

'Triangular project' – Zoom classes in October 2020

Final version Oct 30, 2020, thore.egeland@gmail.com

Contents and practical information

The Zoom lectures (links will be provided by the organisers) introduce the necessary statistical background and software for Disaster Victim Identification (DVI). The likelihood ratio based approach is emphasized. The freely available programs Familias and FamLinkX are exemplified. The participants should have the latest versions of the mentioned software installed, Familias, version 3.2.8, from <https://familias.no/english/download/> (here's a guide to [running Familias on MacOS](#)) and FamLinkX version 2.9.2 https://famlink.se/fx_download.html. We also recommend participants to install R from <https://cran.r-project.org/bin/windows/base/> (optional). Selected parts of the [Tutorial](#) will be presented. Furthermore, we will do *some* of these [exercises](#). They are from the [book](#) 'Relationship Inference with Familias and R', by Egeland, Kling and Mostad. Input files for exercises can be downloaded as zip files: [Chapter 2](#), [Chapter 3](#) and [Chapter 4](#). There are [solutions all exercises](#).

Please email Franco franco.lmarsico@gmail.com or Thore thore.egeland@gmail.com in case you have problems installing the software. Note that installation is typically only possible if you are administrator on your laptop. Lectures will be recorded and links will be provided by the organisers. Also, there are some videos that you can watch to prepare for the lectures. You are encouraged to watch videos 1 and 2 linked below before the Oct 8 lecture:

1. [Introduction to Familias](#) (Video 18:17 minutes),
2. [Introduction to Blind Search](#) (Video 13:27 minutes).

Here's a list of [videos](#). The ones relevant for this course are linked below.

Program¹. All times below are Norwegian (GMT +02:00)

- Oct 8 16-18:30: Thore Egeland and Mariana Herrera
16:00 -16:15 Event opening
Introduction to Familias: [Tutorial](#) pp. 1-21
Introduction to Blind Search: [Tutorial](#) pp. 41-47
[Case Study \(pp. 1-4\)](#)
Exercises for Oct 15: 2.1, 2.2, 2.3, 2.9, 3.2 from [exercises](#)
- Oct 15 16-18: Thore Egeland and Mariana Herrera
Exercise **2.2** and **2.3** from Oct 8 discussed in class.
[Solutions all exercises](#)
Video solutions: [2.1 \(14:47\)](#), [2.2 \(6:10\)](#) [[Mutations](#)], [2.3 \(8:24\)](#) [[Simulation, 20:07](#)],
[2.9 \(11:17\)](#), [3.2 \(9:09\)](#)

¹ There will be a breakout session Oct 8 18:00 – 18:15 . Thore is lecturing unless specified otherwise, with Mariana as a co-teacher taking care of the chat. Break 17:00 -17:05.

DVI: [Tutorial](#) pp. 48-59

[Case Study](#) (pp. 5-14)

[Exercises for Oct 22](#): 3.1, 3.3 from [exercises](#). [Exercise E1: Conditional simulation](#)

- Oct 22 16-18: Thore Egeland and Mariana Herrera
16-17 [Marcadores STRs del Cromosoma X y su uso forense](#) (Mariana)
17:05-17:30 Exercises from Oct 15 discussed in class. [Solutions](#) are available, also videos: [3.1](#) (12:22) , 3.3 ([first part](#) 13:39, [second part](#) 6:02). [Exercise E1](#) (15:18, [written solution](#)).
17:30-18:00 [Incest case](#) involving X-chromosomal markers
[Exercises for Oct 29](#): Watch video on [plotting pedigrees](#) and FamLinkX [introduction video](#) based on Exercise 4.12 (21:02, [presentation](#) used in video), 4.12, 4.13 from [exercises](#)
- Oct 29 16:00-18:00: Thore Egeland, Mariana Herrera and Franco Marsico
16:00-17:00 [Presentation of FOGSA](#), (Franco)
17:05-18:00 Exercises discussed in class: [Modified GHEP-2019 eExercise](#) continued. Video solutions: [4.12](#) (21:02) [4.13](#) (7:30). Written [Solutions](#).
Review of lectures. Discussion.

Bonus material

In response to questions and comments, I have added some material:

- [Mutation models \(advanced\)](#)
- ["Which mutation model should I use?"](#).
- [Fundamentos básicos \(Lourdes Prieto\)](#)
- [Use Extra persons or not to define pedigrees?](#)
- Exclude extremely influential markers? It may happen, as in Exercise 2.3, that one marker gives a very large LR. It is good practice to check the LR for the individual markers, but I don't recommend to exclude a marker unless something is wrong, for instance a misspecified allele frequency.
- Bug reporting: Please email daniel.l.kling@gmail.com with copy to thore.egeland@gmail.com should you encounter problems with Familias or FamLinkX. Please include the Familias (fam-file) or FamLinkX (sav-file) that creates the problem and a description like a screen shot. Also, indicate the version you are using.
- [parentela](#). Blog: [genetica forense y probabilidad](#).
- "Prioritising family members for genotyping in missing person cases: A general approach combining the statistical power of exclusion and inclusion", [Vigeland et al.](#), FSI Genetics, 2020
- Some [Exercises in Spanish](#) with written [solutions](#), translated by Manuel García Magariños. Manuel also recorded [Introduccion Familias 3](#) (2015).