

# GHEP-ISFG Forensic Advanced Theoretical Challenge 2025

## Questionnaire: *General questions on your current casework practice*

Please fill out this questionnaire. After completing this questionnaire, you can start with the exercises.

### 1. Laboratory ID:

#### DNA profiling

### 2. Please indicate all autosomal STR amplification kit(s) that are validated and used in your laboratory for DNA mixtures (check all that apply).

- ☐ Applied Biosystems AmpFLSTR Identifier
- ☐ Applied Biosystems AmpFLSTR Identifier Plus
- ☐ Applied Biosystems AmpFLSTR Profiler
- ☐ Applied Biosystems AmpFLSTR Profiler Plus
- ☐ Applied Biosystems GlobalFiler
- ☐ Promega Powerplex 16
- ☐ Promega Powerplex 16 HS
- ☐ Promega Powerplex Fusion 5C
- ☐ Promega Powerplex Fusion 6C
- ☐ Qiagen Investigator 24plex
- ☐ Other (specify)

### 3. Please indicate which autosomal STR amplification kit is by default used in your laboratory.

Please specify the validated amplification cycle settings specified by your guidelines.

- ☐ Applied Biosystems AmpFLSTR Identifier (specify amp cycles)
- ☐ Applied Biosystems AmpFLSTR Identifier Plus (specify amp cycles)
- ☐ Applied Biosystems AmpFLSTR Profiler (specify amp cycles)
- ☐ Applied Biosystems AmpFLSTR Profiler Plus (specify amp cycles)
- ☐ Applied Biosystems GlobalFiler (specify amp cycles)
- ☐ Promega Powerplex 16 (specify amp cycles)
- ☐ Promega Powerplex 16 HS (specify amp cycles)
- ☐ Promega Powerplex Fusion 5C (specify amp cycles)
- ☐ Promega Powerplex Fusion 6C (specify amp cycles)
- ☐ Qiagen Investigator 24plex (specify amp cycles)
- ☐ Other (specify kit and number of amplification cycles)

### 4. Please indicate the CE instrument that is by default used for mixture casework in your laboratory.

Please specify the default voltage and injection time settings for your default STR kit as specified by your guidelines.

- ☐ Applied Biosystems 3100 (specify voltage(s) and injection time(s))
- ☐ Applied Biosystems 3130 (specify voltage(s) and injection time(s))
- ☐ Applied Biosystems 3130xl (specify voltage(s) and injection time(s))

- ☐ Applied Biosystems 3500 (specify voltage(s) and injection time(s))
- ☐ Applied Biosystems 3500xl (specify voltage(s) and injection time(s))
- ☐ Applied Biosystems 3700 (specify voltage(s) and injection time(s))
- ☐ Applied Biosystems 3730 (specify voltage(s) and injection time(s))
- ☐ Promega Spectrum (specify voltage(s) and injection time(s))
- ☐ Other (specify name, voltage and injection time...)

## LR calculation software

### 5. Please indicate all LR calculation software that are validated and used for mixture casework in your laboratory (check all that apply).

- ☐ Armed Xpert
- ☐ CEESIt
- ☐ DNAMix
- ☐ DNA View Mixture Solution
- ☐ DNAxs/DNAstatistX
- ☐ EuroForMix
- ☐ EFMrep
- ☐ Final Forensic Genetics (GFF)
- ☐ CaseSolver
- ☐ LabRetriever
- ☐ likeLTD
- ☐ LiRaHT
- ☐ LRmix/LRmix Studio
- ☐ MixCal
- ☐ PopStats
- ☐ Soft Genetics MaSTR
- ☐ STRmix
- ☐ TrueAllele
- ☐ Own calculation sheet
- ☐ Other (specify)

### 6. Please indicate the LR calculation software that is by default used for mixture casework in your laboratory. 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)
- ☐ Own calculation sheet (specify name and version number)
- ☐ Other (specify name and version number)

### Internal interpretation guidelines

The following questions relate to the internal guidelines for trace profiles obtained with your laboratory's current default STR typing kit (and default PCR cycles, CE settings and profile analysis).

**7. Do you have a minimum DNA quantity at which you will perform amplification?**

- ☐ Yes (specify minimum DNA quantity)
- ☐ No

**8. Do you have an internally validated stochastic threshold?**

- ☐ Yes (specify height (RFU) of the stochastic threshold)
- ☐ No

**9. Do you use a minimum number of loci/ allele callings required to continue with analysis of a DNA profile?**

- ☐ Yes (specify)
- ☐ No

**10. Do you have a maximum number of contributors at which you will continue with analysis of a DNA profile?**

- ☐ Yes (specify max. number of contributors in a mixture profile that will be analysed in your laboratory)
- ☐ No

**11. Do you have a maximum numbers of mismatches (i.e. unseen alleles/ drop-outs) between reference and trace profiles allowed to continue with analysis of a DNA profile?**

- ☐ Yes (specify)
- ☐ No

**12. Do you use an LR threshold below which you will not report? (e.g. a lower threshold of LR 100 means that LRs lower than 100 are not reported)**

- ☐ Yes (specify lower LR threshold)
- ☐ No

**13. Do you use an upper threshold for reporting LRs? (e.g. upper threshold of 1 billion means that all LRs larger than  $10^9$  are reported as 'more than a billion' instead of providing the actual LR values, such as  $10^{23}$ )**

- ☐ Yes (specify upper LR threshold)
- ☐ No

### Comments

**14. Any other aspects of your casework practice that may be important for us to know?**