Appendix S3. Detailed results of LRMix Studio for each suspected male: Global Composite (ADO 0.55).

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
Date and time of analysis: 2016/09/01 15:27:39
Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
MJ4	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05
Theta correction: 0.03
Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	9,95500E-003	1,96023E-001	5,07849E-002
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	9,44775E-001	5,95266E-001	1,58715E000
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	9,44680E-001	6,42542E-001	1,47022E000
MU11	9,44775E-001	6,19291E-001	1,52558E000
MU15	9,40448E-001	8,51280E-001	1,10475E000
MU23	5,22499E-001	4,97658E-001	1,04992E000
MU50	1,51646E-002	1,89039E-001	8,02193E-002
MU59	9,39391E-001	8,61193E-001	1,09080E000
Overall Likelihood Ratio			1,62201E-003

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
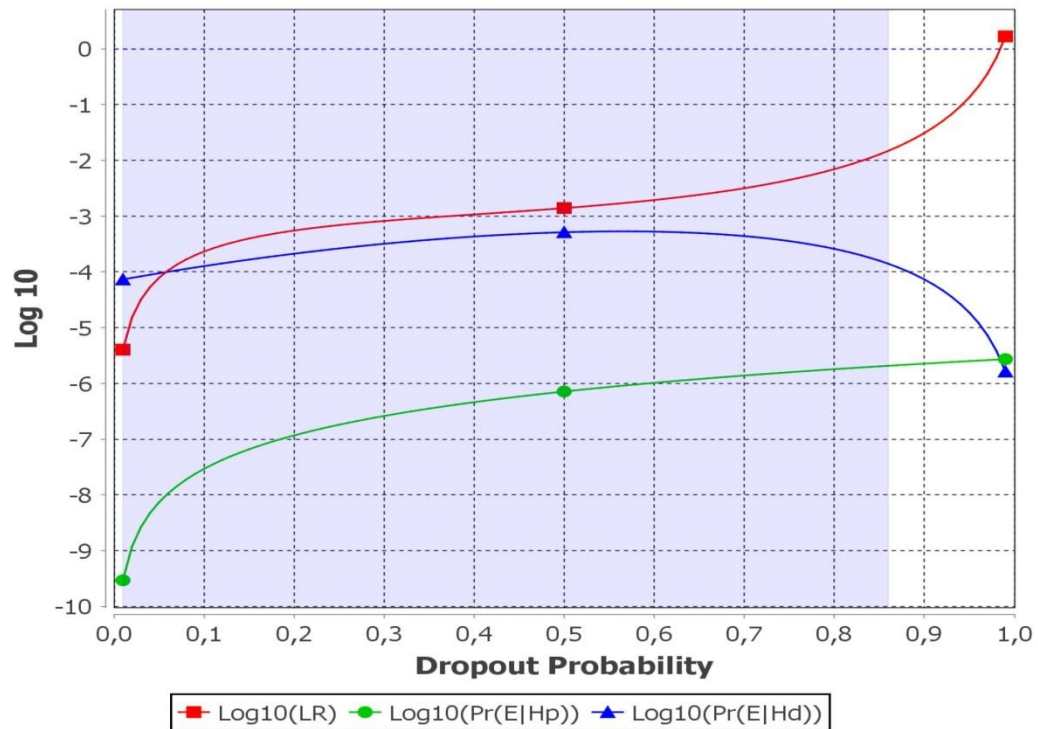Date and time of analysis: 2016/09/01 15:27:39
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of MJ4 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.01 ~ 0.86

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-5.394758	-9.5309464686462099	-4.1361881090024219
0.10	-3.636077	-7.5333126492845234	-3.8972359888262015
0.20	-3.259177	-6.9338842283645973	-3.6747068309235819
0.30	-3.087303	-6.58433589710170701	-3.4970332433559394
0.40	-2.970542	-6.3370952324229321	-3.3665534475712939
0.50	-2.856449	-6.1459146419025607	-3.2894653715801864
0.60	-2.711823	-5.9901942175428724	-3.2783712574737804
0.70	-2.500288	-5.8589453435555185	-3.3586569618960142
0.80	-2.158058	-5.7456087977268346	-3.5875511294182480
0.90	-1.510411	-5.6459537491421656	-4.1355430910146226
0.99	0.2225749	-5.5655556441203488	-5.7881305777029981

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
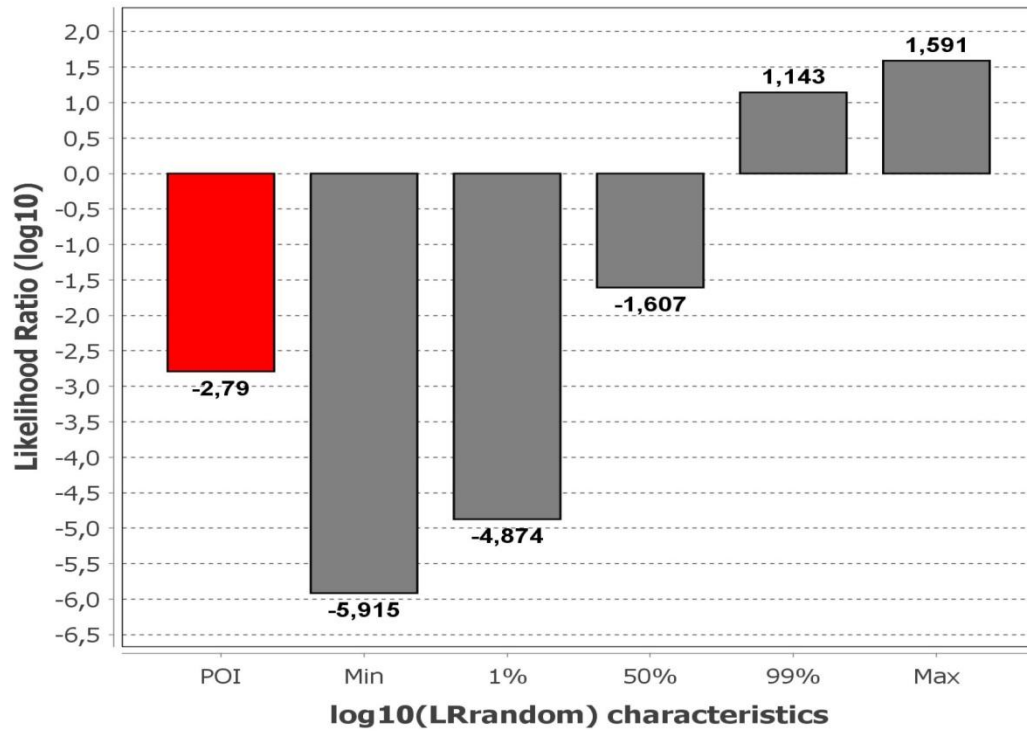Date and time of analysis: 2016/09/01 15:27:39
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing MJ4 with randomly generated profiles over 1000 iterations.
LRs>1: 12% (129).   LRs>LR(POI): 75% (750).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:27:39

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.01	0.69
Defense	0.26	0.86
Overall	0.01	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:27:39

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\01_Input_Sospetto_MJ4.csv	MJ4

The reference profiles MJ5, DG2, KJ2G2, MJ2G1, DJ1G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	MJ4
CXX20	118 118	118 118	118 118	118 120
G10M	117 119	117 123	119 123	117 123
G10P	151 171	171 171	171 171	151 171
G10X	139 143	133 139	133 143	133 143
G1D	102 116	102 106	102 116	102 106
MU11	88 88	78 88	88 88	78 88
MU15	136 142	136 146	136 146	136 146
MU23	120 122	120 122	120 122	118 120
MU50	98 104	98 98	102 104	98 102
MU59	103 123	111 123	101 103	101 111

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:30:07

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
MJ5	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	9,47126E-001	5,95414E-001	1,59070E000
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	9,40406E-001	6,42385E-001	1,46393E000
MU11	5,19626E-001	6,02407E-001	8,62584E-001
MU15	9,44680E-001	8,51457E-001	1,10949E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	1,51653E-002	1,89040E-001	8,02227E-002
MU59	9,39391E-001	8,61193E-001	1,09080E000
Overall Likelihood Ratio			1,14779E-002

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
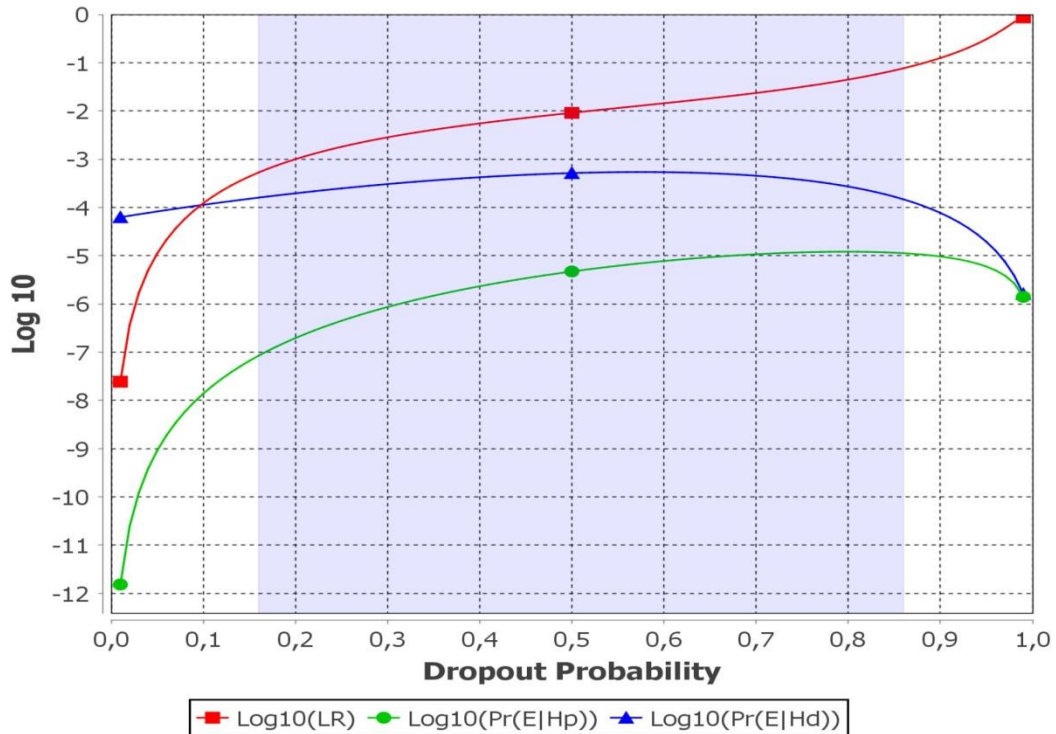Date and time of analysis: 2016/09/01 15:30:07
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of MJ5 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.16 ~ 0.86

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-7.612104	-11.815224101994301	-4.2031204250773175
0.10	-3.912403	-7.8586347719938816	-3.9462316954093039
0.20	-3.000563	-6.7079941389122845	-3.7074314191647279
0.30	-2.547646	-6.0640370334399804	-3.5163915073831857
0.40	-2.258959	-5.6337341520244645	-3.3747751161500065
0.50	-2.039546	-5.3278701006265745	-3.2883245164944048
0.60	-1.841384	-5.1107396038008596	-3.2693551592050882
0.70	-1.627523	-4.9706656700451192	-3.3431422089384352
0.80	-1.350509	-4.9176539912292165	-3.5671448324218864
0.90	-0.9034265	-5.0170295118485821	-4.1136030013592135
0.99	-0.06113539	-5.8541968060019060	-5.7930614131825688

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
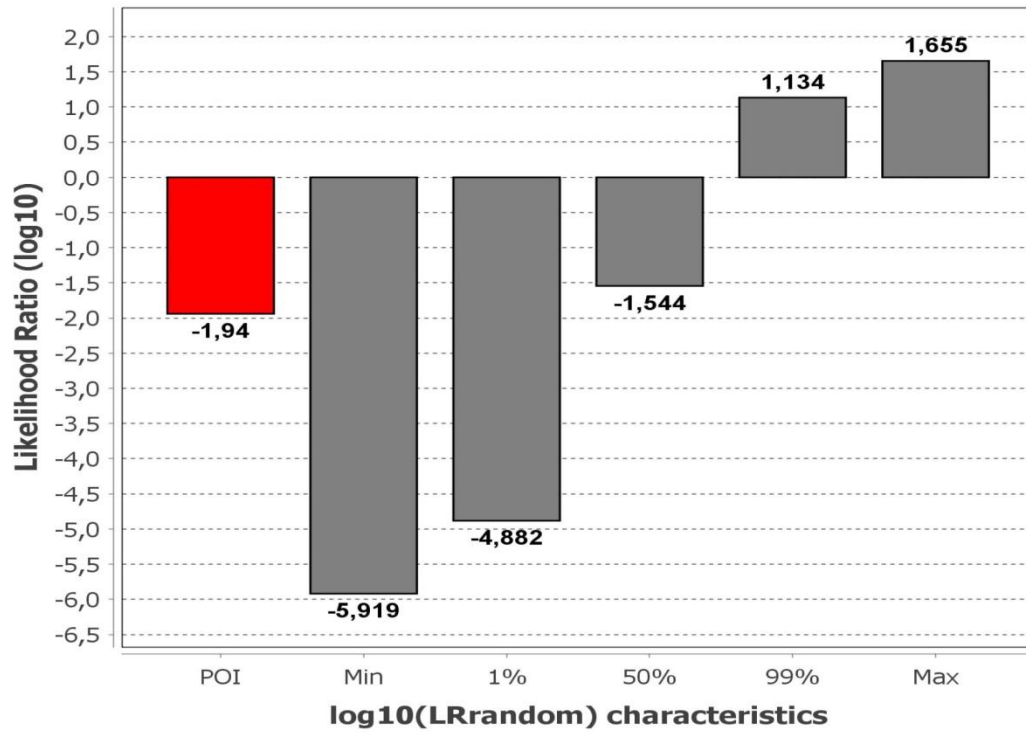Date and time of analysis: 2016/09/01 15:30:07
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing MJ5 with randomly generated profiles over 1000 iterations.
LRs>1: 13% (131).　　LRs>LR(POI): 56% (567).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:30:07

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.16	0.77
Defense	0.25	0.86
Overall	0.16	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:30:07

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\02_Input_Sospetto MJ5.csv	MJ5

The reference profiles MJ4, DG2, KJ2G2, MJ2G1, DJ1G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	MJ5
CXX20	118 118	118 118	118 118	130 134
G10M	117 119	117 123	119 123	117 123
G10P	151 171	171 171	171 171	151 151
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	102 102
MU11	88 88	78 88	88 88	78 86
MU15	136 142	136 146	136 146	136 142
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	102 104
MU59	103 123	111 123	101 103	101 111

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:31:37

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
DG2	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
                         Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	2,84501E-001	5,62235E-001	5,06019E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	2,84473E-001	6,08235E-001	4,67702E-001
MU11	2,84501E-001	5,85612E-001	4,85819E-001
MU15	5,17246E-001	8,31522E-001	6,22047E-001
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	8,30316E-003	1,86530E-001	4,45138E-002
MU59	9,39391E-001	8,61193E-001	1,09080E000
Overall Likelihood Ratio			2,04391E-004

Analysis performed by: davoli

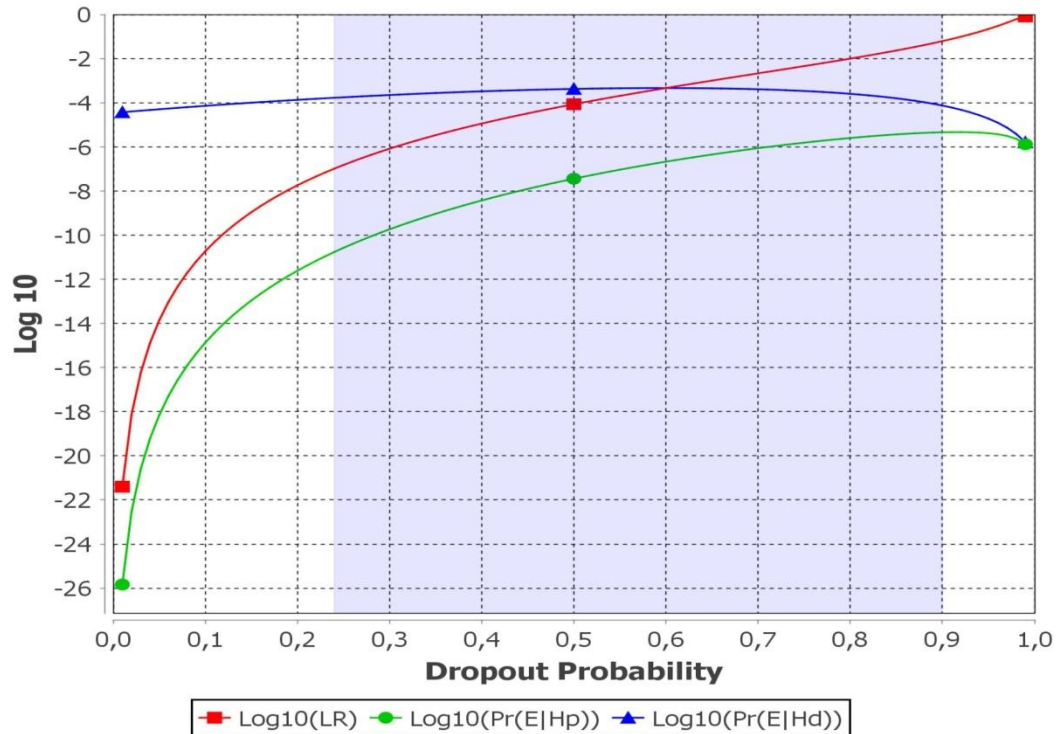Date and time of analysis: 2016/09/01 15:31:37

Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis

Varying dropout of DG2 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.

■ Dropout Estimation 0.24 ~ 0.90

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-21.40121	-25.832510461327895	-4.4312970862095371
0.10	-10.73254	-14.874708758825549	-4.1421641170793304
0.20	-7.743906	-11.615427280906144	-3.8715210436034306
0.30	-6.085147	-9.7373122025431424	-3.6521655333455305
0.40	-4.945630	-8.4308305878393348	-3.4852006854051169
0.50	-4.068985	-7.4449002649958480	-3.3759155730345629
0.60	-3.335459	-6.6717160232790204	-3.3362569895213454
0.70	-2.669942	-6.0611404051172126	-3.3911979345705587
0.80	-2.002275	-5.6002214597241302	-3.5979468508755014
0.90	-1.210949	-5.3394758036887290	-4.1285266235417781
0.99	-0.09037569	-5.8849689090139962	-5.7945932220793174

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
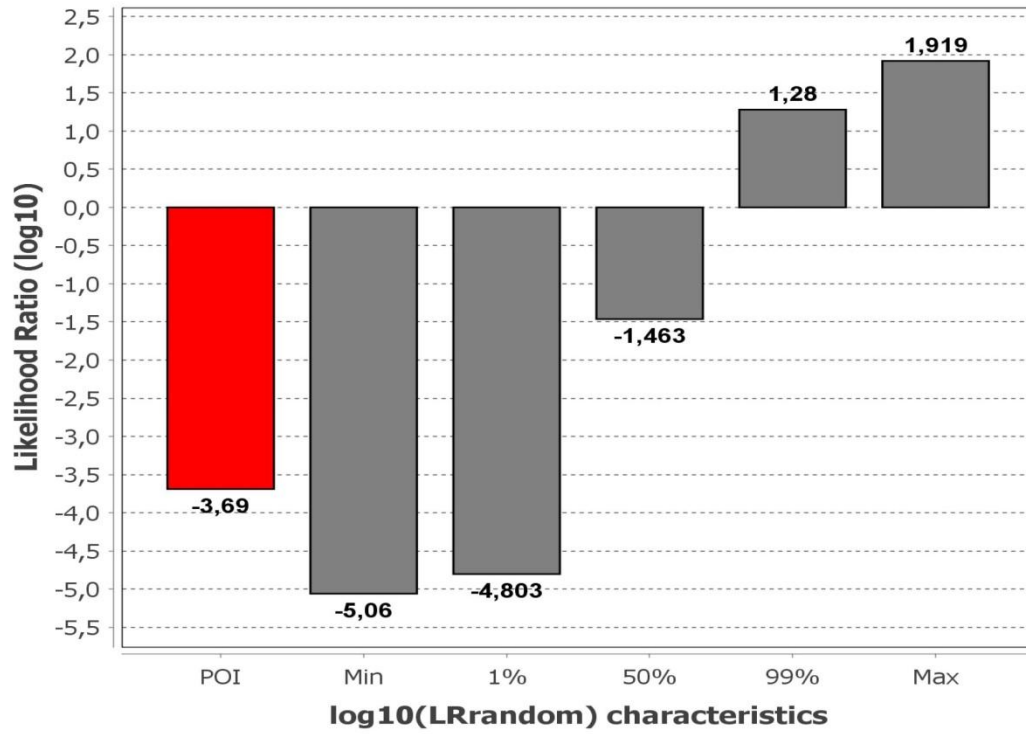Date and time of analysis: 2016/09/01 15:31:37
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing DG2 with randomly generated profiles over 1000 iterations.
LRs>1: 13% (134).   LRs>LR(POI): 92% (927).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:31:37

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.50	0.90
Defense	0.24	0.86
Overall	0.24	0.90

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:31:37

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\03_Input_Sospetto DG2.csv	DG2

The reference profiles MJ4, MJ5, KJ2G2, MJ2G1, DJ1G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	DG2
CXX20	118 118	118 118	118 118	120 134
G10M	117 119	117 123	119 123	119 123
G10P	151 171	171 171	171 171	165 169
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	108 108
MU11	88 88	78 88	88 88	80 90
MU15	136 142	136 146	136 146	132 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	104 106
MU59	103 123	111 123	101 103	101 111

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:33:18

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
KJ2G2	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	6,62625E-001	2,27868E-001	2,90793E000
G10M	4,27391E-001	2,23092E-001	1,91576E000
G10P	5,17275E-001	5,78561E-001	8,94072E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	5,17223E-001	6,25196E-001	8,27298E-001
MU11	5,19626E-001	6,02407E-001	8,62584E-001
MU15	9,44722E-001	8,51459E-001	1,10953E000
MU23	5,22499E-001	4,97658E-001	1,04992E000
MU50	8,30279E-003	1,86530E-001	4,45119E-002
MU59	9,30993E-001	8,60839E-001	1,08149E000
Overall Likelihood Ratio			2,34099E-001

Analysis performed by: davoli
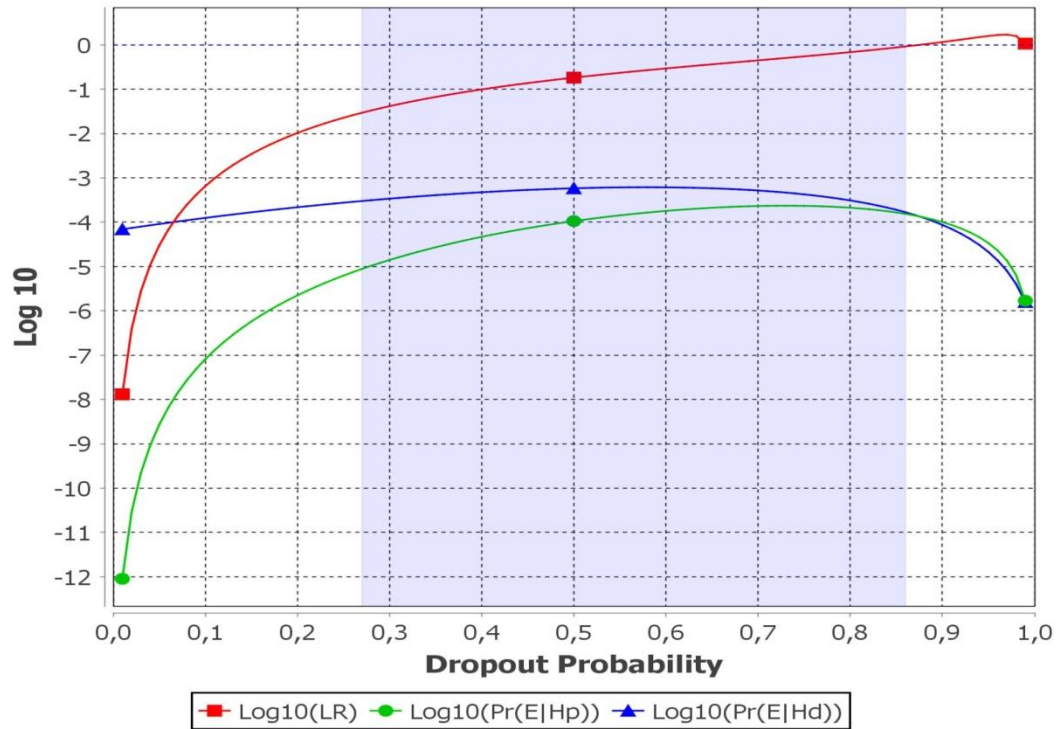Date and time of analysis: 2016/09/01 15:33:18
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis

Varying dropout of KJ2G2 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.

■ Dropout Estimation 0.27 ~ 0.86

Legend: ■ Log10(LR) ● Log10(Pr(E|Hp)) ▲ Log10(Pr(E|Hd))

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-7.883423	-12.043757481521451	-4.1603343061548478
0.10	-3.187083	-7.0902772700651732	-3.9031944082606999
0.20	-1.987791	-5.6505398579803447	-3.6627490921811824
0.30	-1.382946	-4.8522023049626241	-3.4692565518118771
0.40	-1.005301	-4.3301153464605608	-3.3248141689087882
0.50	-0.7393866	-3.9748632546283402	-3.2354766153893179
0.60	-0.5318050	-3.7456479088978338	-3.2138429436654556
0.70	-0.3497820	-3.6353629566984282	-3.2855809696254980
0.80	-0.1646029	-3.6736634987949008	-3.5090606230019276
0.90	0.06298067	-3.9973820075510442	-4.0603626815978586
0.99	0.02902730	-5.7711318656323129	-5.8001591672849714

Analysis performed by: davoli
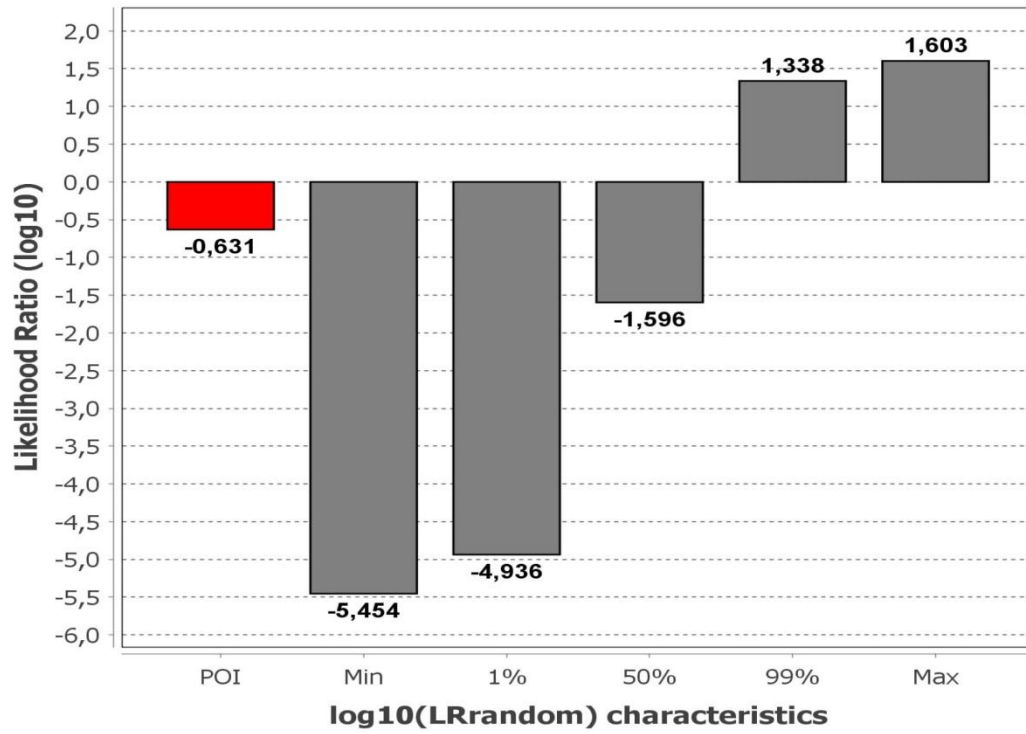
Date and time of analysis: 2016/09/01 15:33:18

Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results

Replacing KJ2G2 with randomly generated profiles over 1000 iterations.
LRs>1: 12% (125).   LRs>LR(POI): 21% (219).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:33:18

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.32	0.84
Defense	0.27	0.86
Overall	0.27	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:33:18

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\04_Input_Sospetto KJ2G2.csv	KJ2G2

The reference profiles MJ4, MJ5, DG2, MJ2G1, DJ1G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	KJ2G2
CXX20	118 118	118 118	118 118	134 134
G10M	117 119	117 123	119 123	111 123
G10P	151 171	171 171	171 171	165 171
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	102 108
MU11	88 88	78 88	88 88	78 86
MU15	136 142	136 146	136 146	142 146
MU23	120 122	120 122	120 122	118 120
MU50	98 104	98 98	102 104	98 106
MU59	103 123	111 123	101 103	103 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:35:04

Trace Analysed: R1234_Ua6797-98-99-800

Analysis 1 of 1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
MJ2G1	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies: C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	9,95500E-003	1,96023E-001	5,07849E-002
G10M	4,27391E-001	2,23092E-001	1,91576E000
G10P	5,19626E-001	5,78709E-001	8,97906E-001
G10X	5,22367E-001	7,89345E-001	6,61773E-001
G1D	2,84473E-001	6,08235E-001	4,67702E-001
MU11	2,84501E-001	5,85612E-001	4,85819E-001
MU15	9,40448E-001	8,51280E-001	1,10475E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	8,30316E-003	1,86530E-001	4,45138E-002
MU59	9,35182E-001	8,61004E-001	1,08615E000
Overall Likelihood Ratio			4,17954E-004

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
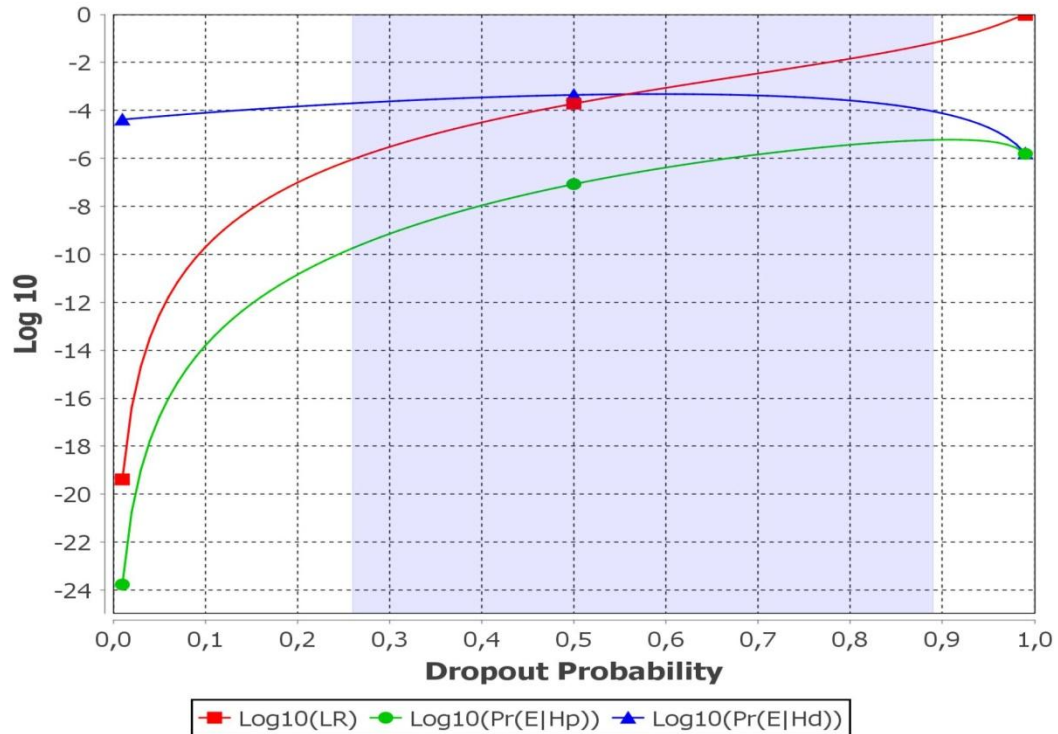Date and time of analysis: 2016/09/01 15:35:04
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of MJ2G1 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.26 ~ 0.89

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-19.38127	-23.763802937592487	-4.3825338699627645
0.10	-9.705314	-13.805997365504852	-4.1006829090575473
0.20	-7.010870	-10.847741583668963	-3.8368712657258279
0.30	-5.522417	-9.1457134647377493	-3.6232964162198388
0.40	-4.502887	-7.9641662869749199	-3.4612792648674810
0.50	-3.718864	-7.0751416774287410	-3.3562778486530255
0.60	-3.060759	-6.3811343820053592	-3.3203752948841254
0.70	-2.458836	-5.8375012536765558	-3.3786653461395563
0.80	-1.846075	-5.4345699554201196	-3.5884951521888752
0.90	-1.102775	-5.2249725219476284	-4.1221980216053877
0.99	-0.01899275	-5.8118544424979603	-5.7928616928033704

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
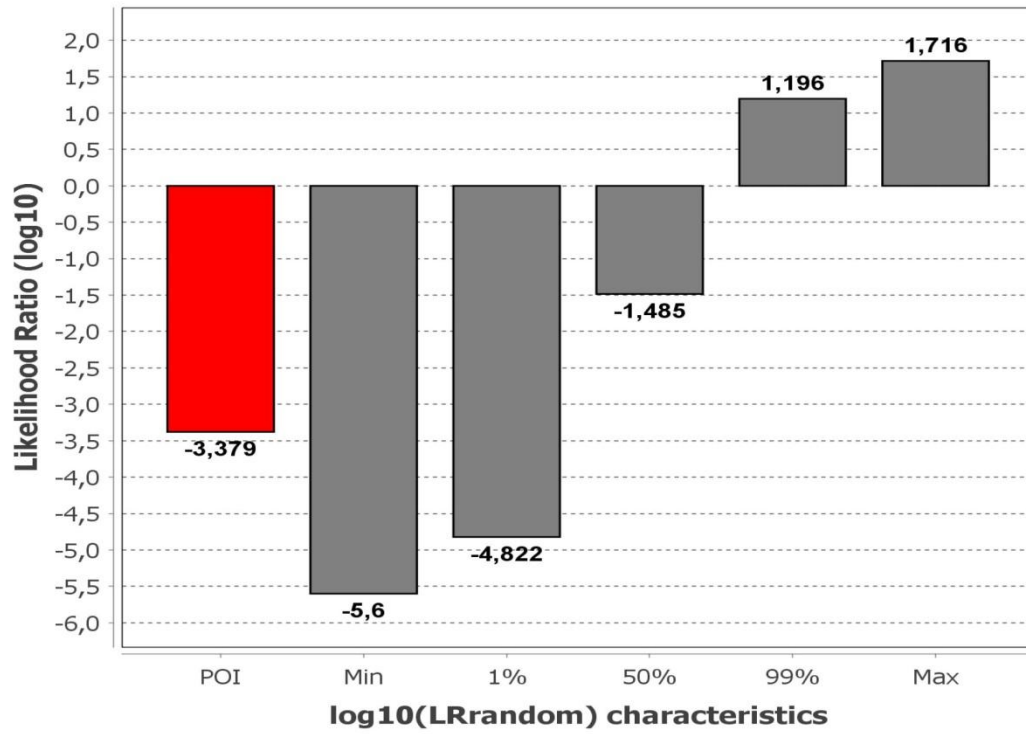
Date and time of analysis: 2016/09/01 15:35:04

Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing MJ2G1 with randomly generated profiles over 1000 iterations.
LRs>1: 15% (150).   LRs>LR(POI): 88% (882).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:35:04

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.47	0.89
Defense	0.26	0.86
Overall	0.26	0.89

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:35:04

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\05_Input_Sospetto MJ2G1.csv	MJ2G1

The reference profiles MJ4, MJ5, DG2, KJ2G2, DJ1G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	MJ2G1
CXX20	118 118	118 118	118 118	118 130
G10M	117 119	117 123	119 123	111 123
G10P	151 171	171 171	171 171	151 165
G10X	139 143	133 139	133 143	133 153
G1D	102 116	102 106	102 116	108 114
MU11	88 88	78 88	88 88	80 86
MU15	136 142	136 146	136 146	136 146
MU23	120 122	120 122	120 122	118 118
MU50	98 104	98 98	102 104	104 106
MU59	103 123	111 123	101 103	101 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:36:55

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
DJ1G1	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	5,47525E-003	1,93102E-001	2,83542E-002
G10M	1,54464E-002	2,05228E-001	7,52647E-002
G10P	5,17275E-001	5,78561E-001	8,94072E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	5,17223E-001	6,25196E-001	8,27298E-001
MU11	9,47126E-001	6,19433E-001	1,52902E000
MU15	9,44722E-001	8,51459E-001	1,10953E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	4,23201E-001	2,05698E-001	2,05740E000
MU59	9,35182E-001	8,61004E-001	1,08615E000
Overall Likelihood Ratio			4,18670E-003

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
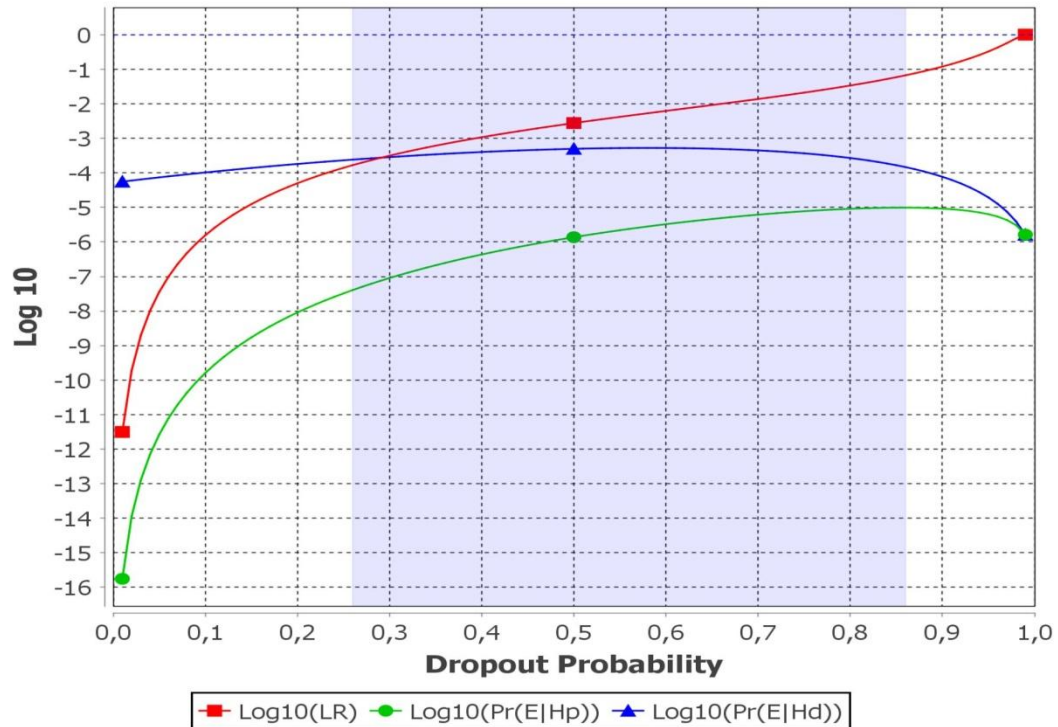Date and time of analysis: 2016/09/01 15:36:55
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of DJ1G1 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.26 ~ 0.86

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-11.50042	-15.753736499087262	-4.2533129653692611
0.10	-5.807791	-9.7959743542803572	-3.9881829197321136
0.20	-4.300590	-8.0419701789171753	-3.7413799839814338
0.30	-3.501193	-7.0445265561825047	-3.5433332229877456
0.40	-2.967508	-6.3630417515896180	-3.3955336974676959
0.50	-2.558459	-5.8620527707899929	-3.3035935503271782
0.60	-2.205522	-5.4852544224407386	-3.2797323230361969
0.70	-1.860817	-5.2099810913322341	-3.3491642491594193
0.80	-1.470333	-5.0396792391827993	-3.5693465721361592
0.90	-0.9227077	-5.0354429716164181	-4.1127353118269152
0.99	0.003209002	-5.7886484276730856	-5.7918574292756543

Analysis performed by: davoli
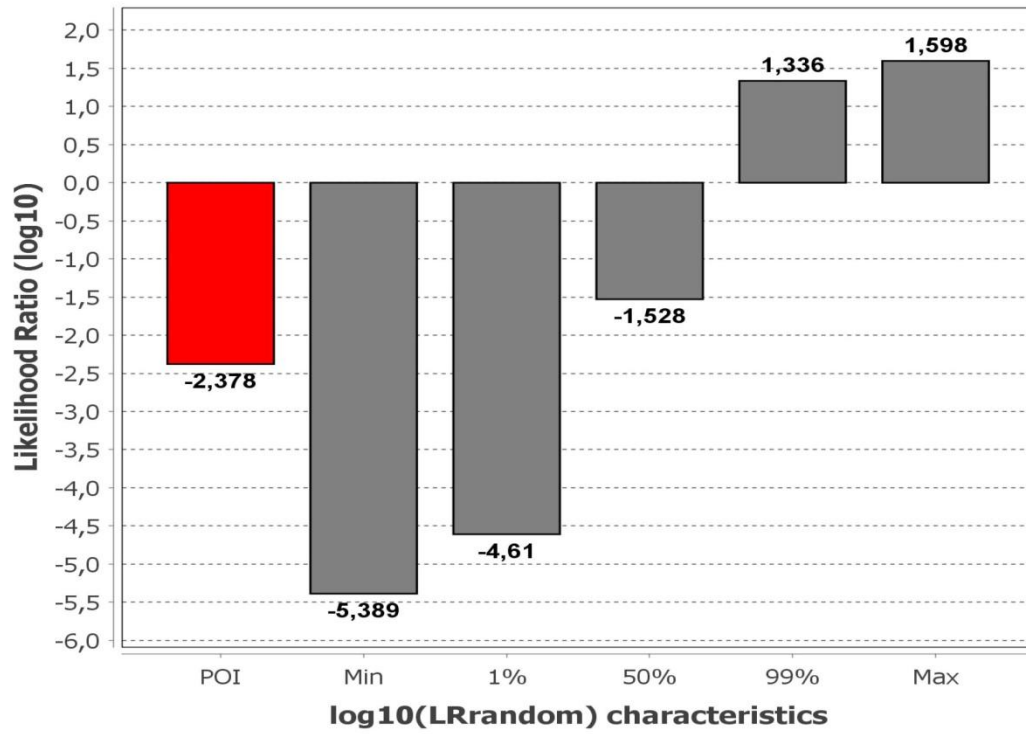
Date and time of analysis: 2016/09/01 15:36:55

Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results

Replacing DJ1G1 with randomly generated profiles over 1000 iterations.
LRs>1: 14% (141).   LRs>LR(POI): 66% (660).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:36:55

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.26	0.83
Defense	0.26	0.86
Overall	0.26	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:36:55

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\06_Input_Sospetto DJ1G1.csv	DJ1G1

The reference profiles MJ4, MJ5, DG2, KJ2G2, MJ2G1, M1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	DJ1G1
CXX20	118 118	118 118	118 118	130 130
G10M	117 119	117 123	119 123	123 123
G10P	151 171	171 171	171 171	165 171
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	102 108
MU11	88 88	78 88	88 88	78 78
MU15	136 142	136 146	136 146	142 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	84 104
MU59	103 123	111 123	101 103	101 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:39:05

Trace Analysed: R1234_Ua6797-98-99-800

Analysis 1 of 1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M1	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	4,27391E-001	2,23092E-001	1,91576E000
G10P	2,84501E-001	5,62235E-001	5,06019E-001
G10X	2,87289E-001	7,70217E-001	3,72997E-001
G1D	2,84473E-001	6,08235E-001	4,67702E-001
MU11	5,19626E-001	6,02407E-001	8,62584E-001
MU15	9,40448E-001	8,51280E-001	1,10475E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	6,55932E-001	2,22170E-001	2,95239E000
MU59	9,30993E-001	8,60839E-001	1,08149E000
Overall Likelihood Ratio			3,42601E-001

Analysis performed by: davoli

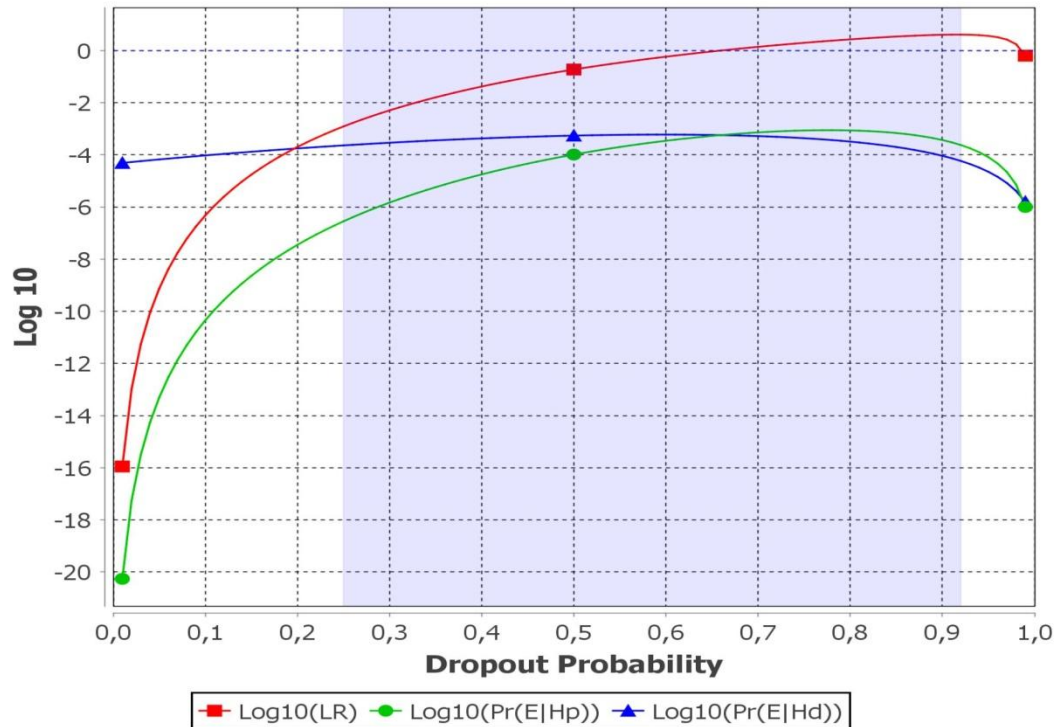Date and time of analysis: 2016/09/01 15:39:05

Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis

Varying dropout of M1 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.

■ Dropout Estimation 0.25 ~ 0.92

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-15.94906	-20.258076753697221	-4.3090139260557975
0.10	-6.323576	-10.345590251724368	-4.0220141116795131
0.20	-3.698160	-7.4514116639452234	-3.7532521102468110
0.30	-2.294742	-5.8301656066810156	-3.5354240561103287
0.40	-1.380089	-4.7498871618231843	-3.3697978045228555
0.50	-0.7269670	-3.9888212201765345	-3.2618542345248320
0.60	-0.2363423	-3.4601641876368729	-3.2238218974988095
0.70	0.1415797	-3.1396381146732155	-3.2812178435221883
0.80	0.4290717	-3.0636238311912999	-3.4926954820469213
0.90	0.6043691	-3.4321629322142999	-4.0365320191667990
0.99	-0.1960836	-5.9985468743143215	-5.8024632424340767

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

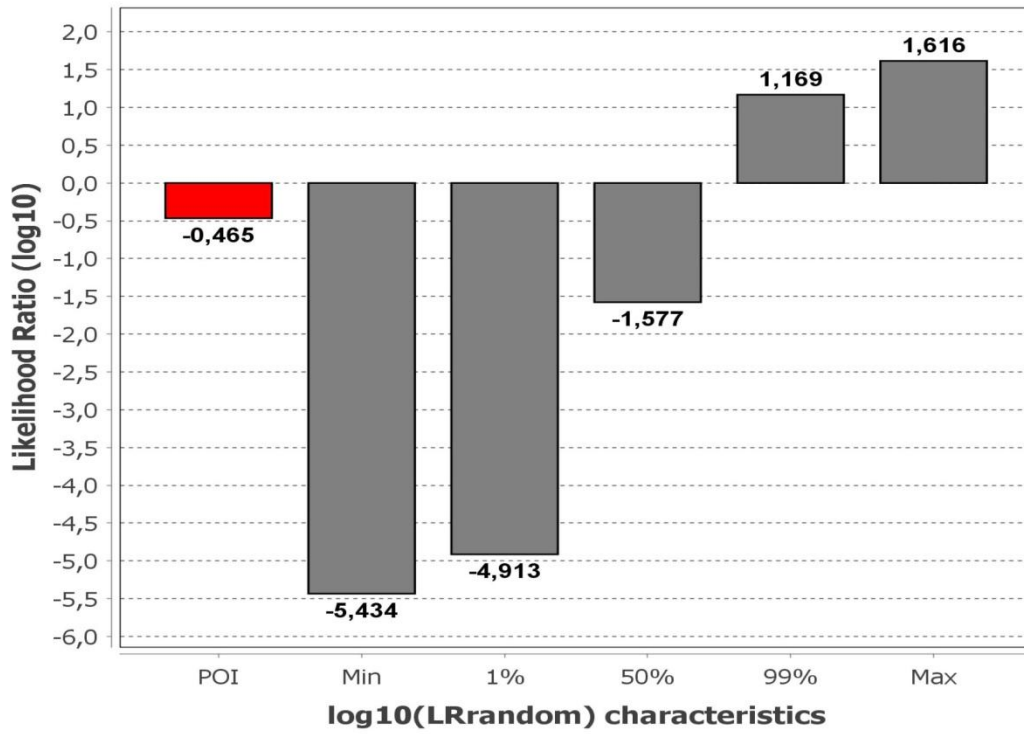Date and time of analysis: 2016/09/01 15:39:05

Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M1 with randomly generated profiles over 1000 iterations.
LRs>1: 13% (139).   LRs>LR(POI): 19% (192).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:39:05

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.55	0.92
Defense	0.25	0.86
Overall	0.25	0.92

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:39:05

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\07_Input_Sospetto_M1.csv	M1

The reference profiles MJ4, MJ5, DG2, KJ2G2, MJ2G1, DJ1G1, M3, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M1
CXX20	118 118	118 118	118 118	130 134
G10M	117 119	117 123	119 123	111 123
G10P	151 171	171 171	171 171	165 169
G10X	139 143	133 139	133 143	131 153
G1D	102 116	102 106	102 116	108 108
MU11	88 88	78 88	88 88	78 86
MU15	136 142	136 146	136 146	136 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	84 84
MU59	103 123	111 123	101 103	103 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

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Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:40:59

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M3	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

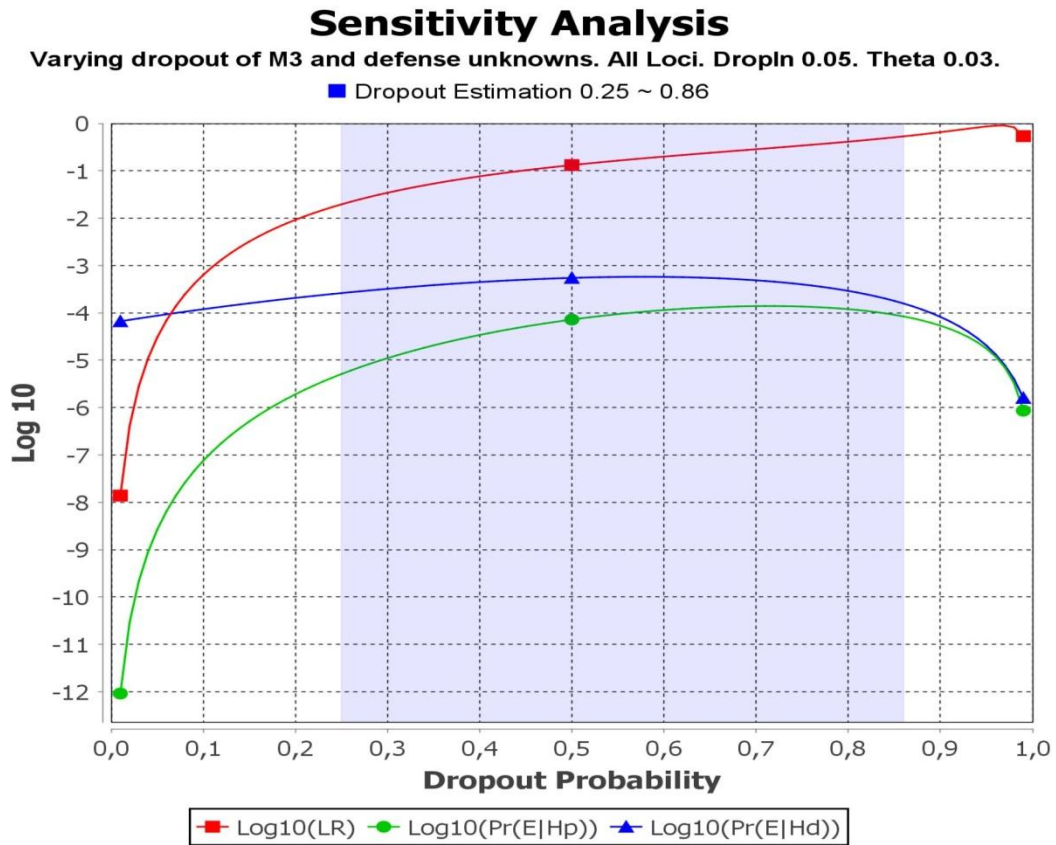| Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	5,19626E-001	5,78709E-001	8,97906E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	9,40406E-001	6,42385E-001	1,46393E000
MU11	5,17275E-001	6,02265E-001	8,58883E-001
MU15	5,19574E-001	8,31697E-001	6,24715E-001
MU23	5,22499E-001	4,97658E-001	1,04992E000
MU50	4,23182E-001	2,05697E-001	2,05731E000
MU59	9,37467E-001	8,61167E-001	1,08860E000
Overall Likelihood Ratio			1,63853E-001

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
Date and time of analysis: 2016/09/01 15:40:59
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of M3 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.25 ~ 0.86

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-7.859998	-12.038141834468994	-4.1781443292156046
0.10	-3.198719	-7.1217680795827487	-3.9230495436061345
0.20	-2.035316	-5.7199408328925516	-3.6846249426176811
0.30	-1.463697	-4.9565739667955135	-3.4928764839066346
0.40	-1.117071	-4.4669673790754194	-3.3498965845549428
0.50	-0.8803325	-4.1420614879767274	-3.2617290286339839
0.60	-0.7004080	-3.9413453693163291	-3.2409373716479636
0.70	-0.5448633	-3.8579476750391692	-3.3130843741800406
0.80	-0.3855176	-3.9217182794409137	-3.5362006698226644
0.90	-0.1848919	-4.2696529203899959	-4.0847610675469692
0.99	-0.2681135	-6.0642398775348445	-5.7961263454040006

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
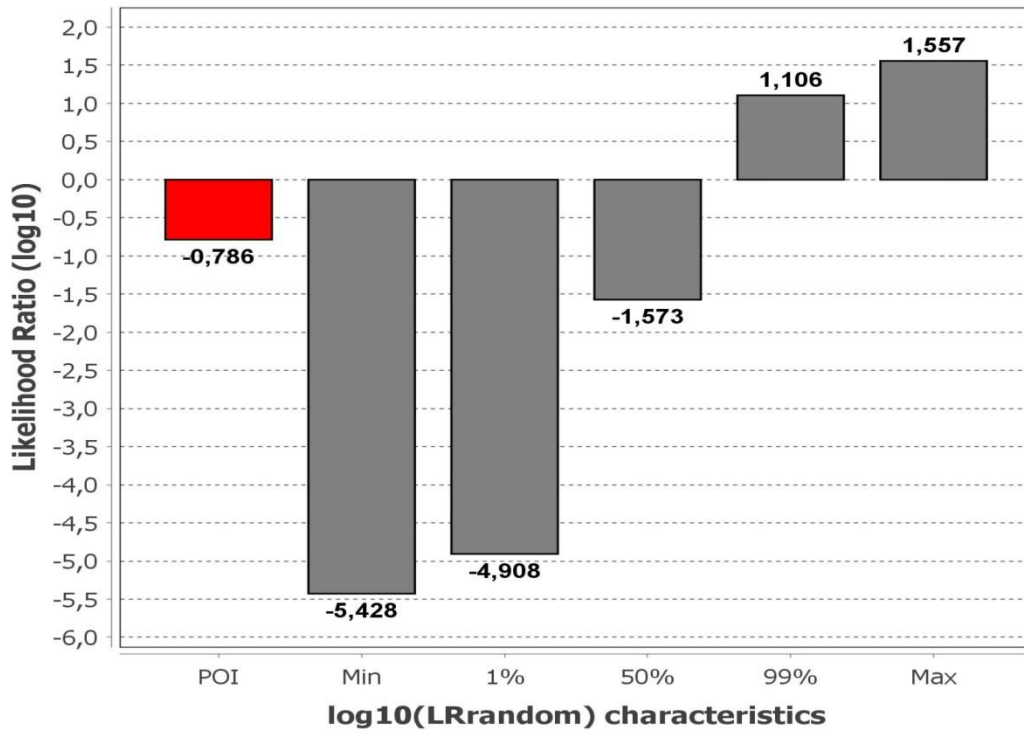Date and time of analysis: 2016/09/01 15:40:59
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M3 with randomly generated profiles over 1000 iterations.
LRs>1: 12% (125).   LRs>LR(POI): 22% (226).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:40:59

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.29	0.83
Defense	0.25	0.86
Overall	0.25	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:40:59

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\08_Input_Sospetto M3.csv	M3

The reference profiles MJ4, MJ5, DG2, KJ2G2, MJ2G1, DJ1G1, M1, M4, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M3
CXX20	118 118	118 118	118 118	130 134
G10M	117 119	117 123	119 123	117 123
G10P	151 171	171 171	171 171	151 167
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	102 102
MU11	88 88	78 88	88 88	86 88
MU15	136 142	136 146	136 146	138 142
MU23	120 122	120 122	120 122	120 124
MU50	98 104	98 98	102 104	84 98
MU59	103 123	111 123	101 103	101 101

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:43:06

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M4	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	5,17275E-001	5,78561E-001	8,94072E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	5,19574E-001	6,25351E-001	8,30852E-001
MU11	2,84501E-001	5,85612E-001	4,85819E-001
MU15	9,47031E-001	8,51633E-001	1,11202E000
MU23	9,49999E-001	5,13126E-001	1,85139E000
MU50	1,50960E-002	1,89014E-001	7,98668E-002
MU59	9,30993E-001	8,60839E-001	1,08149E000
Overall Likelihood Ratio			6,34071E-003

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
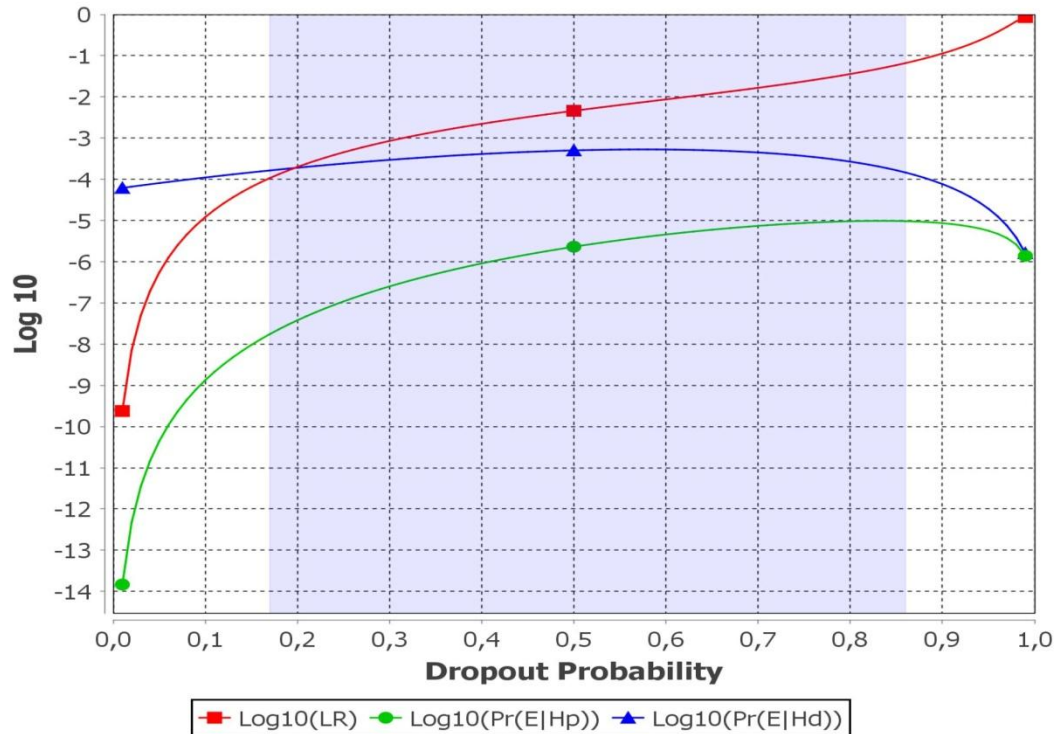Date and time of analysis: 2016/09/01 15:43:06
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of M4 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.17 ~ 0.86

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-9.623068	-13.832466595457253	-4.2093986079060581
0.10	-4.917590	-8.8743168187287455	-3.9567268791749943
0.20	-3.700905	-7.4209107148424093	-3.7200053221801407
0.30	-3.069839	-6.5991251397545669	-3.5292859224240635
0.40	-2.655252	-6.0421445722512485	-3.3868921337422364
0.50	-2.338642	-5.6376298159350559	-3.2989874463486223
0.60	-2.061418	-5.3395756351990399	-3.2781577381623039
0.70	-1.780958	-5.1308107244652596	-3.3498531473407577
0.80	-1.446414	-5.0180611582964962	-3.5716467186119000
0.90	-0.9486838	-5.0645364595118413	-4.1158526301747446
0.99	-0.06545058	-5.8587366364229929	-5.7932860564045132

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
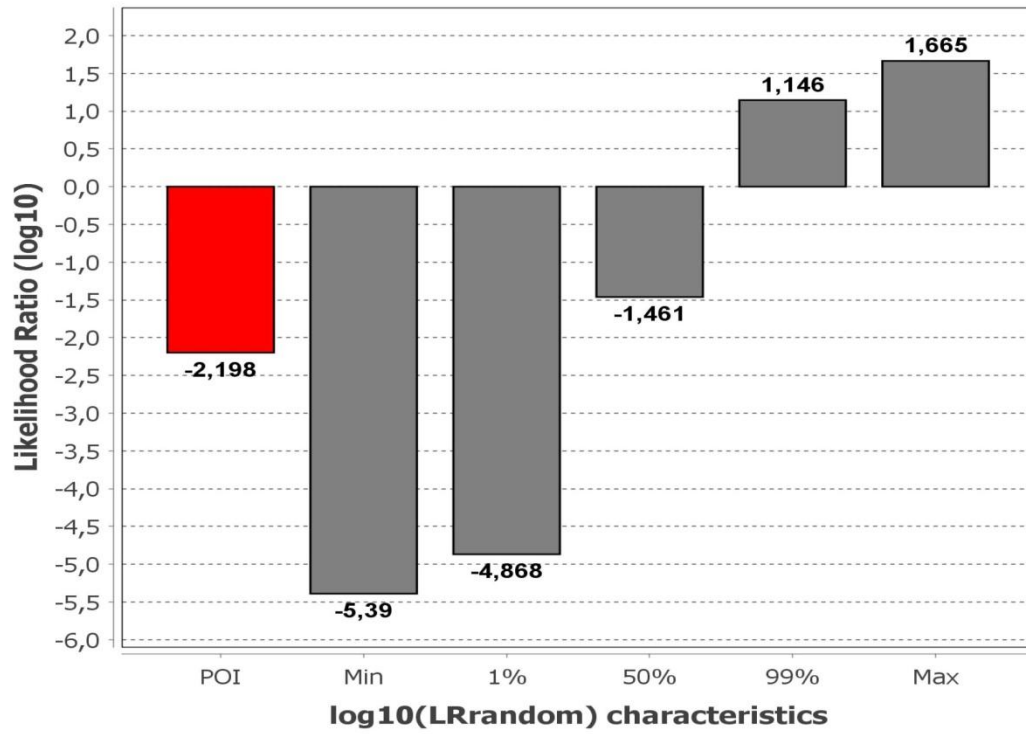Date and time of analysis: 2016/09/01 15:43:06
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M4 with randomly generated profiles over 1000 iterations.
LRs>1: 15% (154).   LRs>LR(POI): 64% (649).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:43:06

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

	Dropout Probability	
Hypothesis	Minimum (5%)	Maximum (95%)
Prosecution	0.17	0.79
Defense	0.25	0.86
Overall	0.17	0.86

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:43:06

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\09_Input_Sospetto M4.csv	M4

The reference profiles MJ4, MJ5, DG2, KJ2G2, MJ2G1, DJ1G1, M1, M3, M7, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M4
CXX20	118 118	118 118	118 118	130 134
G10M	117 119	117 123	119 123	117 123
G10P	151 171	171 171	171 171	167 171
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	106 108
MU11	88 88	78 88	88 88	86 86
MU15	136 142	136 146	136 146	142 142
MU23	120 122	120 122	120 122	120 120
MU50	98 104	98 98	102 104	98 98
MU59	103 123	111 123	101 103	103 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:45:44

Trace Analysed: R1234_Ua6797-98-99-800

Analysis 1 of 1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M7	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies: C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	4,27391E-001	2,23092E-001	1,91576E000
G10P	5,19626E-001	5,78709E-001	8,97906E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	5,17223E-001	6,25196E-001	8,27298E-001
MU11	9,44775E-001	6,19291E-001	1,52558E000
MU15	9,44722E-001	8,51459E-001	1,10953E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	4,23201E-001	2,05698E-001	2,05740E000
MU59	5,12023E-001	8,41070E-001	6,08776E-001
Overall Likelihood Ratio			2,35923E000

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
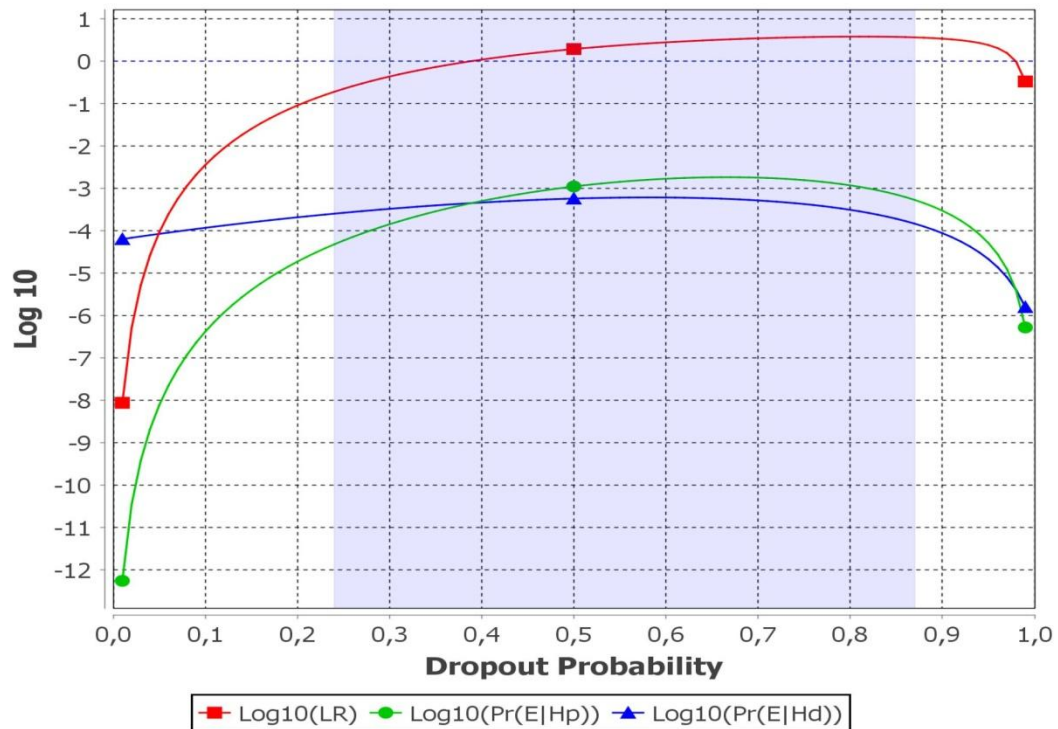Date and time of analysis: 2016/09/01 15:45:44
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of M7 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.24 ~ 0.87

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-8.057261	-12.253669385221366	-4.1964083984498667
0.10	-2.448564	-6.3790441722800954	-3.9304803169829298
0.20	-1.045119	-4.7276527079477688	-3.6825336837205790
0.30	-0.3632202	-3.8464132452280623	-3.4831929961829661
0.40	0.03510404	-3.2989547561487442	-3.3340587943484449
0.50	0.2844907	-2.9563732915525728	-3.2408639710750368
0.60	0.4426529	-2.7733520458722096	-3.2160049516540163
0.70	0.5372182	-2.7478250284158192	-3.2850432334603678
0.80	0.5768852	-2.9294859557975598	-3.5063711611850161
0.90	0.5295188	-3.5270009644297584	-4.0565197747463468
0.99	-0.4805225	-6.2798521286102522	-5.7993296291938474

Case Number: GlobalComp10Loci_ADO055

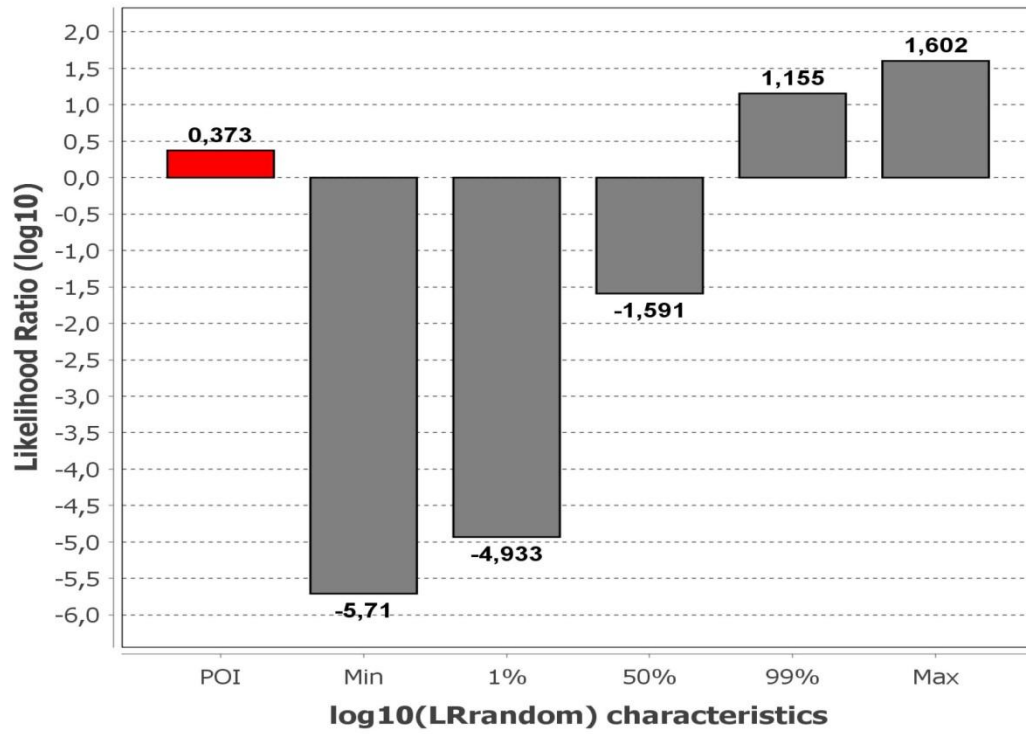Analysis performed by: davoli
Date and time of analysis: 2016/09/01 15:45:44
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M7 with randomly generated profiles over 1000 iterations.
LRs>1: 13% (134).   LRs>LR(POI): 7% (79).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:45:44

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.40	0.87
Defense	0.24	0.86
Overall	0.24	0.87

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:45:44

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\10_Input_Sospetto M7.csv	M7

The reference profiles MJ4, MJ5, DG2, KJ2G2, MJ2G1, DJ1G1, M1, M3, M4, M8, M9 were disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M7
CXX20	118 118	118 118	118 118	120 134
G10M	117 119	117 123	119 123	111 119
G10P	151 171	171 171	171 171	151 165
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	102 108
MU11	88 88	78 88	88 88	78 88
MU15	136 142	136 146	136 146	142 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	84 104
MU59	103 123	111 123	101 103	113 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:50:50

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M8	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	2,35125E-001	2,10366E-001	1,11769E000
G10M	4,27391E-001	2,23092E-001	1,91576E000
G10P	5,19626E-001	5,78709E-001	8,97906E-001
G10X	9,49801E-001	8,08703E-001	1,17447E000
G1D	5,19574E-001	6,25351E-001	8,30852E-001
MU11	9,47126E-001	6,19433E-001	1,52902E000
MU15	9,40448E-001	8,51280E-001	1,10475E000
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	8,30316E-003	1,86530E-001	4,45138E-002
MU59	5,14327E-001	8,41233E-001	6,11397E-001
Overall Likelihood Ratio			5,13779E-002

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
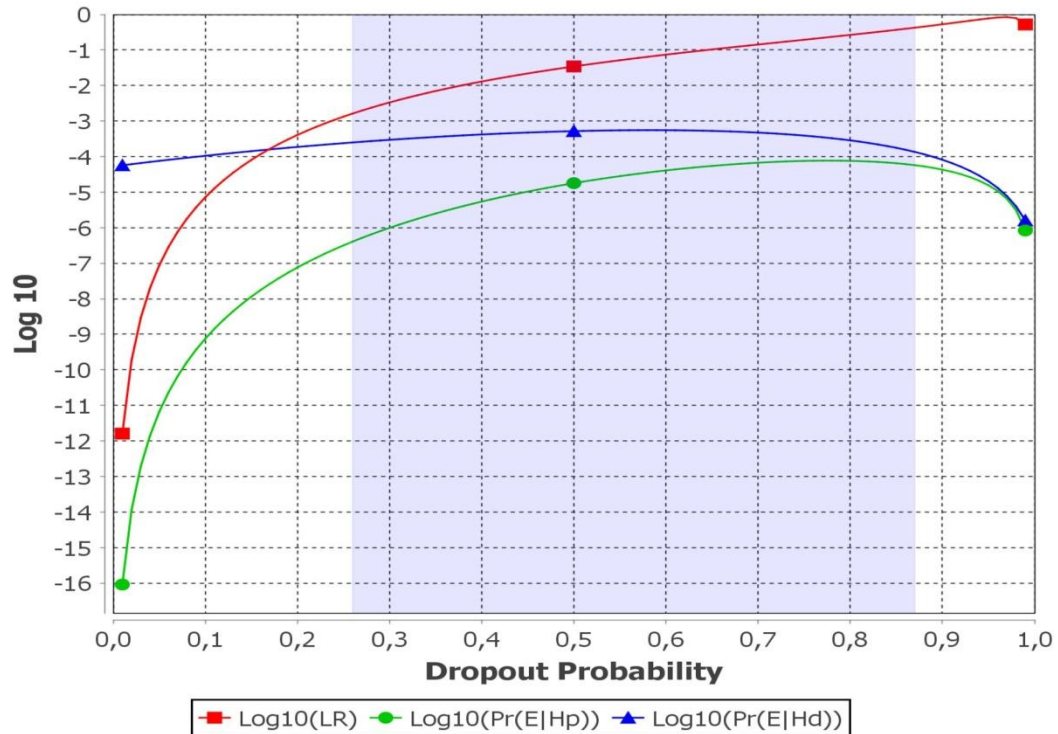Date and time of analysis: 2016/09/01 15:50:50
Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of M8 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.26 ~ 0.87

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-11.79494	-16.039436967685311	-4.2444924645989265
0.10	-5.145894	-9.1234581582351808	-3.9775640920491945
0.20	-3.391453	-7.1200101537029647	-3.7285568193185105
0.30	-2.476717	-6.0049004303751472	-3.5281838586803058
0.40	-1.887843	-5.2658564585888134	-3.3780135329272851
0.50	-1.463840	-4.7475710597719205	-3.2837310744131014
0.60	-1.131285	-4.3889333973421562	-3.2576486477800132
0.70	-0.8469368	-4.1720835030407048	-3.3251467241490022
0.80	-0.5761973	-4.1203120245208095	-3.5441146817540269
0.90	-0.2774990	-4.3663838642940904	-4.0888848355738138
0.99	-0.2818783	-6.0785838411518753	-5.7967055626123995

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli
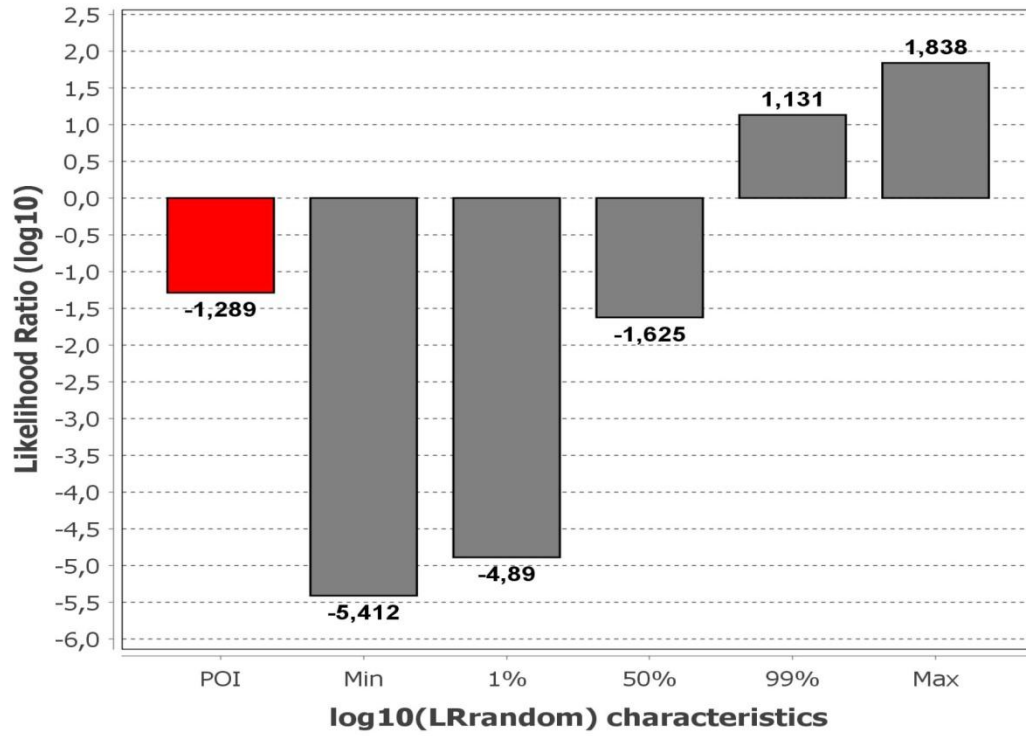
Date and time of analysis: 2016/09/01 15:50:50

Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M8 with randomly generated profiles over 1000 iterations.
LRs>1: 13% (132).   LRs>LR(POI): 41% (417).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:50:50

Trace Analysed: R1234_Ua6797-98-99-800

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

	Dropout Probability	
Hypothesis	Minimum (5%)	Maximum (95%)
Prosecution	0.40	0.87
Defense	0.26	0.86
Overall	0.26	0.87

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:50:50

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\11_Input_Sospetto M8.csv	M8

The reference profile M9 was disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M8
CXX20	118 118	118 118	118 118	120 134
G10M	117 119	117 123	119 123	111 119
G10P	151 171	171 171	171 171	151 165
G10X	139 143	133 139	133 143	139 143
G1D	102 116	102 106	102 116	106 108
MU11	88 88	78 88	88 88	78 78
MU15	136 142	136 146	136 146	136 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	104 106
MU59	103 123	111 123	101 103	101 113

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005

LRmix Studio

version 2.1.3-CommunityEdition

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:52:23

Trace Analysed: R1234_Ua6797-98-99-800

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
M9	0.55
0 Unknown	

Defense Hypothesis

Profile	Dropout Probability
BJ1	0.01
M33	0.01
F22	0.01
1 Unknown	0.55

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.03

Allele Frequencies   C:\Users\davoli\Documents\Lavoro\Analisi
                         Infanticidio\LRMixStudio\Input\Input_Freq_LRmix.csv

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
CXX20	5,47525E-003	1,93102E-001	2,83542E-002
G10M	1,54468E-002	2,05228E-001	7,52663E-002
G10P	5,17275E-001	5,78561E-001	8,94072E-001
G10X	5,22367E-001	7,89344E-001	6,61773E-001
G1D	2,84473E-001	6,08235E-001	4,67702E-001
MU11	5,19626E-001	6,02407E-001	8,62584E-001
MU15	5,17246E-001	8,31522E-001	6,22047E-001
MU23	2,87374E-001	4,82421E-001	5,95692E-001
MU50	8,30316E-003	1,86530E-001	4,45138E-002
MU59	5,12023E-001	8,41070E-001	6,08776E-001
Overall Likelihood Ratio			5,11524E-006

Analysis performed by: davoli

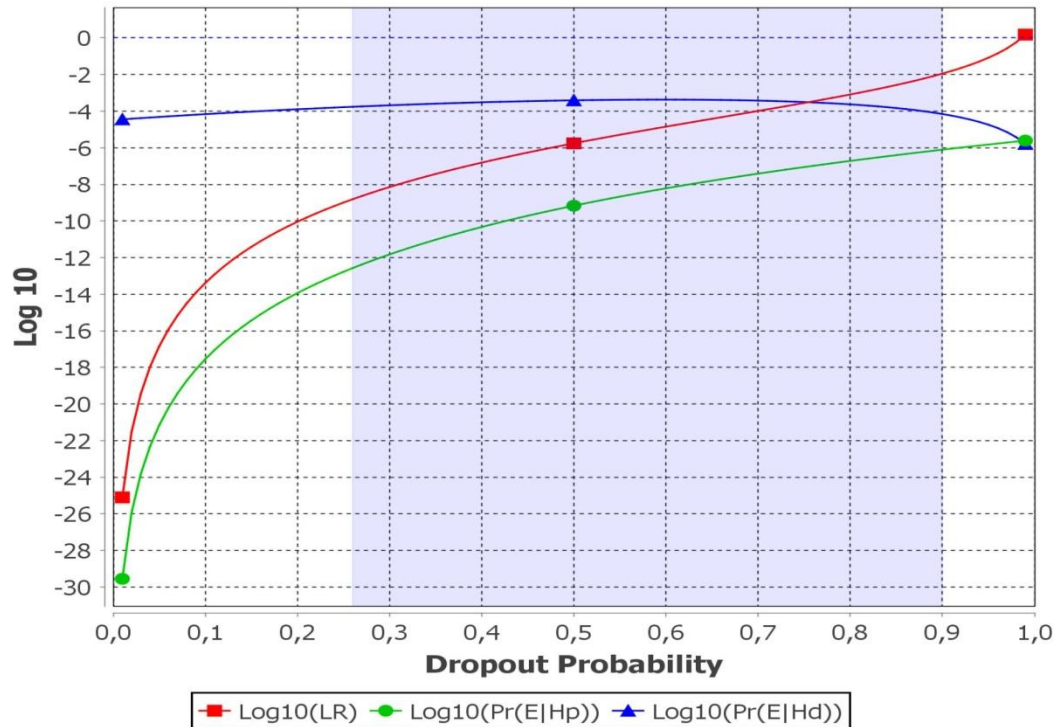Date and time of analysis: 2016/09/01 15:52:23

Trace Analysed: R1234_Ua6797-98-99-800

Sensitivity Analysis

Sensitivity Analysis
Varying dropout of M9 and defense unknowns. All Loci. DropIn 0.05. Theta 0.03.
■ Dropout Estimation 0.26 ~ 0.90

The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-25.10469	-29.552512060084755	-4.4478186898734834
0.10	-13.38917	-17.552926592273884	-4.1637569724612184
0.20	-10.04356	-13.941027649308848	-3.8974658983115668
0.30	-8.147067	-11.828393981941104	-3.6813271053607299
0.40	-6.812971	-10.329591021114769	-3.5166202483846817
0.50	-5.758373	-9.1671331815419723	-3.4087606585778873
0.60	-4.847662	-8.2174209844253933	-3.3697590470415921
0.70	-3.989979	-7.4145227041270844	-3.4245440794385100
0.80	-3.089101	-6.7190829763637740	-3.6299818084512169
0.90	-1.949462	-6.1057167845524498	-4.1562546317486512
0.99	0.1809016	-5.6094226107497480	-5.7903241743195392

Analysis performed by: davoli
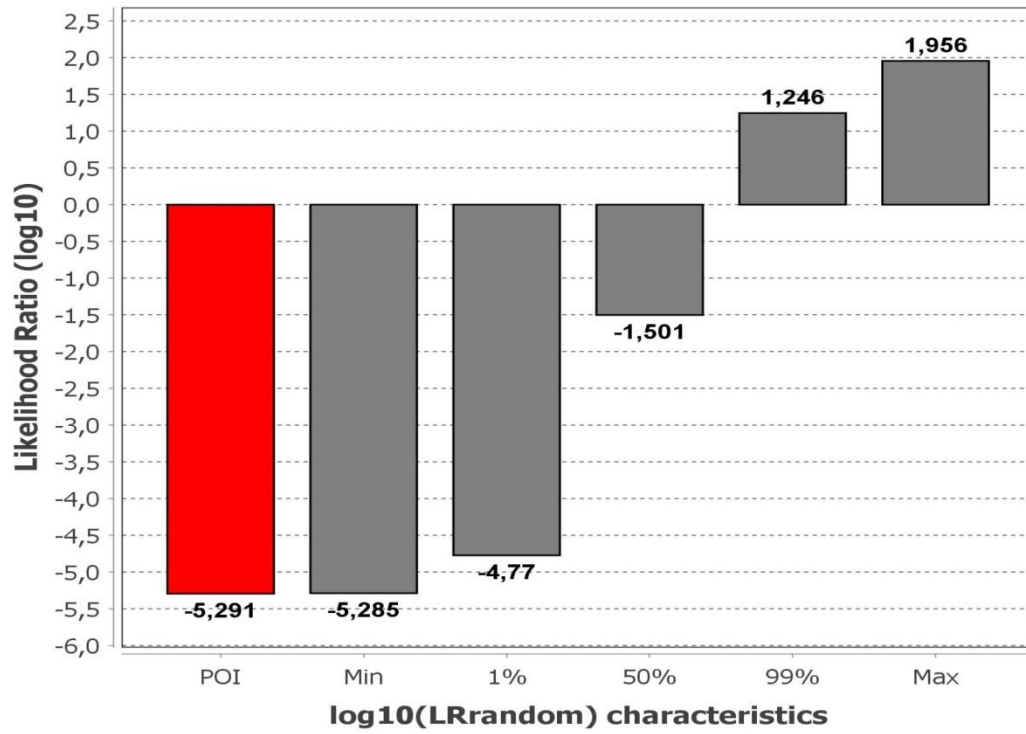Date and time of analysis: 2016/09/01 15:52:23
Trace Analysed: R1234_Ua6797-98-99-800

Non-contributor test

Non-contributor test results
Replacing M9 with randomly generated profiles over 1000 iterations.
LRs>1: 12% (122).   LRs>LR(POI): 100% (1000).

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:52:23

Trace Analysed: R1234_Ua6797-98-99-800

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Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 29 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.49	0.90
Defense	0.26	0.86
Overall	0.26	0.90

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\0_Input_SWABS_GlobalComp10Loci_010916.txt	R1234_Ua6797-98-99-800

The contents of the profiles is listed below:

	R1234_Ua6797-98-99-800
CXX20	118 134
G10M	111 117 119 123
G10P	151 171
G10X	133 139 143
G1D	102 106 116
MU11	78 88
MU15	136 142 146
MU23	120 122
MU50	84 98 102 104
MU59	101 103 111 123

Case Number: GlobalComp10Loci_ADO055

Analysis performed by: davoli

Date and time of analysis: 2016/09/01 15:52:23

Trace Analysed: R1234_Ua6797-98-99-800

Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	BJ1
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	M33
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\Input_Vittime_040716.csv	F22
C:\Users\davoli\Documents\Lavoro\Analisi Infanticidio\LRMixStudio\Input\12_Input_Sospetto M9.csv	M9

The reference profile M8 was disabled for this analysis.

The contents of the reference profiles is listed below:

	BJ1	M33	F22	M9
CXX20	118 118	118 118	118 118	120 130
G10M	117 119	117 123	119 123	119 123
G10P	151 171	171 171	171 171	165 171
G10X	139 143	133 139	133 143	143 153
G1D	102 116	102 106	102 116	108 108
MU11	88 88	78 88	88 88	78 80
MU15	136 142	136 146	136 146	132 146
MU23	120 122	120 122	120 122	118 124
MU50	98 104	98 98	102 104	104 106
MU59	103 123	111 123	101 103	113 123

More Information

For more information about the probabilistic model implemented in LRmix Studio see:

- P. Gill & H.Haned. A new methodological framework to interpret complex DNA profiles using likelihood ratios. Forensic Sci. Int. Genet. (2013).

- H. Haned, et al., Exploratory data analysis for the interpretation of low template DNA mixtures, Forensic Sci. Int. Genet. (2012).

- P. Gill et al, DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR-typing results that may include drop-out and/or drop-in using probabilistic methods, Forensic Sci. Int. Genetics (2012).

- Haned, H. & Gill, P. Analysis of complex DNA mixtures using the Forensim package, Forensic Sci. Int. Genetics. Supplement Series (2011).

- P. Gill, A. Kirkham and J. Curran, LoComatioN: a software tool for the analysis of low copy number DNA-profiles, Forensic Sci. Int., (2007).

- J.M. Curran, P. Gill and M.R. Bill, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, Forensic Sci. Int., (2005).

- Buckleton, J.; Triggs, C. M. & Walsh, S. J. Forensic DNA evidence interpretation, Chapter 4: 'Relatedness', CRC PRESS, 2005