

# **PRE-CONGRESS WORKSHOP**

## **Disaster Victim Identification**

Monday, September 9, 2024 – 14:00-18:15h

### Aim of the workshop

The main objective of the workshop is to provide an understanding of the challenges in **DNA matching and statistical analysis** that are relevant for large-scale human identification. The success of DNA supported large-scale human identification depends on many factors (e.g. collecting and managing samples, DNA analysis methods, etc.). The interpretation of DNA results, database management and DNA matching are also crucial for any possible identification. We will focus on aSTR results and will show examples and exercises of DVI scenarios of varying complexity.

We encourage you to register for the workshop! We will all learn a great deal, for sure!

#### **Technical requirements**

Participants must bring a laptop (Windows OS) with the following software installed (freely available):

- *Familias 3*, <u>http://familias.no/english/download/</u> (preferably v3.3, released 2021-12-09)
- *R*, preferably version 4.2.x or higher, <u>https://cran.r-project.org/bin/windows/base/</u>.

Please note that installation is typically only possible if you are the administrator on your laptop (this is required).

**Participants are invited and encouraged to present their own cases.** There will be a session available for this purpose.

#### **Tentative programme**

**14:00-14:30h Brief introduction – Complexity of DVI scenarios** *Number of victims, individual vs. comingled human remains, closed vs. open scenarios, single vs. several related victims, primary vs. secondary graves.* 

**14:30-15:00h Post-mortem profiles**: problems (partial profiles, drop-out/in), types of comparisons (direct and kinship), false positives and false negatives. An example will be given by using Familias software.

**15:00-16:00h Ante-mortem profiles**: non-conditional simulations, pedigree check, conditional simulations, problems (distant relatives, errors in pedigrees, mutations, non-paternity events). An example will be given by using Familias software.

#### 16:00-16:15h Short Break

**16:15-17:15h AM-PM comparisons**: types of comparisons (direct and kinship), problems (false positives and negatives), Bayes theorem, prior probabilities, types of approaches (one to one, PM-driven, AM-driven, Joint approach).

17:15-18:15h Cases from participants, Exercises using Familias.