



Case Number: Example_2A

Analysis performed by: pc

Date and time of analysis: 2020/05/19 19:20:43

Trace Analysed: C10.5.19

Analysis 1 of 1

Prosecution Hypothesis

Profile	Dropout Probability
C10.AC.19	0.12
1 Unknown	0.12

Defense Hypothesis

Profile	Dropout Probability
2 Unknown	0.12

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

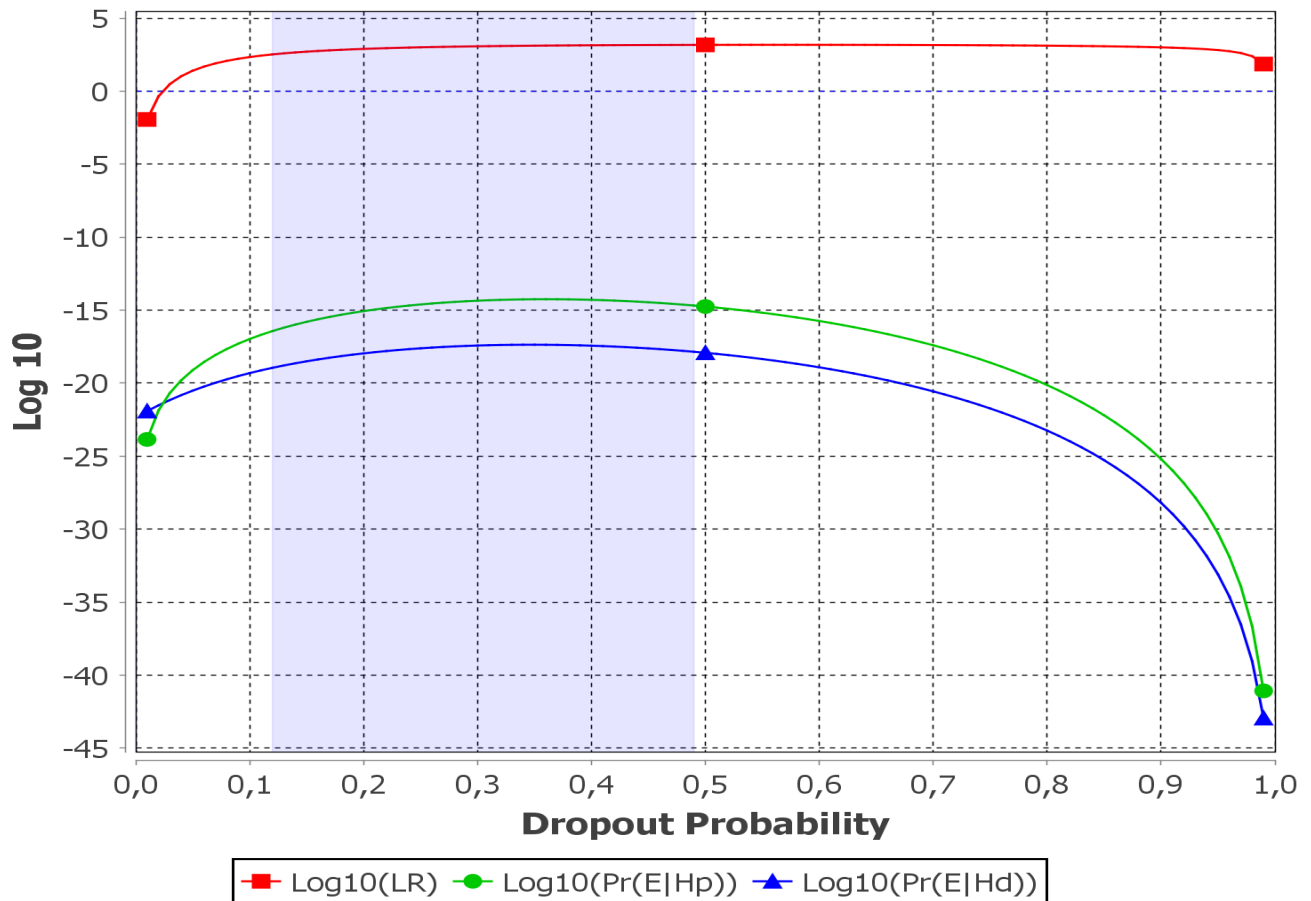
Locus	Pr(E Hp)	Pr(E Hd)	LR
D10S1248	8,50200E-002	6,24531E-002	1,36134E000
D16S539	2,41975E-002	1,01790E-002	2,37719E000
D8S1179	1,74787E-002	2,36076E-002	7,40384E-001
D18S51	6,48488E-004	3,65190E-003	1,77576E-001
D22S1045	3,59115E-001	9,00467E-002	3,98810E000
TH01	3,36810E-002	2,46650E-003	1,36554E001
D2S441	1,98763E-001	1,53152E-002	1,29782E001
D3S1358	4,08370E-003	1,23017E-003	3,31963E000
D1S1656	1,60596E-004	4,87066E-004	3,29722E-001
Overall Likelihood Ratio			3,29148E002

Sensitivity Analysis

Sensitivity Analysis

Varying dropout of C10.AC.19 and all unknowns. All Loci. DropIn 0.05. Theta 0.01.

■ Dropout Estimation 0.12 ~ 0.49



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

	Log10(LR)	Log10(Pr(E Hp))	Log10(Pr(E Hd))
0.01	-1.941641	-23.856795779461549	-21.915154282553373
0.10	2.335422	-16.977749222076333	-19.313171438259470
0.20	2.894670	-15.068105327375054	-17.962775509220882
0.30	3.071411	-14.353902640896205	-17.425313353646920
0.40	3.142237	-14.294287782606847	-17.436525107207494
0.50	3.169646	-14.754156820198938	-17.923802329526743
0.60	3.173252	-15.744812730923648	-18.918064459353910
0.70	3.157739	-17.407650659274427	-20.565389921139978
0.80	3.115741	-20.134275534849606	-23.250016908037476
0.90	3.000372	-25.196061969535080	-28.196433747005634
0.99	1.860114	-41.085459159986221	-42.945572889368143

Case Number: Example_2A

Analysis performed by: pc

Date and time of analysis: 2020/05/19 19:20:43

Trace Analysed: C10.5.19

Dropout Estimation

Below are listed the 5% and 95% percentiles of the empirical drop-out distribution, determined using 1000 Monte-Carlo simulations with the 21 alleles observed in average across the 1 replicates.

Hypothesis	Dropout Probability	
	Minimum (5%)	Maximum (95%)
Prosecution	0.18	0.49
Defense	0.12	0.46
Overall	0.12	0.49

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_1_rep.txt	C10.5.19

The contents of the profiles is listed below:

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

Case Number: Example_2A

Analysis performed by: pc

Date and time of analysis: 2020/05/19 19:20:43

Trace Analysed: C10.5.19

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