

Expanding the use of DNA matches to better understand criminal networks and co-offending. A bridge between forensic science and criminology.

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In Canada local criminal DNA databases are in operation since 2000. They have played a central role in forensic identification, with thousands of DNA matches collected to date, between traces from different caseworks. Matches between caseworks in local databases and with the convicted offenders at the national database, to which personal identification data is eventually connected, constitute important tactical/operational tool for investigations. Beyond this conventional use, it is thought that the administrative data contained in casework matches bears a huge, yet unexploited, potential for intelligence-led policing and criminology. Previous studies (e.g., conducted in Belgium and in the Netherlands) have shown the interest of studying criminal trajectories and co-offending by examining DNA match data.

In this study, we apply a social network analysis (SNA) to forensic DNA matches data accumulated over 15 years in Québec, hereby shedding light on co-offending patterns and trajectories. Thus, the administrative data associated with these matches was retrieved from the database of the biology department of the Laboratoire de sciences judiciaires et de médecine légale du Québec. Key sensitive data were anonymized and structured in an appropriate format for SNA using an R script. Then, we examined the consequences of integrating to SNA unknown individuals that emerge in DNA matches and that are necessarily absent in traditional arrestees files. The Gephi software was used to evaluate the relationships among individuals using standard SNA measures (i.e. degree centrality; betweenness centrality; strength of dyadic relations).

A total of 1,250 graph components were identified, each comprising between two and 37 individuals, for a total of 3,242 individuals involved in 4,503 criminal caseworks. At the operational level, the visualization of components, including unknown individuals (i.e. known only by their DNA profile), is crucial information for investigators. These results also show that the absence of information about unknown individuals in traditional SNA has a non-negligible effect on the results. As one or more unknown individuals were present in 386 (30%) of the components, each of them has the potential to modify the estimated proportion or classification of co-offenders (two individuals working together, three or more). More precisely, without DNA match data 60% of the components with one or more unknowns would have not been detected in some subset of co-offender (2 or 3 individuals). The remaining 40% would simply fall in a different, and smaller, subset of components. We also show that SNA measurements represent key statistical information for the general evaluation of DNA networks.

Our results suggest that the study of co-offending, both for intelligence and research, would greatly benefit from a wider collaboration between forensic science and criminology. We thus expect new cross-discipline

bridges linking DNA and traditional data opening a new era for SNA and an expanded use of DNA matches.

DNA database, social networks analysis