

2026 GHEP-ISFG Forensic Advanced Theoretical Challenge

Case 1

Case circumstances

Date: 1 April, 2026

Summary:

During the final phase of a highly anticipated Advanced Theoretical Challenge (ATC) on forensic DNA mixture interpretation, a security incident is discovered. The official answer key — meticulously prepared and stored under restricted access — is missing from a secured safe at the forensic institute in the Netherlands. Without the answer key, participants' results cannot be validated.

The exterior surface of the safe door was sampled for biological traces, and a DNA profile was obtained. The objective of the forensic investigation is to assess from whom the detected DNA may have originated. Three persons of interest have been identified in connection with access to the secured area.

Available data

- Trace profile: 1.2026Trace#01.csv (including peak heights), 1.2026Trace#01.txt (without peak heights), 1.2026Trace#01.pdf (pdf of the electropherogram)
- Person of interest 1's reference profile: 1.POI1#01.txt
- Person of interest 2's reference profile: 1.POI2#01.txt
- Person of interest 3's reference profile: 1.POI3#01.txt
- Population frequency file: Fusion 6C_Holland2.csv

General information

Please see document '*01_2026_GHEP-ISFG_ATC_Instructions*' for details on DNA profile generation and weight of evidence calculations.

Mixture interpretation

Please interpret the DNA profile(s) and answer the questions below. We are aware that the DNA profiles may differ from your casework practice and will keep in mind the answers you provided in the document '*02_2026_GHEP-ISFG_ATC_General questions on casework practice*'. If you believe there is additional information we should know, please provide this at the end of this exercise.

Trace profile interpretation

1. How would you report the number of contributors (NoC) in this trace profile?

In other words, how would you report the number of contributors to this DNA trace profile if you encountered this profile in casework? Would you be able to assess the number of contributors given this DNA profile? If so, would you report an *exact/single estimate* of number of contributors (e.g., 3 contributors), would you report a *range* of possible numbers of contributors (e.g., 3-4 contributors or minimum of 3 contributors/maximum of 4 contributors), or would you report a *minimum number* of contributors (e.g., at least 3 contributors)?

- a. I would report an exact number of contributors.
- b. I would report a range of possible numbers of contributors
- c. I would report a minimum number of contributors
- d. The mixture is too complex to determine the number of contributors (Skip to Q3)
- e. Other (Please specify: _____)

2. Provide your NoC estimate based on your selection in question 1.

- a. Enter value:

Suitability

3. Under your current laboratory practices and guidelines, do you deem this profile suitable for conducting manual and/or statistical comparisons?

- a. Yes (for the entire mixture and all contributors)
- b. Yes, but only for a subset of the contributors (e.g., major(s))
- c. Yes, but only for a subset of loci (and all contributors)
- d. Yes, but only for a subset of loci, and only for a subset of the contributors
- e. No

4. For which comparisons do you deem this profile suitable?

- a. Manual analysis
- b. Statistical analysis
- c. Manual and statistical analysis
- d. Neither

LR calculations

Independent of your answer in the previous question and of whether you would compute LR in casework for such a DNA mixture and POIs, we ask you to run LR calculations. We ask you to compute LR using various approaches and propositions, but using your estimated NOC and the LR software you have in use in your laboratory.

5. Please indicate the LR calculation software that you use to compute LR in this exercise. Please specify the version number.

- ☐ Armed Xpert (specify version number)
- ☐ CEESIt (specify version number)
- ☐ DNAMix (specify version number)
- ☐ DNA View Mixture Solution (specify version number)
- ☐ DNAXs/DNAStatistX (specify version number)
- ☐ EuroForMix (specify version number)
- ☐ EFMrep (specify version number)
- ☐ Final Forensic Genetics (GFF) (specify version number)
- ☐ CaseSolver (specify version number)
- ☐ LabRetriever (specify version number)
- ☐ likeLTD (specify version number)
- ☐ LiRaHT (specify version number)
- ☐ LRMix/LRMix Studio (specify version number)
- ☐ MixCal (specify version number)
- ☐ PopStats (specify version number)
- ☐ Soft Genetics MaSTR (specify version number)
- ☐ STRmix (specify version number)
- ☐ TrueAllele (specify version number)

- ☐ Own calculation sheet (specify name and version number)
- ☐ Other (specify name and version number)

6. Compute an LR using the following hypotheses (i.e. propositions):

H1: POI1 + (Estimated NOC - 1)

H2: Estimated NOC

Please provide the \log_{10} LR value, rounded to two decimal places (e.g., 6.25).

- a. \log_{10} LR POI1:

7. Compute an LR using the following hypotheses:

H1: POI2 + (Estimated NOC - 1)

H2: Estimated NOC

Please provide the \log_{10} LR value, rounded to two decimal places (e.g., 6.25).

- a. \log_{10} LR POI2:

8. Compute an LR using the following hypotheses:

H1: POI3 + (Estimated NOC - 1)

H2: Estimated NOC

Please provide the \log_{10} LR value, rounded to two decimal places (e.g., 6.25).

- a. \log_{10} LR POI3:

9. Compute an LR using the following (compound) propositions approach:

H1: POI1 + POI2 + POI3 + (estimated NOC-3)

H2: Estimated NOC.

Please provide the \log_{10} LR value, rounded to two decimal places (e.g., 6.25).

- a. \log_{10} LR:

Exhaustive propositions/ multiple propositions approach

Compute LRs using the exhaustive propositions/ multiple propositions approach and fill out the provided Excel spreadsheet '*Multiple propositions tool for combined weight of evidence_ENG_2026_Case 1*'. For instructions and information on the multiple propositions approach, please view the e-learning material: <https://nfi.cappagile.com/s/nSrKP3ot0T93vfQsrB3i9w> (~18 minutes).

10. Calculate LRs using each hypothesis against a default alternative. Make sure that all POI are loaded into the software, also for those hypotheses that do not include all POI. List the resulting LRs in the yellow marked cells in the Excel spreadsheet. Assess the evidence per POI. This is done in the Excel sheet by summing all LRs for hypotheses that assume presence of the POI and dividing this by the summed LR for hypotheses not assuming presence of the POI. Based on this approach, is there support for contribution of DNA of POI1?

- a. Yes
- b. No
- c. I do not know

11. Based on this approach, is there support for contribution of DNA of POI2?

- a. Yes
- b. No
- c. I do not know

12. Based on this approach, is there support for contribution of DNA of POI3?

- a. Yes

- b. No
- c. I do not know

13. If there is no support for inclusion of a POI, omit the hypotheses including this POI and re-assess the evidence per (remaining) POI. Define the hypothesis that overall best supports the data:

- a. ...

14. Based on the exhaustive propositions approach, is there support for joint contribution of two out of the three POI?

- a. Yes
- b. No

15. Based on the exhaustive propositions approach, is there support for joint contribution of all three POI?

- c. Yes
- d. No

Additional comments

16. Do you have any comments/notes that you would like to share based on this exercise?

- a. ...

17. Do you have any comments/questions/suggestions/tips about this case/design of the research in general? (you may think of: profile, scenario, etc.) Or is there anything else you would like to share or believe is important for us to know?

- a. ...