

## TECHNOLOGY

## DNA has nowhere to hide

For many years, forensic scientists wanting to determine whether an individual was present at the scene of a crime have had to laboriously test a suboptimal biological sample with a handful of DNA markers. A new report promises to end this challenging state of affairs — it shows that SNP genotyping arrays can detect trace quantities of a suspect's DNA in a complex mixture containing hundreds of other individuals.

High-density SNP genotyping has transformed the identification of disease-associated gene variants, yet its uses were never extended to person identification owing to the belief that individuals within a pooled sample would be impossible to resolve. The authors of this paper have reversed this assumption — first by investigating the feasibility of using hundreds and thousands of SNPs to genotype individuals in a complex mix, then by probing the limitations of the approach through simulations, and finally by testing the idea in a real-life context.

The basic approach involves determining the SNP allele frequencies

of the sample (as inferred from allele probe intensities) and then calculating whether the frequency profile seen in a suspect is closer to the profile seen in the sample than in the reference population. How well does the theory hold? This question was initially addressed in a simulation in which the allele frequencies, the fraction of the suspect's DNA in a sample and experimental noise were modelled on a random sample of over 1,400 individuals of known genotype. The results are striking: by genotyping only 50,000 SNPs, single individuals can be detected even when each one makes up only 0.1% of the sample. By contrast, the amount of noise only marginally affects accuracy. These values were then confirmed experimentally when the framework was applied to real data — on a series of eight mixtures made up of varying proportions of HapMap individuals that were typed using Affymetrix or Illumina platforms.

The ability to identify individuals in a complex mixture promises to transform the field of forensics.

Although the results are impressive, the method comes with a few caveats, not least the need to account for any differences in ancestry between the reference and the experimental populations. And it is not just criminals who risk being unmasked: individuals whose DNA is pooled for research purposes — for example, in genome-wide association studies — are at risk of having their anonymity unveiled by such probing analyses. Although such a risk is currently low, the National Institutes of Health and the Wellcome Trust have responded to this work by removing some of their genetic data from public view.

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**ORIGINAL RESEARCH PAPER** Homer, N. *et al.* Resolving individuals contributing trace amounts of DNA to highly complex mixtures using high-density SNP genotyping microarrays. *PLoS Genet.* **4**, e1000167 (2008)

**FURTHER READING** Jobling, M. A. & Gill, P. Encoded evidence: DNA in forensic analysis. *Nature Rev. Genet.* **5**, 739–751 (2004) | Weir, B. S. *et al.* Genetic relatedness analysis: modern data and new challenges. *Nature Rev. Genet.* **7**, 771–780 (2006) | McCartney, C. LCN DNA: proof beyond reasonable doubt? *Nature Rev. Genet.* **9**, 325 (2008)

