

Netherlands Forensic Institute Ministry of Security and Justice

Performance tests

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Case of interest # 2012xxxx

- (a) Prosecution hypothesis The suspect Mr. X and one unknown person are the sources of the crime-sample.
- (b) Defence hypothesis Two unknown individuals, unrelated to Mr.X, are the sources of the crime-sample.

- ➤ If LR > 1, evidence is more supportive of (a) than (b)
- ➤ If LR < 1, evidence is more supportive of (b) than (a)
- ➤ If LR=1, evidence is neutral



Case of interest # 2012xxxx

- Complex two-person mixture
- The profile is not ideal (low DNA levels), but it can be analysed
- To do this, we use a LR model when calculating the likelihood ratio of hypotheses (a) and (b)



DNA commission

International Society for Forensic Genetics (2012)

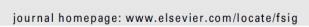


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DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods

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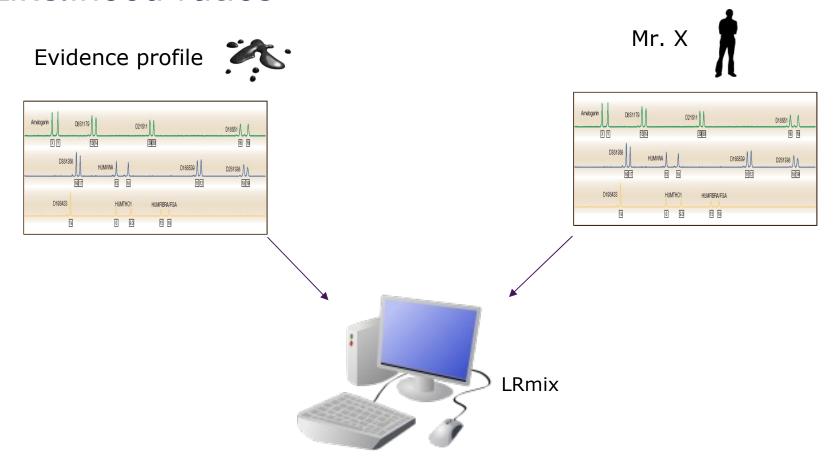


All models rely on assumptions

- ➤ Level 1: Propositions described by the forensic expert
 - The crime-sample came from the suspect
 - The crime-sample came from an unknown (unrelated) person
- ➤ Level 2: Model parameters
 - allele frequencies
 - theta correction
 - drop-out probability
 - drop-in probability
 - ...



Likelihood ratios





Statement

I have evaluated the proposition that (a) Mr. X and one unknown unrelated person are the contributors to the crime stain compared to the alternative proposition that (b) two unknown persons are the contributors to the crime stain using the conditions defined in the LR model.

The evidence is **10.000** times more likely if the first proposition (a) is true, compared to the alternative described by (b).



Value of DNA evidence further evaluated

We are now able to test the *performance* of the model, one way to do this, is to replace the person of interest (suspect) by a non-contributor



Step 1: Simulate large number of males, from the Dutch allele frequencies data-base



10.000 DNA profiles



Step 2: evaluate the hypotheses and replace Suspect by random men

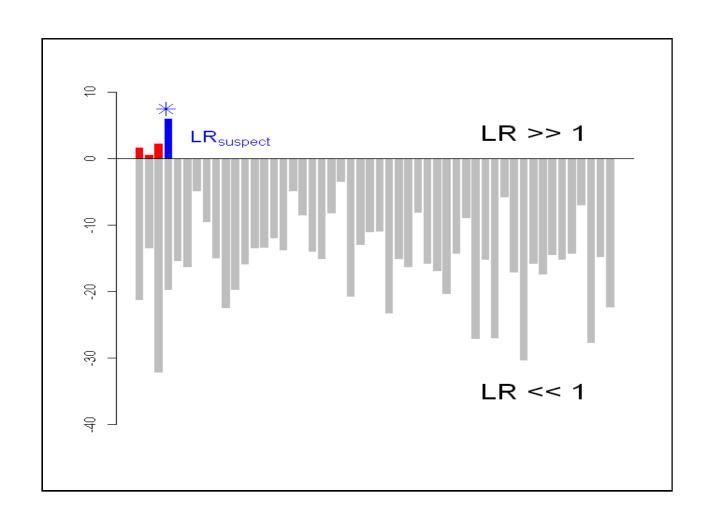


10.000 DNA profiles



LRs are calculated for each simulated individual



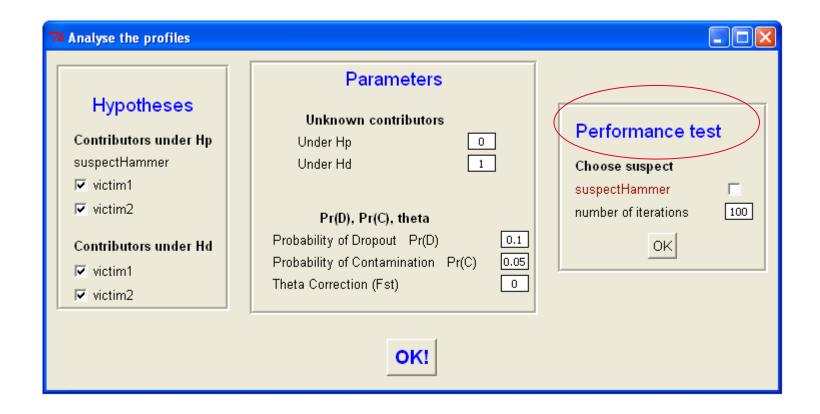




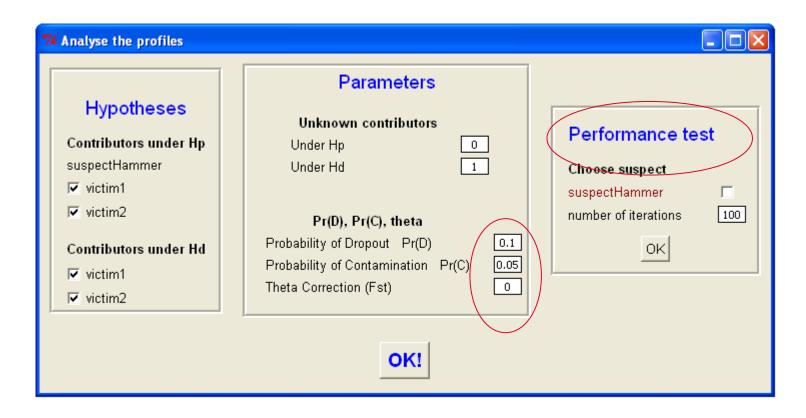
Step 3: Statement

The likelihood ratio can be evaluated with a **test of performance**. To do this we replace Mr. X with a random unrelated individual and we repeat the measurement of the likelihood ratio. We do this a total of 10.000 times, with a different random individual each time. When this was carried out the greatest likelihood ratio observed was of the order of 160.



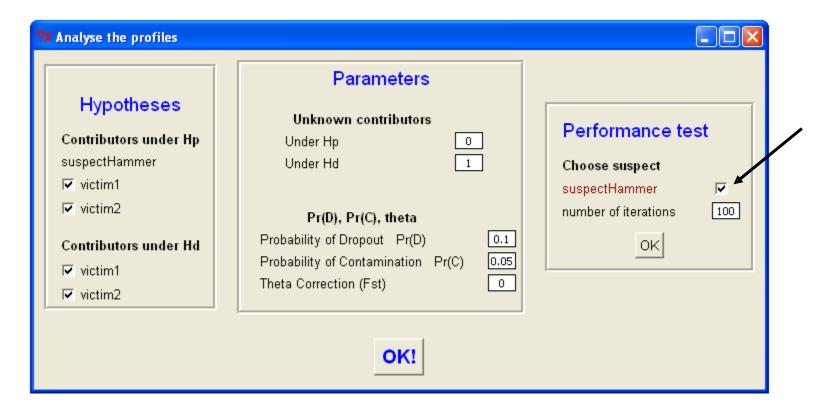






Performance test relate to a set of parameters







LRmix creates a File and paste it to your working folder, open to get the percentiles of the performance test

