## Report on the Peter M. Schneider ISFG Fellowship stay at the National Board of Forensic Medicine, Linköping

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As a recipient of the Peter M. Schneider ISFG Fellowship, I had the opportunity to spend a research stay at the Department of Forensic Genetics and Forensic Toxicology at the National Board of Forensic Medicine (NBFM) in Linköping, Sweden, from August 26<sup>th</sup> to August 30<sup>th</sup> 2024. The main purpose of the stay was to gain hands-on experience with bioinformatical tools and analytical strategies used in forensic genetic casework, with a particular focus on applications relevant to kinship analysis.

During my stay, I received training in a range of bioinformatical tools routinely used at NBFM for processing massively parallel sequencing data. This included instruction on how to generate output suitable for complex kinship assessments, such as genotype likelihoods from degraded or historical samples. These tools were applied to a set of bone samples dating back to the 18th century, with the aim of extracting reliable genetic information despite the challenging condition of the material. For the alleged living relatives, genotype imputation was performed using bioinformatical tools to increase marker overlap and improve comparability with the historical samples.

The generated data were subsequently used in kinship comparisons. Importantly, the statistical framework used for this analysis had not previously been applied to real historical case data. This provided a unique opportunity to evaluate the practical utility of these methods and to contribute new insights to the field of forensic genetics.

The work carried out during this fellowship stay will lead to a scientific publication, and the results have also been presented at the 2024 ISFG Congress in Santiago de Compostela. This experience significantly enriched my doctoral research and fostered new collaborations that will be valuable for my future career in forensic genetics.