

## Computers Interpret DNA Mixtures Better Than Human Experts

DNA is the forensic gold standard for human identification. But having DNA evidence does not mean having a match statistic for court. Much DNA today is too complex (mixtures, touch or degraded samples) for human experts to interpret effectively. This DNA data is under-reported (lower match statistics) or never reported at all ("inconclusive" result). When DNA evidence is unused, the guilty go free and innocents are harmed.

Modern computing can interpret this new DNA, and provide accurate match statistics. Innovated by Cybergenetics, the TrueAllele® Casework system can *thoroughly* examine millions of alternative identification scenarios. The computer is entirely *objective*, since it never sees the suspect when solving a problem. The TrueAllele computer is accurate and reliable, and regularly used in court.

Cybergenetics website has much information about the TrueAllele system (articles, courses, news, newsletters, presentations). The articles linked below are all downloadable from the "[www.cybgen.com/information](http://www.cybgen.com/information)" Publications page.

### Magazine Articles

[Perlin, M.W. "Forensic science in the information age." \*Forensic Magazine\*, 9\(2\): 17-21, 2012.](#)

[Perlin, M.W. and Galloway, J. "Computer DNA evidence interpretation in the Real IRA Massereene terrorist attack". \*Evidence Technology Magazine\*, 10\(3\):20-3, 2012.](#)

[Perlin, M.W. "Easy reporting of hard DNA: computer comfort in the courtroom." \*Forensic Magazine\*, 9\(4\):32-37, 2012.](#)

### Book Chapters and Cases

[Perlin, M.W. "The Blairsville Slaying and the Dawn of DNA Computing," In \*Death Needs Answers: The Cold-Blooded Murder of Dr. John Yelenic\*, A. Niapas, Ed., New Kensington, PA: Grelin Press, 2013.](#)

[Perlin, M.W. "DNA Identification Science." In \*Forensic Sciences\*, vol. 3, C.H. Wecht, Ed. Albany, NY: LexisNexis Matthew Bender; Chapter 37C, 2012.](#)

[Perlin, M.W. "When good DNA goes bad." \*Journal of Forensic Research\*, 2013.](#)

### Scientific Validations

[Perlin, M.W. and Sinelnikov, A. "An information gap in DNA evidence interpretation." \*PLoS ONE\*, 4\(12\):e8327, 2009.](#)

[Perlin, M.W., Legler, M.M., Spencer, C.E., Smith, J.L., Allan, W.P., Belrose, J.L., and Duceman, B.W. "Validating TrueAllele® DNA mixture interpretation." \*Journal of Forensic Sciences\*, 56\(6\):1430-47, 2011.](#)

[Perlin, M.W., Belrose, J.L., and Duceman, B.W. "New York State TrueAllele® Casework validation study." \*Journal of Forensic Sciences\*. 58\(6\):in press, 2013.](#)