



Case Number: Exercise_1

Analysis performed by: pc

Date and time of analysis: 2020/05/19 19:02:25

Trace Analysed: C29.FD.14

Analysis 1 of 1

Prosecution Hypothesis

Profile	Dropout Probability
C23.AB.15	0.01
1 Unknown	0.01

Defense Hypothesis

Profile	Dropout Probability
2 Unknown	0.01

The defense hypothesis specifies that one unknown contributor is the Sibling of C23.AB.15

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_1\LRmix\pop_freq.txt

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Results

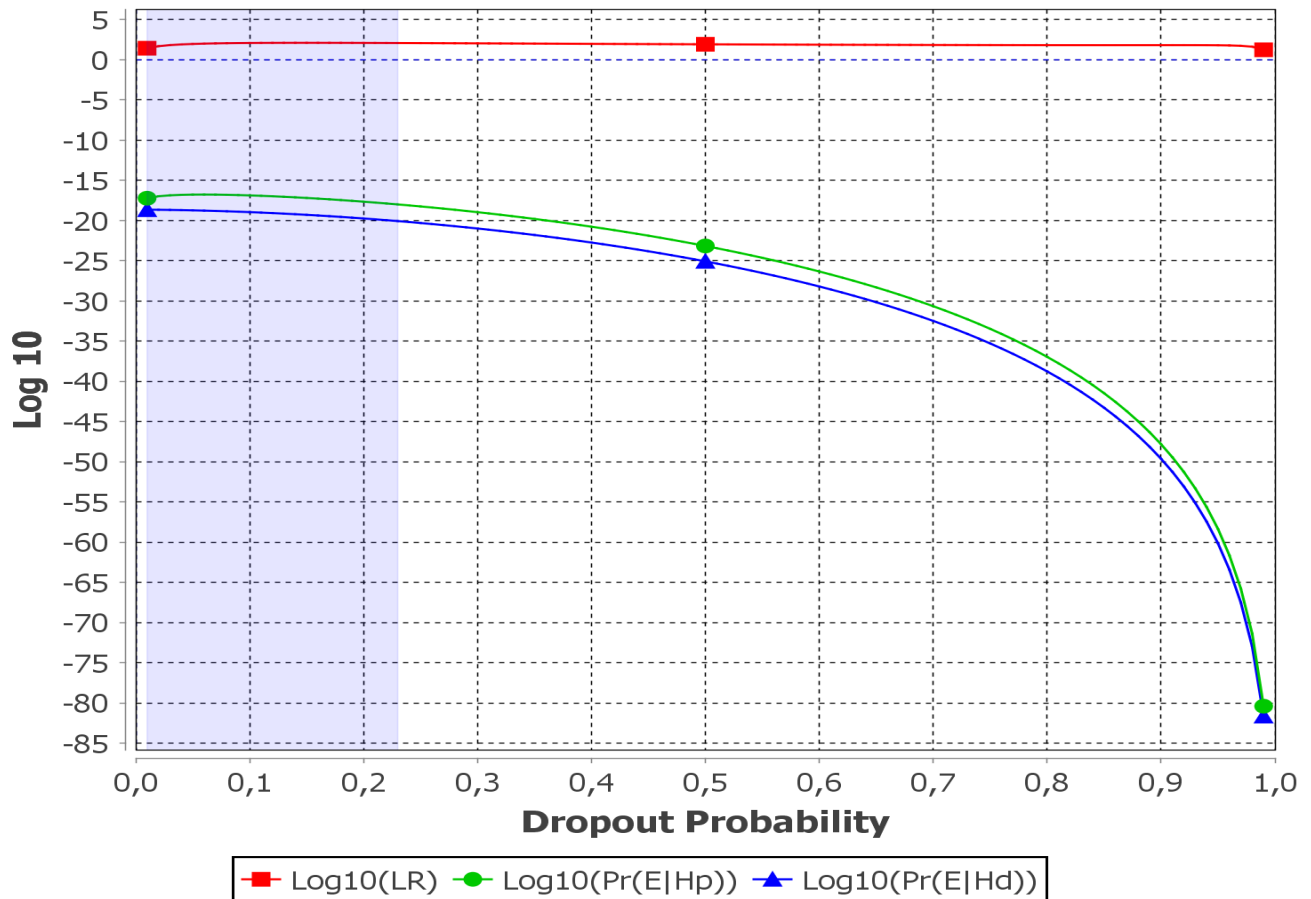
Locus	Pr(E Hp)	Pr(E Hd)	LR
VWA	6,04901E-002	6,22344E-002	9,71971E-001
D16S539	8,11300E-002	1,15431E-001	7,02845E-001
D2S1338	1,01006E-001	4,94592E-002	2,04221E000
D8S1179	3,05113E-002	2,15119E-002	1,41834E000
D21S11	1,23147E-001	5,50980E-002	2,23505E000
D18S51	7,97174E-004	1,10921E-002	7,18687E-002
D19S433	2,48111E-002	1,18378E-002	2,09593E000
TH01	1,52597E-001	7,27247E-002	2,09828E000
FGA	1,29449E-001	6,00586E-002	2,15538E000
D3S1358	2,56500E-001	1,41192E-001	1,81667E000
D7S820	6,66281E-002	6,11668E-002	1,08929E000
CSF1PO	2,53139E-001	1,76742E-001	1,43225E000
D13S317	8,91996E-002	5,57673E-002	1,59950E000
TPOX	3,89501E-001	2,57483E-001	1,51273E000
D5S818	5,41977E-002	4,24238E-002	1,27753E000
Overall Likelihood Ratio			2,63962E001

Sensitivity Analysis

Sensitivity Analysis

Varying dropout of C23.AB.15 and all unknowns. All Loci. DropIn 0.05. Theta 0.01.

■ Dropout Estimation 0.01 ~ 0.23



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

	Log10(LR)	Log10(Pr(E Hp))	Log10(Pr(E Hd))
0.01	1.421541	-17.227101973504399	-18.648642582255412
0.10	2.078874	-16.876463243597303	-18.955337292161708
0.20	2.086549	-17.658239429034757	-19.744788584719575
0.30	2.031639	-18.962004341296424	-20.993643797937597
0.40	1.969815	-20.769793365756690	-22.739608399045426
0.50	1.913233	-23.166581639931187	-25.079815132314124
0.60	1.865607	-26.338337941768156	-28.203944977071031
0.70	1.829228	-30.656332310212267	-32.485560725785703
0.80	1.808051	-36.956872800508349	-38.764924131776687
0.90	1.808571	-47.819792951728352	-49.628363568324388
0.99	1.227109	-80.402526126997003	-81.629635169688071

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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 42 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.01	0.20
Defense	0.02	0.23
Overall	0.01	0.23

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\Exercise_1\LRmix\C29.FD.14_stain_input_LRmix.txt	C29.FD.14

The contents of the profiles is listed below:

	C29.FD.14
VWA	15 17 18
D16S539	11 12 13
D2S1338	17 20 25
D8S1179	11 13 14 15
D21S11	29 32.2
D18S51	13 14
D19S433	10 12 14 15
TH01	7 8 9
FGA	20 21 24
D3S1358	15 16
D7S820	8 11 12
CSF1PO	10 11
D13S317	8 12
TPOX	8 9
D5S818	10 11 12 13

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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\Exercise_1\LRmix\C23.AB.15_suspect_input_LRmix.txt	C23.AB.15

The contents of the reference profiles is listed below:

	C23.AB.15
VWA	18 18
D16S539	11 11
D2S1338	17 25
D8S1179	13 15
D21S11	29 32.2
D18S51	13 15
D19S433	10 14
TH01	7 8
FGA	20 24
D3S1358	15 16
D7S820	12 12
CSF1PO	10 10
D13S317	12 12
TPOX	9 9
D5S818	11 13

Notes:

C23.AB.15 loci converted to homozygotic: [VWA, D16S539, D7S820, CSF1PO, D13S317, TPOX]

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