

2025 GHEP-ISFG Forensic Advanced Theoretical Challenge

Exercise 4

Case circumstances

A woman reports sexual assault by a masked man during a break-in. A vaginal swab is collected and DNA profile generated. The purpose of this research is to determine who the DNA in the sample may have come from. Intelligence information leads police to suspect two brothers known for robberies in the local area. References are provided for the victim and suspects.

Available data

- Trace profile: 4.Trace#01.csv (including peak heights), 4.Trace#01.txt (without peak heights), 4.Trace#01.pdf (pdf of the electropherogram)
- Victim's reference profile: 4.Victim#01 (.csv and .txt)
- Suspect 1's reference profile: 4.Suspect1#01 (.csv and .txt)
- Suspect 2's reference profile: 4.Suspect2#01 (.csv and .txt)

General information

Please see document '01_2025_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_2025_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)?

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

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

- Enter value:

3. Are you able to identify any major contributors?

In other words, would you consider one (or more) contributors to be major contributors according to the criteria in your guidelines (e.g., based upon peak height ratios or RFU percentages). If your guidelines do not permit you to differentiate between major and minor contributors, please indicate as such.

- a. There are no contributors I would consider majors
- b. There is one major contributor
- c. There are two or more major contributors
- d. We do not differentiate between major and minor contributors
- e. Other (Please specify: _____)

Comparison and conclusions

4. 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

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

- a. Manual analysis (Skip to Q7)
- b. Statistical analysis (Skip to Q7)
- c. Manual and statistical analysis (Skip to Q7)
- d. Neither (go to Q6 and then Q19)

6. If the trace profile is NOT suitable for comparison and/or statistical analysis. Why is this profile unsuitable for comparison and statistical analysis? (check all that apply; check at least one)

- a. Not enough alleles or loci suitable for analysis
- b. DNA template levels too low overall
- c. Sample too degraded
- d. Sample too inhibited
- e. Too many contributors
- f. Too much uncertainty in the number of contributors
- g. Mixture proportions/contributor ratios
- h. Beyond our internal guidelines for interpretation (Please specify: _____)
- i. Other (Please specify: _____)

(Skip to Q19)

7. Based on manual analysis, what is your conclusion regarding Suspect 1 (POI) as a potential contributor to the trace sample?

- a. *Included*— the POI is considered a possible contributor (also known as consistent with, support for inclusion, cannot be excluded/eliminated)
- b. *Inconclusive*— the POI can neither be included nor excluded as a potential contributor (also known as uninformative)
- c. *Excluded*— the POI is NOT a possible contributor (also known as eliminated, support for exclusion)
- d. We do not use categorical conclusions

- 8. Based on manual analysis, what is your conclusion regarding Suspect 2 (POI) as a potential contributor to the trace sample?**
- a. *Included*— the POI is considered a possible contributor (also known as consistent with, support for inclusion, cannot be excluded/eliminated)
 - b. *Inconclusive*— the POI can neither be included nor excluded as a potential contributor (also known as uninformative)
 - c. *Excluded*— the POI is NOT a possible contributor (also known as eliminated, support for exclusion)
 - d. We do not use categorical conclusions

- 9. Have you performed one or more statistical analyses on this profile?**
- a. Yes
 - b. No (Skip to Q19)

10. What software did you use to perform this calculation?

Specify parameters used if these are not mentioned in, or differ from, parameters presented in the document '01_2025_GHEP-ISFG_ATC_Instructions'.

- a. I did my calculations manually, or used an in-house software or in-house workbook
- b. Armed Xpert
- c. CEESIt
- d. DNA View Mixture Solution
- e. DNAMix
- f. DNAXs/DNAStatistX
- g. EuroForMix
- h. EFMrep
- i. Final Forensic Genetics (GFF)
- j. LabRetriever
- k. likeLTD
- l. LiRaHT
- m. LRmix/LRmix Studio
- n. MixCal
- o. PopStats
- p. Soft Genetics MaSTR
- q. STRmix
- r. TrueAllele
- s. Other (Please specify...)

11. How many statistical analyses (e.g. number of LR calculations) have you performed on this trace profile to reach your conclusion?

- a. Enter value:

12. Specify your propositions (can be multiple), including NoCs, conditioning on contributors etc

For example, Hypothesis 1: Suspect + x unknowns vs Hypothesis 2: x unknowns

LR= ...

13. Would you report a weight of evidence for Suspect 1?

- a. Yes (skip to Q15)
- b. No (go to Q14 and then skip to Q16)

14. Why did you decide not to report a weight of evidence for Suspect 1?

a. ...
(Skip to Q16)

15. Specify your reported weight of evidence for Suspect 1

Please mention if this is e.g. LR or Log₁₀ LR.

a. ...

16. Would you report a weight of evidence for Suspect 2?

- a. Yes (skip to Q18)
- b. No (go to Q17 and then skip to Q19)

17. Why did you decide not to report a weight of evidence for Suspect 2?

a. ...
(Skip to Q19)

18. Specify your reported weight of evidence for Suspect 2

Please mention if this is e.g. LR or Log₁₀ LR.

a. ...

19. What would you report as your conclusion(s)?

In other words, what is your statement conclusion? For example:

"The probability of the evidence is more than xxx times more likely if proposition *a* (specify) is true, compared to the alternative described by *b* (specify)."

And/or

"This analysis provides xxx support for the proposition that Suspect *X* is a contributor to the DNA obtained from item *I*."

a. ...

Additional comments

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

a. ...

21. 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. ...