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INFERENCE ABOUT RELATIONSHIPS FROM DNA MIXTURES

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DNA is now routinely used in criminal and civil investigations. DNA samples are of varying quality and therefore present challenging problems for their interpretation.
We present a statistical model for the quantitative peak information obtained from an electropherogram (EPG) of a forensic DNA sample and illustrate its potential use for the analysis of civil and criminal cases. In contrast to most previously used methods, we directly model the peak height information and incorporate important artefacts associated with the production of the EPG. The model has a number of unknown parameters, that can be estimated in the presence of multiple unknown contributors; the computations exploit a Bayesian network representation of the model.
We illustrate real casework examples from a criminal case and a disputed paternity case, where in both cases part of the evidence was from a DNA mixture. We present methods for inference about the relationships between contributors to a DNA mixture of unknown genotype and other individuals of known genotype. Following commonly accepted practice, the evidence for such a relationship is presented as the likelihood ratio for the specified relationship versus the alternative that there is no such relationship. Our methods are based on the statistical model for DNA mixtures, in which a Bayesian network is used as a computational device for efficiently computing likelihoods; the present work builds on that approach, but makes more explicit use of the Bayesian network in the modelling. The R code for the analyses presented is freely available as supplementary material.
We find that taking full account of the uncertainty inherent in a DNA mixture can yield likelihood ratios very close to what one would obtain if we had a single source DNA profile. Furthermore, the methods can be readily extended to analyse different scenarios as our methods are not limited to the particular genotyping kits used in the examples, to the allele frequency databases used, to the numbers of contributors assumed, to the number of traces analysed simultaneously, nor to the specific hypotheses tested.