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LRmix update

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Statistical methods in forensic genetics 20-23 May 2013, Copenhagen

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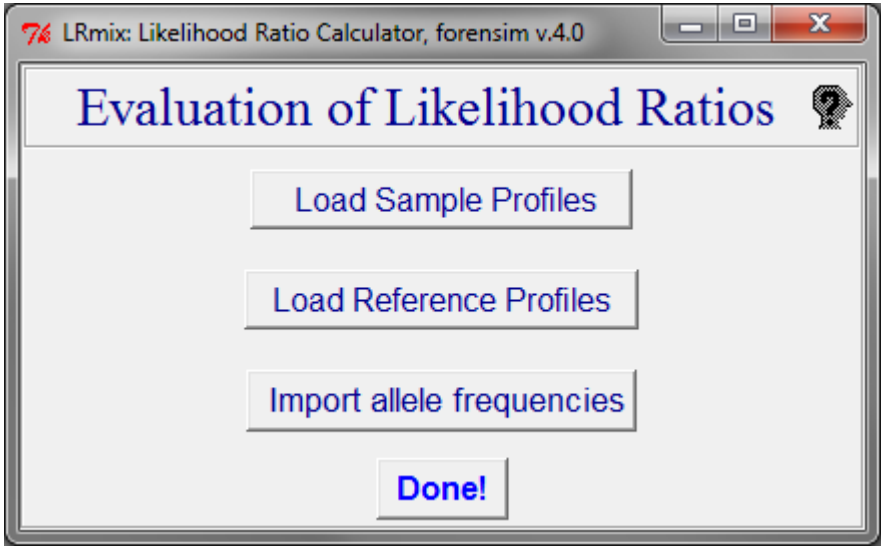
Current version

Current version on CRAN* is **forensim** version 4.3 including **LRmixTK** version 4.0 (2013-09-15)



* i.e. available from the package menu in Windows RGui

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Problems and reminders

Decimal separator/delimiter problem

- Comma separated value files (CSV) can cause problem in countries where semi-colon (;) is used instead of the comma (,)*
- Tab separated TXT files behave the same in different locales
- Never use spaces in your column names, or in the sample names

* However there is a global Windows locale setting to change the list separator:
http://office.microsoft.com/en-001/excel-help/import-or-export-text-txt-or-csv-files-HP010099725.aspx

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CSV file example

```
SampleName,Marker,Allele1,Allele2
Suspect1,AMEL,X,Y
Suspect1,D3S1358,16,17
Suspect1,VWA,16,18
Suspect1,D16S539,12,13
Suspect1,D2S1338,19,20
Suspect1,D8S1179,9,13
Suspect1,D21S11,28,32
Suspect1,D18S51,12,15
Suspect1,D19S433,12,16
Suspect1,TH01,6,9.3
Suspect1,FGA,19,21
Suspect2,AMEL,X,Y
Suspect2,D3S1358,15,17
Suspect2,VWA,18,19
Suspect2,D16S539,12,12
Suspect2,D2S1338,17,18
Suspect2,D8S1179,13,13
Suspect2,D21S11,30,30
Suspect2,D18S51,12,20
Suspect2,D19S433,12,15
Suspect2,TH01,6,9.3
Suspect2,FGA,20,21
```

CSV file opened in a raw 'non-destructive' text editing program like Notepad or Notepad++

	A	B	C	D
1	SampleName	Marker	Allele1	Allele2
2	Suspect1	AMEL	X	Y
3	Suspect1	D3S1358	16	17
4	Suspect1	VWA	16	18
5	Suspect1	D16S539	12	13
6	Suspect1	D2S1338	19	20
7	Suspect1	D8S1179	9	13
8	Suspect1	D21S11	28	32
9	Suspect1	D18S51	12	15
10	Suspect1	D19S433	12	16
11	Suspect1	TH01	6	9.3
12	Suspect1	FGA	19	21
13	Suspect2	AMEL	X	Y
14	Suspect2	D3S1358	15	17
15	Suspect2	VWA	18	19
16	Suspect2	D16S539	12	12
17	Suspect2	D2S1338	17	18
18	Suspect2	D8S1179	13	13
19	Suspect2	D21S11	30	30
20	Suspect2	D18S51	12	20
21	Suspect2	D19S433	12	15
22	Suspect2	TH01	6	9.3
23	Suspect2	FGA	20	21

CSV file opened in a spread-sheet program like Microsoft Excel or Libre Office Calc. Depending on the settings you may have to use a function like "Text to columns" and separate by comma (,).

If editing in a spread-sheet program be careful to save the file as a CSV file.

NB! Beware in countries using comma as decimal separator.

S11	30	30
S51	12	20
S433	12	15
1	6	09.mar
	20	21

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Problems and reminders

Known profiles must be encoded as follows

SampleName	Marker	Allele1	Allele2
Suspect	TH01	6	8
Suspect	D21S11	30	32.2
Suspect	D18S51	15	16
Suspect	D10S1248	13	13
Suspect	D1S1656	13	17.3
Suspect	D2S1338	19	21

NB! homozygotes

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Problems and reminders

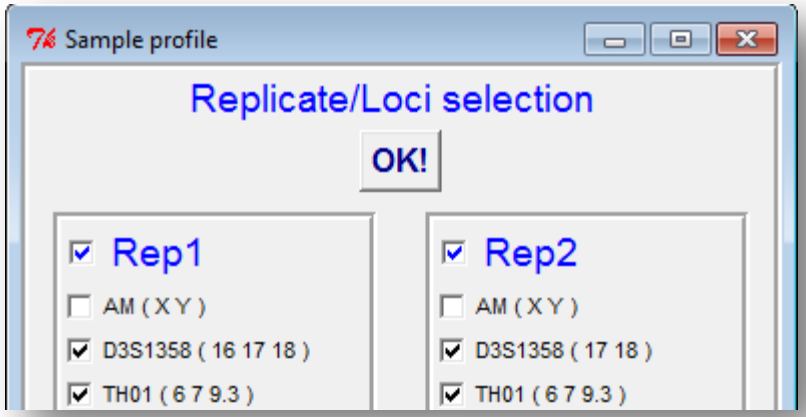
Do not provide the Amelogenin locus in the evidence

- Can cause an error

```
[1] "AM"
Error in appelC(Repliste, T, V, x, theta, prDHet, prDHom, prC, freq, sortieR) :
  NA/NaN/Inf in foreign function call (arg 1)
```

- However ‘AMEL’ is hard-coded to be dropped

- A workaround is to manually exclude the amelogenin locus if present in the file



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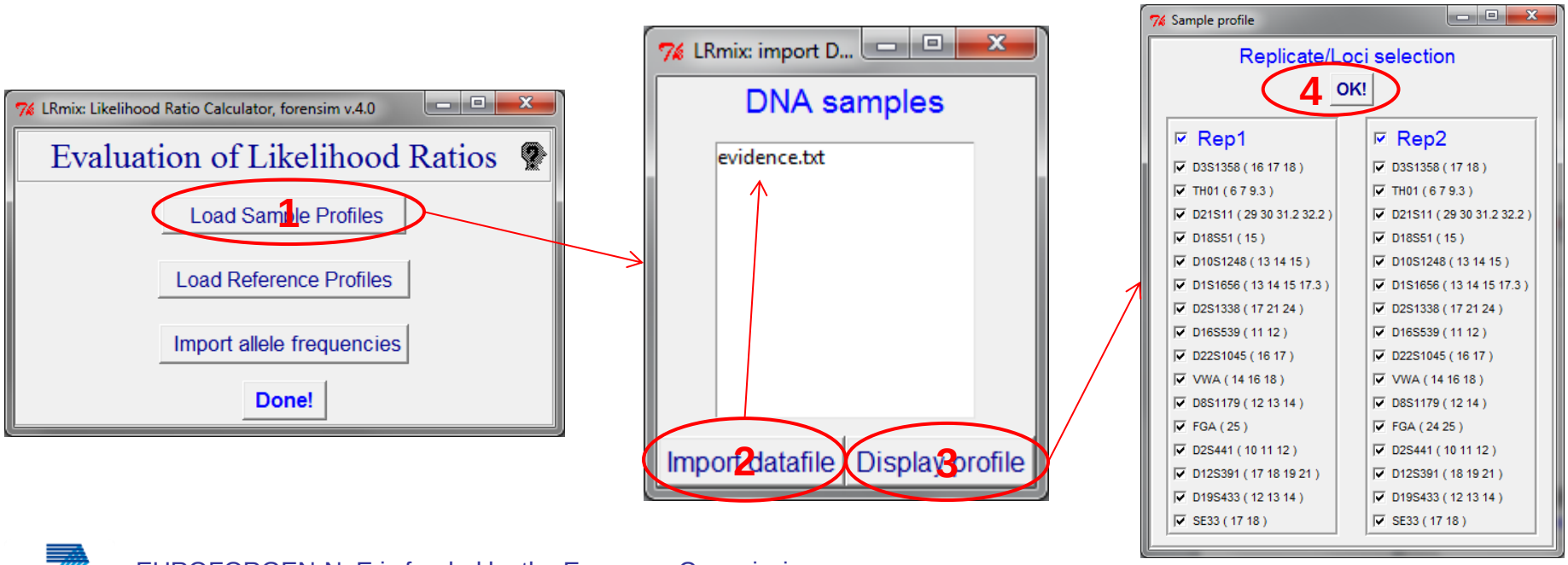
Problems and reminders

Load the evidence

1. Click the “Load Sample Profiles” button
2. Click the “Import datafile” button and locate the evidence file
3. Click the “Display profile” button
4. Click “Ok” to load the evidence into LRmix



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Problems and reminders

- LRmix should not be used for more than 3 unknowns under each hypothesis (performance)

- Three contributors work, but takes quite some time (± 1 hour for 1 replicate)

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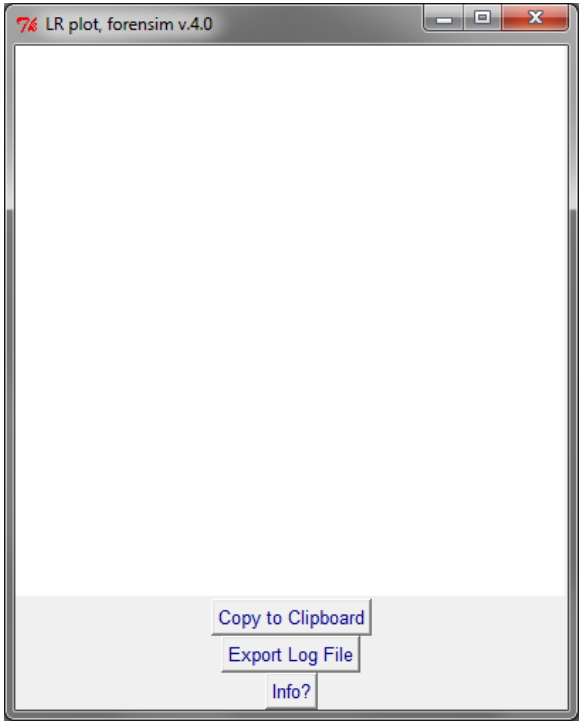
Problems and reminders

Probability of contamination

Do not set Pr(C) = 0 as it can lead to an empty sensitivity plot and an error message in R

```
Error in plot.window(...) : need finite 'ylim' values
In addition: Warning messages:
1: In min(x) : no non-missing arguments to min; returning Inf
2: In max(x) : no non-missing arguments to max; returning -Inf
```



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Problems and reminders

Allele frequency file

- The file should contain the entire allele frequency database* (usually the frequency of the alleles in each marker sums to 1)

- Rare alleles (i.e. not in the database) are currently hard-coded to use freq. 1/(2*2085) = 0.00024

- The marker names are case sensitive and must match the names in the samples (e.g. vWA ≠ VWA)

- There should be an equal number of columns for each row in the file (count the number of commas/tabs)

* Or can cause the error “Ranges of drop-out could not be determined with the chosen LR parameters. Please check that the hypothesised contributors are sufficient to explain the X observed alleles”

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Collaborative Exercise

Forensic Science International: Genetics 9 (2014) 47–54

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Euroforgen-NoE collaborative exercise on LRmix to demonstrate standardization of the interpretation of complex DNA profiles

L. Prieto [a], H. Haned [b], A. Mosquera [c], M. Crespillo [d], M. Alemañ [e], M. Aler [f], F. Álvarez [a], C. Baeza-Richer [g], A. Dominguez [h], C. Doutremepuich [i], M.J. Farfán [j,k], M. Fenger-Grøn [l], J.M. García-Ganivet [m], E. González-Moya [k], L. Hombreiro [n], M.V. Lareu [c], B. Martínez-Jarreta [o], S. Merigioli [p], P. Milans del Bosch [q], N. Morling [l], M. Muñoz-Nieto [d], E. Ortega-González [r], S. Pedrosa [s], R. Pérez [d], C. Solís [a], I. Yurrebaso [t], P. Gill [u,v,*]

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Collaborative Exercise

- Little consistency in reporting practices of mixtures between laboratories because operating with different rules

- The Euroforgen-NoE has held training courses in mixture interpretation methodology and software

- Participants on the “Interpretation on mixtures and complex DNA profiles” course in Madrid 2012 organised an inter-laboratory exercise to find out if standardization could be demonstrated

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Collaborative Exercise

2.1. Exercise 1 circumstances (rape case)

A woman was raped in Madrid. The pathologist took a sample from the vagina of the victim and sent it to the DNA Laboratory. A suspect was detained following police investigations. The judge asked the scientist to determine if the suspect could have contributed to the vaginal sample from the victim.

2.2. Exercise 2 circumstances (homicide case)

The dismembered body of a woman was found in the countryside on the outskirts of a Spanish village. The police suspect that her husband (a butcher) committed the murder. Apart from other evidence, the body parts were perfectly separated from each other (indicating "professional" quartering) and the suspect also has a cut in his right hand. The police interrogated the man and he admitted that he had cut his hand with a knife. The apparently clean knife (evidence) was sent to the DNA Laboratory to be analyzed. Reference samples from the victim and the suspect were taken. The judge asked the scientist if DNA from the victim was present on the knife.

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Collaborative Exercise I

Table 3A

Exercise 1 results from 18 participating laboratories (Labs). Laboratory number 8 performed 3 independent tests taking into account the same pair of hypothesis. *Key*: Hp = contributors to the unknown sample under prosecutor hypothesis; Hd = contributors to the unknown sample under the defense hypothesis; LR before sensitivity = likelihood ratio before estimating the drop-out probability given the profile characteristics (an initial $Pr(D)$ of 0.5 was fixed in order to remove variability in the results); estimated $Pr(D)$ = probability of drop-out estimated to obtain the lower LR; LR after sensitivity = likelihood ratio after estimating the drop-out probability; $Pr(D)$ under Hp 5% and 95% percentiles = percentiles 5 and 95 of the distribution of the drop-out probability conditioned on the expected number of alleles observed relative to the genotype of the hypothesized contributors under Hp. $Pr(D)$ under Hd 5% and 95% percentiles = percentiles 5 and 95 of the distribution of the drop-out probability conditioned on the expected number of alleles observed relative to the genotype of the hypothesized contributors under Hd. Hypotheses wrongly formulated highlighted in grey. Drop-out probabilities wrongly selected to calculate the final LR highlighted in grey.

A	B		C	D	E	F			
Labs	Hp	Hd	LR before sensitivity	Estimated $Pr(D)$	LR after sensitivity	$Pr(D)$ under Hp 5% percentile	$Pr(D)$ under Hp 95% percentile	$Pr(D)$ under Hd 5% percentile	$Pr(D)$ under Hd 95% percentile
1	V+S	V+U	4.862×10^{15}	0.19	6.508×10^{16}	0.01	0.11	0.01	0.19
2	V+S	V	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.13	0.01	0.15
3	V+S	V+U	4.862×10^{15}	0.01	1.032×10^{17}	0.01	0.13	0.01	0.17
4	V+S	V+U	4.86×10^{15}	0.17	7.86×10^{16}	0.01	0.11	0.01	0.17
5	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.13	0.01	0.15
6	V+S	V+U	4.86×10^{15}	0.17	7.86×10^{16}	0.01	0.15	0.01	0.17
7	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.11	0.01	0.15
8	V+S	V+U	4.86×10^{15}	0.17	7.86×10^{16}	0.01	0.11	0.01	0.17
	V+S	V+U	4.86×10^{15}	0.01	1.032×10^{17}	0.01	0.13	0.01	0.13
	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.11	0.01	0.15
9	V+S	V+U	4.862×10^{15}	0.01	1.032×10^{17}	0.01	0.11	0.01	0.17
10	V+S	V+U	4.862×10^{15}	0.17	7.857×10^{16}	0.01	0.11	0.01	0.17
11	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.13	0.01	0.15
12	V+S	V+U	4.862×10^{15}	0.17	7.857×10^{16}	0.01	0.13	0.01	0.17
13	V+S	V+U	4.86×10^{15}	0.15	9.49×10^{16}	0.01	0.13	0.01	0.15
14	S	U	4.862×10^{15}	0.01	1.032×10^{17}	0.01	0.09	0.01	0.13
15	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.11	0.01	0.15
16	V+S	V+U	4.862×10^{15}	0.01	1.032×10^{17}	0.01	0.11	0.01	0.13
17	V+S	V+U	4.862×10^{15}	0.17	7.857×10^{16}	0.01	0.11	0.01	0.17
18	V+S	V+U	4.862×10^{15}	0.15	9.492×10^{16}	0.01	0.13	0.01	0.15

V = victim; S = Suspect; U = Unknown

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Collaborative Exercise II

Table 3B
Exercise 2 results from 18 participating laboratories (Labs). Laboratories number 4 and 7 performed 2 independent tests taking into account 2 different pairs of hypotheses. Laboratory number 8 performed 2 independent tests taking into account the same pair of hypotheses. Key: the same as in Table 3A. Hypotheses wrongly formulated highlighted in grey. Dropout probabilities wrongly selected to calculate the final LR highlighted in grey.

A	B		C	D	E	F			
Lab	Hp	Hd	LR before sensitivity	Estimated $Pr(D)$	LR after sensitivity	$Pr(D)$ under Hp 5% percentile	$Pr(D)$ under Hp 95% percentile	$Pr(D)$ under Hd 5% percentile	$Pr(D)$ under Hd 95% percentile
Set 1 propositions									
1	$S+V$	$S+U$	7.14×10^5	0.19	2.195×10^5	0.19	0.43	0.19	0.43
2	$S+V$	S	7.145×10^5	0.19	2.195×10^5	0.19	0.39	0.23	0.43
4	$S+V$	$S+U$	7.14×10^5	0.17	1.52×10^5	0.17	0.41	0.19	0.43
6	$S+V$	$S+U$	7.14×10^5	0.21	2.93×10^5	0.21	0.43	0.21	0.45
7	$S+V$	$S+U$	7.145×10^5	0.17	1.52×10^5	0.17	0.43	0.19	0.45
8	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.43	0.19	0.43
8	$S+V$	$S+U$	7.145×10^5	0.17	1.52×10^5	0.17	0.43	0.21	0.45
9	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.43	0.21	0.45
10	$S+V$	$S+U$	1.178×10^{6a}	0.15	3.634×10^{5a}	0.15	0.41	0.19	0.45
11	$S+V$	$S+U$	7.145×10^5	0.17	1.52×10^5	0.17	0.43	0.25	0.45
12	$S+V$	$S+U$	7.145×10^5	0.21	2.93×10^5	0.21	0.43	0.21	0.47
13	$S+V$	$S+U$	7.145×10^5	0.21	2.93×10^5	0.21	0.43	0.21	0.47
15	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.41	0.19	0.45
16	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.43	0.21	0.43
17	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.41	0.21	0.47
18	$S+V$	$S+U$	7.145×10^5	0.19	2.195×10^5	0.19	0.43	0.19	0.43
Set 2 propositions									
4	$S+V$	$U+U$	8.99×10^{16a}	0.43	1.6×10^{17a}	0.19	0.41	0.19	0.43
5	$S+V$	$U+U$	8.992×10^{16a}	0.45	1.359×10^{17a}	0.15	0.39	0.17	0.45
18	$S+V$	$U+U$	8.992×10^{16a}	0.41	1.89×10^{17a}	0.17	0.41	0.19	0.41
Set 3 propositions									
7	$U+V$	$U+U$	5759	0.21	1091	0.21	0.49	0.21	0.43
Set 4 propositions									
14	V	U	2.083×10^{14}	0.42	4.683×10^{14}	0.19	0.41	0.21	0.45
3	$S+V$	$V+U$	2.083×10^{14}	0.21	6.897×10^{15}	0.19	0.43	0.21	0.45

V = victim; S = suspect; U = unknown.
[a] LRs without SE33 marker.

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Conclusions

- A high level of standardization was obtained
- No major deviations in allele designations
- Similar statistical results were obtained
- With suitable tools and training are provided standardization of probabilistic interpretation is possible

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