LRmix Studio

version 2.1.3-CommunityEdition

Case Number: Example_2B

Analysis performed by: pc

Date and time of analysis: 2020/05/19 19:24:25

Traces Analysed: C10.5.19, C10.5.19bis

Analysis   1 of   1

Prosecution Hypothesis

Profile	Dropout Probability
C10.AC.19	0.20
1 Unknown	0.20

Defense Hypothesis

Profile	Dropout Probability
2 Unknown	0.20

Match Parameters

Probability of dropin: 0.05

Theta correction: 0.01

Allele Frequencies   C:\Users\pc\Desktop\didattica_da_2018\Lezioni_2019-20\BIO\workshop_1_solutions\Exercise_2\LRmix_data\pop_freq.txt

Results

Locus	Pr(E|Hp)	Pr(E|Hd)	LR
D10S1248	3,83029E-002	2,67793E-002	1,43032E000
D16S539	1,91895E-003	7,37056E-004	2,60353E000
D8S1179	5,57794E-005	5,76910E-005	9,66865E-001
D18S51	2,35682E-005	3,31218E-005	7,11563E-001
D22S1045	2,20641E-002	6,81663E-003	3,23680E000
TH01	2,50974E-003	1,72690E-004	1,45332E001
D2S441	8,47143E-002	6,27031E-003	1,35104E001
D3S1358	4,95851E-004	2,25562E-004	2,19829E000
D1S1656	1,25148E-006	1,64933E-006	7,58779E-001
Overall Likelihood Ratio			2,71594E003

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Sensitivity Analysis

Sensitivity Analysis
Varying dropout of C10.AC.19 and all unknowns. All Loci. DropIn 0.05. Theta 0.01.
■ Dropout Estimation 0.20 ~ 0.56
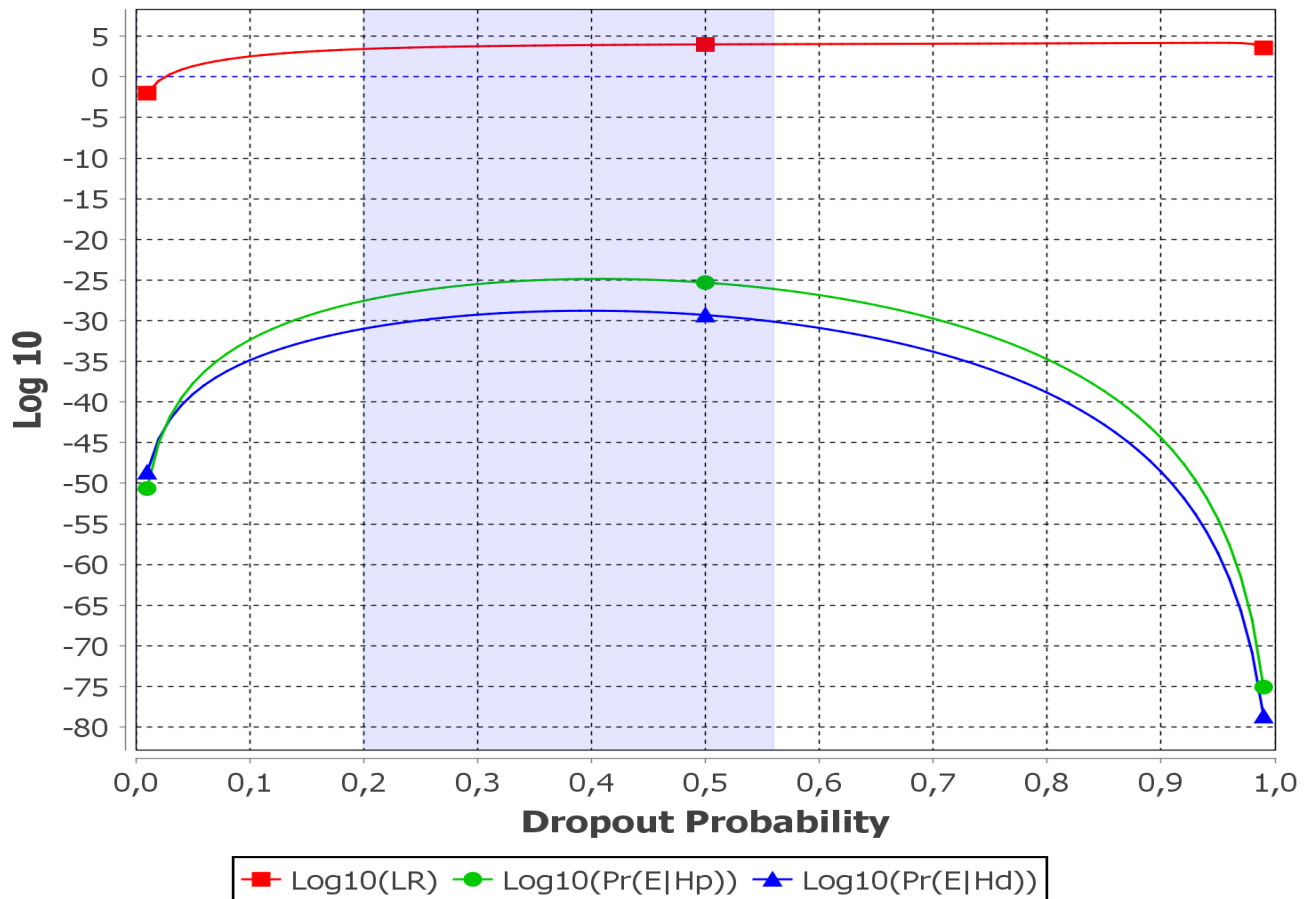
The following table contains some of the values for the graph above.

	Log10(LR)	Log10(Pr(E|Hp))	Log10(Pr(E|Hd))
0.01	-2.004784	-50.647077916401762	-48.642293849360250
0.10	2.516223	-32.356974731050250	-34.873197558969309
0.20	3.433921	-27.550859747304336	-30.984780397404318
0.30	3.767922	-25.492492164185996	-29.260414166796639
0.40	3.916230	-24.854917363120161	-28.771147073629453
0.50	3.994328	-25.307942702424583	-29.302270414240268
0.60	4.043259	-26.845238701790641	-30.888497829065141
0.70	4.081296	-29.729886428147029	-33.811182873381689
0.80	4.120256	-34.731884450532831	-38.852140778901159
0.90	4.171705	-44.409828738288112	-48.581533796919636
0.99	3.570473	-75.074032635694621	-78.644505906088269

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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 19 alleles observed in average across the 2 replicates.

	Dropout Probability	
Hypothesis	Minimum (5%)	Maximum (95%)
Prosecution	0.25	0.56
Defense	0.20	0.53
Overall	0.20	0.56

Rare Alleles

All observed alleles are present in the population statistics.

Replicates

The following replicates were loaded for this analysis:

Filename	Replicate
C:\Users\pc\Desktop\didattica_da_2018\Lezioni_2019-20\BIO\workshop_1_solutions\Exercise_2\LRmix_data\stain_2_reps.txt	C10.5.19
C:\Users\pc\Desktop\didattica_da_2018\Lezioni_2019-20\BIO\workshop_1_solutions\Exercise_2\LRmix_data\stain_2_reps.txt	C10.5.19bis

The contents of the profiles is listed below:

	C10.5.19	C10.5.19bis
D10S1248	14 15 16	14 15 16
D16S539	9 10 11 12	9 11 12
D8S1179	13	null
D18S51	13	14
D22S1045	15 16 17	15 17
TH01	8 9 9.3 10	9 9.3 10
D2S441	10 11 15	10 11 15
D3S1358	14	14
D1S1656	17	11 14

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Reference Profiles

The following reference profiles were loaded for this analysis:

Filename	Reference Profile
C:\Users\pc\Desktop\didattica_da_2018\Lezioni_2019-20\BIO\workshop_1_solutions\Exercise_2\LRmix_data\suspect.txt	C10.AC.19

The contents of the reference profiles is listed below:

	C10.AC.19
D10S1248	16 16
D16S539	9 12
D8S1179	10 13
D18S51	12 14
D22S1045	16 17
TH01	9 10
D2S441	10 15
D3S1358	14 17
D1S1656	11 17.3

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