

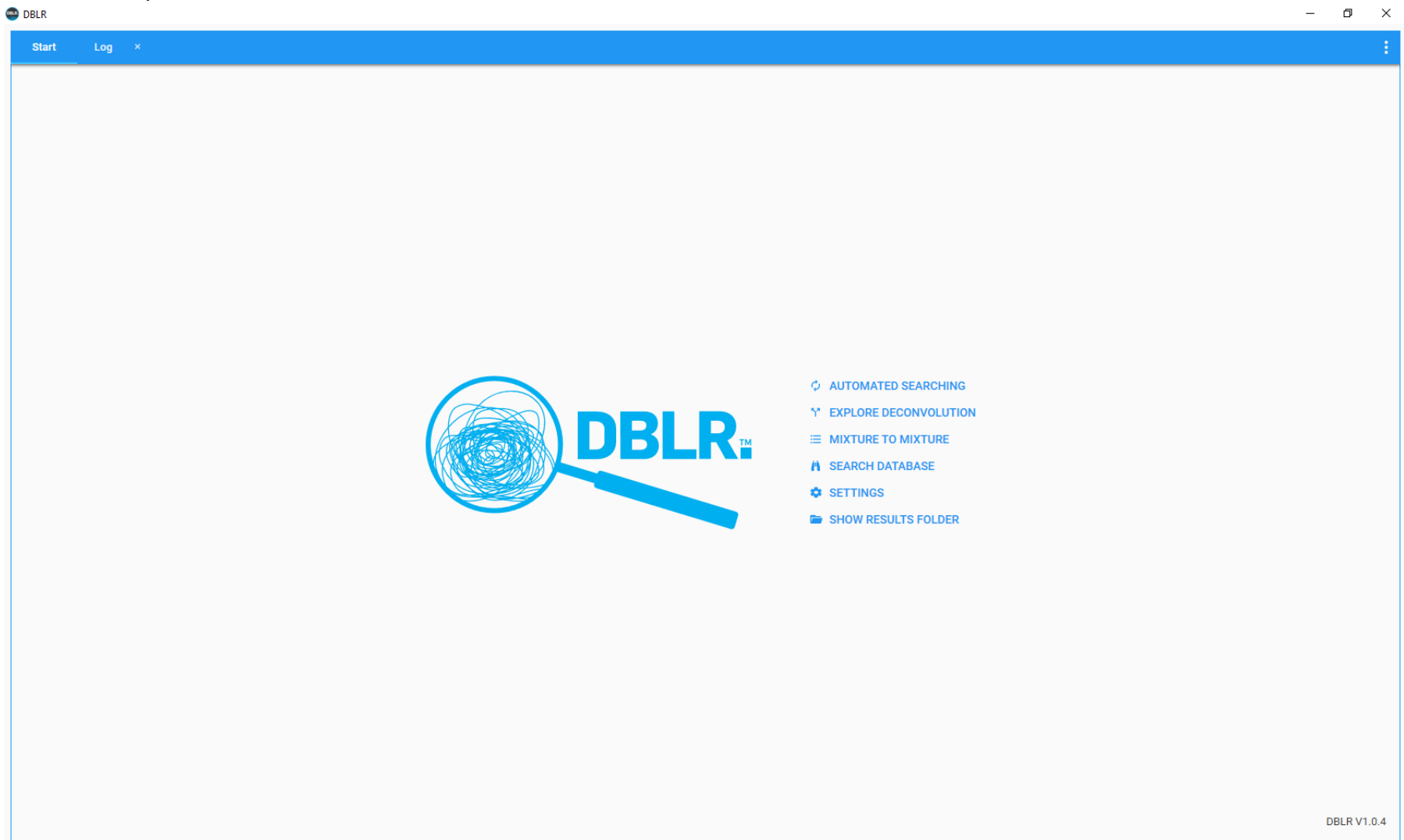
STRmix.™
**RESOLVE
MORE DNA
MIXTURES.**

www.STRmix.com

DBLR™

Database likelihood ratios

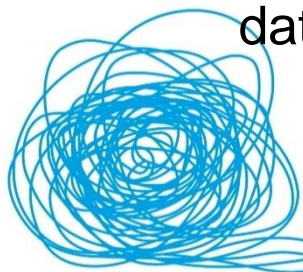




Standalone software for the calculation of LR_s using STRmix™ deconvolutions

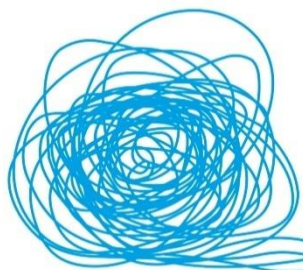
Functionality

- Automated searching
 - Save and manage deconvolutions and profile databases and generate matches
- Explore deconvolution
 - What are the expected LRs given different propositions?
- Mixture to mixture
 - Match one or more mixtures with other mixtures to find common donors
- Search database
 - Undertake one off searches of a deconvolution to a profile database including contributor matching, familial etc



Settings

- Add allele frequency files (STRmix™ format)
- Create new search strategies
 - Flexible propositions
 - LR thresholds
 - Allele frequencies
 - Profile databases



Automated searching

Profile Databases

Deconvolutions

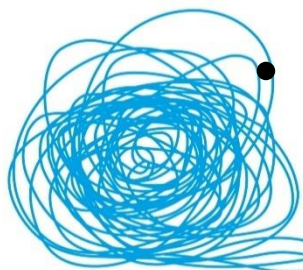
Automated Searches

Queued Automated Searches

Results

Name	Number of Profiles	Number of Loci	Date Added	Date Modified
TC database	245	24	15/02/2019 9:34:20 AM	15/02/2019 9:34:20 AM
GF 10 million	10,000,000	23	16/02/2019 10:40:55 AM	16/02/2019 10:40:55 AM
QIAGEN Hp true	5	24	16/02/2019 10:43:48 AM	16/02/2019 10:43:48 AM

- Load new profile databases
- Load new profiles to existing databases
- Delete database
- Delete profiles from a database
- 1 to millions of profiles within each database, any number of databases



Automated searching

Profile Databases

Deconvolutions

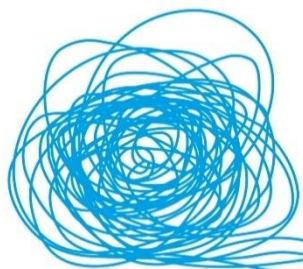
Automated Searches

Queued Automated Searches

Results

Case Number	Sample Name	Number of contributors	Date loaded	# Linked Searches	# Matches	Default Contributor
QIAGEN 60rfu	CMIX_2-1_C06_3500 Instrument_Investigator 24_plex.hid	3	16/02/2019 10:47:22 AM	2	3	<input checked="" type="checkbox"/> 1 <input checked="" type="checkbox"/> 2
QIAGEN 60rfu	CMIX_3-1_E06_3500 Instrument_Investigator 24_plex.hid	3	16/02/2019 10:47:23 AM	2	3	<input checked="" type="checkbox"/> 1 <input checked="" type="checkbox"/> 2
QIAGEN 60rfu	CMIX_5-2_C07_3500 Instrument_Investigator 24_plex.hid	3	16/02/2019 10:47:24 AM	2	3	<input checked="" type="checkbox"/> 1 <input checked="" type="checkbox"/> 2

- Save STRmix™ deconvolutions
- Select contributors of interest
- Link deconvolution to profile database for matching
- Delete deconvolutions



Automated searching

Profile Databases

Deconvolutions

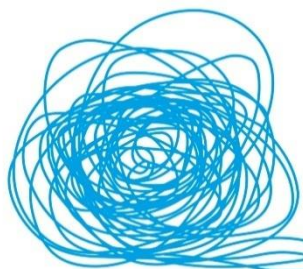
Automated Searches

Queued Automated Searches

Results

Name	Relationship (H1)	Relationship (H2)	Population	Use Log10(LR) Threshold?	Log10(LR) Threshold	Profile Database	# Linked
Familial Half sibs	Half sibling of contributor	Unrelated	Cauc	<input checked="" type="checkbox"/>	0	GF 10 million	0
Familial PC	Parent or child of contributor	Unrelated	Cauc	<input checked="" type="checkbox"/>	0	GF 10 million	0
GlobalFiler 10 million	Contributor	Unrelated	Cauc	<input checked="" type="checkbox"/>	0	GF 10 million	67

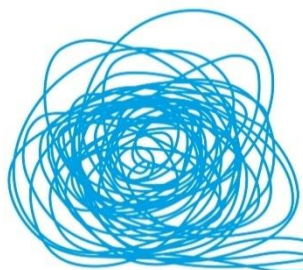
- Create search strategies with varying LR propositions, LR thresholds, allele frequencies, profile databases



Automated searching

Profile Databases		Deconvolutions		Automated Searches		Queued Automated Searches	Results
	ID	Search Name	Profile Database	# Deconvolutions	# Matches	Date Matched	
➤	3	QIAGEN Hp	QIAGEN Hp true	67	199	16/02/2019 11:02:51 AM	
➤	2	GlobalFiler 10 million	GF 10 million	67	1,713,002	16/02/2019 10:48:58 AM	
➤	1	TC offender search	TC database	2	3	15/02/2019 9:39:25 AM	

- New decons and profiles are queued ready for matching
- On completion of match, all results are saved ready for inspection





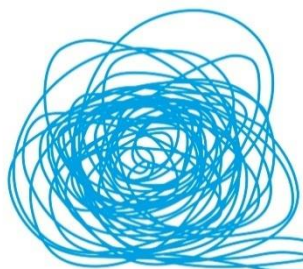
Automated Search Report

DETAILS

SEARCH NAME:	TC offender search
USER:	jbright
VERSION:	DBLR V1.0.4
RUN AT:	15 Feb 2019 09:39
# DECONVOLUTIONS:	2
# MATCHES:	3

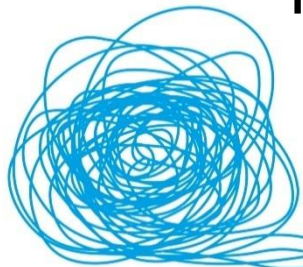
SEARCH CONFIGURATION

LOG10(LR) THRESHOLD:	6
POPULATION:	Cauc

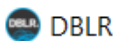


Explore deconvolution

- H1 and H2 true experiments
- Sample 10,000 to 10 million profiles given a set of propositions
 - Contributors
 - Non contributors (“random man”)
 - Relatives of contributors etc
- Profiles are sampled based on genotype weights and allele frequencies
- Calculate likelihood ratios for the sampled profiles
- Plot to inform suitability of profile component for comparison to a POI or database



Explore deconvolution settings



Start

Log



Automated Searching



Add deconvolutions



Explore (QIAGEN 60rfu CMIX_2-1_C06_



Simulation

Search configuration

Search type

Custom

H1

H2

Relationship

Contributor

Relationship

Unrelated

Contributor position



1



2



3

Population

Include loci



TH01



D3S1358



vWA



D21S11



TPOX



DYS391



D1S1656



SE33



D10S1248



D22S1045



D19S433



D8S1179



D2S1338



D18S51



FGA



D16S539



CSF1PO



D13S317



D5S818



D7S820

DESELECT ALL

Explore deconvolution settings

DBLR

Start

Log

Automated Searching

Add deconvolutions

Explore (QIAGEN 60rfu CMIX_2-1_C06_)

☒ Log10(LR) threshold

6

Simulation parameters

Sample

☒ H1 true

☒ H2 true

☐ Additional hypothesis (H3)

Seed

☒ Random

543027

Number of samples

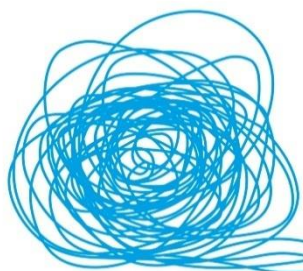
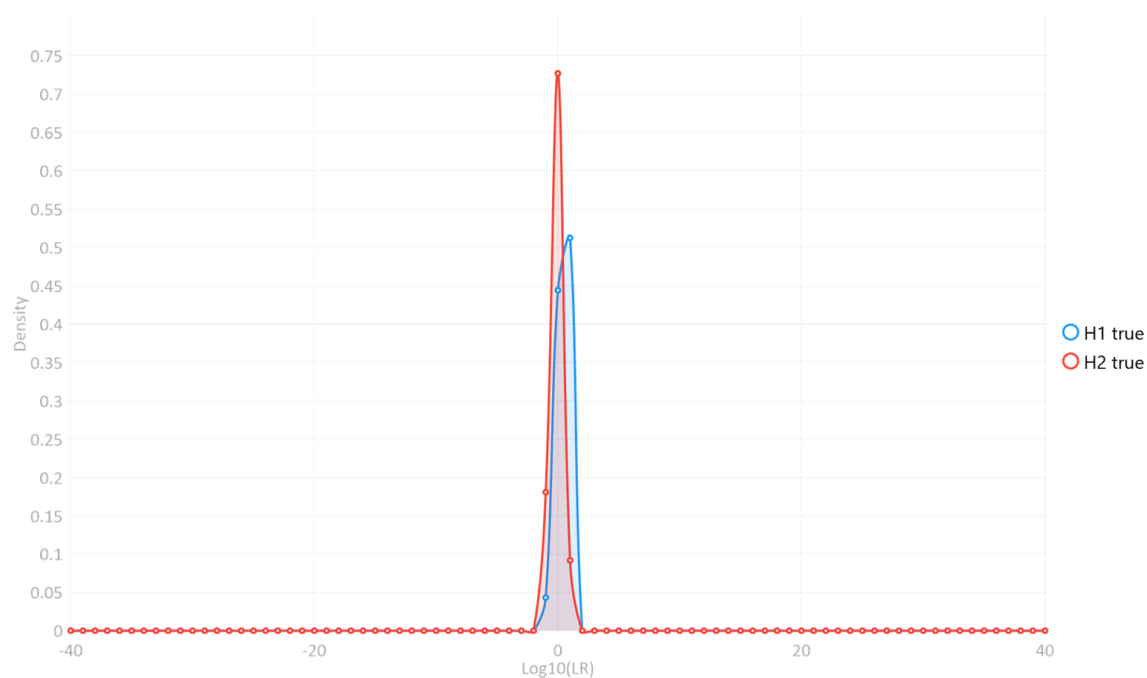
100,000

☐ Importance Sampling

SAMPLE LIKELIHOOD RATIOS

Explore deconvolution results

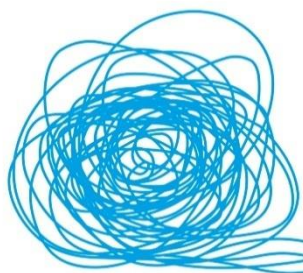
Low level single source profile
Not suitable for comparison



Explore deconvolution results

Complex 4 person mixture

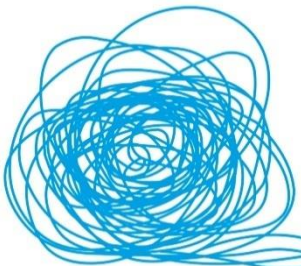
Major contributor suitable for comparison



Exceedance probabilities

- Based on naïve sample or using importance sampling
- Flexible threshold
- For example: The probability of a logLR greater than 0 (i.e. inclusionary LR) given the profile is compared to a true contributor (H1) = 1
- Probability of inclusionary LR for a non-contributor (H2) = 0

Probability	Monte Carlo estimate
$P(\text{Log}_{10}\text{LR} \geq 0 \mid H1)$	1
$P(\text{Log}_{10}\text{LR} \geq 0 \mid H2)$	0



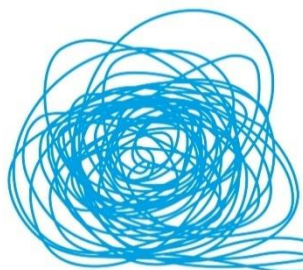
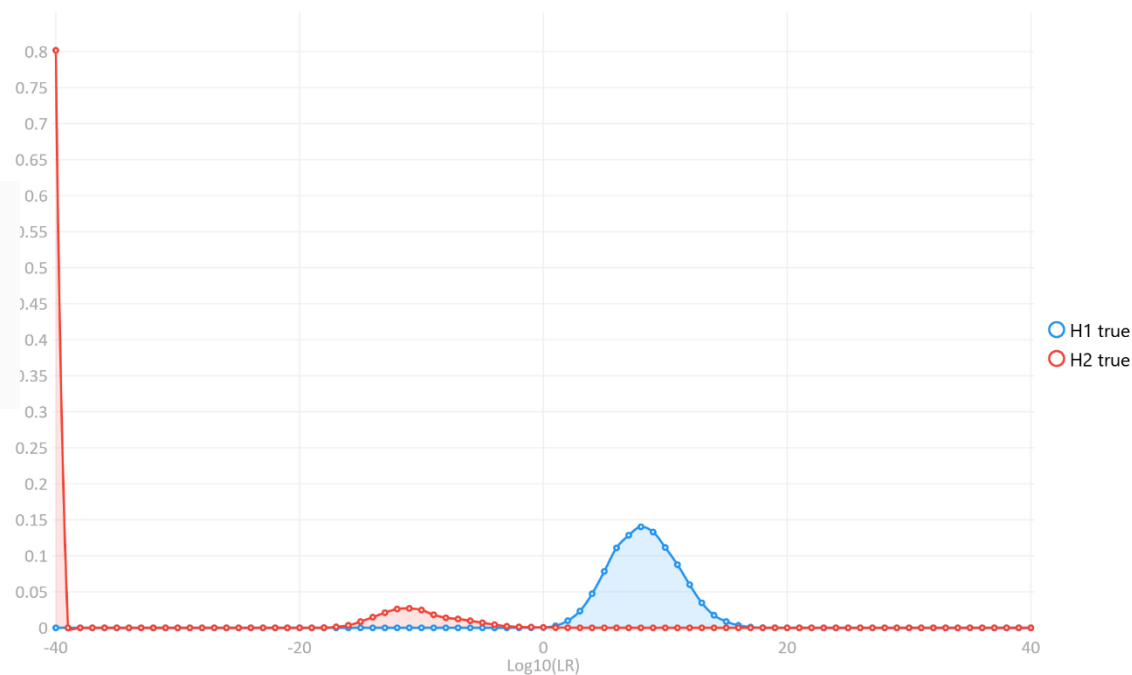
Explore deconvolution results

Complex 4 person mixture

Minor contributor may be suitable for comparison

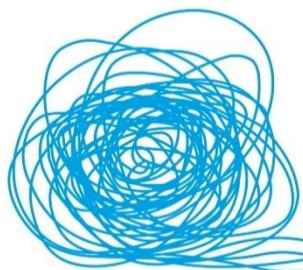
Exceedance probabilities:

Probability	Monte Carlo estimate
$P(\text{Log}_{10}\text{LR} \geq 6 \mid H_1)$	0.78509
$P(\text{Log}_{10}\text{LR} \geq 6 \mid H_2)$	0



Mix to mix matching

- Compares all components within one mixture to all components in a second mixture and calculates an LR
- The average across all components:
 - H1: The two mixtures share one common contributor
 - H2: All contributors to both mixtures are unrelated



Mix to mix matching

DBLR

— □ ×

Start Log × Mixture to Mixture ×



Mixture to Mixture

Select Inputs

Showing 4 items

Case Number	Sample Name	# contributors
D	D	2
C	C	2
B	B	2
A	A	2

Add profiles here...

[BROWSE](#) [DELETE](#) [DELETE ALL](#)

← →

Showing 4 items

Case Number	Sample Name	# contributors
D	D	2
C	C	2
B	B	2
A	A	2

And some profiles here...

[BROWSE](#) [DELETE](#) [DELETE ALL](#)

Ready to compare 6 pairs of deconvolutions

[CONFIRM INPUTS](#)

Mix to mix results

- Per component LRs and average across contributors
- PDF and csv reporting options

DBLR

— □ ×

Start Log × Mixture to Mixture ×



Mixture to Mixture

Results

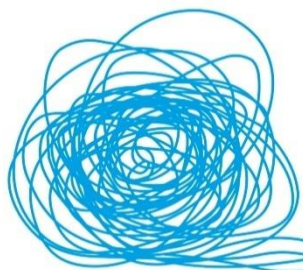
Mixture 1 Case Number	Mixture 1 Sample Name	Mixture 2 Case Number	Mixture 2 Sample Name	Contributor Mixture 1	Contributor Mixture 2	LR	Log(10)
D	D	C	C	1	1	2.24874E25	2.53519 ↑
D	D	C	C	1	2	2.88363E23	2.34599
D	D	C	C	2	1	2.39422E23	2.33792
D	D	C	C	2	2	1.45859E25	2.51639
D	D	C	C	Stratified	Stratified	9.40027E24	2.49731
D	D	B	B	1	1	1.52957E25	2.51846
D	D	B	B	1	2	5.01334E23	2.37001
D	D	B	B	2	1	4.37222E23	2.36407
D	D	B	B	2	2	9.25920E24	2.49666

BACK

SAVE RESULTS

Search database

- One off search of deconvolution against a chosen profile database
- Flexible propositions, allele frequencies, and LR thresholds
- PDF, csv, xml reporting options



Search database results

Search Report



DETAILS

PROFILE: QIAGEN 60rfu
CMIX_8-1_H07_3500
Instrument_Investigator
24_plex.hid

SEARCH RUN: 22 Feb 2019 20:26

USER: jbright

VERSION: DBLR V1.0.4

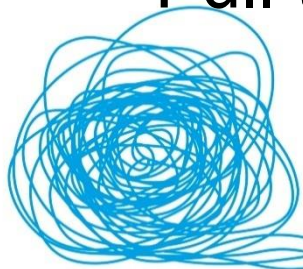
DECONVOLUTION RUN: 24 Oct 2018 20:08:13

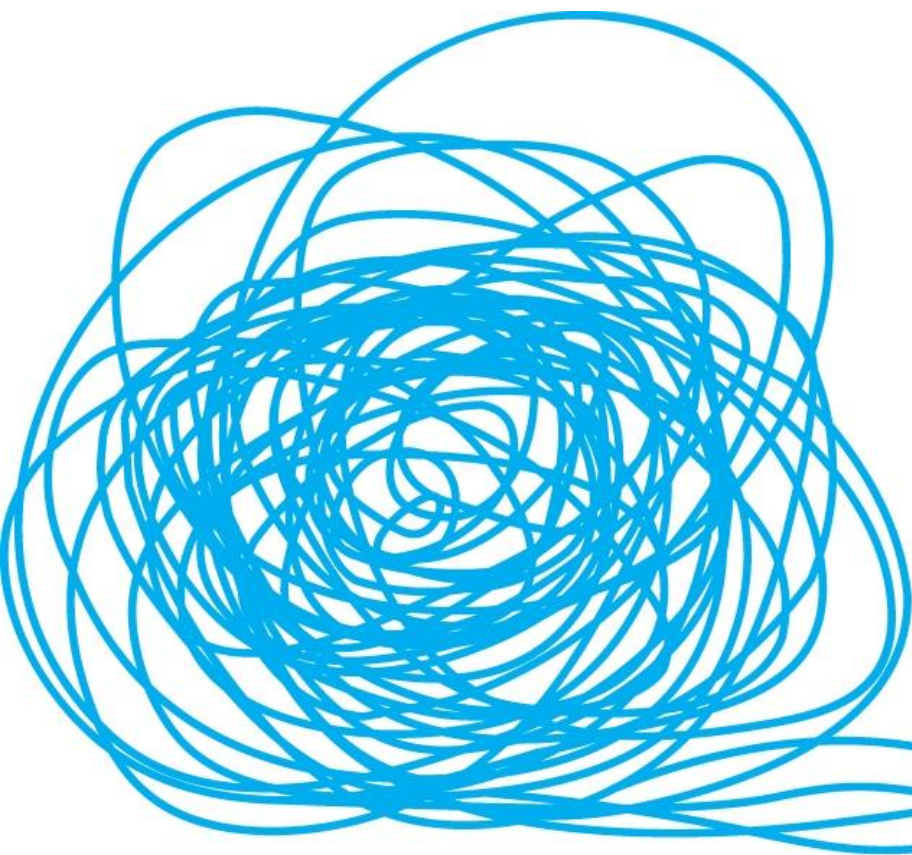
USER: Samson

VERSION: STRmix 2.6.0

Support

- Exploring the probative value of mixed DNA profiles, Kruijver et al. Under review
- The efficacy of DNA mixture to mixture matching, Bright et al. Accepted FSI:Gen
- Inter-sample contamination detection using mixture deconvolution comparison, Taylor et al. Accepted FSI:Gen
- Full user's manual
- Full training and support available





STRmix.™
**RESOLVE
MORE DNA
MIXTURES.**

www.STRmix.com