Canadian Scientific Working Group on DNA Analysis Methods

March 7, 2022

Response to the Law Commission of Ontario's "AI Case Study: Probabilistic Genotyping DNA Tools in Canadian Criminal Courts" by Canadian SWGDAM

The Canadian Scientific Working Group on DNA Analysis Methods (CanSWGDAM) hereby wishes to comment on the Law Commission of Ontario (LCO) report entitled "Artificial Intelligence Case Study: Probabilistic Genotyping DNA Tools in Canadian Criminal Courts", published in June 2021. Canadian SWGDAM is comprised of senior managers and scientific technical leaders of four entities: the DNA divisions of the three government forensic laboratories in Canada, including the Centre of Forensic Sciences (CFS) in Ontario, the Laboratoire de Sciences Judiciaires et de Médecine Légale (LSJML) in Quebec, the National Forensic Laboratory Services (NFLS) of the Royal Canadian Mounted Police (RCMP), serving the remaining provinces and territories, as well as the National DNA Data Bank (NDDB), also of the RCMP. CanSWGDAM is a platform for discussion and sharing of Canadian best practices in forensic biology.

CanSWGDAM members are familiar with probabilistic genotyping and its use in Canada, as this approach has been in operation in two of the three forensic laboratories for several years (the CFS began using the system in 2016 while the LSJML began in 2018) and is also currently under validation in the third. We therefore consider it appropriate to clarify and correct a number of assertions in the LCO report.

Probabilistic Genotyping

Probabilistic genotyping (PG) is the use of statistical methods and mathematical algorithms for DNA profile interpretation in a forensic context. It is an approach that provides a mathematical breakdown of a DNA result. It can be similarly applied to a DNA result coming from one individual (i.e. single-source profile), as well as to a DNA result coming from several individuals (i.e. a DNA mixture). The software determines, according to the biological model and the parameters of each laboratory, which genetic profile or profiles (genotypes) can explain the observed result. The software then assigns weights to each genotype or set of genotypes according to their probabilities (i.e. how best they explain the observed result). These probabilities are then used, in a second operation, to calculate the Likelihood Ratio (LR), according to the chosen hypotheses and the relevant population databases.

Thus, PG does not reveal what "kind" of suspect is being sought, as claimed on page 11 of the report. Rather, it considers the possible genotypes of whichever contributor(s) could explain the DNA result obtained, independent of the profile of any specific individual. Therefore, PG tools are not intended to "produce potentially very inculpatory evidence" as written on page 8 of the report; they are intended to resolve the DNA result, regardless of the outcome. These tools can thus allow for the exclusion as well as

the inclusion of a given individual. Furthermore, whether the DNA profile is single-source or a DNA mixture, the calculations have the same level of rigor and validity.

Disclosure, Black Boxes and Transparency

Like any technology, PG software requires thorough validation prior to being implemented in a forensic laboratory. This process typically requires several months and is performed by competent scientists in each of the laboratories where PG operates. As a laboratory accredited to international quality standards, which all three Canadian public forensic laboratories are, audits are performed by independent, impartial scientists external to the organization during which validations are scrutinized and evaluated to ensure that they meet appropriate standards. Thus, there is no barrier to transparency regarding validation data, as implied by the authors. Furthermore, validation summaries from Canadian laboratories are available to legal counsel, upon request and where relevant.

The CFS has disclosed its validation summaries several times in preparation for potential challenges. On page 18 of the report, a case is referenced in which a defendant was denied access to PG validation documents following a disclosure request in Quebec. In this case, while the court did not consider the documentation relevant, the laboratory nevertheless proposed that some data could be released and that the remainder could be reviewed on site. It should be noted that this same validation, performed by the LSJML, was also the subject of a peer-reviewed publication in 2019 [1], which may be consulted by all.

Finally, the Institute of Environmental Science and Research of New Zealand (ESR), the manufacturer of the PG software used by the three CanSWGDAM forensic laboratories, offers legal counsel and others a mechanism for access to the code and details of the algorithms used, upon request and free of charge (https://www.strmix.com/news/strmix-updates-defense-access-policy/).

Scientific Validity and Bias

As a result of the validations performed in Canada and in at least 90 international laboratories, it is possible to affirm that PG is an objective approach that is valid for its intended use. It allows all aspects of a DNA result to be considered in a consistent, mathematical manner and does so without knowledge of the suspect's profile. The only non-mathematical input is the assessment of the number of contributors represented by the result. This is a core element of DNA interpretation, for which experts are duly trained and qualified, and has been occurring long before PG was available.

PG allows for an even more objective analysis than methods previously employed. It is the reason why the authors of the 2016 PCAST report [2], which is discussed in the LCO report, encourage its use. Their concern was only in respect of those contributions of DNA present in small proportions (defined by them as less

than 20% of the total) for which, at the time of writing the report, little data had been formally published. However, publications since then, as well as several unpublished validations, have demonstrated that LRs obtained regarding contributors in such low proportions appropriately reflect the strength of an association and are thus reliable [1, 3, 4].

Likelihood Ratios

The Likelihood Ratio (LR) is extensively referenced in the LCO report. It is important to note, however, that use of the LR is not exclusive to PG. The significance of forensic DNA test results has been expressed as a LR, long before the advent of PG, in relation to some mixtures of DNA as well as in paternity cases and others involving familial comparisons, in both civil and criminal matters. The Random Match Probability (RMP) itself, upheld as a gold standard in the LCO report and in use across Canada for nearly 30 years, can be readily expressed as a LR when it is used in relation to single-source profiles. Like the LR, the RMP is an assessment of probabilities weighed against each other. It contrasts the probability of the DNA result under two mutually exclusive hypotheses and requires no assumption of any prior probabilities (i.e. non-DNA information). In the case of the RMP, only two hypotheses may be formulated: 1) the individual in question is the contributor 2) the individual in question is not the contributor, but rather someone else, taken at random from the population, is the contributor.

When the LR is calculated for a mixed DNA result, the number of possible hypotheses is dependent on the number of contributors represented by the DNA result. Most often, at the time the LR is calculated, the so-called “defence” hypothesis is not known. The expert must therefore choose the hypotheses used. In most cases, the two hypotheses leading to the most conservative (lowest) LR will be those selected. In some instances, an individual will be assumed (what is called conditioning) to be a contributor when, for example, one is dealing with a sample taken from an individual’s body and the detection of their DNA is expected. The expert therefore chooses the hypotheses by being conservative, and in consideration of the context of the case. In addition, each laboratory indicates, either in the test report or in information documents available to the parties, that the LR can be calculated according to other hypotheses that may be proposed, upon request.

The LR is an assessment of the probability of the observed DNA result under two hypotheses and must ultimately be evaluated by the trier of fact in the context of the rest of the evidence in the case. For example, the DNA evidence (LR) in a particular case may provide support for the assertion that the suspect is a contributor to a mixed profile, but if the suspect was not in the country at the time of the crime, has never been to the scene of the crime, and has not had contact with anyone who has, these factors clearly need to be taken into account, although not by the forensic scientist, in evaluating the veracity of the assertion. The very same can be said, whether the DNA evidence is expressed as a LR or as a RMP.

The authors of the LCO report are not wrong in stating that presenting the LR to the court can be challenging. However, these challenges are not unique to PG nor to the LR but to the inherent complexities of scientific evidence in general. It is the expert's role to convey the evidence clearly and to neither overstate nor understate it. Major forensic science associations, including the US SWGDAM, the International Society for Forensic Genetics (ISFG) and the European Network of Forensic Science Institutes (ENFSI), all endorse the use of the LR in a forensic context.

In conclusion, we hope that the clarifications provided will be considered useful and taken into account when reading the LCO report.

Sincerely,

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1. Noël S, Noël J, Granger D, Lefebvre JF, Séguin S. STRmix™ put to the test: 300 000 non-contributor profiles compared to four contributor DNA mixtures and the impact of replicates. Forensic Sci. Int. Genet. 2019;41:24-31. doi: 10.1016/j.fsigen.2019.03.017.

2. President's Council of Advisors on Science and Technology, PCAST releases Report on Forensic Science in Criminal Courts. 2016.

3. Moretti TR, Just RS, Kehl SC, Willis LE, Buckleton JS, Bright JA, Taylor DA, Onorato AJ. Internal validation of STRmix™ for the interpretation of single source and mixed DNA profiles. Forensic Sci. Int. Genet. 2017;29:126–144. doi: 10.1016/j.fsigen.2017.04.004.

4. Bright JA, Richards R, Kruijver M, Kelly H, McGovern C, Magee A, et al. Internal validation of STRmix™ – a multi laboratory response to PCAST. Forensic Sci. Int. Genet. 2018;34:11–24. doi: 10.1016/j.fsigen. 2018.01.003.