A partial DNA profile (see pdf copy of epg “stain\_first\_rep”) is obtained from a baseball cap used by a bank-robber.

A suspect is identified (see pdf copy of epg “suspect”)

With LRmix (input files for stain “stain\_1\_rep” and suspect “suspect”, as well as population frequencies file are provided in “LRmix data” folder), calculate the LR of the following alternative hypotheses:

Hp: the DNA profile obtained from the cap comes from the suspect + 1 unknown donor

Hd: the DNA profile obtained from the cap comes from 2 unknown donors

Report the LR value for the most conservative drop-out value (within the range of most likely drop-out values): 329.1

A replicate PCR from a remaining aliquot of DNA isolated from the baseball cap is performed (see pdf copy of epg “stain\_first\_rep”).

With LRmix, recalculate LR (same as above, but using the “stain\_2\_reps” input file, instead of “stain\_1\_rep” input file) using replicate data (input file for stain …): 2715.9

With EFM (STR kit: ESSplexSEQS), using the two replicates (input files and population frequencies file provided in the “EFM data folder), report -loglik values (Hd) for the different combinations of parameter models, by first considering the following competing hypotheses

Hp: the DNA profile obtained from the cap comes from the suspect + 1 unknown donor

Hd: the DNA profile obtained from the cap comes from 2 unknown donors

and the

Hp: the DNA profile obtained from the cap comes from the suspect + 2 unknown donor

Hd: the DNA profile obtained from the cap comes from 3 unknown donors

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| CONTRIBUTORS | DEGRADATION | STUTTER | -loglik | PENALIZATION |
| SUSPECT + 1 UNK | NO | NO | -359.7 | 0 |
| SUSPECT + 1 UNK | YES | NO | -301.9 | 1 |
| SUSPECT + 1 UNK | NO | YES | -359.2 | 1 |
| SUSPECT + 1 UNK | YES | YES | -299.8 | 2 |
| SUSPECT + 2 UNK | NO | NO | -359 | 1 |
| SUSPECT + 2 UNK | YES | NO | -299.7 | 2 |
| SUSPECT + 2 UNK | NO | YES | -359.2 | 2 |
| SUSPECT + 2 UNK | YES | YES | -299.7 | 3 |

Report the maximum likelihood estimation of LR for the best combination of models (according to -loglik values): 124817