Expert Systems and Cognitive Bias

David H. Kaye
Penn State Law &
Forensic Science Program

Forensic MAGAZINE

Drug Identification Software

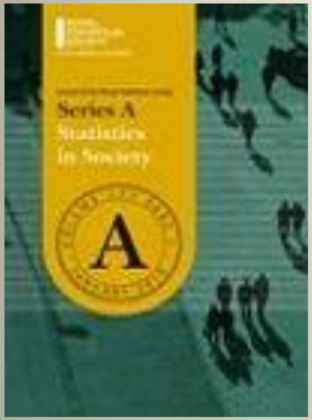
- Tue, Apr. 29, 2014, Centice Corporation

- Centice Corporation has released version 5.5 of its drug identification software … .
- Centice's products enable law enforcement, narcotic squads, and drug task forces to quickly and easily perform drug identification without destroying any evidence. Based on Raman spectroscopy technology the system rapidly scans any unknown substance or pill and identifies its unique spectral fingerprint, comparing it to a custom library of over 3,800 narcotics, prescription pills, precursors, cutting agents, and synthetic drugs.

CENTICE

Computer Program Could Help Solve Arson Cases

- Tue, Apr. 29, 2014, Bev Betkowski, Univ. of Alberta
- A computer program developed by U of A Faculty of Science professor James Harynuk, his team of … researchers and the Royal Canadian Mounted Police National Forensic Laboratory Services, can cut the need for extra levels of human analysis, reducing the waiting time to find out the cause of a deliberately set fire.
- Currently, an RCMP forensic scientist examines data from a sample, which is then re-examined by a second scientist to see whether they agree on the findings—a process that can take hours per sample. The average arson investigation yields three or four samples.
- The technology … would allow the first scientist to run findings through the computer program, getting an answer in seconds. Only if the computer gave a result different from that of the scientist would the debris sample go to a second human analyst.



Quantifying the Weight of Evidence from a Forensic Fingerprint Comparison: A New Paradigm

- Neumann, Evett & Skerrett, JRSS(A), 2012

- For each mark, we therefore obtained a triplet of data: mark—corresponding print from the UK—most similar non-corresponding print from the USA.
- (a) very few instances of $LR(H_d)>1$ were observed and most of them would be filtered out because of the presence of a small numerator,
- (b) even fewer instances of $LR(H_p)<1$ are observed, most of them for configurations with lower numbers of minutiae, and, in all cases, low values for $LR(H_p)$ are provoked by an extreme distortion of the mark or by a mislabelling of the mark or the print,

International Association for Identification

The Worlds Oldest and Largest
Forensic Science
Identification Association

Resolution 2010-18

- The use of mathematically based models to assess the associative value of the evidence may provide a scientifically sound basis for supporting the examiner’s opinion. **Examiners shall only use mathematically based models that have been accepted as valid by the IAI** in partnership with the relevant scientific community and in which they have been trained to competency.

Subjectivity and Bias in Forensic DNA Mixture Interpretation

- Dror & Hampikian, Sci & Just, 2011

- “the first experimental study exploring DNA interpretation”
- “When 17 North American expert DNA examiners were asked for their interpretation of data from an adjudicated criminal case in that jurisdiction, they produced inconsistent interpretations. Furthermore, the majority of 'context free' experts disagreed with the laboratory's pre-trial conclusions, suggesting that the extraneous context of the criminal case may have influenced the interpretation of the DNA evidence, thereby showing a biasing effect of contextual information in DNA mixture interpretation.”

New Kiwi Crime Tool Unravels Mixed DNA

- Ian Steward, Jan. 6, 2014

- A Kiwi backyard invention is changing crime scene investigations around the world. For the first time, police can take samples that contain more than one person's DNA and unravel the strands. …
- In the past all this evidence would have been discarded. Mixed DNA was useless DNA. There was no way to separate out the strands of genetic code. But now, with a tool developed in the "backyard" of some Kiwi scientists, the problem that has long stymied international forensic scientists has been solved.
- The software, called STRmix, has already been sold to the US Army, and the FBI is in talks to acquire the rights.

Euroforgen-NoE Collaborative Exercise on LRmix

- Prieto et al., FSI: Genetics, 2014
- The interpretation of mixtures is not solely a matter of using some software to provide ‘an answer’. An assessment … will usually begin with a consideration of the circumstances of a crime. Assumptions made about the numbers of contributors follow from an examination of the electropherogram(s) – and these may differ between the prosecution and the defence hypotheses. ... Once the hypotheses are formulated, the mathematical analysis … can only be accomplished [with] specialist software. [I]t is essential that scientists are trained … but also in the methodology to understand the likelihood ratio concept … . ... Recently, 18 different laboratories … trained in the methodology … were asked to independently analyze … cases with partial mixture DNA evidence … . We show … for the first time, that a high degree of standardization, leading to uniformity of results can be achieved … .

PLOS | ONE

TrueAllele Casework on Virginia DNA Mixture Evidence: Computer and Manual Interpretation

- Perlin et al., PLoS ONE, 2014
- Mathematical modeling can … allow a computer to assess the relative likelihood of alternative solutions. The result is a genotype probability distribution that is objectively derived from the data, independent of known comparison genotypes. Subsequent comparison of this evidence genotype with a reference genotype, relative to a human population, produces a DNA match statistic that measures identification information. By using all of the quantitative DNA mixture data, and thoroughly considering all feasible genotype alternatives, computer modeling can preserve more identification information than manual review.

Conclusions

Automated (expert) systems can supplement, guide, or replace human analysis.

They can operate free of domain irrelevant cues and expectation effects.

They should be validated against a realistic range of input to ascertain accuracy (and that they have no built-in biases).