed			
n N Apply Stutter		Normal			
Sampler Warmup		Uniform			
ins		Bounded Normal			
		Symmetric Dirichlet			
		Beta Marker Fixed 1 -			
SAVE SAVE AS		Standard Deviation			
			0.2		
		Lower			
			0.5		
		Input Value +	1.5		
			DELETE	SAVE	

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

	our Log	
Your Institu	ution's Nar	ne
Results of Rape		
Protocol Set BU_Identifiler	Created By researcher	
Panel Identifiler	ID 5b6ae2ae1d58ce0	01c105fdb
Frequency Hill_et_al (2013)	Queue Time 8/8/2018, 12:31:42	PM
Model Standard_10k_8chains	Start Time 8/8/2018, 12:31:47	PM
Coancestry Adjustment NRCII Recommendation 4.1	End Time 8/8/2018, 12:48:50	PM
Coancestry Value 0.01	Duration 17 minutes, 3 seco	nds
Name RapeCase_twoAccused	Memory Usage 179 MB	
Comments		
Contributors 2	Γ	Table of Contents
Signal ID_2_SAB_NG0.5_R1,1_A1_V1.txt		Likelihood Ratios
Reference		Genotype Set Results
B_ind_genotype.txt		Ratio Plots
Known A_ind_genotypet.txt		Degradation Plots
Alternate		Protocol Set / SOP
C_ind_genotype.txt		Stutter
		Variance
		Panel
		Frequency

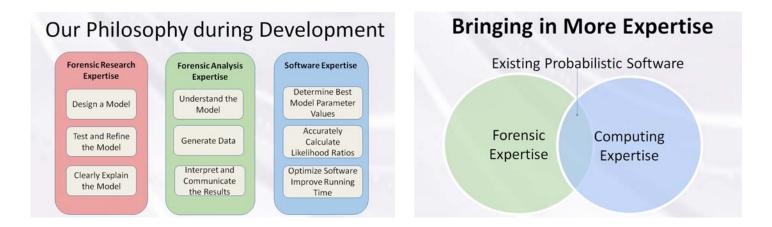
Likelihood Ratios	3
Genotype Set Results	11
Ratio Plots	
Degradation Plots	27
Protocol Set / SOP	
Stutter	32
Variance	
Panel	40
Frequency	
Model	
Signal	
Reference	91
Known	
Alternate	93

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.

Download Report for 'Ra	apeCase_twoAc	cused'		
Organization Your Institution's Name	Sections		Populations	
	Likelihood Ratios	\checkmark	All data	
Your Logo	Genotype Set Results	\checkmark	AfAm	\checkmark
Tour Logo	Ratio Plots	\checkmark	Cauc	\checkmark
	Degradation Plots	\checkmark	Hisp	\checkmark
	Protocol Set / SOP		Asian	
	Stutter	\checkmark		
	Variance	\checkmark		
	Panel	\checkmark		
	Frequency	\checkmark		
	Model	\checkmark		
	Signal			
	Reference	\checkmark		
	Known	\checkmark		
	Alternate	\checkmark		
				<u>.</u>
				DOWNLOAD

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)
 - \circ 4-core CPU
 - \circ 16 GB of RAM
 - \circ Solid-State Drive (SSD) for storage
 - \circ 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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