

Curriculum Vitae

Mark W. Perlin, PhD, MD, PhD
DNA evidence interpretation and the likelihood ratio

Cybergenetics, Corp.
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Positions Held

Cybergenetics, Corp.	chief scientist & executive	1996-present	Comput. Bioscience
Carnegie Mellon University	senior research scientist	1995-1996	Computer Science
Carnegie Mellon University	research computer scientist	1992-1995	Computer Science
Carnegie Mellon University	research associate	1988-1992	Computer Science
Carnegie Mellon University	visiting researcher	1986-1988	Computer Science
Pittsburgh NMR Institute	research scientist	1985-1986	Comput. Radiology
Mercy Hospital, Pittsburgh, PA	transitional resident	1984-1985	Medicine/Radiology
IBM/Watson Research Yorktown, NY	post-doctoral fellow	1984-1984	Mathematics

Education and Training

Carnegie Mellon University, Pittsburgh, PA	Ph.D.	1991	Computer Science
The University of Chicago Pritzker School of Medicine	M.D.	1984	Medicine
City University of New York Graduate School	Ph.D.	1982	Mathematics
Harpur College/SUNY, Binghamton, NY	B.A.	1977	Chemistry

Professional Societies

American Academy of Forensic Sciences, Fellow (Criminalistics)
American Society of Human Genetics
American Statistical Association
Duquesne University Forensic Science and Law, Scholar in Residence

Honors and Awards

Noteworthy Article chosen by the Journal of Forensic Sciences, 2020
Innovation Award for Forensic Science, Pittsburgh Business Times, 2017
Pittsburgh Smart 50 Impact Award, Smart Business Magazine, 2017
Solution Provider of the Year: Innovative Technology, Pittsburgh Technology Council, 2017
Paul Chapman Justice Award, Foundation for Improvement of Justice, 2017
Keynote Speaker, International Conference on Forensic Inference and Statistics, 2014
Keynote Speaker, International Conference on Forensic Research and Technology, 2012
Keynote Speaker, Duquesne University Summer Research Symposium, 2010
Keynote Speaker, ACM Symposium on Software Reusability, 2001
Keynote Speaker, SRI Biotechnology Conference, 1997
CUNY Alumnus Achievement Award, 1990
Phi Beta Kappa, 1977
Eagle Scout, 1974

Dr. Mark W. Perlin

Bausch and Lomb Science Award, 1973

Patents

- M. W. Perlin, "Method, apparatus and computer software program for determining probability of error in identifying evidence," U.S. Patent #10,489,233, Nov. 2019
- M. W. Perlin, "Method and system for DNA mixture analysis," U.S. Patent #9,708,642, Jul. 2017
- M. W. Perlin, "Method and system for DNA mixture analysis," U.S. Patent #8,898,021, Nov. 2014
- M. W. Perlin, "Method and system for DNA mixture analysis," E.P.O. Patent #1,229,135, Jan. 2014
- M. W. Perlin, "Method for DNA mixture analysis," U.S. Patent #6,807,490, Oct. 2004
- M. W. Perlin, "Method and system for genotyping," U.S. Patent #6,750,011, Jun. 2004
- M. W. Perlin, "Method and system for sequencing genomes," U.S. Patent #6,068,977, May 30, 2000.
- M. W. Perlin, "Method and system for genotyping," U.S. Patent #6,054,268, Apr. 15, 2000.
- M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,876,933, Mar. 2, 1999.
- M. W. Perlin, "A system and method for producing maps and cloning genes therefrom," U.S. Patent #5,622,823, Apr. 22, 1997.
- M. W. Perlin, "Method and system for sequencing genomes," U.S. Patent #5,604,100, Feb. 18, 1997.
- M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,580,728, Dec. 3, 1996.
- M. W. Perlin, "Method and system for genotyping," U.S. Patent #5,541,067, Jul. 30, 1996.

Publications

Journal (33)

- D. W. Bauer, N. Butt, J. Hornyak, and M. W. Perlin. "Validating TrueAllele[®] interpretation of DNA mixtures containing up to ten unknown contributors." *Journal of Forensic Sciences*, 65(2):380-398, 2020.
- M. W. Perlin. "Efficient construction of match strength distributions for uncertain multi-locus genotypes." *Heliyon*, 4(10):e00824, 2018.
- M. W. Perlin. "Inclusion probability for DNA mixtures is a subjective one-sided match statistic unrelated to identification information." *Journal of Pathology Informatics*, 6(1):59, 2015.
- M. W. Perlin, J. Hornyak, G. Sugimoto, and K. Miller. "TrueAllele[®] genotype identification on DNA mixtures containing up to five unknown contributors." *Journal of Forensic Sciences*, 60(4):857-868, 2015.
- M. W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood, and S. Greenspoon, "TrueAllele[®] Casework on Virginia DNA mixture evidence: computer and manual interpretation in 72 reported criminal cases." *PLoS ONE*, 9(3):e92837, 2014.
- M. W. Perlin, J. L. Belrose, and B. W. Duceman, "New York State TrueAllele[®] Casework validation study." *Journal of Forensic Sciences*, 58(6):1458-1466, 2013.
- J. Ballantyne, E. K. Hanson, and M. W. Perlin. "DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information." *Science & Justice*, 53(2):103-114, 2013.
- M. W. Perlin, "When good DNA goes bad," *Journal of Forensic Research*, S11:003, DOI 10.4172/2157-7145.S11-003, 2013.

Dr. Mark W. Perlin

M. W. Perlin, M. M. Legler, C. E. Spencer, J. L. Smith, W. P. Allan, J. L. Belrose, and B. W. Duceman. "Validating TrueAllele[®] DNA mixture interpretation." *Journal of Forensic Sciences*, 56(6) 1430-1447, 2011.

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

M. W. Perlin, J. B. Kadane, and R. W. Cotton, "Match likelihood ratio for uncertain genotypes." *Law, Probability and Risk*, 8(3):289-302, 2009.

S. Y. Hill, S. Shen, N. Zezza, E. K. Hoffman, M. W. Perlin, and W. Allan. "A genome wide search for alcoholism susceptibility genes." *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics* 128B(1): 102-113, 2004.

M. W. Perlin and B. Szabady, "Determining sequence length or content in zero, one, and two dimensions," *Human Mutation*, 19(4), 2002.

M. W. Perlin and B. Szabady, "Linear mixture analysis: a mathematical approach to resolving mixed DNA samples," *Journal of Forensic Sciences*, 46(6), pp. 1372-77, 2001.

B. Pálsson, F. Pálsson, M. Perlin, H. Gubjartsson, K. Stefánsson, and J. Gulcher, "Using quality measures to facilitate allele calling in high-throughput genotyping," *Genome Research*, 9(10): 1002-1012, 1999.

G. Lancia and M. Perlin, "Genotyping of pooled microsatellite markers by combinatorial optimization techniques," *Discrete Applied Math.*, vol. 88, no. 1-3, pp. 291-314, 1998.

M. W. Perlin, "Reliable genome maps from unreliable data: BIN-SORT mapping of cloned DNA fragments," *Math. Model. Sci. Comp.*, 1998.

M. W. Perlin, "Rapid construction of genome maps," *Nature Med.*, vol. 3, no. 9, pp. 1046-1048, 1997.

C. Andrews, B. Devlin, M. Perlin, and K. Roeder, "Binning clones by hybridization with complex probes: statistical refinement of an inner product mapping method," *Genomics*, vol. 41, no. 2, pp. 141-154, 1997.

M. W. Perlin, G. Lancia, and S.-K. Ng, "Toward fully automated genotyping: genotyping microsatellite markers by deconvolution," *Am. J. Hum. Genet.*, vol. 57, no. 5, pp. 1199-1210, 1995.

M. W. Perlin, D. J. Duggan, K. Davis, J. E. Farr, R. B. Findler, M. J. Higgins, N. J. Nowak, G. A. Evans, S. Qin, J. Zhang, T. B. Shows, M. R. James, and C. W. Richard III, "Rapid construction of integrated maps using inner product mapping: YAC coverage of human chromosome 11," *Genomics*, vol. 28, no. 2, pp. 315-327, 1995.

H. Kobayashi, T. C. Matise, M. W. Perlin, H. G. Marks, and E. P. Hoffman, "Towards fully automated genotyping: use of an X linked recessive spastic paraplegia family to test alternative analysis methods," *Hum. Genet.*, vol. 95, pp. 483-490, 1995.

M. W. Perlin, M. B. Burks, R. C. Hoop, and E. P. Hoffman, "Towards fully automated genotyping: allele assignment, pedigree construction, phase determination, and recombination detection in Duchenne muscular dystrophy," *Am. J. Hum. Genet.*, vol. 55, no. 4, pp. 777-787, 1994.

M. W. Perlin, "Visualizing dynamic artificial intelligence algorithms and applications," *Artificial Intelligence Tools*, vol. 3, no. 2, pp. 289-307, 1994.

Dr. Mark W. Perlin

T. C. Matise, M. W. Perlin, and A. Chakravarti, "Automated construction of genetic linkage maps using an expert system (MultiMap): application to 1268 human microsatellite markers," *Nature Genetics*, vol. 6, no. 4, pp. 384-390, 1994.

M. W. Perlin and A. Chakravarti, "Efficient construction of high-resolution physical maps from yeast artificial chromosomes using radiation hybrids: inner product mapping," *Genomics*, vol. 18, no. 2, pp. 283-289, 1993.

M. W. Perlin, "Factored arc consistency for RETE match," *Artificial Intelligence Tools*, 1993.

E. Kanal and M. Perlin, "Computer-based magnetic resonance imaging tutorial," *Amer. J. Neuroradiology*, vol. 13, pp. 1527-1534, 1992.

M. W. Perlin, "Arc consistency for factorable relations," *Artificial Intelligence*, vol. 53, no. 2-3, pp. 329-342, 1992.

M. W. Perlin, "Transforming recursive processes into efficient algorithms: call-graph caching for artificial intelligence," *Artificial Intelligence Tools*, vol. 1, 1992.

M. W. Perlin, "Transforming conjunctive match into RETE: a call-graph caching approach," *Int. Journal of Software Engineering and Knowledge Engineering*, vol. 1, no. 4, 1991.

M. W. Perlin, "Topologically traversing the RETE network," *Applied Artificial Intelligence*, vol. 4, pp. 155-177, 1990.

E. F. Feig, F. Greenleaf, and M. W. Perlin, "Magnetic resonance imaging with non-uniform fields," *Physics in Medicine and Biology*, vol. 10, pp. 1091-1099, 1986.

Conference (19)

M. W. Perlin. "Objective DNA mixture information in the courtroom: relevance, reliability and acceptance," *Presented at International Symposium on Forensic Science Error Management: Detection, Measurement and Mitigation, National Institute of Standards and Technology, Arlington, VA, 2015.*

M. W. Perlin, "DNA mapping the crime scene: do computers dream of electric peaks?," *in the Proceedings of Promega's Twenty Third International Symposium on Human Identification, Nashville, TN, 2012.*

M. W. Perlin. "Combining DNA evidence for greater match information." *Forensic Science International: Genetics Supplement Series*, 3(1):e510–e511, 2011.

M. W. Perlin. "Investigative DNA databases that preserve identification information." *Forensic Science International: Genetics Supplement Series*, 3(1):e484–e485, 2011.

M. W. Perlin, "Explaining the likelihood ratio in DNA mixture interpretation," *in the Proceedings of Promega's Twenty First International Symposium on Human Identification. San Antonio, TX, 2010.*

M. W. Perlin, "Scientific validation of mixture interpretation methods," *in the Proceedings of Promega's Seventeenth International Symposium on Human Identification. Nashville, TN, 2006.*

Dr. Mark W. Perlin

M. W. Perlin, "Real-time DNA investigation," in the Proceedings of *Promega's Sixteenth International Symposium on Human Identification*. Dallas, TX, 2005.

M. W. Perlin, "Simple reporting of complex DNA evidence: automated computer interpretation," in the Proceedings of *Promega's Fourteenth International Symposium on Human Identification*. Phoenix, AZ, 2003.

M. W. Perlin, D. Coffman, C.A. Crouse, F. Konotop, and J.D. Ban, "Automated STR data analysis: validation studies," in the Proceedings of *Promega's Twelfth International Symposium on Human Identification*. Biloxi, MS, 2001.

M. W. Perlin, "An expert system for scoring DNA database profiles," in the Proceedings of *Promega's Eleventh International Symposium on Human Identification*. Biloxi, MS, 2000.

M. W. Perlin, "Computer automation of STR scoring for forensic databases". In First International Conference on Forensic Human Identification in The Millennium, London, UK, The Forensic Science Service, 1999.

M. W. Perlin, and D. R. Richards, "Quantitative analysis of gel electrophoresis data for automated genotyping applications (Abstract)," *Amer. J. Hum. Genet.*, 57(4 Supplement): A26, 1995.

D. K. Pathak, E. P. Hoffman, and M. W. Perlin, "Intelligent molecular diagnostics using PCR-based linked genetic markers," in *Second International Conference on Intelligent Systems for Molecular Biology*, Stanford, CA, pp. 331-339, 1994.

D. K. Pathak and M. W. Perlin, "Automatic computation of genetic risk," in *Proceedings of the Tenth Conference on Artificial Intelligence for Applications*, San Antonio, Texas, pp. 164-170, 1994.

M. W. Perlin, "Principled animation of artificial intelligence algorithms," in *Fifth Int. Conf. on Tools for Artificial Intelligence*, Boston, MA, IEEE Computer Society, 1993.

M. W. Perlin, "Incremental binding-space match: The linearized MatchBox algorithm," in *Third Int. Conf. on Tools for Artificial Intelligence*, San Jose, CA, IEEE Computer Society, November, 1991.

M. W. Perlin, "LR recursive transition networks for Earley and Tomita parsing," in *Proceedings of the 29th Association for Computational Linguistics Meeting*, Berkeley, CA, June, 1991."

M. W. Perlin, E. Kanal, and A. John, "A user interface for visualizing concepts in Magnetic Resonance Imaging," in *First Conference on Visualization in Biomedical Computing*, Atlanta, GA, May, 1990.

M. W. Perlin, "Call-Graph Caching: transforming programs into networks," in *Proc. of the Eleventh Int. Joint Conf. on Artificial Intelligence*, Detroit, Michigan, Morgan Kaufmann, August, 1989, pp. 122-128.

Magazine (8)

M. W. Perlin, "Good answers to bad questions about DNA match statistics." *Forensic Magazine*, 16(1):32-34, 2019.

M. W. Perlin, "Suspect-centric bias in DNA mixture interpretation." *Forensic Magazine*, 15(3):10-13, 2018.

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M. W. Perlin, "When DNA is not a gold standard: failing to interpret mixture evidence." *The Champion*, 42(4):50-56, May, 2018.

M. W. Perlin, "Hidden DNA evidence: exonerating the innocent." *Forensic Magazine*, 15(1):10-12, 2018.

M. W. Perlin and K. W. P. Miller, "Kern County resolves the DNA mixture crisis." *Forensic Magazine*, 11(4):8-12, 2014.

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

M. W. Perlin and J. Galloway, "Computer DNA evidence interpretation in the Real IRA Massereene terrorist attack." *Evidence Technology Magazine*, 10(3):20-23, 2012.

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

Book chapter (4)

M. W. Perlin, "DNA identification science: an introduction for lawyers," in *Forensic Sciences*, volume 3. C. H. Wecht, Ed., Albany, NY: LexisNexis Matthew Bender, Chapter 37C, 2017.

M. W. Perlin, "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.

M. W. Perlin, "Identifying human remains using TrueAllele® technology." *Forensic Investigation and Management of Mass Disasters*. M. I. Okoye and C. H. Wecht. Tucson, AZ, Lawyers & Judges Publishing Co: 31-38, 2007.

M. W. Perlin, "Mass casualty identification through DNA analysis: overview, problems and pitfalls." *Forensic Investigation and Management of Mass Disasters*. M. I. Okoye and C. H. Wecht. Tucson, AZ, Lawyers & Judges Publishing Co: 23-30, 2007.

Newsletter (5)

M. W. Perlin. "DNA done right." *FHC Experts for Law: Experts Forum Newsletter*, (5):4-7, 2013.

M. W. Perlin. "Cybergenetics TrueAllele technology enables objective analysis of previously unusable DNA evidence." *MathWorks Newsletters: Technical Article*. 1-4, 2013.

M. W. Perlin. "DNA intelligence and forensic failure: ^{[[SEP]]}what you don't know can kill you." *Cybergenetics: The DNA Investigator™ Newsletter*, Winter, 2011.

M. W. Perlin. "Validating DNA mixture interpretation methods." *Cybergenetics: The DNA Investigator™ Newsletter*, Spring, 2010.

M. W. Perlin. "Same data, more information – murder, match and DNA." *Cybergenetics: The DNA Investigator™ Newsletter*, Fall, 2009.

Thesis (2)

M. W. Perlin, "Automating the construction of efficient Artificial Intelligence algorithms", Doctoral Dissertation, School of Computer Science, Carnegie Mellon University, 1991.

Dr. Mark W. Perlin

M. W. Perlin, "Random Graphs Applied to the Immune Network," Doctoral Dissertation, Mathematics Department, City University of New York, 1982.

Presentations

M. W. Perlin, "Eliminating bias in forensic algorithms and statistics", *American Academy of Forensic Sciences 73rd Annual Meeting, Interdisciplinary Symposium*, 2021.

M. W. Perlin, "Human factors in automated forensic DNA examination", *Expert Working Group on Human Factors in Forensic DNA Interpretation: Probabilistic Genotype Software*, National Institute of Standards and Technology, National Institute of Justice, 2021.

M. W. Perlin, "Forensic validation, error, and reporting: a unified approach", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

G. Hampikian and M. W. Perlin, "The first five exonerations using TrueAllele® statistical software: how labs can review and correct old cases", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

J. Donahue* and M. W. Perlin, "Genotype information criteria for forensic DNA databases", *American Academy of Forensic Sciences 71th Annual Meeting*, Baltimore, MD, 2019.

L. Gumbs, E. Kanal, M. W. Perlin, G. Shannon, "CERT Data Science in Cybersecurity Symposium", Panel, *Software Engineering Institute, Carnegie Mellon University*, Arlington, VA, 2018.

M. W. Perlin, "Solving sexual assault cases using DNA mixture evidence", *National Sexual Assault Kit Initiative (SAKI)*, National Institute of Justice, Webinar, 2018.

N. Butt*, D. Bauer* and M. W. Perlin, "Validating TrueAllele® interpretation of DNA mixtures containing up to ten unknown contributors", *American Academy of Forensic Sciences 70th Annual Meeting*, Seattle, WA, 2018.

M. W. Perlin, "Distorting DNA evidence: methods of math distraction", *American Academy of Forensic Sciences 70th Annual Meeting*, Seattle, WA, 2018.

J. Donahue* and M. W. Perlin, "Using computers to overcome forensic DNA testing bottlenecks and improve recovery from complex samples", *American Academy of Forensic Sciences 70th Annual Meeting*, Seattle, WA, 2018.

M. W. Perlin, "Forensic match information: exact calculation and applications", *Tenth International Conference on Forensic Inference and Statistics (ICFIS)*, Minneapolis, MN, 2017.

J. Hornyak* and M. W. Perlin, "To include or not to include: the extent is the question", *Mid-Atlantic Association of Forensic Scientists Annual Meeting*, Pittsburgh, PA, 2017.

D. Bauer* and M. W. Perlin, "Validating TrueAllele® genotyping on ten contributor DNA mixtures", *Mid-Atlantic Association of Forensic Scientists Annual Meeting*, Pittsburgh, PA, 2017.

W. P. Allan* and M. W. Perlin, "Machines can work it out: automated TrueAllele® workflow", *Mid-Atlantic Association of Forensic Scientists Annual Meeting*, Pittsburgh, PA, 2017.

Dr. Mark W. Perlin

M. W. Perlin, "Transforming DNA evidence into reliable information: computers, science and society", *Pathology Informatics Summit, Association for Pathology Informatics*, Pittsburgh, PA, 2017.

M. W. Perlin, "Error in the likelihood ratio: false match probability", *American Academy of Forensic Sciences 69th Annual Meeting*, New Orleans, LA, 2017.

M. W. Perlin, W. P. Allan and C. Hughes, "On the threshold of injustice: manipulating DNA evidence", *American Academy of Forensic Sciences 69th Annual Meeting*, New Orleans, LA, 2017.

M. W. Perlin, F. Watson and G. Hampikian, "When DNA alone is not enough: exoneration by computer interpretation", *American Academy of Forensic Sciences 69th Annual Meeting*, New Orleans, LA, 2017.

M. W. Perlin, "Transparency in DNA evidence", *President's Council of Advisors on Science and Technology (PCAST)*, Washington, DC, 2016.

M. W. Perlin, "Justice denied: Mr. Hopkins invisible semen", *Annual Conference, American Investigative Society of Cold Cases*, St. Louis, MO, 2016.

M. W. Perlin, "Forensic stasis in a world of flux", *Quattrone Center Spring Symposium on Technology in Criminal Justice Reform, Penn Law School*, Philadelphia, PA, 2016.

M. W. Perlin, "DNA investigation: across the universe", *Spring Training Conference, Pennsylvania Homicide Investigators Association*, State College, PA, 2016.

M. W. Perlin, "Overcoming bias in DNA mixture interpretation", Presented by Dr. Ria David at the *American Academy of Forensic Sciences 68th Annual Meeting*, Las Vegas, NV, 2016.

M. W. Perlin and G. Sugimoto, "Separating DNA mixtures by computer to identify and convict a serial rapist", Presented by Dr. David Bauer at the *American Academy of Forensic Sciences 68th Annual Meeting*, Las Vegas, NV, 2016.

M. W. Perlin. "Objective DNA mixture information in the courtroom: relevance, reliability and acceptance", *International Symposium on Forensic Science Error Management: Detection, Measurement and Mitigation, National Institute of Standards and Technology*, Arlington, VA, 2015.

R. David, M. Bowkley* and M. W. Perlin, "Separating familial mixtures, one genotype at a time", *Northeastern Association of Forensic Scientists 40th Annual Meeting*, Hershey, PA, 2014.

M. W. Perlin, "Solving cold cases by TrueAllele® analysis of DNA evidence", *Finding Closure: The Science, Law and Politics of Cold Case Investigations, Cyril H. Wecht Institute of Forensic Science and Law 14th Annual Symposium*, Pittsburgh, PA, 2014.

J. Hornyak, W. Allan and M. W. Perlin, "Using TrueAllele® Casework to separate DNA mixtures of relatives", *DNA Workshop, 124th California Association of Criminalists*, San Francisco, CA, 2014.

M. Bowkley* and M. W. Perlin, "Compute first, ask questions later: an efficient TrueAllele® workflow", *Midwestern Association of Forensic Scientists 43rd Annual Fall Meeting*, St. Paul, MN, 2014.

J. Hornyak*, W. P. Allan and M. W. Perlin, "TrueAllele® Casework validation on PowerPlex® 21 mixture data", *Twenty Second International Symposium on the Forensic Sciences of the Australia and New Zealand Forensic Science Society (ANZFSS)*, Adelaide, Australia, 2014.

Dr. Mark W. Perlin

M. W. Perlin, "TrueAllele[®] interpretation of DNA mixture evidence", Keynote talk, *Ninth International Conference on Forensic Statistics and Inference (ICFIS)*, Leiden, The Netherlands, 2014.

M. W. Perlin, "Solving crimes using MCMC to analyze previously unusable DNA evidence", *American Statistical Association, Joint Statistical Meetings (JSM)*, Boston, MA, 2014.

M. W. Perlin, "Preventing rape in the military through effective DNA computing", *Forensic Europe Expo, Forensic Seminar Theatre*, London, UK, 2014.

M. W. Perlin, "Cracking the DNA mixture code – computer analysis of UK crime cases", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2014.

M. W. Perlin and M. M. Legler, "Coding a safer society through computer interpretation of DNA evidence", *MATLAB Virtual Conference*, Europe and North America, 2014.

M. W. Perlin, "Getting past first Bayes with DNA mixtures", *American Academy of Forensic Sciences 66th Annual Meeting*, Seattle, WA, 2014.

M. W. Perlin, "DNA knowledge, DNA power: how computers interpret evidence", *Cybergenetics Webinar*, Pittsburgh, PA, 2013.

M. W. Perlin, "Unleashing forensic DNA through computer intelligence", *Forensic Europe Expo, Forensic Innovation Conference*, London, UK, 2013.

M. W. Perlin, "Finding truth in DNA mixture evidence", *Innocence Network Conference, Advanced DNA*, Charlotte, NC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, L. Schiermeier-Wood, and S. Greenspoon, "Virginia TrueAllele[®] validation study: casework comparison", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, K. Dormer, J. Hornyak, T. Meyers, and W. Lorenz, "How inclusion interpretation of DNA mixture evidence reduces identification information", *American Academy of Forensic Sciences 65th Annual Meeting*, Washington, DC, 2013.

M. W. Perlin, "DNA mapping the crime scene: do computers dream of electric peaks?", *Promega's Twenty Third International Symposium on Human Identification*, Nashville, TN, 2012.

M. W. Perlin, "When good DNA goes bad," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "Forensic thinking, fast and slow," *International Conference on Forensic Research and Technology*, Chicago, IL, 2012.

M. W. Perlin, "The Massereene touch DNA evidence", *Twenty First International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Hobart, Tasmania, 2012. (Talk presented by DCI John McVea of the Police Service of Northern Ireland.)

M. W. Perlin, "Combining DNA evidence for greater match information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

Dr. Mark W. Perlin

M. W. Perlin, "Investigative DNA databases that preserve identification information", *American Academy of Forensic Sciences 64th Annual Meeting*, Atlanta, GA, 2012.

R. David* and M. W. Perlin, "Creating informative DNA libraries using computer reinterpretation of existing data", *Northeastern Association of Forensic Scientists 2011 Annual Meeting*, Newport, RI, 2011.

J. Ballantyne and M. W. Perlin, "DNA mixture deconvolution by binomial sampling of individual cells", *Eighth International Conference on Forensic Inference and Statistics*, Seattle, WA, 2011.

M. W. Perlin, "Computer interpretation of uncertain DNA evidence", *National Institute of Justice (NIJ) Conference*, Arlington, VA, 2011.

M. W. Perlin, "Taming uncertainty in forensic DNA evidence", *European Network of Forensic Science Institutes (ENFSI) DNA Working Group meeting*, Brussels, Belgium, 2011.

M. W. Perlin, "Sherlock Holmes and the DNA likelihood ratio", *American Academy of Forensic Sciences 63rd Annual Meeting*, Chicago, IL, 2011.

M. W. Perlin, "The science of quantitative DNA mixture interpretation", *Scientific Working Group on DNA Analysis Methods (SWGDM)*, Fredericksburg, VA, 2011.

M. W. Perlin, "Reliable interpretation of stochastic DNA evidence", *Canadian Society of Forensic Sciences 57th Annual Meeting*, Toronto, ON, 2010.

M. W. Perlin, "Overcoming DNA stochastic effects", *Northeastern Association of Forensic Scientists 2010 Annual Meeting*, Manchester, VT, 2010.

M. W. Perlin, "Inclusion probability is a likelihood ratio: implications for DNA mixtures" (poster), *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

M. W. Perlin, "Explaining the likelihood ratio in DNA mixture interpretation", *Promega's Twenty First International Symposium on Human Identification*, San Antonio, TX, 2010.

R. David* and M. W. Perlin, "More informative DNA identification: computer reinterpretation of existing data", *Midwestern Association of Forensic Scientists*, Kansas City, MO, 2010.

M. W. Perlin and K. E. Williams, "Preserving DNA information", *National Association of Medical Examiners 2010 Annual Meeting*, Cleveland, OH, 2010.

M. W. Perlin and B. W. Duceman, "Profiles in productivity: greater yield at lower cost with computer DNA interpretation", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.

M. W. Perlin and M. Greenhalgh, "Scientific combination of DNA evidence: a handgun mixture in eight parts", *Twentieth International Symposium on the Forensic Sciences of the Australian and New Zealand Forensic Science Society*, Sydney, Australia, 2010.

M. W. Perlin, "DNA identification science: the search for truth", *Duquesne University 2010 Summer Research Symposium Keynote Address*, Pittsburgh, PA, 2010.

M. W. Perlin, "Statistical computation for forensic DNA evidence", *University of Pittsburgh Department of Human Genetics*, Pittsburgh, PA, 2010.

Dr. Mark W. Perlin

M. W. Perlin and R. W. Cotton, "Three match statistics, one verdict," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin and B. W. Duceman, "Casework validation of genetic calculator mixture interpretation," *American Academy of Forensic Sciences 62nd Annual Meeting*, Seattle, WA, 2010.

M. W. Perlin, J. B. Kadane and R. W. Cotton, "A match likelihood ratio for DNA comparison," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, A. Sinelnikov, E. Vey, M. Legler and M. Clarke, "Identifying victim remains from uncertain data," *American Academy of Forensic Sciences 61st Annual Meeting*, Denver, CO, 2009.

M. W. Perlin, J. B. Kadane and R. W. Cotton. "Forensic DNA inference," *Seventh International Conference on Forensic Inference and Statistics*, Lausanne, Switzerland, 2008.

M. W. Perlin, "Exploring forensic scenarios with TrueAllele[®] mixture automation," *American Academy of Forensic Sciences 59th Annual Meeting*, San Antonio, TX, 2007.

M. W. Perlin, "Scientific validation of mixture interpretation methods," *Promega's Seventeenth International Symposium on Human Identification*. Nashville, TN, 2006.

M. W. Perlin, "Real-time DNA investigation," *Promega's Sixteenth International Symposium on Human Identification*. Dallas, TX, 2005.

M. W. Perlin, "Simple reporting of complex DNA evidence: automated computer interpretation," *Promega's Fourteenth International Symposium on Human Identification*. Phoenix, AZ, 2003.

M. W. Perlin, "Expert systems for automated STR analysis," *Scientific Working Group on DNA Analysis Methods (SWGAM)*, Quantico, VA, 2003.

M. W. Perlin, "Automated interpretation of forensic STR data," *DNA Forensics Conference, Cambridge Healthtech Institute*. Washington, DC, 2002.

M. W. Perlin, "Automated interpretation of forensic DNA data," *Third Annual DNA Grantees' Workshop, National Institute of Justice (NIJ)*, Washington, DC, 2002.

M. W. Perlin, "Automated interpretation of forensic DNA data," *Attorney General's Initiative on DNA Laboratory Backlogs (AGID-LAB), U.S. Department of Justice*, Washington, DC, 2002.

M. W. Perlin, D. Coffman, C.A. Crouse, F. Konotop, and J.D Ban, "Automated STR data analysis: validation studies," *Promega's Twelfth International Symposium on Human Identification*. Biloxi, MS, 2001.

M. W. Perlin, "Automating STR analysis," *Federal Bureau of Investigation (FBI), Scientific Working Group on DNA Analysis Methods (SWGAM)*. Quantico, VA, 2001.

M. W. Perlin, "Automated STR analysis for DNA databases," *Second Annual DNA Grantees' Workshop, National Institute of Justice (NIJ)*, Washington, DC, 2001.

M. W. Perlin, "Automating STR analysis," *Sixth CODIS User's Conference, Federal Bureau of Investigation (FBI)*, Washington, DC, 2001.

Dr. Mark W. Perlin

M. W. Perlin, "Fully automated computer analysis of forensic STR data," *STR Analysis Workshop, 53rd Annual Meeting of the American Association of Forensic Sciences (AAFS)*, Seattle, WA, 2001.

M. W. Perlin, "An expert system for scoring DNA database profiles," *Promega's Eleventh International Symposium on Human Identification*. Biloxi, MS, 2000.

M. W. Perlin, "Computer automation of STR scoring for forensic databases," *First International Conference on Forensic Human Identification in The Millennium*, London, UK, The Forensic Science Service, 1999.

Courses

Legal Education

M. W. Perlin, "The role of truth in science and law," *Legal Medicine & Forensic Science, Duquesne University School of Law*, Pittsburgh, PA, March, 2021.

M. W. Perlin, "Complex mixtures & probabilistic genotyping software," *Forensic Science, Santa Clara University School of Law*, San Jose, CA, March, 2021.

M. W. Perlin, "The impact of government policy on forensic DNA science," *Legal Medicine & Forensic Science, Duquesne University School of Law*, Pittsburgh, PA, April, 2020.

M. W. Perlin, "Working with the expert witness," *Trial Advocacy, University of Pittsburgh, School of Law*, Pittsburgh, PA, April, 2020.

M. W. Perlin, "Mining the mixture - a DNA analyst explains," *Judicial Summer Seminars, New York State Judicial Institute*, Rye Brook, NY, June, 2019.

M. W. Perlin, "Probabilistic genotyping in theory and practice," *Brooklyn Defender Services*, Brooklyn, NY, April, 2019.

M. W. Perlin, "Bayesian reasoning for complex DNA evidence," *Quantitative Reasoning in the Law, Northwestern Pritzker School of Law*, Chicago, IL, April, 2019.

M. W. Perlin, "DNA mixtures in sexual assault: evidence and admissibility," *Legal Medicine & Forensic Science, Duquesne University School of Law*, Pittsburgh, PA, March, 2019.

M. W. Perlin, "DNA transfer for lawyers," *Allegheny County Courthouse - Continuing Legal Education*, Pittsburgh, PA, February, 2019. (Mock trial panel: W. P. Allan, D. W. Bauer, J. M. Hornyak)

M. W. Perlin and M. J. Machen, "DNA evidence and transfer," *CLE at Beaver County Bar Association*, Beaver, PA, December, 2018.

M. W. Perlin and J. Mulholland, "TrueAllele® preparation and testimony for a Daubert/Harper hearing," *Georgia District Attorneys Association, Fall Meeting*, Athens, GA, November, 2018.

M. W. Perlin, "Daubert in practice," Lecture in *Evidence* class, *Penn State University Law School*, State College, PA, November, 2018.

Dr. Mark W. Perlin

M. W. Perlin, "Probabilistic genotyping: bad, good & ugly," *Minnesota DNA Defenders*, Minneapolis, MN, October, 2018.

M. W. Perlin, "Probabilistic genotyping to the rescue for Pinkins and Glenn," *Wrongful Conviction Day, Indiana University McKinney School of Law*, Indianapolis, IN, October, 2018.

M. W. Perlin, "DNA science, systems and strategy," *Full day CLE for New York City Legal Aid Society public defenders*, New York, NY, August, 2018.

M. W. Perlin, "TrueAllele[®] science and court," *Half day CLE for Cuyahoga County prosecutors, with crime lab scientists*, Cleveland, OH, July, 2018.

M. W. Perlin, "TrueAllele for DNA mixtures," *Georgia District Attorneys Association, Spring Meeting*, Savannah, GA, May, 2018.

M. W. Perlin, "Getting away with murder: forensic science and society," *Duquesne University School of Law*, Pittsburgh, PA, April, 2018.

M. W. Perlin, "Presenting TrueAllele[®] evidence in the courtroom," *Twelve hour joint workshop for Baltimore City prosecutors and scientists*, Baltimore, MD, February, 2018.

M. W. Perlin, "Detecting and denying DNA evidence: a history of forensic identification", *Pioneers of Forensic Science, Duquesne University*, Pittsburgh, PA, June, 2017.

M. W. Perlin, "DNA: TrueAllele[®] statistical analysis, probabilistic genotyping", *Indiana Prosecuting Attorneys Council, IPAC Winter Conference*, Indianapolis, IN, December, 2016.

M. W. Perlin and M. J. Machen, "Forensic failures: the ethics of unfounded science in the courtroom", *Duquesne University Ethics and Eats Seminar*, Pittsburgh, PA, December, 2016.

M. W. Perlin, "Fighting for DNA justice: genotyping software in the Hillary acquittal", *Questioning Forensics: Inside the Black Box, Legal Aid Society*, New York, NY, October, 2016.

M. W. Perlin, "Solving serious crime with TrueAllele technology", *DA Roundtable, Annual Summer Meeting, Pennsylvania District Attorneys Association*, Bedford, PA, July, 2016.

M. W. Perlin, "The probative power of DNA mixtures", *The Balancing Act of Justice, 39th Annual Conference, Louisiana District Attorneys Association*, Destin, FL, June, 2016.

M. W. Perlin, "How to defend yourself against DNA mixtures", *National Forensic College, National Association of Criminal Defense Lawyers*, Cardozo School of Law, New York, NY, June, 2016.

M. W. Perlin, "Issues with DNA evidence, past and future", *Washington County Bar Association*, Washington, PA, March, 2016.

M. W. Perlin, "Understanding DNA evidence", *Beaver County Courthouse*, Beaver, PA, March, 2016.

M. W. Perlin, "Understanding complex DNA evidence", *New York Legal Aid Society*, New York, NY, March, 2016.

M. W. Perlin, "Understanding DNA", *Pennsylvania Conference of State Trial Judges*, Philadelphia, PA, February, 2016.

Dr. Mark W. Perlin

M. W. Perlin, "DNA mixture evidence", *Penn State University Dickinson Law School*, State College, PA, February, 2016.

M. W. Perlin, "Mix & match: getting comfortable with DNA reporting", *Duquesne University Forensic Fridays*, Pittsburgh, PA, October, 2015.

M. W. Perlin. "Cutting edge DNA strategies", *Forensic Science and Criminal Law, Pennsylvania Association of Criminal Defense Lawyers*, Pittsburgh, PA, September, 2015.

M. W. Perlin, "Challenging DNA Evidence", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2015.

M. W. Perlin, "Shedding light on inconclusive DNA: TrueAllele[®] computer analysis", *Office of the Onondaga County District Attorney*, Syracuse, NY, November, 2014.

M. W. Perlin, "TrueAllele computing: all the DNA, all the time", *NSW Office of the Director of Public Prosecutions, Continuing Professional Development*, Sydney, Australia, March, 2014.

M. W. Perlin. "TrueAllele[®] interpretation of Allegheny County DNA mixtures", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2014.

M. W. Perlin, "No DNA left behind: when 'inconclusive' really means 'informative'", *Office of the Schenectady County District Attorney*, Schenectady, NY, January, 2014.

M. W. Perlin, "Understanding DNA mixtures" & "How to convict an innocent man using DNA mixtures" *DNA in the 21st Century*, *New Jersey Office of the Public Defender*, Trenton, NJ, October, 2013.

J. Butler, A. Mitchell, M. W. Perlin, A. M. Schubert, J. Friedman and J. Spriggs, "DNA mixture interpretations and statistics – to include or exclude", *Prescription for Criminal Justice Forensics, American Bar Association Criminal Justice Section*, New York, NY, June, 2013.

M. W. Perlin, "DNA mixture statistics", *Virginia Spring Institute, Commonwealth's Attorneys' Services Council*, Richmond, VA, March, 2013.

G. Hampikian, V. Weedn, M. W. Perlin, A. Blumstein, J. Rangos, K. Mains, L. Irwin, A. Adepoju and W. Oliver, "Whose DNA is it anyway?", *Duquesne University Forensic Fridays, Continuing Legal Education Program on DNA Access*, Pittsburgh, PA, March, 2013.

M. W. Perlin, "Reanimating Zombie[™] DNA", *Penn State Dickinson Law School*, State College, PA, September, 2012.

M. W. Perlin, "DNA evidence: computer interpretation, case investigation and court presentation", *Kern County District Attorney's Office, Continuing Legal Education*, Bakersfield, CA, April, 2012.

M. W. Perlin, J. Galloway and M. Agnew, "Investigation and trial in the Massereene case", *Police, Public Prosecution and Forensic Services of Northern Ireland, Continuing Professional Development*, Belfast, Northern Ireland, March, 2012.

M. W. Perlin and J. Galloway, "Touch DNA and the Massereene Barracks attack investigation", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, February, 2012.

Dr. Mark W. Perlin

R. Freeman, M. W. Perlin and R. Harmon, "The science of DNA search", *Duquesne University Forensic Fridays, Continuing Legal Education Program on Familial Search*, Pittsburgh, PA, May, 2011.

M. W. Perlin and A. Krastek, "Forensic DNA analysis: a CLE introduction", *Allegheny County Courthouse, Continuing Legal Education*, Pittsburgh, PA, March, 2011.

M. W. Perlin, A. Krastek and M. Collins, "Forensic DNA analysis: an introduction", *Duquesne University Forensic Fridays, Continuing Legal Education*, Pittsburgh, PA, October, 2010.

M. W. Perlin, "Objective interpretation of DNA evidence: automation and admissibility", *Arizona State University Law School*, Tempe, AZ, April, 2003.

M. W. Perlin, "Automated computer analysis of forensic DNA data," *DNA and the Law: Reining in the Revolution*, Wecht Institute of Forensic Science and Law & Duquesne University School of Law, Pittsburgh, PA, 2001.

Forensic Science

M. W. Perlin, "TrueAllele® validation: computer interpretation of DNA mixture evidence," *Undergraduate and Graduate Seminars, Duquesne University, Forensic Science and Law*, April, 2021.

M. W. Perlin, "Reliable computer interpretation of DNA mixture evidence," *Forensic Biology, West Virginia University, Forensic and Investigative Science*, April, 2021.

M. W. Perlin, "TrueAllele® interpretation of complex DNA evidence," *South African Police Service*, Cape Town, South Africa, February, 2020.

M. W. Perlin, "Probabilistic genotyping of evidentiary DNA typing results: TrueAllele® admissibility," *Federal Bureau of Investigation & National Institute of Justice Webinar*, June, 2019.

M. W. Perlin, "Probabilistic genotyping of evidentiary DNA typing results: TrueAllele® technology," *Federal Bureau of Investigation & National Institute of Justice Webinar*, May, 2019.

M. W. Perlin, "Forensic DNA in criminal justice: science and society," *Osher Lifelong Learning Institute, Carnegie Mellon University*, Pittsburgh, PA, March – April, 2019.

M. W. Perlin, "Reporting match error: casework, validation & language," *Cybergenetics Webinar*, December, 2018.

M. W. Perlin, "Forensic DNA in criminal justice: science and society," *Osher Lifelong Learning Institute, Carnegie Mellon University*, Pittsburgh, PA, September – October, 2018.

M. W. Perlin, "Expert DNA testimony," *University of Pittsburgh*, Pittsburgh, PA, April, 2018.

M. W. Perlin, "Solving serious crime using effective DNA evidence," *Allegheny County Police Department*, Pittsburgh, PA, March, 2018.

M. W. Perlin, "TrueAllele® science and testimony," *Two-day Georgia Bureau of Investigation course for DNA analysts*, Decatur, GA, January, 2018.

M. W. Perlin, "Science & sorcery in forensic DNA evidence," *Science in our world: certainty & controversy*, Penn State Beaver, Monaca, PA, April, 2017.

Dr. Mark W. Perlin

M. W. Perlin, "Forensic DNA evidence," *University of Pennsylvania*, Philadelphia, PA, February, 2016.

M. W. Perlin, "How TrueAllele® Works, Part 4: Genotype database and DNA investigation," *Cybergenetics Webinar*, January, 2015.

M. W. Perlin, "How TrueAllele® Works, Part 3: Kinship, paternity and missing persons," *Cybergenetics Webinar*, December, 2014.

M. W. Perlin, M. Bowkley and M. Legler, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Workshop*, Cuyahoga County Medical Examiner's Office, Cleveland, OH, December, 2014.

M. W. Perlin, "How TrueAllele® Works, Part 2: Degraded DNA and allele dropout," *Cybergenetics Webinar*, November, 2014.

M. W. Perlin, "How TrueAllele® Works, Part 1: Genotype modeling and the likelihood ratio," *Cybergenetics Webinar*, October, 2014.

M. W. Perlin, "TrueAllele® Casework", *Almost Everything You Wanted to Know About Probabilistic Software (But Were Afraid to Ask)*, *Promega's Twenty Fifth International Symposium on Human Identification*, Phoenix, AZ, September, 2014.

M. W. Perlin, "Computer interpretation of touch DNA mixtures", *Seminar for Chiefs of Police in Western Pennsylvania, CSI Investigators Series*, Pittsburgh, PA, May, 2014.

M. W. Perlin, "Revolutionising DNA analysis in major crime investigations", *The Investigator, Full Day DNA Workshop*, Aylesbury, Buckinghamshire, UK, May, 2014.

M. W. Perlin, "DNA-led investigation through computer interpretation of evidence", *Workshop for Criminal Investigation Assessment*, Pennsylvania State Police Academy, Hershey, PA, April, 2014.

M. W. Perlin, M. Legler, J. Hornyak and L. Ferrara, "Science & Software: DNA mixture interpretation", *Cybergenetics Forensic Science Student Workshop*, George Washington University, Washington, DC (distance learning), October, 2013.

M. W. Perlin, "Revolutionising DNA analysis in major crime investigations", *Workshop for Investigators*, The Investigator Conferences, Rothley, Leicestershire, UK, April, 2013.

Part 1. The DNA information pathway

Part 2. TrueAllele® case studies

Part 3. The way forward in the UK

M. W. Perlin, "TrueAllele® mixture interpretation", *9th Annual DNA Technology Educational Seminar*, Centre of Forensic Sciences and the Promega Corporation, Toronto, ON, November, 2012.

M. W. Perlin, "TrueAllele® challenges in court and culture", *9th Annual DNA Technology Educational Seminar*, Centre of Forensic Sciences and the Promega Corporation, Toronto, ON, November, 2012.

M. W. Perlin, M. Legler and J. Hornyak, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, New York State Police (NYSP), Albany, NY (distance learning), October, 2012.

Dr. Mark W. Perlin

M. W. Perlin, M. Legler, J. Hornyak and K. Dormer, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Duquesne University, Pittsburgh, PA, Fall, 2012.

M. W. Perlin, M. Legler and J. Kos, "Science & Software: DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, New York State Police (NYSP), Albany, NY (distance learning), May, 2012.

M. W. Perlin, M. Legler and J. Kos, "DNA expert system software" (with hands-on computer laboratory), *TrueAllele® Workshop*, California Association of Criminalists (CAC), Bakersfield, CA, May, 2012.

M. W. Perlin, M. Legler and J. Kos, "Probabilistic genotyping for DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Science Workshop*, National Institute of Standards and Technology (NIST), Gaithersburg, MD, April, 2012.

M. W. Perlin, M. Legler and W. Allan, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Virginia Division of Forensic Sciences (DFS), Richmond, VA, August, 2011.

M. W. Perlin, "DNA mixture interpretation", *Cybergenetics Forensic Scientist Training Course*, Oman Royal Police, Muscat, Oman, December, 2010.

M. W. Perlin, M. Legler and W. Allan, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, National Institute of Standards and Technology (NIST), Pittsburgh, PA, October, 2010.

M. W. Perlin, M. Legler and W. Allan, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Allegheny County Crime Laboratory, Pittsburgh, PA, August, 2010.

M. W. Perlin, M. Legler, J. Staub and E. Turo, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Workshop*, Joint New York State Crime Laboratories, Albany, NY, April, 2010.

M. W. Perlin, M. Legler and E. Turo, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Massachusetts State Police (MSP), Maynard, MA, January, 2010.

M. W. Perlin and W. Allan, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, Australian Biology Specialist Advisory Group (BSAG), Melbourne, Australia, April, 2009.

M. W. Perlin and W. Allan, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, New South Wales Police (NSWP), Sydney, Australia, April, 2009.

M. W. Perlin, M. Legler and E. Turo, "DNA mixture interpretation" (with hands-on TrueAllele® computer laboratory), *Cybergenetics Forensic Scientist Training Course*, New York State Police (NYSP), Albany, NY, February, 2009.

Dr. Mark W. Perlin

M. W. Perlin, "Automated and objective DNA mixture analysis," *Workshop on Practical Applications of DNA Profiling Technology, Sixteenth Meeting of the International Association of Forensic Sciences (IAFS)*, Montpellier, France, 2002.

Reviews

BioTechniques
F1000Research
Forensic Science International: Genetics
Journal of Forensic Sciences
Journal of Pathology Informatics
Journal of the Royal Statistical Society
Proceedings of the National Academy of Sciences
Science and Justice

M. W. Perlin, W. P. Allan, and M. A. Clarke. Discussion on 'Analysis of DNA mixtures with artefacts' (by R. G. Cowell, T. Graversen, S. L. Lauritzen and J. Mortera). *Journal of the Royal Statistical Society, Series C Applied Statistics*. 64(1):38-40, 2015.

M. W. Perlin, Referee Report For: Analysis of red autofluorescence (650-670nm) in epidermal cell populations and its potential for distinguishing contributors to 'touch' biological samples. *F1000Research*, 5:180, 2016.

Grants

Source National Institute of Justice (NIJ) - Cooperative Agreement
Identifier NIJ 2001-IJ-CX-K003
Title Automated STR Mixture Analysis
Dates 2001 - 2003
Objectives The major goal is to fully automate the computer analysis of mixed DNA samples in forensic casework.

Source National Institute of Justice (NIJ) - Cooperative Agreement
Identifier NIJ 2000-IJ-CX-K005
Title Automated STR Analysis for DNA Databases
Dates 2000 - 2002
Objectives The major goal is to rapidly introduce validated intelligent data analysis systems for eliminating tedious human STR analysis.

Source National Institutes of Health (NIH); National Cancer Institute (NCI) - SBIR Phase I
Identifier NIH 1R43 CA84679
Title Automated Multiplex Genetic Analysis Technology
Dates 2000 - 2002
Objectives The major goal is to greatly reduce the cost and time of using gene expression data in cancer research and patient care.

Source National Inst. of Health (NIH); Nat. Human Genome Research Inst. (NHGRI)- SBIR Phase I
Identifier NIH 1R43 HG002005
Title Computer Scoring of Gridded Data
Dates 2000 - 2002
Objectives The major goal is to eliminate the human time, cost, error, and effort associated with data scoring, accelerating very high-throughput DNA technology for diverse genetic problems.

Dr. Mark W. Perlin

Source National Institutes of Health (NIH) - University of Pittsburgh Subcontract
Identifier NIH 1R01 AA11304, Subcontract 100084-2
Title Molecular Genetic Analyses of Multiplex Families
Dates 1997 - 2002
Objectives The major goal is to perform a genetic linkage analysis of alcoholism in order to elucidate its underlying genetic etiology.

Source National Institutes of Health (NIH); National Human Genome Research Institute (NHGRI)
Identifier NIH 1R43 HG001568
Title Automated Microsatellite Genotyping
Dates 1996 - 1997
Objectives The major goal is to determine the feasibility of automated microsatellite genotyping with low error on data from automated DNA sequencers and using pooled DNA material.

Source National Inst. of Health (NIH); National Inst. of Neurological Disorders & Stroke (NINDS)
Identifier NIH 1R01NS032084
Title Automated PCR-Based Disease Gene Mapping
Dates 1993 - 1996
Objectives The major goal is to develop an automation system that localizes disease genes anywhere on the X chromosome.

Source National Institutes of Health (NIH); National Human Genome Research Institute (NHGRI)
Identifier NIH 5R21 HG000856
Title Inner Product Mapping
Dates 1993 - 1995
Objectives The major goal is to determine the effectiveness and utility of the Inner Product Mapping (IPM) algorithm, and to develop software that assists investigators in the use of IPM.

Source National Institutes of Health (NIH); National Library of Medicine (NLM)
Identifier NIH 1R29 LM004707
Title CONTRAST: A Computer Consultant for Optimal NMR Imaging
Dates 1987 - 1992
Objectives The major goal is to apply existing methods of artificial intelligence and knowledge engineering in order to construct a first prototype expert system for medical NMR imaging.

Cases

Reported on TrueAllele[®] results in about a thousand criminal cases. Gave expert DNA testimony in about a hundred court proceedings. Selected cases:

Prosecution

California v Billy Ray Johnson
Florida v Pablo Ibar
Georgia v Thaddus Nundra
Indiana v Vaylen Glazebrook
Louisiana v Christopher Hutsell
Maryland v Nelson Clifford
Nebraska v Charles Simmer
New York v John Wakefield
Pennsylvania v Kevin Foley

Dr. Mark W. Perlin

Virginia v Michael Gardner
Washington v Emanuel Fair
United States v Cory Harris

Defense

California v Charles Merritt
Georgia v Johnny Lee Gates
Maryland v William Jamison
Michigan v Jennifer Heavlin
New York v Michael Robinson
Pennsylvania v Gregory Scott Hopkins

Exonerations & Post-Conviction

Connecticut v. Ralph Birch
Connecticut v. Shawn Henning
Georgia v. Johnny Lee Gates
Georgia v. Jimmy Meders
Georgia v. Kerry Robinson
Idaho v. Christopher Tapp
Indiana v. Roosevelt Glenn
Indiana v. Darryl Pinkins
Montana v. Paul Jenkins
Montana v. Freddie Lawrence
New Mexico v. Gregory Hobbs
Texas v. Lydell Grant