ISFG report Short Term Fellowship 2023

Applicant: Marisa Mariano Faustino, PhD student at Faculty of Sciences of the University of Porto (FCUP), Institute for Research and Innovation in Health (i3S)

Research visit to the Department of Forensic Toxicology, National Board of Forensic Medicine, Linköping, Sweden, from September 8th to October 2nd, 2023

The main goal of the visit was to extend the mathematical framework developed previously for independent X-chromosomal markers Faustino et al. (2023, under review) to linked ones, in pairwise kinship analysis when one of the individuals exhibits a non-mosaic X chromosome aneuploidy (Trisomy X, Klinefelter syndrome, or Turner syndrome).

The unique features of the X chromosome can be crucial to complement autosomal profiling or to disentangle complex kinship problems, providing for some pedigrees a similar or even greater power than the one obtained by autosomes in paternity/maternity investigations. While theoretical and informatics approaches for pairwise X-linked kinship analyses are well established for individuals with a regular number of chromosomes, these are still lacking for individuals with an X chromosome aneuploidy. Indeed, our work was motivated by a real forensic case involving the evaluation of X-chromosomal markers to compare the hypotheses of two women being related either as paternal half-sisters or as unrelated, one of them showing a trisomy X (47, XXX). Besides, greater statistical power may be obtained when quantifying the evidence of linked X-chromosomal markers instead of considering only independent ones.

During my visit we were able to develop R programs, specifically one implementing the mathematical framework (under review) for pairwise kinship problems considering independent X-chromosomal markers and two females, one of them with a Trisomy X. Intending to expand the framework to linked markers, first, we established the inheritance patterns for kinship hypotheses commonly analyzed in forensic casework, and then we developed a new program, which considered the transition probabilities between the hidden states in the Markov chain for genetic markers. This probability is now being investigated for the female with Trisomy X.

This short-term fellowship allowed me, not only to learn how to program in R, but also to improve and expand my research work in pairwise kinship analyses involving individuals with an X chromosome aneuploidy for linked markers. We hope these efforts will result in an informatics and statistical framework, which will be disseminated within the forensic genetics community through an international, peer reviewed, publication.

References:
Faustino, M., Gusmão, L., Amorim, A., Kling, D., & Pinto, N. (2023). A Mathematical Framework for Genetic Relatedness Analysis Involving X Chromosome Aneuploidies. In Review. Forensic Science International: Genetics.