Likelihood ratios in practice

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Mixture classification scheme

A Exclusion

B Match with statistical evaluation: the alleles from all (hypothesized) donors are recovered in the sample (RMNE, RMP, LR)

C Match without statistical evaluation: If not all the alleles of all the donors can be identified

D No exclusion or match: In such cases essential information required to enable the forensic scientist to pronounce an exclusion or match is missing from the profile obtained.

Meulenbroek et al, FSIG supp. series. 2011

The purpose of a model is to provide an appreciation of the value of the evidence, regardless of the category the DNA profile

Software an as interpretation tool

- The software is there to assist the reporting officers
- It is the software that is used to explore the profiles, and not the profiles that are used to explore the software
- The limitations of the software should not dictate what is feasible in terms of interpretation
- The expert cannot be replaced!

The software is a tool, it should not become a straitjacket

Workflow

1. Quality of the profiles?
2. Order new tests?
3. Compare with reference profiles/search the national DNA database
4. Hypotheses formulation (# contributors)
5. Calculate the LR
6. Optional: performance test to compare several sets of hypotheses
7. Decision and statement

Reporting 1/4: Verbal scale

LR	Verbal scale	Translation
1	equally likely	no support
$1 - 10$	somewhat likely	weak support
$10 - 100$	likely	moderate support
$100 - 10,000$	much more likely	moderately strong support
$10,000 - 1,000,000$	very much more likely	very strong support
$> 1,000,000$	extremely high likelihood	extremely strong support

Reporting 2/4: describe method

- There can be uncertainty on the true composition of the sample
- Stochastic effects are well-known and well-documented
- We are able to evaluate the strength of the evidence, while accounting for these effects
- We use the likelihood ratio framework, which is the preferred way for reporting results of DNA testing
- The methods used are published in a peer –review journal and are well accepted by the forensic community

Reporting 3/4: cite literature

- H. Haned, et al, Exploratory data analysis for the interpretation of low template DNA mixtures, FSIG (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, FSIG (2012).
- P. Gill et al, LoComatioN: a software tool for the analysis of low copy number DNA profiles, FSI (2007).
- J.M. Curran et al, Interpretation of repeat measurement DNA evidence allowing for multiple contributors and population substructure, FSI (2005).

Reporting 4/4: statement

It is much more likely to observe the DNA profile if hypothesis I is true, compared to its alternative, described by hypothesis II.

Current status

- Evaluation of 'non-exclusion' with complex mixture upon request
- March 2012 – July 2013: 150+ 'non-exclusions' evaluated
- LRmix robust and can be used for most complex DNA profiles
- $\approx 1/3$ cases 'SplitDrop' was used
- Accepted in court