

Relatedness inference with forensic applications

Thore Egeland

What does it mean to be related? This question is surprisingly subtle, and its answer depends on the context. The definition "being connected by a pedigree" suffices for some applications, but -- counterintuitively -- does not imply genetic relatedness. I begin my talk by discussing definitions of relatedness and formulating relevant statistical models. Recent years have seen a rapid development in methods and computer implementations for relatedness inference. I will present two applications based on the Ped Suite, a unified collection of R packages for pedigree analysis described in the book "Pedigree analysis in R" by the developer Vigeland (Elsevier, 2021).

The first application is the famous set of missing person cases commonly referred to as the "Missing grandchildren of Argentina". Several hundred children abducted during the military dictatorship 1976–1983 are still unaccounted for. The search for these children, organized by the 'Banco Nacional de Datos Geneticos' in Buenos Aires, poses important scientific challenges and has motivated recent developments in the statistical analysis of missing person cases.

The second example addresses DNA-based identification of victims in the aftermath of disasters. Until recently, methods and software for such identification typically considered each victim individually. This leads to suboptimal statistical power and potentially to inconsistencies in the identifications. As I will show, these problems are resolved by performing identification of all victims simultaneously.