

Citation Index

Peer-reviewed and scientific articles that cite TrueAllele® publications

May, 2024

Number of unique citations: 667

M.W. Perlin. "DNA Identification Science." In: C.H. Wecht (ed) *Forensic Sciences*. Albany, NY: LexisNexis Matthew Bender; Chapter 37C, 2021.

H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.

J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.

D.W. Bauer, N. Butt, J.M. 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.

K. Chen, R. Tao, Y. Qu, J. Lu, Y. Ping, Y. Zhang, P. Chen, and C. Li. "Validation and forensic application of a new 36 X-STR loci multiplex system." *Forensic Sciences Research*, 2024 (in press).

H.R. Dash, K.M. Elkins, and N.R. Al-Snan. "Statistical Interpretation of Forensic DNA Evidence." In: H.R. Dash, K.M. Elkins, and N.R. Al-Snan (eds) *Advancements in Forensic DNA Analysis*. Springer, Singapore, 105-117, 2023.

D. Taylor and D. Abarno. "A lights-out forensic DNA analysis workflow for no-suspect crime." *Forensic Science International: Genetics*, 66:102907, 2023.

K. Huffman and J. Ballantyne. "Single cell genomics applications in forensic science: Current state and future directions." *iScience*, 26, 2023.

M. Susik and I.F. Sbalzarini. "Analysis of the Hamiltonian Monte Carlo genotyping algorithm on PROVEDIt mixtures including a novel precision benchmark." *Forensic Science International: Genetics*, 64:102840, 2023.

D. Orozco. "TrueAllele® and STRmix™: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis, 2023.

- W.C. Thompson. "Uncertainty in probabilistic genotyping of low template DNA: A case study comparing STRMix™ and TrueAllele™." *J Forensic Sci.*, 68(3): 1049-1063, 2023.
- J.M. Butler. "Recent advances in forensic biology and forensic DNA typing: INTERPOL review 2019–2022." *Forensic Science International: Synergy*, 6:100311, 2023.
- K. Huffman and J. Ballantyne. "Probabilistic Genotyping of Single Cell Replicates from Mixtures Involving First-Degree Relatives Prevents the False Inclusions of Non-Donor Relatives." *Genes*, 13(9):1658, 2022.
- M. Susik, H. Schönborn, and I.F. Sbalzarini. "Hamiltonian Monte Carlo with strict convergence criteria reduces run-to-run variability in forensic DNA mixture deconvolution." *Forensic Science International: Genetics*, 60:102744, 2022.
- S.K. Sinha, H. Brown, H. Holt, M. Khan, R. Brown, J.B. Sgueglia, A. Loftus, G. Murphy, and A. Montgomery. "Development and validation of a novel method "SpermX™" for high throughput differential extraction processing of sexual assault kits (SAKs) for DNA analysis." *Forensic Science International: Genetics*, 59:102690, 2022.
- K. Huffman, E. Hanson, and J. Ballantyne. "Probabilistic genotyping of single cell replicates from complex DNA mixtures recovers higher contributor LR's than standard analysis." *Science & Justice*, 62(2):156-163, 2022.
- H. Miller Coyle. "Quality Control Measures in Short Tandem Repeat (STR) Analysis." In: H.R. Dash, P. Shrivastava, J.A. Lorente (eds) *Handbook of DNA Profiling*. Springer, Singapore, 1107-1124, 2022.
- K. Slooten. "The analogy between DNA kinship and DNA mixture evaluation, with applications for the interpretation of likelihood ratios produced by possibly imperfect models." *Forensic Science International: Genetics*, 52:102449, 2021.
- D. McNevin, K. Wright, M. Barash, S. Gomes, A. Jamieson, and J. Chaseling. "Proposed Framework for Comparison of Continuous Probabilistic Genotyping Systems amongst Different Laboratories." *Forensic Sciences*, 1(1):33-45, 2021.
- D. Taylor, J.A. Bright, L. Scandrett, D. Abarno, S.I. Lee, R. Wivell, H. Kelly, and J. Buckleton. "Validation of a top-down DNA profile analysis for database searching using a fully continuous probabilistic genotyping model." *Forensic Science International: Genetics*, 52:102479, 2021.
- E.M. Anderson. "Evaluation of DNA Extraction Efficiencies of Promega's DNA IQ™ Methods and Casework Extraction Kit for Low Template Samples." Master's thesis. Virginia Commonwealth University, April 2021.

L. Ostojic, C. O'Connor, and E. Wurmbach. "Micromanipulation of single cells and fingerprints for forensic identification." *Forensic Science International: Genetics*, 51:102430, 2021.

E.J. Imwinkelried. "The Admissibility of Scientific Evidence: Exploring the Significance of the Distinction between Foundational Validity and Validity as Applied." *Syracuse Law Review*, 70:817-849, 2020.

C. McGovern, K. Cheng, H. Kelly, A. Ciecko, D. Taylor, J.S. Buckleton, and J.A. Bright. "Performance of a method for weighting a range in the number of contributors in probabilistic genotyping." *Forensic Science International: Genetics*, 48:102352, 2020.

K. Newland. "Evaluation of the Performance of Probabilistic Genotyping Software on Complex Mixture Samples." Master's Thesis. West Virginia University, 2020.

M.W. Perlin. "Efficient construction of match strength distributions for uncertain multi-locus genotypes." *Heliyon*, 4(10):e00824, 2018.

S. Myers. "Searching CODIS with binary conversions of STRmix interpretations." *Forensic Science International: Genetics*, 55, 2021.

N.A. Stokes, C.E. Stanciu, E.R. Brocato, C.J. Ehrhardt, and S.A. Greenspoon. "Simplification of complex DNA profiles using front end cell separation and probabilistic modeling." *Forensic Science International: Genetics*, 36:205-212, 2018.

J. Hogg, A.C.W. Vandepoele, N. Zaccheo, J. Schulte, I. Schulz, J. Dubois, M. Frank, and M.A. Marciano. "Targeted recovery of male cells in a male and female same-cell mixture." *Journal of Forensic Sciences*, 2024 (in press).

K. Huffman, M. Kruijver, J. Ballantyne, and D. Taylor. "Carrying out common DNA donor analysis using DBLR™ on two or five-cell mini-mixture subsamples for improved discrimination power in complex DNA mixtures." *Forensic Science International: Genetics*, 66, 2023.

C.A. Filipe. "Comparing likelihood ratios of degraded DNA mixture profiles using DNA-view mixture solution." Master's thesis. Boston University, 2023.

K. Huffman and J. Ballantyne. "Validation of Probabilistic Genotyping Software for Single Cell STR Analysis." *Genes*, 14(3):674, 2023.

K. Huffman, E. Hanson, and J. Ballantyne. "Y-STR mixture deconvolution by single-cell analysis." *Journal of Forensic Sciences*, 68(1):275-288, 2023.

J.M. Miller, C. Lee, S. Ingram, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Use of hormone-specific antibody probes for differential labeling of contributor cell populations in trace DNA mixtures." *International Journal of Legal Medicine*, 136(6):1551-1564, 2022.

K. Huffman, E. Hanson, and J. Ballantyne. "Probabilistic genotyping of single cell replicates from complex DNA mixtures recovers higher contributor LR's than standard analysis." *Science & Justice*, 62(2):156-163, 2022.

K. Huffman, E. Hanson, and J. Ballantyne. "Cell Subsampling Recovers Probative DNA Profile Information from Unresolvable/Undetectable Minor Donors in Mixtures." *Genes*, 13(7):1117, 2022.

K. Huffman. "Complex DNA Mixture Deconvolution by Single Cell Genomics: Direct Physical Cell Subsampling and High Sensitivity DNA Typing." Doctoral Dissertation. University of Central Florida, 2022.

J. Ge, J.L. King, A. Smuts, and B. Budowle. "Precision DNA Mixture Interpretation with Single-Cell Profiling." *Genes*, 12(11):1649, 2021.

M. Diepenbroek, B. Bayer, and K. Anslinger. "Pushing the Boundaries: Forensic DNA Phenotyping Challenged by Single-Cell Sequencing." *Genes*, 12(9):1362, 2021.

K. Huffman, E. Hanson, E. and J. Ballantyne. "Recovery of single source DNA profiles from mixtures by direct single cell subsampling and simplified micromanipulation." *Science & Justice*, 61(1):13-25, 2021.

J.M. Miller, E.R. Brocato, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Testing Hormone-specific Antibody Probes for Presumptive Detection and Separation of Contributor Cell Populations in Trace DNA Mixtures." *bioRxiv*, 2019.

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

R. Abebe, M. Hardt, A. Jin, J. Miller, L. Schmidt, and R. Wexler. "Adversarial Scrutiny of Evidentiary Statistical Software." In the Proceedings of the 2022 ACM Conference on Fairness, Accountability, and Transparency. Seoul Republic of Korea, June 2022.

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

J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.

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.

C.A. Filipe. "Comparing likelihood ratios of degraded DNA mixture profiles using DNA-view mixture solution." Master's thesis. Boston University, 2023.

S. Ravichandran. "A Little Right of Center": Carceral Feminism and the Expansion of Biosurveillance." *Feminist Formations*, 34(2):43-68, 2022.

H.R. Dash, N. Rawat, K. Vajpayee, P. Shrivastava, and S. Das. "Useful autosomal STR marker sets for forensic and paternity applications in the Central Indian population." *Annals of Human Biology*, 48(1):37-48, 2021.

P. Lafargue-Molina. "Marker development for the traceability of certified sustainably produced cacao (*Theobroma cacao*) in the chocolate industry." Doctoral dissertation. Faculty of Health and Applied Sciences, Centre for Research in Biosciences. University of the West of England, 2021.

D. McNevin, K. Wright, M. Barash, S. Gomes, A. Jamieson, and J. Chaseling. "Proposed Framework for Comparison of Continuous Probabilistic Genotyping Systems amongst Different Laboratories." *Forensic Sciences*, 1(1):33-45, 2021.

K. Newland. "Evaluation of the Performance of Probabilistic Genotyping Software on Complex Mixture Samples." Master's Thesis. West Virginia University, 2020.

A.E. Kirby, J. Chance-Johnson, and H.M. Coyle. "The effect of the analytical threshold on the loss and gain of data for single source and mixed dna samples." *International Research Journal of Computer Science (IRJCS)*, 8(4):50-55, 2017.

A. Santurtún, J.A. Riancho, J. Arozamena, M. López-Duarte, and M.T. Zarrabeitia. "Indel analysis by droplet digital PCR: a sensitive method for DNA mixture detection and chimerism analysis." *International Journal of Legal Medicine*, 131(1):67-72, 2017.

S.A. Greenspoon, L. Schiermeier-Wood, and B.C. Jenkins. "Establishing the limits of TrueAllele Casework: a validation study." *Journal of Forensic Sciences*, 60(5):1263-1276, 2015.

- C.A. Filipe. "Comparing likelihood ratios of degraded DNA mixture profiles using DNA-view mixture solution." Master's thesis. Boston University, 2023.
- W.C. Thompson. "Uncertainty in probabilistic genotyping of low template DNA: A case study comparing STRMix™ and TrueAllele™." *J Forensic Sci.*, 68(3): 1049-1063, 2023.
- K. Huffman. "Complex DNA Mixture Deconvolution by Single Cell Genomics: Direct Physical Cell Subsampling and High Sensitivity DNA Typing." Doctoral Dissertation. University of Central Florida, 2022.
- H. Miller Coyle. "Quality Control Measures in Short Tandem Repeat (STR) Analysis." In: H.R. Dash, P. Shrivastava, J.A. Lorente (eds) *Handbook of DNA Profiling*. Springer, Singapore, 1107-1124, 2022.
- A.E. Scherr. "Ineffective Assistance of Counsel in DNA Cases: A Re-Appraisal of the Effectiveness of Strickland v. Washington Judges." *Loyola of Los Angeles Law Review*, 55(2):527-608, 2022.
- N. Hashemi. "Protected but Prejudiced: Redefining a Corporation's Ability to Pursue or Defend Litigation Without Counsel." *Loyola of Los Angeles Law Review*, 55(2):373-403, 2022.
- J.M. Miller, C. Lee, S. Ingram, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Use of hormone-specific antibody probes for differential labeling of contributor cell populations in trace DNA mixtures." *International Journal of Legal Medicine*, 136(6):1551-1564, 2022.
- M.S. Adamowicz, T.N. Rambo, and J.L. Clarke. "Internal Validation of MaSTR™ Probabilistic Genotyping Software for the Interpretation of 2–5 Person Mixed DNA Profiles." *Genes*, 13(8):1429, 2022.
- R.M. Gutierrez. "Alternative Sample Processing Techniques for Rootless Hair Shafts and Other Challenging Samples." Doctoral thesis. Sam Houston State University, July 2021.
- C.M. McCaughan. "PowerPlex® Fusion 6C System versus PowerPlex® Fusion 5C: A Comparison of Performance Metrics." Master's thesis. Virginia Commonwealth University, 2021.
- E.M. Anderson. "Evaluation of DNA Extraction Efficiencies of Promega's DNA IQ™ Methods and Casework Extraction Kit for Low Template Samples." Master's thesis. Virginia Commonwealth University, April 2021.

M.H. Lin, J.A. Bright, S.N. Pugh, and J.S. Buckleton. "The interpretation of mixed DNA profiles from a mother, father, and child trio." *Forensic Science International: Genetics*, 44:102175, 2020.

J.S. Buckleton, J.A. Bright, A. Ciecko, M. Kruijver, B. Mallinder, A. Magee, S. Malsom, T. Moretti, S. Weitz, T. Bille, S. Noël, R.H. Oefelein, B. Peck, T. Kalafut, and D.A. Taylor. "Response to: Commentary on: Bright et al. (2018) Internal validation of STRmix™ – A multi laboratory response to PCAST, Forensic Science International: Genetics, 34: 11–24." *Forensic Science International: Genetics*, 44, 2020.

J.M. Miller, E.R. Brocato, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Testing Hormone-specific Antibody Probes for Presumptive Detection and Separation of Contributor Cell Populations in Trace DNA Mixtures." *bioRxiv*, 2019.

B. Stiffelman. "No Longer the Gold Standard: Probabilistic Genotyping Is Changing the Nature of DNA Evidence in Criminal Trials." *Berkeley J. Crim. L.*, 24:110, 2019.

J.A. Bright and M. Coble. *Forensic DNA Profiling: A Practical Guide to Assigning Likelihood Ratios*. CRC Press, 2019.

M.D. Coble and J.A. Bright. "Probabilistic genotyping software: An overview." *Forensic Science International: Genetics*, 38:219-224, 2019.

P.C. Lynch and R.W. Cotton. "Determination of the possible number of genotypes which can contribute to DNA mixtures: Non-computer assisted deconvolution should not be attempted for greater than two person mixtures." *Forensic Science International: Genetics*, 37:235-240, 2018.

K.E. Lohmueller and K. Inman. "Advancing Probabilistic Approaches to Interpreting Low-template DNA Profiles and Mixtures: Developing Theory, Implementing Practice." *2013-DN-BX -K029 Cumulative Technical Report*, July 2018.

K.M. Webb, E. Rogers, ed., A.W. Stern, ed. "DNA Evidence Collection and Analysis." *Veterinary Forensics: Investigation, Evidence Collection, and Expert Testimony*, 2017.

Y. Tan, L. Wang, H. Wang, H. Tian, Z. Li, Q. Wang, H. Jian, S. Cao, W. Liang, and L. Zhang. "An investigation of a set of DIP-STR markers to detect unbalanced DNA mixtures among the southwest Chinese Han population." *Forensic Science International: Genetics*, 31:34-39, 2017.

A. Conway. "A Validation of STRmix™ for Forensic Casework." Master's thesis. University of North Texas Health Science Center Graduate School of Biomedical Sciences, 2017.

K.C. Peters. "Characterizing low copy DNA signal using simulated and experimental data." Master's thesis. Boston University School of Medicine, 2017.

E.J. Imwinkelried. "Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques." *DePaul Law Review*, Forthcoming; UC Davis Legal Studies Research Paper No. 487, 2016.

Ø. Bleka, C.C. Benschop, G. Storvik, and P. Gill. "A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles." *Forensic Science International: Genetics*, 25:85-96, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

M.W. Perlin, J. Hornyak, G. Sugimoto, and K.W.P. Miller. "TrueAllele Genotype Identification on DNA Mixtures Containing Up to Five Unknown Contributors." *Journal of Forensic Sciences*, 60(4):857-868, 2015.

K. Chen, R. Tao, Y. Qu, J. Lu, Y. Ping, Y. Zhang, P. Chen, and C. Li. "Validation and forensic application of a new 36 X-STR loci multiplex system." *Forensic Sciences Research*, 2024 (in press).

K.R. Duffy, D.S. Lun, M.M. Mulcahy, L. O'Donnell, N. Sheth, and C.M. Grgicak. "Evidentiary evaluation of single cells renders highly informative forensic comparisons across multifarious admixtures." *Forensic Science International: Genetics*, 64, 102852, 2023.

M.M. Mulcahy. "Forensic Interpretation of Grouped and Ungrouped Single-Cell Electropherograms." Master's thesis. Rutgers University, May 2023.

D. Orozco. "TrueAllele[®] and STRmix[™]: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis, 2023.

W.C. Thompson. "Uncertainty in probabilistic genotyping of low template DNA: A case study comparing STRmix[™] and TrueAllele[™]." *J Forensic Sci.*, 68(3): 1049-1063, 2023.

J.M. Miller, C. Lee, S. Ingram, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Use of hormone-specific antibody probes for differential labeling of contributor cell populations in trace DNA mixtures." *International Journal of Legal Medicine*, 136(6):1551-1564, 2022.

M.S. Adamowicz, T.N. Rambo, and J.L. Clarke. "Internal Validation of MaSTR™ Probabilistic Genotyping Software for the Interpretation of 2–5 Person Mixed DNA Profiles." *Genes*, 13(8):1429, 2022.

A.E. Scherr. "Ineffective Assistance of Counsel in DNA Cases: A Re-Appraisal of the Effectiveness of Strickland v. Washington Judges." *Loyola of Los Angeles Law Review*, 55(2):527-608, 2022.

N. Hashemi. "Protected but Prejudiced: Redefining a Corporation's Ability to Pursue or Defend Litigation Without Counsel." *Loyola of Los Angeles Law Review*, 55(2):373-403, 2022.

E. Rogers, R. Aranda, P.M. Spencer, and D.R. Myers. "DNA Mixture Study: Novel metrics to quantify the intra- and inter-laboratory variability in forensic DNA mixture interpretation." (Report # 304317), 2022.

H. Miller Coyle. "Quality Control Measures in Short Tandem Repeat (STR) Analysis." In: H.R. Dash, P. Shrivastava, J.A. Lorente (eds) *Handbook of DNA Profiling*. Springer, Singapore, 1107-1124, 2022.

N.N. Phan, A. Chattopadhyay, T.T. Lee, H.I. Yin, T.P. Lu, L.C. Lai, H.L. Hwa, M.H. Tsai, and E.Y. Chuang. "High-performance deep learning pipeline predicts individuals in mixtures of DNA using sequencing data." *Briefings in Bioinformatics*, 22(6), 2021.

J. Valtl, U.J. Mönich, D.S. Lun, J. Kelley, and C.M. Grgicak. "A series of developmental validation tests for Number of Contributors platforms: Exemplars using NOCI and a neural network." *Forensic science international: Genetics*, 54:102556, 2021.

D. Taylor, J.A. Bright, L. Scandrett, D. Abarno, S.I. Lee, R. Wivell, H. Kelly, and J. Buckleton. "Validation of a top-down DNA profile analysis for database searching using a fully continuous probabilistic genotyping model." *Forensic Science International: Genetics*, 52:102479, 2021.

C. McGovern, K. Cheng, H. Kelly, A. Cieccko, D. Taylor, J.S. Buckleton, and J.A. Bright. "Performance of a method for weighting a range in the number of contributors in probabilistic genotyping." *Forensic Science International: Genetics*, 48, 102352:2020.

C.M. Grgicak, S. Karkar, X. Yearwood-Garcia, L.E. Alfonse, K.R. Duffy, and D.S. Lun. "A large-scale validation of NOCI's A Posteriori Probability of the number of contributors and its integration into forensic interpretation pipelines." *Forensic Science International: Genetics*, 47:102296, 2020.

- E. Alamoudi, R. Mehmood, A. Albeshri, and T. Gojobori. "A Survey of Methods and Tools for Large-Scale DNA Mixture Profiling." In: R. Mehmood, S. See, I. Katib, I. Chlamtac (eds) *Smart Infrastructure and Applications. EAI/Springer Innovations in Communication and Computing*. Springer, Cham, 2020.
- H.L Hwa, M.Y. Wu, J.C.I. Lee, H.I. Yin, P.M. Hsu, S.F. Li, W.L. Hwu, and C.W. Su. "Analysis of nondegraded and degraded DNA mixtures of close relatives using massively parallel sequencing." *Legal Medicine*, 42:101631, 2020.
- S. Karkar, L.E. Alfonse, C.M. Grgicak, and D.S. Lun. "Statistical modeling of STR capillary electrophoresis signal." *BMC Bioinformatics*, 20(584), 2019.
- H.M. Coyle. "DNA Mixture Interpretation: Effect of the Hypothesis on the Likelihood Ratio." *Int Res J Comput Sci*, 8(6), 672-675, 2019.
- J.A. Bright, M. Jones Dukes, S.N. Pugh, I.W. Evett, and J.S. Buckleton. "Applying calibration to LR's produced by a DNA interpretation software." *Australian Journal of Forensic Sciences*, 53(2):147-153, 2019.
- D. Taylor, E. Rowe, M. Kruijver, D. Abarno, J. Bright, and J. Buckleton. "Inter-sample contamination detection using mixture deconvolution comparison." *Forensic Science International: Genetics*, 40:160-167, 2019.
- S. Karkar, L.E. Alfonse, C.M. Grgicak, and D.S. Lun. "Statistical Modeling of Short-Tandem Repeat Capillary Electrophoresis Profiles." *Proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE, 2018.
- E. Rogers. "A novel method for cluster analysis of RNA structural data." Doctoral thesis. Georgia Institute of Technology, August 2018.
- K.E. Lohmueller and K. Inman. "Advancing Probabilistic Approaches to Interpreting Low-template DNA Profiles and Mixtures: Developing Theory, Implementing Practice." *2013-DN-BX -K029 Cumulative Technical Report*, July 2018.
- S. Norsworthy, D.S. Lun, and C.M. Grgicak. "Determining the number of contributors to DNA mixtures in the low-template regime: Exploring the impacts of sampling and detection effects." *Legal Medicine*, 32:1-8, 2018.
- L.E. Alfonse, A.D. Garrett, D.S. Lun, K.R. Duffy, and C.M. Grgicak. "A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt." *Forensic Science International: Genetics*, 32:62-70, 2018.
- J.G. Cino. "Deploying the Secret Police: The Use of Algorithms in the Criminal Justice System." *Ga. St. UL Rev.* 34:1073, 2017.

K.M. Webb, E. Rogers, ed., A.W. Stern, ed. "DNA Evidence Collection and Analysis." *Veterinary Forensics: Investigation, Evidence Collection, and Expert Testimony*, 2017.

B.F.B. Algee-Hewitt, J. Kim, and C.E. Hughes. "Thinking Computationally about Forensics: Anthropological Perspectives on Advancements in Technologies, Data, and Algorithms." *Human Biology*, Project MUSE, muse.jhu.edu/article/705545, 2017.

C.M. Grgicak and D.S. Lun. "A Tool for Determining the Number of Contributors: Interpreting Complex, Compromised Low-Template DNA Samples." *Technical Report*, September 2017.

O. Hansson and P. Gill. "Characterisation of artefacts and drop-in events using STR-validator and single-cell analysis." *Forensic Science International: Genetics*, 30:57-65, 2017.

D. Russell, W. Christensen, and T. Lindsey. "A simple unconstrained semi-continuous model for calculating likelihood ratios for complex DNA mixtures." *Forensic Science International: Genetics Supplement Series*, 5:e37-e38, 2015.

E.J. Imwinkelried. "Computer Source Code: A Source of the Growing valisy Over the Reliability of Automated Forensic Techniques." *DePaul Law Review*, Forthcoming; UC Davis Legal Studies Research Paper No. 487, 2016.

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.

D. Orozco. "TrueAllele® and STRmix™: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis, 2023.

A.V. Cronin. "Interpretation and Presentation of Statistical Methods: Understanding Statistical Evidence in the Australian Criminal Justice System." Doctoral thesis. Queensland Universtiy of Technology, 2023.

J.M. Miller, C. Lee, S. Ingram, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Use of hormone-specific antibody probes for differential labeling of contributor cell populations in trace DNA mixtures." *International Journal of Legal Medicine*, 136(6):1551-1564, 2022.

- G.J.A. Knoops. "Probabilistic Genotyping: A Possible New Legal Avenue to Prevent and Redress Miscarriages of Justice." In: I. Freckelton (ed) *Forensic Analysis: Scientific and Medical Techniques and Evidence under the Microscope*. IntechOpen, London, UK, 2021.
- R. Alaeddini, M. Yang, and B. Puza. "Bayesian regression analysis of stutter in DNA mixtures." *Communications In Statistics – Theory and Methods*, 50(17):4066-4080, 2021.
- K. Newland. "Evaluation of the Performance of Probabilistic Genotyping Software on Complex Mixture Samples." Master's Thesis. West Virginia University, 2020.
- E. Alamoudi, R. Mehmood, A. Albeshri, and T. Gojobori. "A Survey of Methods and Tools for Large-Scale DNA Mixture Profiling." In: R. Mehmood, S. See, I. Katib, I. Chlamtac (eds) *Smart Infrastructure and Applications. EAI/Springer Innovations in Communication and Computing*. Springer, Cham, 2020.
- J.M. Miller, E.R. Brocato, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Testing Hormone-specific Antibody Probes for Presumptive Detection and Separation of Contributor Cell Populations in Trace DNA Mixtures." *bioRxiv*, 2019.
- G. Hampikian. "Correcting forensic DNA errors." *Forensic Science International: Genetics*, 41:32-33, 2019.
- E. Alamoudi, R. Mehmood, A. Albeshri, and T. Gojobori. "DNA Profiling Methods and Tools: A Review." In: R. Mehmood, B. Bhaduri, I. Katib, I Chlamtac (eds) *Smart Societies, Infrastructure, Technologies and Applications. SCITA 2017. Lecture Notes of the Institute for Computer Sciences, Social Informatics and Telecommunications Engineering*, vol 224. Springer, Cham, 2018.
- K.E. Lohmueller and K. Inman. "Advancing Probabilistic Approaches to Interpreting Low-template DNA Profiles and Mixtures: Developing Theory, Implementing Practice." *2013-DN-BX -K029 Cumulative Technical Report*, July 2018.
- H. Swaminathan, A. Garg, C.M. Grgicak, M. Medard, and D.S. Lun. "CEESIt: A computational tool for the interpretation of STR mixtures." *Forensic Science International: Genetics*, 22:149-160, 2016.
- C.D. Marsden, N. Rudin, K. Inman, and K.E. Lohmueller. "An assessment of the information content of likelihood ratios derived from complex mixtures." *Forensic Science International: Genetics*, 22:64-72, 2016.
- Ø. Bleka, C.C. Benschop, G. Storvik, and P. Gill. "A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles." *Forensic Science International: Genetics*, 25:85-96, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

H.M. Coyle. "Touch DNA in a Complicated Alleged Child Abuse Case." *Austin Journal of Forensic Science and Criminology*, 2:1042, 2015.

A. Garg. "Development of a computational tool for forensic DNA analysis." Doctoral dissertation, Rutgers University-Camden Graduate School, 2015.

H.M. Coyle. "Sources of Computational Error in Probabilistic Genotyping Software Used for DNA Mixture Interpretation." *International Research Journal of Computer Science*, 5(2):12-16, 2015.

G. Tejada. "Evaluating a peak height based method to determine the number of contributors in a DNA mixture and a study of DNA recovery using laser microdissection." Doctoral Dissertation, Boston University, 2015.

R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.

M.W. Perlin, J.L. Belrose, and B.W. Duceaman. "New York State TrueAllele Casework validation study." *Journal of Forensic Sciences*, 58(6):1458-1466, 2013.

J. Alfieri, M.D. Coble, C. Conroy, A. Dahl, D.R. Hares, B.S. Weir, C. Wolock, E. Zhao, H. Kingston, and T.W. Zolandz. "A new implementation of a semi-continuous method for DNA mixture interpretation." *Forensic Science International: Reports*, 6, 2022.

M.S. Adamowicz, T.N. Rambo, and J.L. Clarke. "Internal Validation of MaSTR™ Probabilistic Genotyping Software for the Interpretation of 2–5 Person Mixed DNA Profiles." *Genes*, 13(8):1429, 2022.

H.M. Coyle. "DNA Mixture Interpretation: Effect of the Hypothesis on the Likelihood Ratio." *Int Res J Comput Sci*, 8(6), 672-675, 2019.

L. Bennett, F. Oldoni, K. Long, S. Cisana, K. Madella, S. Wootton, J. Chang, R. Hasegawa, R. Lagace, K.K. Kidd, and D. Podini. "Mixture deconvolution by massively parallel sequencing of microhaplotypes." *International Journal of Legal Medicine*, 1-11, 2019.

E.J. Imwinkelried. "Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques." *DePaul Law Review*, Forthcoming; UC Davis Legal Studies Research Paper No. 487, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

J.M. Butler. "The future of forensic DNA analysis." *Phil. Trans. R. Soc. B*, 370(1674), 2015.

H. Haned and P. Gill. "Expert Systems in DNA Interpretation." *Wiley Encyclopedia of Forensic Science*, 2015.

T.J. Verdon, R.J. Mitchell, W. Chen, K. Xiao, and R.A. van Oorschot. "FACS separation of non-compromised forensically relevant biological mixtures." *Forensic Science International: Genetics*, 14:194-200, 2015.

R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.

C.D. Steele and D.J. Balding. "Statistical Evaluation of Forensic DNA Profile Evidence." *Annual Review of Statistics and Its Application*, 1:361-384, 2014.

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.

J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.

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.

K. Huffman and J. Ballantyne. "Single cell genomics applications in forensic science: Current state and future directions." *iScience*, 26, 2023.

K. Huffman, M. Kruijver, J. Ballantyne, and D. Taylor. "Carrying out common DNA donor analysis using DBLR™ on two or five-cell mini-mixture subsamples for improved discrimination power in complex DNA mixtures." *Forensic Science International: Genetics*, 66, 2023.

S.K. Alketbi. "The role of DNA in forensic science: A comprehensive review." *International Journal of Science and Research Archive*. 9(2):814-829, 2023.

K. Huffman and J. Ballantyne. "Validation of Probabilistic Genotyping Software for Single Cell STR Analysis." *Genes*, 14(3):674, 2023.

T. Bille, M.D. Coble, and J.A. Bright. "Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation." *Australian Journal of Forensic Sciences*, 54(5):584-595, 2022.

K. Huffman, E. Hanson, and J. Ballantyne. "Cell Subsampling Recovers Probative DNA Profile Information from Unresolvable/Undetectable Minor Donors in Mixtures." *Genes*, 13(7):1117, 2022.

K. Huffman. "Complex DNA Mixture Deconvolution by Single Cell Genomics: Direct Physical Cell Subsampling and High Sensitivity DNA Typing." Doctoral Dissertation. University of Central Florida, 2022.

K. Huffman, E. Hanson, and J. Ballantyne. "Probabilistic genotyping of single cell replicates from complex DNA mixtures recovers higher contributor LR's than standard analysis." *Science & Justice*, 62(2):156-163, 2022.

M.M. Holland, T.M. Tiedge, A.J. Bender, S.A. Gaston-Sanchez, and J.A. McElhoe. "MaSTR™: an effective probabilistic genotyping tool for interpretation of STR mixtures associated with differentially degraded DNA." *International Journal of Legal Medicine*, 136(2):433-446, 2022.

L. Ostojic, C. O'Connor, and E. Wurmbach. "Micromanipulation of single cells and fingerprints for forensic identification." *Forensic Science International: Genetics*, 51, 102430, 2021.

K. Huffman, E. Hanson, E, and J. Ballantyne. "Recovery of single source DNA profiles from mixtures by direct single cell subsampling and simplified micromanipulation." *Science & Justice*, 61(1):13-25, 2021.

S.N. Wright, B.J. Huges, and N.J. Dovichi. "Capillary zone electrophoresis separation and collection of spermatozoa for the forensic analysis of sexual assault evidence." *Electrophoresis*, 41(15):1344-1353, 2020.

D. Taylor, J. Bright, H. Kelly, M. Lin, and J. Buckleton. "A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis." *Forensic Science International: Genetics*, 31:149-154, 2017.

L. Ostojic. "Qualitative and Quantitative Assessment of Biological Traces in Forensic DNA Analysis." Doctoral Dissertation. University of Belgrade. 2017.

L. Ostojic and E. Wurmbach. "Analysis of fingerprint samples, testing various conditions, for forensic DNA identification." *Science & Justice*, 57(1):35-40, 2017.

C.E. Stanciu, M.K. Philpott, E.E. Bustamante, Y.J. Kwon, and C.J. Ehrhardt. "Analysis of red autofluorescence (650-670nm) in epidermal cell populations and its potential for distinguishing contributors to 'touch' biological samples." *F1000Research*, 5:180, 2016.

K.E. Rowan, G.A. Wellner, and C.M. Grgicak. "Exploring the Impacts of Ordinary Laboratory Alterations During Forensic DNA Processing on Peak Height Variation, Thresholds, and Probability of Dropout." *Journal of Forensic Sciences*, 61(1):177-185, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

L.E. Alfonse, A.D. Garrett, H. Swaminathan, K.C. Peters, G. Wellner, X. Yearwood-Garcia, L.M. Taranow, J. Sheehan, S.E. Norsworthy, U. Mönich, D.S. Lun, K.R. Duffy, M. Médard, R.W. Cotton, and C.M. Grgicak. "The Development and Release of a Collection of Computational Tools and a Large-Scale Empirical Data Set for Validation: The PROVEDIt Initiative." International Symposium on Human Identification, 2016.

G. Tejada. "Evaluating a peak height based method to determine the number of contributors in a DNA mixture and a study of DNA recovery using laser microdissection." Doctoral Dissertation, Boston University, 2015.

D. McNevin, J. Edson, J. Robertson, and J.J. Austin. "Reduced reaction volumes and increased Taq DNA polymerase concentration improve STR profiling outcomes from a real-world low template DNA source: telogen hairs." *Forensic Sci Med Pathol*, 11(3): 326-338, 2015.

C.N. Taveira. "Optimizing cell elution conditions for a novel enzymatic DNA extraction technique for spermatozoa on cotton swabs." Master's thesis. Boston University School of Medicine, 2015.

R.W. Cotton and M.B. Fisher. "Review: Properties of sperm and seminal fluid, informed by research on reproduction and contraception." *Forensic Science International: Genetics*, 18:66-77, 2015.

C. Xu, L. Feng, F. Yang, J. Jia, A.Q. Ji, L. Hu, and C.X. Li. "Mucosal Cell Isolation and Analysis from Cellular Mixtures of Three Contributors." *Journal of Forensic Sciences*, 60(3):783-786, 2015.

T.J. Verdon, R.J. Mitchell, W. Chen, K. Xiao, and R.A. van Oorschot. "FACS separation of non-compromised forensically relevant biological mixtures." *Forensic Science International: Genetics*, 14:194-200, 2015.

R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.

J. Bright. "Informing biological models for probabilistic methods of DNA profile interpretation." Doctoral Dissertation. The University of Auckland, 2015.

C.D. Steele, M. Greenhalgh, and D.J. Balding. "Verifying likelihoods for low template DNA profiles using multiple replicates." *Forensic Science International: Genetics*, 13:82-89, 2014.

C.D. Steele and D.J. Balding. "Statistical Evaluation of Forensic DNA Profile Evidence." *Annual Review of Statistics and Its Application*, 1:361-384, 2014.

H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.

L. Barron. "The final frontier." *Science & Justice*, 53(4):373-374, 2013.

J.A. Bright, D. Taylor, J.M. Curran, and J.S. Buckleton. "Degradation of forensic DNA profiles." *Australian Journal of Forensic Sciences*, 45(4):445-449, 2013.

H. Kelly. "The Application of Statistical Modelling to the Interpretation of Complex DNA Profiles." Doctoral thesis. Philosophy in Forensic Science, The University of Auckland, 2013.

J.M. Romeika and F. Yan. "Recent Advances in Forensic DNA Analysis." *Forensic Research*. 2013.

R. Visser and G. Hampikian, "When DNA Won't Work", 49 IDAHO L. REV. 39, 2012.

M.W. Perlin. "When good DNA goes bad". *Journal of Forensic Research*. S11:003, DOI 10.4172/2157-7145.S11-003, 2013.

E.A. Wade. "Determining the number of contributors in a DNA mixture." Master's thesis. Boston University School of Medicine, 2022.

B.W.R. Randolph. "An analysis of Bulletproof as probabilistic genotyping software for forensic DNA analysis casework." Master's thesis. Boston University School of Medicine, 2019.

K.L. Moss. "The Admissibility of TrueAllele: A Computerized DNA Interpretation System." *Wash. & Lee L. Rev.* 72:1033, 2015.

P.L. Marshall. "Improved Tools for the Robust Analysis of Low Copy Number and Challenged DNA Samples." Doctoral dissertation (Biomedical Sciences). University of North Texas Health Science Center, May 2014.

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

H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.

J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.

H. Kelly. "The Application of Statistical Modelling to the Interpretation of Complex DNA Profiles." Doctoral thesis. Philosophy in Forensic Science, The University of Auckland, 2013.

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

B.W.R. Randolph. "An analysis of Bulletproof as probabilistic genotyping software for forensic DNA analysis casework." Master's thesis. Boston University School of Medicine, 2019.

H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.

J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.

H. Kelly. "The Application of Statistical Modelling to the Interpretation of Complex DNA Profiles." Doctoral thesis. Philosophy in Forensic Science, The University of Auckland, 2013.

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

D. Taylor and J. Buckleton. "Can a reference 'match' an evidence profile if these have no loci in common?" *Forensic Science International: Genetics*, 53, 2021.

J. Bright, D. Taylor, J. Curran, and J. Buckleton. "Testing methods for quantifying Monte Carlo variation for categorical variables in Probabilistic Genotyping." *bioRxiv*, 2021.

J. Mortera. "DNA Mixtures in Forensic Investigations: The Statistical State of the Art." *Annual Review of Statistics and Its Application*, 7:111-142, 2020.

T. Graversen, J. Mortera, and G. Lago. "The Yara Gambirasio case: Combining evidence in a complex DNA mixture case." *Forensic Science International: Genetics*, 40:52-63, 2019.

D. Taylor, J. Bright, H. Kelly, M. Lin, and J. Buckleton. "A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis." *Forensic Science International: Genetics*, 31:149-154, 2017.

R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.

J. Ballantyne. "De-convolution of Body Fluid Mixtures: Cell Type Identification and Genetic Profiling of Micro-Dissected Cells." *National Center for Forensic Science, Report*, 2013.

J.M. Romeika and F. Yan. "Recent Advances in Forensic DNA Analysis." *Journal of Forensic Research*, S12:001, doi: 10.4172/2157-7145.S12-001, 2013.

V.L. Pascali and S. Merigioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.

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*. 2011;56(6):1430-1447.

F. Sessa, M. Esposito, G. Cocimano, S. Sablone, M.A.A. Karaboue, M. Chisari, D.G. Albano, and M. Salerno. "Artificial Intelligence and Forensic Genetics: Current Applications and Future Perspectives." *Applied Sciences*, 14(5):2113, 2024.

- H. Hwa, M. Wu, P. Hsu, H. Yin, T. Lee, and C. Su. "DNA mixture analyses of autosomal single nucleotide polymorphisms for individual identification using droplet digital polymerase-chain reaction and massively parallel sequencing in combination with EuroFormix." *Australian Journal of Forensic Sciences*, 2023 (in press).
- S. Inokuchi, H. Nakanishi, A. Takada, and K. Saito. "Effect existence of aging on stutter ratio evaluated via Bayesian inference." *Forensic Science International: Genetics*, 67:102933, 2023.
- D. Taylor and D. Abarno. "A lights-out forensic DNA analysis workflow for no-suspect crime." *Forensic Science International: Genetics*, 66:102907, 2023.
- K. Huffman and J. Ballantyne. "Single cell genomics applications in forensic science: Current state and future directions." *iScience*, 26, 2023.
- K. Huffman, M. Kruijver, J. Ballantyne, and D. Taylor. "Carrying out common DNA donor analysis using DBLR™ on two or five-cell mini-mixture subsamples for improved discrimination power in complex DNA mixtures." *Forensic Science International: Genetics*, 66, 2023.
- M.M. Foley. "Likelihood Ratio Calculation Using LRmix Studio." In: C.C. Connon (ed) *Forensic DNA Analysis: Methods and Protocols*, Springer Link, 307-328, 2023.
- K.R. Duffy, D.S. Lun, M.M. Mulcahy, L. O'Donnell, N. Sheth, and C.M. Grgicak. "Evidentiary evaluation of single cells renders highly informative forensic comparisons across multifarious admixtures." *Forensic Science International: Genetics*, 64, 102852, 2023.
- D. Orozco. "TrueAllele® and STRmix™: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis, 2023.
- D. Taylor. "Evaluation of Observations Given Activity Level Propositions." In: D. Taylor and B. Kokshoorn (eds) *Forensic DNA Trace Evidence Interpretation*. CRC Press, Taylor & Francis Group, 37-66, 2023.
- L. Kulhankova, D.M. González, E. Bindels, D. Kling, M. Kayser, and E. Mulugeta. "Single-cell transcriptome sequencing allows genetic separation, characterization and identification of individuals in multi-person biological mixtures." *Communications Biology*, 6, 2023.
- K. Huffman, E. Hanson, and J. Ballantyne. "Y-STR mixture deconvolution by single-cell analysis." *Journal of Forensic Sciences*, 68(1):275-288, 2023.

N. Galante, R. Cotroneo, D. Furci, G. Lodetti, and M.B. Casali. "Applications of artificial intelligence in forensic sciences: Current potential benefits, limitations and perspectives." *International Journal of Legal Medicine*, 137:445-458, 2022.

J. Alfieri, M.D. Coble, C. Conroy, A. Dahl, D.R. Hares, B.S. Weir, C. Wolock, E. Zhao, H. Kingston, and T.W. Zolandz. "A new implementation of a semi-continuous method for DNA mixture interpretation." *Forensic Science International: Reports*, 6, 2022.

M. Kruijver and J.A. Bright. "A tool for simulating single source and mixed DNA profiles." *Forensic Science International: Genetics*, 60:102746, 2022.

M. Susik, H. Schönborn, and I.F. Sbalzarini. "Hamiltonian Monte Carlo with strict convergence criteria reduces run-to-run variability in forensic DNA mixture deconvolution." *Forensic Science International: Genetics*, 60:102744, 2022.

J.M. Miller, C. Lee, S. Ingram, V.K. Yadavalli, S.A. Greenspoon, and C.J. Ehrhardt. "Use of hormone-specific antibody probes for differential labeling of contributor cell populations in trace DNA mixtures." *International Journal of Legal Medicine*, 136(6):1551-1564, 2022.

M.S. Adamowicz, T.N. Rambo, and J.L. Clarke. "Internal Validation of MaSTR™ Probabilistic Genotyping Software for the Interpretation of 2–5 Person Mixed DNA Profiles." *Genes*, 13(8):1429, 2022.

D. Syndercombe-Court. "DNA: current developments and perspectives." In: J.A.M. Gall and J.J. Payne-James (eds) *Current Practice in Forensic Medicine (volume 3)*, Chapter 6, 2022.

A.E. Woerner, B. Crysap, F.C. Hewitt, M.W. Gardner, M.A. Freitas, and B. Budowle. "Techniques for estimating genetically variable peptides and semi-continuous likelihoods from massively parallel sequencing data." *Forensic Science International: Genetics*, 59:102719, 2022.

T. Kalafut, J.A. Bright, D. Taylor, and J. Buckleton. "Investigation into the effect of mixtures comprising related people on non-donor likelihood ratios, and potential practises to mitigate providing misleading opinions." *Forensic Science International: Genetics*, 59:102691, 2022.

K.K.W. Cheng. "The Application of Modern Statistical Methods to the Advance of Probabilistic Genotyping." Doctoral Dissertation. University of Auckland, 2022.

D. Ward, J. Henry, and D. Taylor. "Analysis of mixed DNA profiles from the RapidHIT™ ID platform using probabilistic genotyping software STRmix™." *Forensic Science International: Genetics*, 58:102664, 2022.

- H. Miller Coyle. "Quality Control Measures in Short Tandem Repeat (STR) Analysis." In: H.R. Dash, P. Shrivastava, J.A. Lorente (eds) *Handbook of DNA Profiling*. Springer, Singapore, 1107-1124, 2022.
- S. Manabe, T. Fukagawa, K. Fujii, N. Mizuno, K. Sekiguchi, A. Akane and K. Tamaki. "Development and validation of *Kongoh* ver. 3.0.1: Open-source software for DNA mixture interpretation in the GlobalFiler system based on a quantitative continuous model." *Legal Medicine*, 54:101972, 2022.
- T. Bille, M.D. Coble, and J.A. Bright. "Exploring the advantages of amplifying the entire extract versus splitting the extract and interpreting replicates using a continuous model of interpretation." *Australian Journal of Forensic Sciences*, 54(5):584-595, 2022.
- K. Huffman, E. Hanson, and J. Ballantyne. "Probabilistic genotyping of single cell replicates from complex DNA mixtures recovers higher contributor LR's than standard analysis." *Science & Justice*, 62(2):156-163, 2022.
- K. Huffman. "Complex DNA Mixture Deconvolution by Single Cell Genomics: Direct Physical Cell Subsampling and High Sensitivity DNA Typing." Doctoral Dissertation. University of Central Florida, 2022.
- N. Sheth, K.R. Duffy, and C.M. Grgicak. "High-quality data from a forensically relevant single-cell pipeline enabled by low PBS and proteinase K concentrations." *J. Forensic Sciences*, 67(2):697-706, 2022.
- K. Watanabe, K. Taniguchi, K. Toyomane, and T. Akutsu. "A new approach for forensic analysis of saliva-containing body fluid mixtures based on SNPs and methylation patterns of nearby CpGs." *Forensic Science International: Genetics*, 56:102624, 2022.
- J. Noël, S. Noël, F. Mailly, D. Granger, J.F. Lefebvre, E. Milot, and D. Séguin. "Total allele count distribution (TAC curves) improves number of contributor estimation for complex DNA mixtures." *Canadian Society of Forensic Science Journal*, 55(3):156-170, 2022.
- A. Lucassen, K. Ehlers, P.J. Grobler, and C.H. Brenner. "Evaluating Mixture Solution™—rapid and non-MCMC probabilistic mixture analysis." *International Journal of Legal Medicine*, 135:2275-2284, 2021.
- J. Ge, J.L. King, A. Smuts, and B. Budowle. "Precision DNA Mixture Interpretation with Single-Cell Profiling." *Genes*, 12(11):1649, 2021.

S. Manabe, K. Fujii, T. Fukagawa, N. Mizuno, K. Sekiguchi, K. Inoue, M. Hashiyada, A. Akane, K. Tamaki. "Evaluation of probability distribution models for stutter ratios in the typing system of GlobalFiler and 3500xL Genetic Analyzer." *Legal Medicine*, 52:101906, 2021.

J. Valtl, U.J. Mönich, D.S. Lun, J. Kelley, and C.M. Grgicak. "A series of developmental validation tests for Number of Contributors platforms: Exemplars using NOCI and a neural network." *Forensic science international: Genetics*, 54:102556, 2021.

P. Gill, C. Benschop, J. Buckleton, Ø. Bleka, and D. Taylor. "A Review of Probabilistic Genotyping Systems: *EuroForMix*, *DNAStatistX* and *STRmix™*." *Genes*, 12(10):1559, 2021.

K. Cheng, Ø. Bleka, P. Gill, J. Curran, J.A. Bright, D. Taylor, and J. Buckleton. "A comparison of likelihood ratios obtained from EuroForMix and STRmix™." *Journal of Forensic Sciences*, 66(6):2138-2155, 2021.

S. Riman, H. Iyer, and P.M. Vallone. "Examining performance and likelihood ratios for two likelihood ratio systems using the PROVEDIt dataset." *PLoS ONE*, 16(9):e0256714, 2021.

J. Ge, J. King, S. Mandape, and B. Budowle. "Enhanced mixture interpretation with macrohaplotypes based on long-read DNA sequencing." *International Journal of Legal Medicine*, 135:2189-2198, 2021.

M. Lin, S. Lee, X. Zhang, L. Russell, H. Kelly, K. Cheng, S. Cooper, R. Wivell, Z. Kerr, J. Morawitz, and J. Bright. "Developmental validation of FaSTR™ DNA: Software for the analysis of forensic DNA profiles." *Forensic Science International: Reports*, 3:100217, 2021.

K. Cheng, M. Lin, L. Moreno, J. Skillman, S. Hickey, D. Cuenca, W.R. Hudlow, R. Just, J. Bright, J. Buckleton, and J.M. Curran. "Modeling allelic analyte signals for aSTRs in NGS DNA profiles." *Journal of Forensic Sciences*, 66(4):1234-1245, 2021.

D. McNevin, K. Wright, M. Barash, S. Gomes, A. Jamieson, and J. Chaseling. "Proposed Framework for Comparison of Continuous Probabilistic Genotyping Systems amongst Different Laboratories." *Forensic Sciences*, 1(1):33-45, 2021.

R. Puch-Solis and S. Pope. "Interpretation of DNA data within the context of UK forensic science—evaluation." *Emerging Topics in Life Sciences*, 5(3):405-413, 2021.

- P. Ferrara, R. Haraksim, and L. Beslay. "Performance Evaluation of Source Camera Attribution by Using Likelihood Ratio Methods." *Journal of Imaging*, 7(7):116, 2021.
- L. O'Donnell. "Clustering Single-Cell Electropherograms by Genotype Through Unsupervised Machine Learning." Master's Thesis. Hamilton Institute Maynooth University, 2021.
- D. Kling, C. Phillips, D. Kennett, and A. Tillmar. "Investigative genetic genealogy: Current methods, knowledge and practice." *Forensic Science International: Genetics*, 52:102474, 2021.
- K. Slooten. "The analogy between DNA kinship and DNA mixture evaluation, with applications for the interpretation of likelihood ratios produced by possibly imperfect models." *Forensic Science International: Genetics*, 52:102449, 2021.
- P.S. Allen, S.N. Pugh, J.A. Bright, D.A. Taylor, J.M. Curran, Z. Kerr, and J.S. Buckleton. "Relaxing the assumption of unrelatedness in the numerator and denominator of likelihood ratios for DNA mixtures." *Forensic Science International: Genetics*, 51:102434, 2021.
- L. Ostojic, C. O'Connor, and E. Wurmbach. "Micromanipulation of single cells and fingerprints for forensic identification." *Forensic Science International: Genetics*, 51:102430, 2021.
- N. Sheth, H. Swaminathan, A.J. Gonzalez, K.R. Duffy, and C.M. Grgicak. "Towards developing forensically relevant single-cell pipelines by incorporating direct-to-PCR extraction: Compatibility, signal quality, and allele detection." *International Journal of Legal Medicine*, 135:727-738, 2021.
- K. Huffman, E. Hanson, E, and J. Ballantyne. "Recovery of single source DNA profiles from mixtures by direct single cell subsampling and simplified micromanipulation." *Science & Justice*, 61(1):13-25, 2021.
- K. Cheng, J.A. Bright, Z. Kerr, D. Taylor, A Cieccko, J. Curran, and J. Buckleton. "Examining the additivity of peak heights in forensic DNA profiles." *Australian Journal of Forensic Sciences*, 53(5):497-511, 2021.
- J.A. Bright, M. Jones Dukes, S.N. Pugh, I.W. Evett, and J.S. Buckleton. "Applying calibration to LR's produced by a DNA interpretation software." *Australian Journal of Forensic Sciences*, 53(2):147-153, 2021.
- B.S. Weir. "DNA frequencies and probabilities." In: D. Banks, K. Kafadar, D.H. Kaye, and M. Tackett (eds) *Handbook of Forensic Statistics*, Chapman and Hall/CRC, 251-264, 2020.

K. Cheng, J. Skillman, S. Hickey, R. Just, L. Moreno, J.A. Bright, H. Kelly, M. Lin, J.M. Curran, and J. Buckleton. "Variability and additivity of read counts for aSTRs in NGS DNA profiles." *Forensic Science International: Genetics*, 48:102351, 2020.

Ø. Bleka, R. Just, J. Le, and P. Gill. "An examination of STR nomenclatures, filters and models for MPS mixture interpretation." *Forensic Science International: Genetics*, 48:102319, 2020.

A. Sharma and P.K. Rao. "Advanced Forensic Models." In: D. Rawtani and C.M. Hussain (eds) *Technology in Forensic Science: Sampling, Analysis, Data and Regulations*, Wiley-VCH GmbH, Boschstr. Chapter 15, 2020.

C. Schuerman, T. Kalafut, C. Buchanan, J. Sutton, and J.A. Bright. "Using the Nondonor Distribution to Improve Communication and Inform Decision Making for Low LR's from Minor Contributors in Mixed DNA Profiles." *J. Forensic Sciences*, 65(4):1072-1084, 2020.

B.J. O'Brien. "Application of Optical Trapping to Obtain Single-Source STR Profiles from Forensically Relevant Body Fluid Mixtures with Modified DNA Analysis Workflow." Master's Thesis. Virginia Commonwealth University, 2020.

J.M. Butler and S. Willis. "Interpol review of forensic biology and forensic DNA typing 2016-2019." *Forensic Science International: Synergy*, 2:352-367, 2020.

A. Kuffel, A. Gray, and N.N. Daeid. "Human Leukocyte Antigen alleles as an aid to STR in complex forensic DNA samples." *Science & Justice*, 60(1):1-8, 2020.

K. Slooten. "A top-down approach to DNA mixtures." *Forensic Science International: Genetics*, 46:102250, 2020.

S. Riman, H. Iyer, L.A. Borsuk, and P.M. Vallone. "Understanding the characteristics of sequence-based single-source DNA profiles." *Forensic Science International: Genetics*, 44:102192, 2020.

S. Karkar, L.E. Alfonse, C.M. Grgicak, and D.S. Lun. "Statistical modeling of STR capillary electrophoresis signal." *BMC Bioinformatics*, 20(584), 2019.

R. Puch-Solis, T. Clayton, and M. Barron. "Evidential evaluation of DNA profiles using a continuous model implemented in the DNA LiRa software." Eurofins Forensic Services, 2019.

F.M. Lucero. "DNA Mixture statistics using a likelihood ratio software tool: effect of variations in drop-out rates and number of contributors." Master's thesis. CUNY John Jay College, 2019.

K.J. van der Gaag. "Development of forensic genomics research toolkits by the use of Massively Parallel Sequencing." Doctoral thesis. Universiteit Leiden, 2019.

J.A. Bright and M. Coble. *Forensic DNA Profiling: A Practical Guide to Assigning Likelihood Ratios*. CRC Press, 2019.

J. Yang, D. Lin, C. Deng, Z. Li, Y. Pu, Y. Yu, K. Li, D. Li, P. Chen, and F. Chen. "The advances in DNA mixture interpretation." *Forensic Science International*, 301:101-106, 2019.

K. Breslin, B. Wills, A. Ralf, M.V. Garcia, M. Kukla-Bartoszek, E. Pospiech, A. Freire-Aradas, C. Xavier, S. Ingold, M. de La Puente, K.J. van der Gaag, N. Herrick, C. Haas, W. Parson, C. Phillips, T. Sijen, W. Branicki, S. Walsh, and M. Kayser. "HirisPlex-S system for eye, hair, and skin color prediction from DNA: Massively parallel sequencing solutions for two common forensically used platforms." *Forensic Science International: Genetics*, 43:102152, 2019.

M.A. Marciano and J.D. Adelman. "Developmental validation of PACE™: Automated artifact identification and contributor estimation for use with GlobalFiler™ and PowerPlex® fusion 6c generated data." *Forensic Science International: Genetics*, 43:102140, 2019.

M. Kruijver, J.A. Bright, H. Kelly, and J. Buckleton. "Exploring the probative value of mixed DNA profiles." *Forensic Science International: Genetics*, 41:1-10, 2019.

S. Noel, J. Noel, D. Granger, J.F. Lefebvre, and D. Seguin. "STRmix™ put to the test: 300 000 non-contributor profiles compared to four-contributor DNA mixtures and the impact of replicates." *Forensic Science International: Genetics*, 41:24-31, 2019.

Ø. Bleka, L. Prieto, and P. Gill. "CaseSolver: An investigative open source expert system based on EuroForMix." *Forensic Science International: Genetics*, 41:83-92, 2019.

J.J.R.B. Rodriguez, J.A. Bright, J.M. Salvador, R.P. Laude, and M.C.A.D. Ungria. "Probabilistic approaches to interpreting two-person DNA mixtures from post-coital specimens." *Forensic Science International*, 300:157-163, 2019.

B.S. Weir. "Forensic Genetics." In: D. Balding, I. Moltke, and J. Marionis (Eds.), *Handbook of Statistical Genomics: Two Volume Set (4th Edition)*, Chapter 18, 2019.

B.W.R. Randolph. "An analysis of Bulletproof as probabilistic genotyping software for forensic DNA analysis casework." Master's thesis. Boston University School of Medicine, 2019.

A.J. Gonzalez. "Developing a forensically relevant single-cell interpretation strategy for human identification." Master's thesis. Rutgers University, 2019.

D.A. Taylor, J.S. Buckleton, and J. Bright. "Comment on "DNA mixtures interpretation—a proof-of-concept multi-software comparison highlighting different probabilistic methods' performances on challenging samples" by Alladio et al." *Forensic Science International: Genetics*, 40:E248-E251, 2019.

T. Bille, S. Weitz, J.S. Buckleton, and J. Bright. "Interpreting a major component from a mixed DNA profile with an unknown number of minor contributors." *Forensic Science International: Genetics*, 40:150-159, 2019.

J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.

D.O. Ricke, P. Fremont-Smith, J. Watkins, S. Stankiewicz, T. Boettcher, and E. Schwoebel. "Estimating Individual Contributions to Complex DNA SNP Mixtures." *Journal of Forensic Sciences*, Available online 22 February 2019.

M.D. Coble and J.A. Bright. "Probabilistic genotyping software: An overview." *Forensic Science International: Genetics*, 38:219-224, 2019.

B.R. McCord, Q. Gauthier, S. Cho, M.N. Roig, G.C. Gibson-Daw, B. Young, F. Taglia, S.C. Zapico, R.F. Mariot, S.B. Lee, and G. Duncan. "Forensic DNA Analysis." *Analytical Chemistry*, 91(1):673-688, 2019.

S. Karkar, L.E. Alfonse, C.M. Grgicak, and D.S. Lun. "Statistical Modeling of Short-Tandem Repeat Capillary Electrophoresis Profiles." *Proceedings of the 2018 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*. IEEE, 2018.

H. Swaminathan, M.O. Quershi, C.M. Grgicak, K. Duffy, and D.S. Lun. "Four model variants within a continuous forensic DNA mixture interpretation framework: Effects on evidential inference and reporting." *PLoS ONE*, 13(11):e0207599, 2018.

J.S. Buckleton, J. Bright, K. Cheng, B. Budowle, and M.D. Coble. "NIST interlaboratory studies involving DNA mixtures (MIX13): A modern analysis." *Forensic Science International: Genetics*, 37:172-179, 2018.

Y. Tan, P. Bai, L. Wang, H. Tian, H. Jian, R. Zhang, Y. Liu, W. Liang, and L. Zhang. "Two-person DNA mixture interpretation based on a novel set of SNP-STR markers." *Forensic Science International: Genetics*, 37:37-45, 2018.

P. Gill, T. Hicks, J.M. Butler, E. Connolly, L. Gusmao, B. Kokshoorn, N. Morling, R.A.H. van Oorschot, W. Parson, M. Prinz, P.M. Schneider, T. Sijen, and D. Taylor. "DNA commission of the International society for forensic genetics:

Assessing the value of forensic biological evidence-Guidelines highlighting the importance of propositions: Part I: evaluation of DNA profiling comparisons given (sub-) source propositions." *Forensic Science International: Genetics*, 36:189-202, 2018.

D. Taylor, B. Kokshoorn, and A. Biedermann. "Evaluation of forensic genetics findings given activity level propositions: A review." *Forensic Science International: Genetics*, 36:34-49, 2018.

R. Tao, S. Wang, J. Zhang, J. Zhang, Z. Yang, X. Sheng, Y. Hou, S. Zhang, and C. Li. "Separation/extraction, detection, and interpretation of DNA mixtures in forensic science." *International Journal of Legal Medicine*, 132(5):1247-1261, 2018.

R.G. Cowell. "Computation of marginal distributions of peak-heights in electropherograms for analysing single source and mixture STR DNA samples." *Forensic Science International: Genetics*, 35:164-168, 2018.

M.A. Marciano, V.R. Williamson, and J.D. Adelman. "A hybrid approach to increase the informedness of CE-based data using locus-specific thresholding and machine learning." *Forensic Science International: Genetics*, 35:26-37, 2018.

R.S. Just and J.A. Irwin. "Use of the LUS in sequence allele designations to facilitate probabilistic genotyping of NGS-based STR typing results." *Forensic Science International: Genetics*, 34:197-205, 2018.

J. Bright, R. Richards, M. Kruijver, H. Kelly, C. McGovern, A. Magee, A. McWhorter, A. Ciecko, B. Peck, C. Baumgartner, C. Buettner, S. McWilliams, C. McKenna, C. Gallacher, B. Mallinder, D. Wright, D. Johnson, D. Catella, E. Lien, C. O'Connor, G. Duncan, J. Bundy, J. Echard, J. Lowe, J. Stewart, K. Corrado, S. Gentile, M. Kaplan, M. Hassler, N. McDonald, P. Hulme, R.H. Oefelein, S. Montpetit, M. Strong, S. Noel, S. Malsom, S. Myers, S. Welti, T. Moretti, T. McMahan, T. Grill, T. Kalafut, M. Greer-Ritzheimer, V. Beamer, D. Taylor, and J.S. Buckleton. "Internal validation of STRmix™—A multi laboratory response to PCAST." *Forensic Science International: Genetics*, 34:12-24, 2018.

B.S. Weir. "Population Genetic Issues for Forensic DNA Profiles." *2011-DN-BX-K541 Final Report*, April 2018.

G.M. Dembinski, C. Sobieralski, and C.J. Picard. "Estimation of the number of contributors of theoretical mixture profiles based on allele counting: Does increasing the number of loci increase success rate of estimates?." *Forensic Science International: Genetics*, 33:24-32, 2018.

L.E. Alfonse, A.D. Garrett, D.S. Lun, K.R. Duffy, and C.M. Grgicak. "A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt." *Forensic Science International: Genetics*, 32:62-70, 2018.

S.E. Cavanaugh and A.S. Bathrick. "Direct PCR amplification of forensic touch and other challenging DNA samples: A review." *Forensic Science International: Genetics*, 32:40-49, 2018.

K.C. Peters, H. Swaminathan, J. Sheehan, K.R. Duffy, D.S. Lun, and C.M. Grgicak. "Production of high-fidelity electropherograms results in improved and consistent DNA interpretation: Standardizing the forensic validation process." *Forensic Science International: Genetics*, 31:160-170, 2017.

D. Taylor, J. Bright, H. Kelly, M. Lin, and J. Buckleton. "A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis." *Forensic Science International: Genetics*, 31:149-154, 2017.

Y. Tan, L. Wang, H. Wang, H. Tian, Z. Li, Q. Wang, H. Jian, S. Cao, W. Liang, and L. Zhang. "An investigation of a set of DIP-STR markers to detect unbalanced DNA mixtures among the southwest Chinese Han population." *Forensic Science International: Genetics*, 31:34-39, 2017.

J. Bright, D. Taylor, S. Gittelsohn, and J. Buckleton. "The paradigm shift in DNA profile interpretation." *Forensic Science International: Genetics*, 31:e24-e32, 2017.

S. Manabe, C. Morimoto, Y. Hamano, S. Fujimoto, and K. Tamaki. "Development and validation of open-source software for DNA mixture interpretation based on a quantitative continuous model." *PLoS ONE*, 12(11):e0188183, 2017.

B. Kokshoorn, B.J. Blankers, J. de Zoete, and C.E.H. Berger. "Activity level DNA evidence evaluation: on propositions addressing the actor or the activity." *Forensic Science International*, 278:115-124, 2017.

L.E. Alfonse, G. Tejada, H. Swaminathan, D.S. Lun, and C.M. Grgicak. "Inferring the Number of Contributors to Complex DNA Mixtures Using Three Methods: Exploring the Limits of Low-Template DNA Interpretation." *Journal of Forensic Sciences*, 62(2):308-316, 2017.

M. Woldegebriel, A. Asten, A. Kloosterman, and G. Vivó-Truyols. "Probabilistic peak detection in CE-LIF for STR DNA typing." *Electrophoresis*, 2017.

O. Hansson and P. Gill. "Characterisation of artefacts and drop-in events using STR-validator and single-cell analysis." *Forensic Science International: Genetics*, 30:57-65, 2017.

T.R. Moretti, R.S. Just, S.C. Kehl, L.E. Willis, J.S. Buckleton, J. Bright, D.A. Taylor, and A.J. Onorato. "Internal validation of STRmix™ for the interpretation of single source and mixed DNA profiles." *Forensic Science International: Genetics*, 2017.

D. Taylor, A. Biedermann, L. Samie, K. Pun, T. Hicks, and C. Champod. "Helping to distinguish primary from secondary transfer events for trace DNA." *Forensic Science International: Genetics*, 28:155-177, 2017.

J. Hoogenboom, K.J. van der Gaag, R.H. de Leeuw, T. Sijen, P. de Knijff, and J.F. Laros. "FDSTools: A software package for analysis of massively parallel sequencing data with the ability to recognise and correct STR stutter and other PCR or sequencing noise." *Forensic Science International: Genetics*, 27:27-40, 2017.

S. Gittelsohn, T.R. Moretti, A.J. Onorato, B. Budowle, B.S. Weir, and J. Buckleton. "The factor of 10 in forensic DNA match probabilities." *Forensic Science International: Genetics*, 28:178-187, 2017.

D. Meuwly, D. Ramos, and R. Haraksim. "A guideline for the validation of likelihood ratio methods used for forensic evidence evaluation." *Forensic Science International*, 276:142-153, 2017.

M.A.C.S.S. Fernando. "Bayesian Models for PCR Stutter." Doctoral Thesis. The University of Auckland, 2017.

Ø. Bleka, G. Storvik, and P. Gill. "EuroForMix: an open source software based on a continuous model to evaluate STR DNA profiles from a mixture of contributors with artefacts." *Forensic Science International: Genetics*, 21: 35-44, 2016.

D. Taylor, J. Bright, C. McGovern, C. Hefford, T. Kalafut, and J. Buckleton. "Validating multiplexes for use in conjunction with modern interpretation strategies." *Forensic Science International: Genetics*, 20:6-19, 2016.

A. Jamieson. "Issues in Forensic DNA." *A Guide to Forensic DNA Profiling*. 2016.

D. Taylor, D. Abarno, T. Hicks, and C. Champod. "Evaluating forensic biology results given source level propositions." *Forensic Science International: Genetics*, 21:54-67, 2016.

H. Swaminathan, A. Garg, C.M. Grgicak, M. Medard, and D.S. Lun. "CEESIt: A computational tool for the interpretation of STR mixtures." *Forensic Science International: Genetics*, 22:149-160, 2016.

C.D. Steele, M. Greenhalgh, and D.J. Balding. "Evaluation of low-template DNA profiles using peak heights." *Statistical Applications in Genetics and Molecular Biology*, 15(5):431-445, 2016.

D. Taylor, J. Buckleton, J. Bright. "Factors affecting peak height variability for short tandem repeat data." *Forensic Science International: Genetics*, 21:126-133, 2016.

F.R. Bieber, J.S. Buckleton, B. Budowle, J.M. Butler, and M.D. Coble. "Evaluation of forensic DNA mixture evidence: protocol for evaluation, interpretation, and statistical calculations using the combined probability of inclusion." *BMC Genetics*, 17(1):125, 2016.

C.E. Stanciu, M.K. Philpott, E.E. Bustamante, Y.J. Kwon, and C.J. Ehrhardt. "Analysis of red autofluorescence (650-670nm) in epidermal cell populations and its potential for distinguishing contributors to 'touch' biological samples." *F1000Research*, 5:180, 2016.

M.D. Coble, J. Buckleton, J.M. Butler, T. Egeland, R. Fimmers, P. Gill, L. Gusmão, B. Guttman, M. Krawczak, N. Morling, W. Parson, N. Pinto, P.M. Schneider, S.T. Sherry, S. Willuweit, and M. Prinz. "DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications." *Forensic Science International: Genetics*, 25:191-197, 2016.

Ø. Bleka, C.C. Benschop, G. Storvik, and P. Gill. "A comparative study of qualitative and quantitative models used to interpret complex STR DNA profiles." *Forensic Science International: Genetics*, 25:85-96, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

C.D. Marsden, N. Rudin, K. Inman, and K.E. Lohmueller. "An assessment of the information content of likelihood ratios derived from complex mixtures." *Forensic Science International: Genetics*, 22:64-72, 2016.

D. Taylor and D. Powers. "Teaching artificial intelligence to read electropherograms." *Forensic Science International: Genetics*, 25:10-18, 2016.

E.J. Imwinkelried. "Computer Source Code: A Source of the Growing Controversy Over the Reliability of Automated Forensic Techniques." *DePaul Law Review*, Forthcoming; UC Davis Legal Studies Research Paper No. 487, 2016.

D. Taylor, J. Bright, and J. Buckleton. "Using probabilistic theory to develop interpretation guidelines for Y-STR profiles." *Forensic Science International: Genetics*, 21:22-34, 2016.

O. Hansson, T. Egeland, and P. Gill. "Characterization of degradation and heterozygote balance by simulation of the forensic DNA analysis process." *International Journal of Legal Medicine*, 1-15, 2016.

- S. Manabe, Y. Hamano, C. Morimoto, C. Kawai, S. Fujimoto, and K. Tamaki. "New stutter ratio distribution for DNA mixture interpretation based on a continuous model." *Legal Medicine*, 19:16-21, 2016.
- C.D. Steele. "Statistical issues surrounding the analysis of forensic low-template DNA samples." Doctoral Dissertation, University College London, 2016.
- J. de Zoete, W. Oosterman, B. Kokshoorn, and M. Sjerps. "Cell type determination and association with the DNA donor." *Forensic Science International: Genetics*, 25:97-111, 2016.
- D. Taylor, D. Abarno, E. Rowe, and L. Rask-Nielsen. "Observations of DNA transfer within an operational Forensic Biology Laboratory." *Forensic Science International: Genetics*, 23:33-49, 2016.
- J.S. Bucklton, J. Bright, and D. Taylor. *Forensic DNA Evidence Interpretation*. (2nd edition). CRC Press – Taylor & Francis Group, 2016.
- J. Tschoche. "Process optimization in forensic expert opinion generation: Development and integration of software solutions in the context of the creation of forensic tracking." Doctoral Dissertation, LMU Munich, 2016.
- R. Wieten, J. De Zoete, B. Blankers, and B. Kokshoorn. "The interpretation of traces found on adhesive tapes." *Law, Probability, and Risk*, 14(4):305-322, 2015.
- G. Tejada. "Evaluating a peak height based method to determine the number of contributors in a DNA mixture and a study of DNA recovery using laser microdissection." Doctoral Dissertation, Boston University, 2015.
- U.J. Monich, K. Duffy, M. Medard, V. Cadambe, L.E. Alfonse, and C. Grgicak. "Probabilistic characterisation of baseline noise in STR profiles." *Forensic Science International: Genetics*, 19:107-122, 2015.
- R.G. Cowell, T. Graverson, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.
- D.J. Balding and C.D. Steele. *Weight-of-Evidence for Forensic DNA Profiles*. (2nd edition). John Wiley & Sons, 2015.
- C.C. Benschop, C.G. Corina, H. Haned, S.Y. Yoo, and T. Sijen. "Evaluation of samples comprising minute amounts of DNA." *Science & Justice*, 55(5):316-322, 2015.
- H. Haned and P. Gill. "Expert Systems in DNA Interpretation." *Wiley Encyclopedia of Forensic Science*. 2015.

- P. Gill, H. Haned, O. Bleka, O. Hansson, G. Dorum, and T. Egeland. "Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches—Twenty years of research and development." *Forensic Science International: Genetics*, 18:100-117, 2015.
- D. Taylor, J. Buckleton, and I Evett. "Testing likelihood ratios produced from complex DNA profiles." *Forensic Science International: Genetics*, 16:165-171, 2015.
- G. Repiská, J. Durdiaková, N. Kamodyová, and G. Minárik. "The Applicability of Autosomal Short Tandem Repeats Genotyping for Minor Contributor DNA Profiling from Mixed Saliva Samples." *Journal of Forensic Research*, 6(1):1-5, 2015.
- S. Cooper, C. McGovern, J.A. Bright, D. Taylor, and J. Buckleton. "Investigating a common approach to DNA profile interpretation using probabilistic software." *Forensic Science International: Genetics*, 16:121-131, 2015.
- H. Haned, C.C. Benschop, P.D. Gill, and T Sijen. "Complex DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model." *Forensic Science International: Genetics*, 16:17-25, 2015.
- T.J. Verdon, R.J. Mitchell, W. Chen, K. Xiao, and R.A. van Oorschot. "FACS separation of non-compromised forensically relevant biological mixtures." *Forensic Science International: Genetics*, 14:194-200, 2015.
- J.A. Bright, I.W. Evett, D. Taylor, J.M. Curran, and J. Buckleton. "A series of recommended tests when validating probabilistic DNA profile interpretation software." *Forensic Science International: Genetics*, 14:125-131, 2015.
- D. Taylor and J. Buckleton. "Do low template DNA profiles have useful quantitative data?" *Forensic Science International: Genetics*, 16: 13-16, 2015.
- T.R. De Wolff, A.J. Kal, C.E.H. Berger, and B. Kokshoorn. "A probabilistic approach to body fluid typing interpretation: an exploratory study on forensic saliva testing." *Law, Probability and Risk*, 14(4):323-339, 2015.
- L.E. Alfonse. "Effects of template mass, complexity, and analysis method on the ability to correctly determine the number of contributors to DNA mixtures." Doctoral Dissertation, Boston University, 2015.
- J. Bright. "Informing biological models for probabilistic methods of DNA profile interpretation." Doctoral Dissertation. The University of Auckland, 2015.

- J. Sutton, T. Kalafut, L. Smith, C. Schuerman, and D. Diekema. "The Dangers of Not Assuming Contributors – Why the Goal of "Conservative" in Forensic DNA Statistics Should Be Dropped in Favor of Being "Informative"." Found on Promega.com, 2015.
- K. Inman, N. Rudin, K. Cheng, C. Robinson, A. Kirschner, L. Inman-Semeran, and K.E. Lohmueller. "Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles." *BMC Bioinformatics*, 16(1):298, 2015.
- T.W. Bille, S.M. Weitz, M.D. Coble, J. Buckleton, and J.A. Bright. "Comparison of the performance of different models for the interpretation of low level mixed DNA profiles." *Electrophoresis*, 35(21-22):3125-3133, 2014.
- D. Taylor, J.A. Bright, and J. Buckleton. "The 'factor of two' issue in mixed DNA profiles." *Journal of Theoretical Biology*, 363:300-306, 2014.
- J.A. Bright, J.S. Buckleton, D. Taylor, M.A.C.S.S. Fernando, and J.M. Curran. "Modeling forward stutter: Toward increased objectivity in forensic DNA interpretation." *Electrophoresis*, 35(21-22):3152-3157, 2014.
- D. Taylor, J.A. Bright, and J. Buckleton. "Interpreting forensic DNA profiling evidence without specifying the number of contributors." *Forensic Science International: Genetics*, 13:269-280, 2014.
- P. Gill, O. Bleka, and T. Egeland. "Does an English appeal court ruling increase the risks of miscarriages of justice when complex DNA profiles are searched against the national DNA database?" *Forensic Science International: Genetics*, 13:167-175, 2014.
- J.A. Bright and J.M. Curran. "Investigation into stutter ratio variability between different laboratories." *Forensic Science International: Genetics*, 13:79-81, 2014.
- D. Taylor, J.A. Bright, and J. Buckleton. "Considering relatives when assessing the evidential strength of mixed DNA profiles." *Forensic Science International: Genetics*, 13:259-263, 2014.
- J.A. Bright, J.M. Curran, and J.S. Buckleton. "The effect of the uncertainty in the number of contributors to mixed DNA profiles on profile interpretation." *Forensic Science International: Genetics*, 12:208-214, 2014.
- D. Taylor. "Using continuous DNA interpretation methods to revisit likelihood ratio behavior." *Forensic Science International: Genetics*, 11:144-153, 2014.
- J.A. Bright, J. Curran, and J. Buckleton. "Modelling PowerPlex® Y stutter and artefacts." *Forensic Science International: Genetics*, 11:126-136, 2014.

- N. Hu, B. Cong, T. Gao, R. Hu, Y. Chen, H. Tang, L. Xue, L. Shujin, and M. Chunling. "Evaluation of parameters in mixed male DNA profiles for the Identifiler® multiplex system." *International J of Molecular Medicine*, 34(1):43-52, 2014.
- J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.
- D. Taylor, J.A. Bright, J. Buckleton, and J. Curran. "An illustration of the effect of various sources of uncertainty on DNA likelihood ratio calculations." *Forensic Science International: Genetics*, 11:56-63, 2014.
- J.A. Bright, D. Taylor, J. Curran, and J. Buckleton. "Searching mixed DNA profiles directly against profile databases." *Forensic Science International: Genetics*, 9:102-110, 2014.
- J.A. Bright, K.E. Stevenson, M.D. Coble, C.R. Hill, J.M. Curran, and J.S. Buckleton. "Characterising the STR locus D6S1043 and examination of its effect on stutter rates." *Forensic Science International: Genetics*, 8(1):20-23, Available online January 2014.
- C.D. Steele and D.J. Balding. "Statistical Evaluation of Forensic DNA Profile Evidence." *Annual Review of Statistics and Its Application*, 1:361-384, 2014.
- H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.
- T.M. Diegoli, A. Linacre, and M.D. Coble. "A gonosomal marker multiplex to aid in mixture interpretation." *Forensic Science International: Genetics Supplement Series*, 4(1):e184-e185, 2013.
- T. Graversen, and S. Lauritzen, S. "Estimation of parameters in DNA mixture analysis." *Journal of Applied Statistics*, 40(11):2423-2436, 2013.
- J. Drábek. "Two Fagan nomograms for the (genetic) evidence in a judicial context." *Australian Journal of Forensic Sciences*, 46(3):266-271, 2014.
- D.J. Balding. "Evaluation of mixed-source, low-template DNA profiles in forensic science." *Proceedings of the National Academy of Sciences*. 2013. July 1. www.pnas.org/cgi/doi/10.1073/pnas.1219739110
- D. Taylor, J. Bright, and J. Buckleton. "The interpretation of single source and mixed DNA profiles." *Forensic Science International: Genetics*. 2013. 7(5):516-528.

- J. Hartevelde, A. Lindenbergh, and T. Sijen. "RNA cell typing and DNA profiling of mixed samples: Can cell types and donors be associated?." *Science & Justice*, 53(3):261-269, 2013.
- J.A. Bright, D. Taylor, J.M. Curran, and J.S. Buckleton. "Degradation of forensic DNA profiles." *Australian Journal of Forensic Sciences*, 45(4):445-449, 2013.
- J.A. Bright, J.M. Curran, and J.S. Buckleton. "Investigation into the performance of different models for predicting stutter." *Forensic Science International: Genetics*, 7(4):422-427, 2013.
- J.A. Bright, D. Taylor, J.M. Curran, and J.S. Buckleton. "Developing allelic and stutter peak height models for a continuous method of DNA interpretation." *Forensic Science International: Genetics*, 7(2):296-304, 2013.
- T. Bille, J.A. Bright, and J. Buckleton. "Application of Random Match Probability Calculations to Mixed STR Profiles." *Journal of Forensic Sciences*, 58(2):474-485, 2013.
- K. Grisedale. "Comment on Kokshoorn, B, and Blankers, BJ 'Response to Grisedale, KS and van Daal, A: comparison of STR profiling from low template DNA extracts with and without the consensus profiling method'." *Investigative Genetics*, 4(1):2, 3 January 2013.
- B. Kokshoorn and B.J. Blankers. "Response to Grisedale and Van Daal: comparison of STR profiling from low template DNA extracts with and without the consensus profiling method." *Investigative Genetics*, 4(1):1, 3 January 2013.
- P. Gill and H. Haned. "A new methodological framework to interpret complex DNA profiles using likelihood ratios." *Forensic Science International: Genetics*, 7(2):251-263, 2013.
- H. Haned, K. Slooten, and P. Gill. "Exploratory data analysis for the interpretation of low template DNA mixtures." *Forensic Science International: Genetics*, 6(6):762-774, December 2012.
- A.A. Mitchell, J. Tamariz, K. O'Connell, N. Ducasse, Z. Budimlija, M. Prinz, and T. Caragine. "Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in." *Forensic Science International: Genetics*, 6(6):749-761, December 2012.
- V.L. Pascali and S. Merigioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.

H. Kelly, J.A. Bright, J.M. Curran, and J. Buckleton. "Modelling heterozygote balance in forensic DNA profiles." *Forensic Science International: Genetics*, 6(6):729-734, December 2012.

J.A. Bright, P. Gill, and J. Buckleton. "Composite profiles in DNA analysis." *Forensic Science International: Genetics*, 6(3):317-321, May 2012.

H. Kelly, J. Bright, J. Curran, and J. Buckleton. "The interpretation of low level DNA mixtures." *Forensic Science International: Genetics*, 6(2):191-197, 2012.

M.F.Z.P. Navarro. "Comparison of the performance of new short tandem repeat (STR) multiplex kits." PhD Dissertation, ResearchSpace@ Auckland, 2012.

Com. v. Foley, 38 A. 3d 882 – Pa: Superior Court 2012

http://scholar.google.com/scholar_case?case=15047633093833393986&hl=en&as_sdt=5,39&scioldt=0,39

J.K. Ryan. "Y STR interpretation". PhD Diss. 2011.

I.E. Dror and G. Hampikian. "Subjectivity and bias in forensic DNA mixture interpretation." *Science & Justice*, 51(4):204-208., 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.

R.C. Maher. "Forensische Audioanalyse." In: S. Weinzierl (ed) *Handbuch der Audiotechnik*, Springer Link, 2020.

A.M. Rodriguez, Z. Geradts, and M. Worring. "Likelihood Ratios for Deep Neural Networks in Face Comparison." *Journal of Forensic Sciences*, 65(4), 1169-1183, 2020.

A. Roth. (2020). "Admissibility of DNA Evidence in Court." In: H.A. Erlich, E. Stover, and T.J. White (eds) *Silent witness: forensic DNA analysis in criminal investigations and humanitarian disasters*. Oxford University Press, New York, NY, 291-310, 2020.

A. Nambiar, A. Bernardino, and J.C. Nascimento. "Gait-based Person Re-identification: A Survey." *ACM Computing Surveys*, 52(2), 2019.

R.C. Maher. "Forensic Interpretation." *Principles of Forensic Audio Analysis, Modern Acoustics and Signal Processing*. Springer, Cham, 2018.

M.A.C.S.S. Fernando. "Bayesian Models for PCR Stutter." Doctoral Thesis. The University of Auckland, 2017.

A.M. Nambiar. "Towards automatic long term Person Re-identification System in video surveillance." Doctoral thesis. Philosophy in Electrical and Computer Engineering, Universidade de Lisboa Instituto Superior Técnico, 2017.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

J. Ballantyne. "De-convolution of Body Fluid Mixtures: Cell Type Identification and Genetic Profiling of Micro-Dissected Cells." *National Center for Forensic Science*, Report, 2013.

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

D. Orozco. "TrueAllele[®] and STRmix[™]: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis, 2023.

D. Taylor. "Evaluation of Observations Given Activity Level Propositions." In: D. Taylor and B. Kokshoorn (eds) *Forensic DNA Trace Evidence Interpretation*. CRC Press, Taylor & Francis Group, 37-66, 2023.

M.D. Coble, T. Bille, and D. Podini. "Mixtures and Probabilistic Genotyping." In: D. Primorac and M. Schanfield (eds) *Forensic DNA Applications: An Interdisciplinary Perspective*. CRC Press, Taylor & Francis Group, 155-178, 2023.

M.S. Adamowicz, T.N. Rambo, and J.L. Clarke. "Internal Validation of MaSTR[™] Probabilistic Genotyping Software for the Interpretation of 2–5 Person Mixed DNA Profiles." *Genes*, 13(8):1429, 2022.

M.D. Edge and J.N. Matthews. "Open practices in our science and our courtrooms." *Trends in Genetics*, 38(2):113-115, 2022.

D. McNevin, K. Wright, M. Barash, S. Gomes, A. Jamieson, and J. Chaseling. "Proposed Framework for Comparison of Continuous Probabilistic Genotyping Systems amongst Different Laboratories." *Forensic Sciences*, 1(1):33-45, 2021.

C.M. Grgicak, S. Karkar, X. Yearwood-Garcia, L.E. Alfonse, K.R. Duffy, and D.S. Lun. "A large-scale validation of NOCI's A Posteriori Probability of the number of contributors and its integration into forensic interpretation pipelines." *Forensic Science International: Genetics*, 47:102296, 2020.

C.C.G. Benschop, A. Nijveld, F.E. Duijs, and T. Sijen. "An assessment of the performance of the probabilistic genotyping software EuroForMix: Trends in likelihood ratios and analysis of Type I & II errors." *Forensic Science International: Genetics*, 42:31-38, 2019.

F.M. Lucero. "DNA Mixture statistics using a likelihood ratio software tool: effect of variations in drop-out rates and number of contributors." Master's thesis. CUNY John Jay College, 2019.

B.A. Young, K.B. Gettings, B. McCord, and P.M. Vallone. "Estimating number of contributors in massively parallel sequencing data of STR loci." *Forensic Science International: Genetics*, 38:15-22, 2019

J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.

P.C. Lynch and R.W. Cotton. "Determination of the possible number of genotypes which can contribute to DNA mixtures: Non-computer assisted deconvolution should not be attempted for greater than two person mixtures." *Forensic Science International: Genetics*, 37:235-240, 2018.

D. Taylor, B. Kokshoorn, and A. Biedermann. "Evaluation of forensic genetics findings given activity level propositions: A review." *Forensic Science International: Genetics*, 36:34-49, 2018.

H. Swaminathan, M.O. Quershi, C.M. Grgicak, K. Duffy, and D.S. Lun. "Four model variants within a continuous forensic DNA mixture interpretation framework: Effects on evidential inference and reporting." *PLoS ONE*, 13(11):e0207599, 2018.

E. Rogers. "A novel method for cluster analysis of RNA structural data." Doctoral thesis. Georgia Institute of Technology, August 2018.

L.E. Alfonse, A.D. Garrett, D.S. Lun, K.R. Duffy, and C.M. Grgicak. "A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt." *Forensic Science International: Genetics*, 32:62-70, 2018.

C.M. Grgicak and D.S. Lun. "A Tool for Determining the Number of Contributors: Interpreting Complex, Compromised Low-Template DNA Samples." *Technical Report*, September 2017.

K.C. Peters, H. Swaminathan, J. Sheehan, K.R. Duffy, D.S. Lun, and C.M. Grgicak. "Production of high-fidelity electropherograms results in improved and consistent DNA interpretation: Standardizing the forensic validation process." *Forensic Science International: Genetics*, 31:160-170, 2017.

D. Taylor, J. Bright, H. Kelly, M. Lin, and J. Buckleton. "A fully continuous system of DNA profile evidence evaluation that can utilise STR profile data produced under different conditions within a single analysis." *Forensic Science International: Genetics*, 31:149-154, 2017.

M. Woldegebriel, A. Asten, A. Kloosterman, and G. Vivó-Truyols. "Probabilistic peak detection in CE-LIF for STR DNA typing." *Electrophoresis*, 2017.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

K.E. Rowan, G.A. Wellner, and C.M. Grgicak. "Exploring the Impacts of Ordinary Laboratory Alterations During Forensic DNA Processing on Peak Height Variation, Thresholds, and Probability of Dropout." *Journal of Forensic Sciences*, 61(1):177-185, 2016.

J.W. de Keijser, M. Malsch, E.T. Luining, M.W. Kranenbarg, and D.J.H.M. Lenssen. "Differential reporting of mixed DNA profiles and its impact on jurists' evaluation of evidence. An international analysis." *Forensic Science International: Genetics*, 23:71-82, 2016.

C.D. Marsden, N. Rudin, K. Inman, and K.E. Lohmueller. "An assessment of the information content of likelihood ratios derived from complex mixtures." *Forensic Science International: Genetics*, 22:64-72, 2016.

Tvedebrink, Torben. "DNA mixtures." In *Handbook of Forensic Genetics*. World Scientific Publishing Co Pte Ltd, 2016.

D.J. Balding and C.D. Steele. *Weight-of-Evidence for Forensic DNA Profiles*. (2nd edition). John Wiley & Sons, 2015.

K. Inman, N. Rudin, K. Cheng, C. Robinson, A. Kirschner, L. Inman-Semerau, and K.E. Lohmueller. "Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles." *BMC Bioinformatics*, 16(1):298, 2015.

C. Hu. "Determining the change in PCR efficiency with cycle number and characterizing the effect of serial dilutions on the DNA signal." Doctoral Dissertation, Boston University, 2015.

U.J. Monich, K. Duffy, M. Medard, V. Cadambe, L.E. Alfonse, and C. Grgicak. "Probabilistic characterisation of baseline noise in STR profiles." *Forensic Science International: Genetics*, 19:107-122, 2015.

- R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.
- R. Hedell, C. Duvfa, R. Ansell, P. Mostad, and J. Hedman. "Enhanced low-template DNA analysis conditions and investigation of allele dropout patterns." *Forensic Science International: Genetics*, 14:61-75, 2015.
- H. Kelly, J.A. Bright, J.S. Buckleton, and J.M. Curran. "A comparison of statistical models for the analysis of complex forensic DNA profiles." *Science & Justice*, 54(1):66-70, 2014.
- C.D. Steele and D.J. Balding. "Statistical Evaluation of Forensic DNA Profile Evidence." *Annual Review of Statistics and Its Application*, 1:361-384, 2014.
- L. Prieto, H. Haned, A. Mosquera, M. Crespillo, M. Alemañ, M.Aler, F. Alvarez, and P. Gill. "EuroforGen-NoE collaborative exercise on LRmix to demonstrate standardization of the interpretation of complex DNA profiles." *Forensic Science International: Genetics*, 9: 47-54, 2014.
- J. Buckleton, J.A. Bright, D. Taylor, I. Evett, T. Hicks, G. Jackson, and J.M. Curran. "Helping formulate propositions in forensic DNA analysis." *Science & Justice*, 54(4):258-261, 2014.
- H. Kelly. "The Application of Statistical Modelling to the Interpretation of Complex DNA Profiles." Doctoral thesis. Philosophy in Forensic Science, The University of Auckland. 2013.
- J.R. Iacona Jr. "Genomic DNA Isolation from Amplified Product for Recursive Genotyping of Low-template DNA Samples." PhD diss., Boston College, 2013.
- J.S. Gordon. "Characterization of Error Tradeoffs in Human Identity Comparisons: Determining a Complexity Threshold for DNA Mixture Interpretation." PhD dissertation. Harvard University School of Medicine, 2012.
- P. Gill and H. Haned. "A new methodological framework to interpret complex DNA profiles using likelihood ratios." *Forensic Science International: Genetics*, 7(2):251-263, 2013.
- A.A. Mitchell, J. Tamariz, K. O'Connell, N. Ducasse, Z. Budimlija, M. Prinz, and T. Caragine. "Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in." *Forensic Science International: Genetics*, 6(6):749-761, December 2012.
- V.L. Pascali and S. Meriglioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.

C.A. Rakay, J. Bregu, and C.M. Grgicak. "Maximizing allele detection: Effects of analytical threshold and DNA levels on rates of allele and locus drop-out." *Forensic Science International: Genetics*, 6(6):723-728, December 2012.

C.C.G. Benschop. "On the effects of sampling, analysis and interpretation strategies for complex forensic DNA research with focus on sexual assault cases." Doctoral thesis. University of Amsterdam, 2012.

M.C. Kline, E.L.R. Butts, C.R. Hill, M.D. Coble, D.L. Duewer, and J.M. Butler. "The new Standard Reference Material® 2391c: PCR-based DNA profiling standard." *Forensic Science International: Genetics Supplement Series*, 3(1):e355-e356, December 2011.

M.C. Kline, C.R.B. Hill, E. L. Butts, D. L. Duewer, M. D. Coble, and J. M. Butler. "Examination of DNA Mixture Proportion Variability Using Multiple STR Typing Kits and NIST Standard Reference Material® 2391c Component D." *Promega's Twenty Second International Symposium on Human Identification*. October 2011.

C.C.G. Benschop, C.P. van der Beek, H.C. Melland, A.G.M. van Gorp, A.A. Westen, and T. Sijen. "Low template STR typing: Effect of replicate number and consensus method on genotyping reliability and DNA database search results." *Forensic Science International: Genetics*, 5(4):316-328, August 2011.

T.A. Brettell, J.M. Butler, and J.R. Almirall. "Forensic Science." *Analytical Chemistry*, 83(12):4539–56, June 2011.

R. van Oorschot, K. Ballantyne, and R. Mitchell. "Forensic trace DNA: a review." *Investigative Genetics*, 1(1):1-17, 2010.

M. Priya. "Evaluation of the Interpretation Guidelines of Low Template DNA Profiles." 2010.

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

W.C. Thompson. "Uncertainty in probabilistic genotyping of low template DNA: A case study comparing STRMix™ and TrueAllele™." *J Forensic Sci.*, 68(3): 1049-1063, 2023.

National Research Council. "Evidence Integration for Hazard Identification." In: *Review of EPA's Integrated Risk Information System (IRIS) Process*. National Academies Press (US), 2014.

A.A. Mitchell, J. Tamariz, K. O'Connell, N. Ducasse, Z. Budimlija, M. Prinz, and T. Caragine. "Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in." *Forensic Science International: Genetics*, 6(6):749-761, December 2012.

D.H. Kaye. "The Report of the Expert Working Group on Human Factors in Latent Print Analysis--Latent Print Examination and Human Factors: Improving the Practice through a Systems Approach." NIST Interagency/Internal Report – (NISTIR) 7842, 2012.

J.R. Acker and R. Bellandi. "Firmament or Folly? Protecting the Innocent, Promoting Capital Punishment, and the Paradoxes of Reconciliation." *Justice Quarterly*, 29(2):287-307, 2011.

R. van Oorschot, K. Ballantyne, and R. Mitchell. "Forensic trace DNA: a review." *Investigative Genetics*, 1(1):1-17, 2010.

C.G.G. Aitken. "Seventh International Conference on Forensic Inference and Statistics, The University of Lausanne, Switzerland, August 2008." *Law, Probability and Risk*. 8(3):193-195, 2009.

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.

V.L. Pascali and S. Merigioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.

H. Haned, "*Forensim*: An open-source initiative for the evaluation of statistical methods in forensic genetics." *Forensic Science International: Genetics*, 5(4):265–268, August 2011.

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.

J.A. Roberts. "An anthropological study of war crimes against children in Kosovo and Bosnia-Herzegovina in the 1990s." Doctoral thesis. College of Medical, Veterinary and Life Sciences, University of Glasgow, 2011.

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

C.A. Ruddock. "Validation." *Wiley Encyclopedia of Forensic Science*, 2016.

J. Bright. "Informing biological models for probabilistic methods of DNA profile interpretation." Doctoral Dissertation. The University of Auckland, 2015.

D.H. Kaye, F.R. Bieber, and D. Primorac. "DNA as Evidence in the Courtroom." Penn State Law Research Paper No. 47, 2014.

D.H. Kaye. "The Double Helix and the Law of Evidence". Cambridge, MA: Harvard UP, 2010.

R. van Oorschot, K. Ballantyne, and R. Mitchell. "Forensic trace DNA: a review." *Investigative Genetics*, 1(1):1-17, 2010.

W.C. Thompson, "Painting the target around the matching profile: The Texas sharpshooter fallacy in forensic DNA interpretation," *Law, Probability and Risk* 8(3):257-276, 2009.

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

N.R. Phillips. "Expert Systems for High Throughput Analysis of Single Source Samples: A Comparison of GeneMarker® HID V1.71 and GeneMapper® ID V3.2 and Validation of GeneMapper® ID V3.2." Master's thesis. University of North Texas Health Science Center, 2009.

A. Christen, R.K. Roby, J.P. Jones, and T. Fenger. The National Institute of Justice's Expert Systems Testbed Project: Phase II, Analysis of Casework Samples. Poster session. In the proceedings of *Promega's Twenty First International Symposium on Human Identification*. Nashville, TN, 2006.

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.

R.C. Rice, D.V. Gil, A.M. Baratta, R.R. Frawley, S.Y. Hill, S.P. Farris, and G.E. Homanics. "Inter- and transgenerational heritability of preconception chronic stress or alcohol exposure: Translational outcomes in brain and behavior." *Neurobiology of Stress*, 29:100603, 2024.

R. Lusk. "The Development of Computational Approaches for Systems Genetics and Alternative Polyadenylation Studies and Their Application in Studying Genetic Predisposition to Alcohol Related Phenotypes." Doctoral thesis. University of Colorado Graduate School, 2021.

G.J. Lydall. "Genetic Association Studies of Alcohol Dependence." Doctoral thesis. University College London, 2019.

MC. Cornelis. "Genetic determinants of beverage consumption: Implications for nutrition and health." In: F. Toldra (ed) *Advances in Food and Nutrition Research*. Academic Press, 2019.

Y. Zhao, Y. Ge, and Z. Zheng. "Brain Imaging-Guided Analysis Reveals DNA Methylation Profiles Correlated with Insular Surface Area and Alcohol Use Disorder." *Alcoholism Clinical and Experimental Research*, 2019.

S. Sanchez-Roige, P. Fontanillas, S.L. Elson, The 23andMe Research Team, J.C. Gray, H. de Wit, L.K. Davis, J. MacKillop, and A.A. Palmer. "Genome-wide association study of alcohol use disorder identification test (AUDIT) scores in 20 328 research participants of European ancestry." *Addiction biology*, 24(1):121-131, 2019.

L. Vlahek. "Neuroznanstveni pristup alkoholizmu". Dissertation. University of Zagreb. School of Medicine. Chair of Psychiatry and Psychological Medicine, 2018.

L.B. Kozell, D. L. Denmark, N.A.R. Walter, and K.J. Buck. "Distinct roles for two chromosome 1 loci in ethanol withdrawal, consumption, and conditioned place preference." *Front. Genet.* 9:323, 2018.

C.K. Erickson. *The Science of Addiction: from Neurobiology to Treatment*. New York: W.W. Norton & Company, 2018.

W. Maier, I. Giegling, and D. Rujescu. "Genetik und Gen-Umwelt-Interaktionen bei psychischen Erkrankungen." In: Möller HJ., Laux G., Kapfhammer HP. (eds) *Psychiatrie, Psychosomatik, Psychotherapie. Springer Reference Medizin*. Springer, Berlin, Heidelberg, 2017.

D.F. Levey. "Towards personalized medicine in psychiatry: focus on suicide" Doctoral Dissertation. Indiana University, 2017.

I.R. Gizer, J.M. Otto, and J.M. Ellingson. "Molecular genetics of the externalizing spectrum." *Oxford Handbook of Externalizing Spectrum Disorders* 149-169, 2016.

L. Sun, C. Wang, and Y. Hu. "Utilizing mutual information for detecting rare and common variants associated with a categorical trait." *PeerJ*, 4:e2139, 2016.

S.Y. Hill, B.L. Jones, S.R. Steinhauer, N. Zezza, and S. Stiffler. "Longitudinal predictors of cannabis use and dependence in offspring from families at ultra high risk for alcohol dependence and in control families." *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, 171(3): 383-395, 2016.

- A.M. Manzardo, A. McGuire, and M.G. Butler. "Clinically relevant genetic biomarkers from the brain in alcoholism with representation on high resolution chromosome ideograms." *Gene*, 560(2):184-194, 2015.
- S.Y. Hill, B.L. Jones, N. Zezza, and S. Stiffler. "ACN9 and alcohol dependence: Family-based association analysis in multiplex alcohol dependence families." *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, 168(3):179-187, 2015.
- S.M. Malone, U. Vaidyanathan, S. Basu, M.B. Miller, M. McGue, and W.G. Iacono. "Heritability and molecular-genetic basis of the P3 event-related brain potential: A genome-wide association study." *Psychophysiology*, 51(12):1246-1258, 2014.
- J.W. O'Brien, S.D. Lichenstein, and S.Y. Hill. "Maladaptive Decision Making and Substance Use Outcomes in High-Risk Individuals: Preliminary Evidence for the Role of 5-HTTLPR Variation." *Journal of Studies on Alcohol and Drugs*, 75(4):643-652, 2014.
- L. Zuo, L. Lu, Y. Tan X. Pan, Y. Cai, X. Wang, J. Hong, C. Zhong, F. Wang, X. Zhang, L.A. Vanderlinden, B. Tabakoff, and X. Luo. "Genome-wide association discoveries of alcohol dependence." *American Journal on Addictions*, 23(6):526-539, 2014.
- G. Goldstein. "Neurocognitive Disorders." In *Adult Psychopathy and Diagnosis*, 2014.
- T.V. Morozova, T.F. Mackay, and R.R. Anholt. "Genetics and genomics of alcohol sensitivity." *Molecular Genetics and Genomics*, 1-17, 2014.
- C.T. Halpern, K.M. Harris and E.A. Whitsel. "Studying family transitions from a systems perspective: The role of biomarkers." *Emerging Methods in Family Research*. Springer International Publishing, 127-144, 2014.
- J. Daw, M. Shanahan, K.M. Harris, A. Smolen, B. Haberstick, and J.D. Boardman. Genetic Sensitivity to Peer Behaviors 5HTTLPR, Smoking, and Alcohol Consumption. *Journal of health and social behavior*, 54(1):92-108, March 2013.
- L.O. Bygren. "Intergenerational Health Responses to Adverse and Enriched Environments." *Annual review of public health*, 34:49-60, March 2013.
- C.B. Fisher and E.L. Harrington McCarthy. "Ethics in Prevention Science Involving Genetic Testing." *Prevention Science*, 14(3):310-318, June 2013.
- D.M. Dick and A. Agrawal. "The Genetics of Alcohol and Other Drug Dependence." *National Institute on Alcohol Abuse and Alcoholism*.
<http://pubs.niaaa.nih.gov/publications/arh312/111-118.htm>

K.J. Buck, L.C. Milner, D.L. Denmark, S.G. Grant, and L.B. Kozell. "Discovering Genes Involved in Alcohol Dependence and Other Alcohol Responses." *National Institute on Alcohol Abuse and Alcoholism*.

<http://pubs.niaaa.nih.gov/publications/arcr343/367-374.htm>

E.F. Saunders, N. Copeland, R.C. McEachin, S. Zöllner, and M.G. McInnis. "Genetic Linkage of Alcohol Abuse and Dependence in Families with Bipolar Disorder." https://portal.ncibi.org/access/content/group/eca0c49d-a5bb-4d9c-80b8-7a37b6d129cd/Bipolar%20Co-morbidity%20Alcohol/Alcohol_Linkage_Erika.pdf

Z. Zhao, A. Guo, E.J. van den Oord, F. Aliev, P. Jia, H.J. Edenberg, B.P. Riley, et al. "Multi-species data integration and gene ranking enrich significant results in an alcoholism genome-wide association study." *BMC Genomics*, 13(Suppl 8):S16, December 2012.

A. Adkins. "From Linkage to GWAS: A Multifaceted Exploration of the Genetic Risk for Alcohol Dependence." Dissertation. Virginia Commonwealth University. December 2012.

M. Rietschel and J. Treutlein. "The genetics of alcohol dependence." *Annals of the New York Academy of Sciences*. 1282:39-70, 2013.

R.H.C. Palmer, J.E. McGeary, S. Francazio, B.J. Raphael, A.D. Lander, A.C. Heath, and V.S. Knopik. "The genetics of alcohol dependence: Advancing towards systems-based approaches." *Drug and Alcohol Dependence*, 125(3):179-191, October 2012.

I.R. Gizer, C.L. Ehlers, C. Vieten, H.S. Feiler, D.A. Gilder, and K.C. Wilhelmsen. "Genome-wide linkage scan of antisocial behavior, depression, and impulsive substance use in the UCSF family alcoholism study." *Psychiatric Genetics*, 22(5):235-244, October 2012.

P. Lin, S.M. Hartz, J.C. Wang, A. Agrawal, T.X. Zhang, N. McKenna, K. Bucholz, A.I. Brooks, J.A. Tischfield, H.J. Edenberg, V.M. Hesselbrock, J.R. Kramer, S. Kuperman, M.A. Schuckit, A.M. Goate, L.J. Bierut, and J.P. Rice. "Copy Number Variations in 6q14. 1 and 5q13. 2 are Associated with Alcohol Dependence." *Alcoholism: Clinical and Experimental Research*, 36(9):1512-1518, September 2012.

S.Y. Hill, D.E. Weeks, B.L. Jones, N. Zezza, and S. Stiffler. "ASTN1 and alcohol dependence: Family-based association analysis in multiplex alcohol dependence families." *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, 159B(4):445-455, June 2012.

- S. Pochareddy and H.J. Edenberg. "Chronic Alcohol Exposure Alters Gene Expression in HepG2 Cells." *Alcoholism: Clinical and Experimental Research*, 36(6):1021-1033, June 2012.
- T.V. Morozova, D. Goldman, T.F. Mackay, and R.R. Anholt. "The genetic basis of alcoholism: multiple phenotypes, many genes, complex networks." *Genome Biology*, 13(2):239, February 2012.
- A.R. Wolen, C.A. Phillips, M.A. Langston, A.H. Putman, P.J. Vorster, N.A. Bruce, T.P. York, R.W. Williams, and M.F. Miles. "Genetic Dissection of Acute Ethanol Responsive Gene Networks in Prefrontal Cortex: Functional and Mechanistic Implications." *PLoS ONE*, 7(4):e33575, 2012.
- U.W. Preuss, C. Walther, and J.W. Wong. "Genetics of Alcohol Dependence in Humans: Recent Findings and Perspectives." *SUCHT-Zeitschrift für Wissenschaft und Praxis/Journal of Addiction Research and Practice*, 58(1):9-21, 2012.
- W.G. Iacono and S.M. Malone. "Developmental Endophenotypes: Indexing Genetic Risk for Substance Abuse With the P300 Brain Event-Related Potential." *Child development perspectives*, 5(4):239-247, December 2011.
- N.M. Zahr, R.L. Bell, H.N. Ringham, E.V. Sullivan, F.A. Witzmann, and A. Pfefferbaum. "Ethanol-induced changes in the expression of proteins related to neurotransmission and metabolism in different regions of the rat brain." *Pharmacology Biochemistry and Behavior*, 99(3):428-436, September 2011.
- M. Kimura and S. Higuchi. "Genetics of alcohol dependence." *Psychiatry and clinical neurosciences*, 65(3):213-225, April 2011.
- S.Y. Hill, K.D. Tessner, and M.D. McDermott. "Psychopathology in offspring from families of alcohol dependent female probands: A prospective study." *Journal of Psychiatric Research*, 45(3):285-294, March 2011.
- J.X. Cao, J. Hu, X.M. Ye, Y. Xia, C.A. Haile, T.R. Kosten, and X.Y. Zhang. "Association between the 5-HTR1B gene polymorphisms and alcohol dependence in a Han Chinese population." *Brain research*, 1376:1-9, February 2011.
- I.R. Gizer, C.L. Ehlers, C. Vieten, K.L. Seaton-Smith, H.S. Feiler, J.V. Lee, S.K. Segall, D.A. Gilder, K.C. Wilhelmsen. "Linkage scan of alcohol dependence in the UCSF Family Alcoholism Study." *Drug and alcohol dependence*, 13(2):125-132, January 2011.
- A.C. Heath, J.B. Whitfield, N.G. Martin, M.L. Pergadia, A.M. Goate, P.A. Lind, B.P. McEvoy, et al. "A quantitative-trait genome-wide association study of alcoholism risk in the community: findings and implications." *Biological psychiatry*. 70 (6):513-518, 2011.

H. Le-Niculescu, N.J. Case, L. Hulvershorn, S.D. Patel, D. Bowker, J. Gupta, R. Bell, H.J. Edenberg, R. Kuczenski, M.A. Geyer, Z.A. Rodd, and A.B. Niculescu. "Convergent functional genomic studies of omega-3 fatty acids in stress reactivity, bipolar disorder and alcoholism." *Translational Psychiatry*, 1:e4, 2011.

Z. Feng, W. W. L. Wong, X. Gao, and F. Schenkel. "Generalized genetic association study with samples of related individuals." *The Annals of Applied Statistics*, 5(3):2109-2130, 2011.

S.Y. Hill, K. Tessner, S. Wang, H. Carter, and M. McDermott. "Temperament at 5years of age predicts amygdala and orbitofrontal volume in the right hemisphere in adolescence." *Psychiatry Research: Neuroimaging*, 182(1):14-21, April 2010.

C.L. Ehlers, I.R. Gizer, C. Vieten, and K.C. Wilhelmsen. "Linkage analyses of cannabis dependence, craving, and withdrawal in the San Francisco family study." *Am. J. of Med. Genet*, 153B(3):802-811, April 2010.

N.K Hansell, A. Agrawal, J.B. Whitfield, K.I. Morely, S.D. Gordon, P.A. Lind, M.L. Pergadia, G.W. Montgomery, P.A.F. Madden, R.D. Todd, A.C. Heath, and N.G. Martin. "Linkage Analysis of Alcohol Dependence Symptoms in the Community." *Alcoholism: Clinical & Experimental Research*, 34(1):158-163, April 2010.

E-C. Tan, L. Lim, J-Y. Leong, J-Y. Lim, A. Lee, J. Yang, C-H. Tan, and M. Winslow. "Alcohol and Aldehyde Dehydrogenase Polymorphisms in Chinese and Indian Populations." *Substance Use & Misuse*, 45(1-2):1-14, January 2010.

S.Y. Hill. "Neural plasticity, human genetics, and risk for alcohol dependence." *International review of neurobiology*, 91:53-94, 2010.

K.D. Tessner and S.Y. Hill. "Neural Circuitry Associated with Risk for Alcohol Use Disorders." *Neuropsychology Review*, 20:1-20, 2010.

C.L. Ehlers, N.A.R. Walter, D.M. Dick, K.J. Buck, and J.C. Crabbe. "A comparison of selected quantitative trait loci associated with alcohol use phenotypes in humans and mouse models." *Addiction Biology*, 15(2):185-199, 2010.

N.J. Case. "Effects of Omega-3 Fatty Acids on Rodent Models of Bipolar Disorder and Alcoholism." Master's thesis. Indiana University, 2010.

D.M. Dick, C. Prescott, and M. McGue. "The Genetics of Substance Use and Substance Use Disorders." *Handbook of Behavior Genetics*. Springer New York:433-453, 2009.

J. Treutlein, S. Cichon, M. Ridinger, N. Wodarz, M. Soyka, P. Zill, W. Maier, R. Moessner, W. Gaebel, N. Dahmen, C. Fehr, N. Scherbaum, M. Steffens, K.U. Ludwig, J. Frank, H.E. Wichmann, S. Schreiber, N. Dragano, W.H. Sommer, F.

Leonardi-Essmann, A. Lourdasamy, P. Gebicke-Haerter, T.F. Wienker, P.F. Sullivan, M.M. Nöthen, F. Kiefer, R. Spanagel, K. Mann, and M. Rietschel. "Genome-wide Association Study of Alcohol Dependence." *Arch Gen Psychiatry*, 66(7):773-784, 2009.

J.D. Grant, A. Agrawal, K.K. Bucholz, P.A.F. Madden, M.L. Pergadia, E.C. Nelson, M.T. Lynskey, R.D. Todd, A.A. Todorov, N.K. Hansell, J.B. Whitfield, N.G. Martin, and A.C. Heath. "Alcohol Consumption Indices of Genetic Risk for Alcohol Dependence." *Biological Psychiatry*, 66(8):795-800, 2009.

S.Y. Hill, S. Wang, B. Kostelnik, H. Carter, B. Holmes, M. McDermott, N. Zezza, S. Stiffler, and M.S. Keshavan. "Disruption of Orbitofrontal Cortex Laterality in Offspring from Multiplex Alcohol Dependence Families." *Biological Psychiatry*, 65(2):129-136, 2009.

S.Y. Hill, S.R. Steinhauser, J. Locke-Wellman, and R. Ulrich. "Childhood Risk Factors for young Adult Substance Dependence Outcome in Offspring from Multiplex Alcohol Dependence Families: A Prospective Study." *Biological Psychiatry*, 66(8):750-757, October 2009.

C.L. Ehlers, D.A. Gilder, I.R. Gizer, and K.C. Wilhelmsen. "GENETIC STUDY: Heritability and a genome-wide linkage analysis of a Type II/B Cluster Construct for cannabis dependence in an American Indian community." *Addict Biol*, 14(3):338-348, July 2009.

A-Y. Guo, B.T. Webb, M.F. Miles, M.P. Zimmerman, K.S. Kendler, and Z. Zhao. "ERGR: An ethanol-related gene resource." *Nucleic Acids Research*, 37(Suppl 1):D840-D845, 2009.

N.K Hansell, A. Agrawal, J.B. Whitfield, K.I. Morely, S.D. Gordon, P.A. Lind, M.L. Pergadia, G.W. Montgomery, P.A.F. Madden, R.D. Todd, A.C. Heath, and N.G. Martin. "Can We Identify Genes For Alcohol Consumption In Samples Ascertained For Heterogeneous Purposes?" *Alcoholism: Clinical & Experimental Research*, 33(4):729-739, April 2009.

C.L. Ehlers, D.A. Gilder, I.R. Gizer, and K.C. Wilhelmsen. "GENETIC STUDY: Heritability and a genome-wide linkage analysis of a Type II/B cluster construct for cannabis dependence in an American Indian community." *Addiction Biology*, 14(3):338-348, 2009.

T. Hallikainen. "Serotonin and dopamine Gene Polymorphisms and Alcohol Consumption." Doctoral Dissertation. University of Kuopio, 2009.

S.Y. Hill, S. Shen, L. Lowers, J. Locke-Wellman, A.G. Matthews, and M. McDermott. "Psychopathology in offspring from multiplex alcohol dependence families with and without parental alcohol dependence: A prospective study during childhood and adolescence." *Psychiatry Research*, 160(2):155-166, 2008.

H-C. Yang, H-Y. Hsieh, and C.S.J. Fann. "Kernel-Based Association Test." *Genetics*, 179:1057-1068, 2008.

S.Y. Hill, E.K. Hoffman, N. Zezza, A. Thalamuthu, D.E. Weeks, A.G. Matthews, and I. Mukhopadhyay. "Dopaminergic mutations: Within-family association and linkage in multiplex alcohol dependence families." *Am. J. Med. Genet*, 147B(4):517-526, 2008.

D. Ball. "Addiction science and its genetics." *Addiction*, 103(3):360-367, 2008.

D.M. Dick, F. Aliev, J.C. Wang, S. Saccone, A. Hinrichs, S. Bertelsen, J. Budde, N. Saccone, T. Foroud, J. Nurnberger Jr., X. Xuei, P.M. Conneally, M. Schuckit, L. Almasy, R. Crowe, S. Kuperman, J. Kramer, J.A. Tischfield, V. Hesselbrock, H.J. Edenberg, B. Porjesz, J.P. Rice, L. Bierut, and A. Goate. "A Systematic Single Nucleotide Polymorphism Screen to Fine-Map Alcohol Dependence Genes on Chromosome 7 Identifies Association With a Novel Susceptibility Gene *ACN9*." *Biological Psychiatry*, 63(11):1047-1053, 2008.

R. Plomin, J.C. DeFries, G.E. McClearn, and P. McGuffin. *Behavioral genetics*. Worth Publishers, 2008.

F. Ducci and D. Goldman. "Genetic approaches to addiction: genes and alcohol." *Addiction*, 103(9):1414-1428, 2008.

H. Le-Niculescu, M.J. McFarland, C.A. Ogden, Y. Balaraman, S. Patel, J. Tan, Z.A. Rodd, M. Paulus, M.A. Geyer, H.J. Edenberg, S.J. Glatt, S.V. Faraone, J.I. Nurnberger, R. Kuczenski, M.T. Tsuang, and A.B. Niculescu. "Phenomic, Convergent Functional Genomic, and biomarker studies in a stress-reactive genetic animal model of bipolar disorder and co-morbid alcoholism." *Am. J. Med. Genet*, 147B(2):134-166, 2008.

S. Roh, S. Matsushita, and S. Higuchi. "Genetic influences on alcohol use and dependence," in *Research on the Neurobiology of Alcohol Use Disorders* (Sher L ed), pp. 291-320. Nova Science Publishers, New York. 2008

Z.A. Rodd, B.A. Bertsch, W.N. Strother, H. Le-Niculescu, Y. Balaraman, E. Hayden, R.E. Jerome, L. Lumeng, J.I. Nurnberger Jr, H.J. Edenberg, W.J. McBride, and A.B. Niculescu. "Candidate genes, pathways and mechanisms for alcoholism: an expanded convergent functional genomics approach." *The Pharmacogenomics Journal*. 7:222-256, 2007.

C.L. Ehlers and K.C. Wilhelmsen. "Genomic screen for substance dependence and body mass index in southwest California Indians." *Genes, Brain, and Behavior*, 6(2):184-191, 2007.

A.G. Matthews, E.K. Hoffman, N. Zezza, S. Stiffler, and S.Y. Hill. "The role of the GABRA2 polymorphism in multiplex alcohol dependence families with minimal comorbidity: Within-family association and linkage analyses." *J. of Studies on Alcohol and Drugs*, 68(5):625-633, 2007.

C.K. Erickson. *The Science of Addiction: from Neurobiology to Treatment*. New York: W.W. Norton &, 2007. Print.

A. Szczepankiewicz, M. Dmitrzak-Weglarz, M. Skibinska, A. Slopian, A. Leszczynska-Rodziewicz, P. Czerski, and J. Hauser. "Study of Dopamine Receptors Genes Polymorphisms in Bipolar Patients with Comorbid Alcohol Abuse." *Alcohol & Alcoholism*, 42(2):70-74, 2007.

H. Le-Niculescu, Y. Balaraman, S. Patel, J. Tan, K. Sidhu, R.E. Jerome, H.J. Edenberg, R. Kuczenski, M.A. Geyer, J.I. Nurnberger, S.V. Faraone, M.T. Tsuang, and A.B. Niculescu. "Towards understanding the schizophrenia code: An expanded convergent functional genomics approach." *Am. J. Med. Genet*, 144B(2):129-158, 2007.

C.A. Prescott, P.F. Sullivan, P-H. Kuo, B.T. Webb, J. Vittum, D.G. Patterson, D.L. Thiselton, J.M. Myers, M. Devitt, L.J. Halberstadt, V.P. Robinson, M.C. Neale, E.J. van den Oord, D. Walsh, B.P. Riley, and K.S. Kendler. "Genomewide linkage study in the Irish affected sib pair study of alcohol dependence: evidence for a susceptibility region for symptoms of alcohol dependence on chromosome 4." *Molecular Psychiatry*, 11(6):603-611, 2006.

B.Q. Doan, A.J.M. Sorant, C.E. Frangakis, J.E. Bailey-Wilson, and Y.Y. Shugart. "Covariate-based linkage analysis: application of a propensity score as the single covariate consistently improves power to detect linkage." *Eur. J. of Human Genetics*, 14:1018-1026, 2006.

C.L. Ehlers and K.C. Wilhelmsen. "Genomic screen for loci associated with tobacco usage in Mission Indians." *BMC Medical Genetics*. 7:9, 2006.

P-H. Kuo, M.C. Neale, B.P. Riley, B.T. Webb, P.F. Sullivan, J. Vittum, D.G. Patterson, D.L. Thiselton, E.J. Van Den Oord, D. Walsh, K.S. Kendler, and C.A. Prescott. "Identification of Susceptibility Loci for Alcohol-Related Traits in the Irish Affected Sib Pair Study of Alcohol Dependence." *Alcoholism: Clin and Exp Res*, 30(11):1807-1816, 2006.

S. Higuchi, S. Matsushita, and H. Kashima. "New findings on the genetic influences on alcohol use and dependence." *Current Opinion in Psychiatry*, 19(3):253-265, 2006.

C.A. Prescott, P.A.F. Madden, and M.C. Stallings. "Challenges in Genetic Studies of the Etiology of Substance Use and Substance Use Disorders: Introduction to the Special Issue." *Behavior Genetics*, 36(4):473-482, 2006.

D.M. Dick and L.J. Bierut. "The genetics of alcohol dependence." *Current Psychiatry Reports*, 8(2):151-157, 2006.

B.Q. Doan, C.E. Frangakis, Y.Y. Shugart, and J.E. Bailey-Wilson. "Application of the propensity score in a covariate-based linkage analysis of the Collaborative Study on the Genetics of Alcoholism." *BMC Genetics*, 6(Supp 1):S33, 2005.

B.H. Reck, N. Mukhopadhyay, H-J. Tsai, and D.E. Weeks. "Analysis of alcohol dependence phenotype in the COGA families using covariates to detect linkage." *BMC Genetics*, 6(Supp 1):S143, 2005.

S.Y. Hill, S. Shen, J.L. Wellman, E. Rickin, and L. Lowers. "Offspring from families at high risk for alcohol dependence: increased body mass index in association with prenatal exposure to cigarettes but not alcohol." *Psychiatry research*, 135(3):203, 2005.

K.C. Wilhelmsen, G.E. Swan, L.S-C. Cheng, C.N. Lessov-Schlaggar, C.I. Amos, H.S. Feiler, K.S. Hudmon, H.Z. Ring, J.A. Andrews, E. Tildesley, N.L. Benowitz, and H. Hops. "Support for Previously Identified Alcoholism Susceptibility Loci in a Cohort Selected for Smoking Behavior." *Alcoholism: Clinical and Experimental Research*, 29(12):2108-2115, 2005.

C.A. Prescott, H.H. Maes, and K.S. Kendler. "Genetics of substance use disorders." In K. S. Kendler, & L. J. Eaves (Eds.), *Psychiatric Genetics*, vol. 24 (pp. 167 – 196). Washington, DC: American Psychiatric Publishing, Inc. 2005.

U.W. Preuss, G. Schultz, W.M. Wong, A.B. Watzke, S. Barnow, and J. Zimmerman. "Current Perspectives in Genetics and Genomics of Alcohol Dependence." *Current Genomics*, 5(7):601-612, November 2004.

K. Kadash, B.E. Kozlowski, L.A. Biega, B.W. and Duceman. "Validation study of the TrueAllele® automated data review system." *Journal of Forensic Sciences*, 49(4):1-8, 2004.

D. Orozco. "TrueAllele® and STRmix™: A Comparison of Two Probabilistic Genotyping Software Programs in Forensic DNA Profile Analysis." Master's thesis. University of California Davis. 2023.

H. Simayijiang and J. Yan. "Recent Developments in Forensic DNA Typing." *Journal of Forensic Science and Medicine*, 9(4):353-359, 2023.

A. Ivanova-Pozdejeva, A. Kivistik, L. Kübarsepp, T. Tähtjärv, A. Tsahkna, E. Droz, and K. Laanemets. "Fingerprinting of potato genotypes from Estonian Genebank collection using SSR markers." *Potato Research*, 65(1): 153-170, 2022.

A. Badiye, N. Kapoor, P. Kathane, and R.K. Shukla. "Quality Control in Forensic DNA Typing." In: P. Shrivastava, H.R. Dash, J.A. Lorente, and J. Imam (eds) *Forensic DNA Typing: Principles, Applications and Advancements*, Springer Link, 585-605, 2020.

M. Prinz and R. Lessig. "Forensic DNA Analysis." *Handbook of Forensic Medicine*, 1141-1183, 2014.

M.M. Holland and W. Parson. "GeneMarker® HID: A Reliable Software Tool for the Analysis of Forensic STR Data." *Journal of Forensic Sciences*, 56(1), 2011.

R.M. Fourney, A.N. DesRoches, and J.L. Buckle. "Biological Evidence and Forensic DNA Profiling." In: *Interpol's Forensic Science Review*. CRC Press, 591-672, 2010.

B. Budowle and A. van Daal. "Extracting evidence from forensic DNA analyses: future molecular biology directions." *BioTechniques*, 46(5), 2009.

N.R. Phillips. "Expert Systems for High Throughput Analysis of Single Source Samples: A Comparison of GeneMarker® HID V1.71 and GeneMapper® ID V3.2 and Validation of GeneMapper® ID V3.2." *Theses and Dissertations*. University of North Texas Health Science Center, 2009.

M.G. Brevnov, H.S. Pawar, J. Mundt, L.M. Calandro, M.R. Furtado, and J.G. Shewale. "Developmental Validation of the PrepFiler™ Forensic DNA Extraction Kit for Extraction of Genomic DNA from Biological Samples," *Journal of Forensic Sciences*, 54(3):599-607, 2009.

T. Power, B. McCabe, and S.A. Harbinson. "FaSTR DNA: A new expert system for forensic DNA analysis." *Forensic Science International: Genetics*, 2(3):159-165, 2008.

D.L. Duewer and J.M. Butler. "Multiplex_QA: An exploratory quality assessment tool for multiplexed electrophoretic assays." *Electrophoresis*, 27(19):3735-3746, 2006.

T.A. Brettell, J.M. Butler, and R. Saferstein. "Forensic Science." *Analytical Chemistry*. 77(12):3839-3860, 2005.

R.K. Roby, J.P. Jones, B. Tincher, A. Christen, A. Webb, and T. Fenger. "The National Institute of Justice's Expert Systems Testbed Project". *In Proceedings of the Sixteenth Symposium on Human Identification*, 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.

R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.

V.L. Pascali and S. Merigioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.

W.C. Thompson, "Painting the target around the matching profile: The Texas sharpshooter fallacy in forensic DNA interpretation," *Law, Probability and Risk* 8(3):257-276, 2009.

B. Leclair and T. Scholl. "Application of automation and information systems to forensic genetic specimen processing." *Expert Review of Molecular Diagnostics*, 5(2):241-250, 2005.

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

R. Wu, H. Chen, R. Li, Y. Zang, X. Shen, B. Hao, Q. Wang, and H. Sun. "Pairwise kinship testing with microhaplotypes: Can advancements be made in kinship inference with these markers?" *Forensic Science International*, 325:110875, 2021.

E.N. Ganesh. "Application of Nanotechnology in Forensic Science." *International Journal of Research in Advanced Technology*, 1(1):1-4, 2016.

P. Fattorini. "Identificazione di linee guida per l'analisi genetico-forense mediante utilizzo di DNA degradati in vitro." Doctoral thesis. Università degli studi di Trieste, 2015.

Y. Chen. "Forensic Applications of Nanotechnology." *Journal of the Chinese Chemical Society*, 58(6):828-835, 2011.

M. Olejniczak and W.J. Krzyzosiak. "Genotyping of simple sequence repeat factors implicated in shadow band generation revisited." *Electrophoresis*, 27(19):3724-3734, 2006.

R.G.H. Cotton. "Mutation detection 2001: Novel technologies, developments and applications for analysis of the human genome." *Human Mutation*, 19(4):313-314, 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.

F. Sessa, M. Salerno, and C. Pomara. "The Interpretation of Mixed DNA Samples: Historical Perspective and Current Developments." In: H.R. Dash, P. Shrivastava, J.A. Lorente (eds) *Handbook of DNA Profiling*. Springer, Singapore, 997-1017, 2022.

S.N. Mandape, U. Smart, J.L. King, M. Muenzler, K.B. Kapema, B. Budowle, and A.E. Woerner. "MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures." *Forensic Science International: Genetics*, 55:102568, 2021.

J. Valtl, U.J. Mönich, D.S. Lun, J. Kelley, and C.M. Grgicak. "A series of developmental validation tests for Number of Contributors platforms: Exemplars using NOCI and a neural network." *Forensic science international: Genetics*, 54:102556, 2021.

C.M. Grgicak, S. Karkar, X. Yearwood-Garcia, L.E. Alfonse, K.R. Duffy, and D.S. Lun. "A large-scale validation of NOCI's A Posteriori Probability of the number of contributors and its integration into forensic interpretation pipelines." *Forensic Science International: Genetics*, 47:102296, 2020.

J. Mortera. "DNA Mixtures in Forensic Investigations: The Statistical State of the Art." *Annual Review of Statistics and Its Application*, 7:111-142, 2020.

H. Park. "Forensic Bioinformatic Study for Human Identification of Crime Scene Evidences." Doctoral thesis. Seoul National University Graduate School, 2019.

F.M. Lucero. "DNA Mixture statistics using a likelihood ratio software tool: effect of variations in drop-out rates and number of contributors." Master's thesis. CUNY John Jay College, 2019.

M.D. Coble and J.A. Bright. "Probabilistic genotyping software: An overview." *Forensic Science International: Genetics*, 38:219-224, 2019.

S. Norsworthy, D.S. Lun, and C.M. Grgicak. "Determining the number of contributors to DNA mixtures in the low-template regime: Exploring the impacts of sampling and detection effects." *Legal Medicine*, 32:1-8, 2018.

H. Swaminathan, M.O. Quershi, C.M. Grgicak, K. Duffy, and D.S. Lun. "Four model variants within a continuous forensic DNA mixture interpretation framework: Effects on evidential inference and reporting." *PLoS ONE*, 13(11):e0207599, 2018.

L.E. Alfonse, A.D. Garrett, D.S. Lun, K.R. Duffy, and C.M. Grgicak. "A large-scale dataset of single and mixed-source short tandem repeat profiles to inform human identification strategies: PROVEDIt." *Forensic Science International: Genetics*, 32:62-70, 2018.

C.M. Grgicak and D.S. Lun. "A Tool for Determining the Number of Contributors: Interpreting Complex, Compromised Low-Template DNA Samples." *Technical Report*, September 2017.

K.R. Duffy, N. Gurrarn, K.C. Peters, G. Wellner, and C.M. Grgicak. "Exploring STR signal in the single-and multicopy number regimes: Deductions from an in silico model of the entire DNA laboratory process." *Electrophoresis*, 38(6):855-868, 2017.

W. Yao, C. Mei, X. Nan, and L. Hui. "Evaluation and comparison of in vitro degradation kinetics of DNA in serum, urine and saliva: A qualitative study." *Gene*, 590(1):142-148, 2016.

K.E. Rowan, G.A. Wellner, and C.M. Grgicak. "Exploring the Impacts of Ordinary Laboratory Alterations During Forensic DNA Processing on Peak Height Variation, Thresholds, and Probability of Dropout." *Journal of Forensic Sciences*, 61(1):177-185, 2016.

L.M. Taranow. "Exploring the sources of peak height reduction during low-template, compromised DNA data analysis." Doctoral Dissertation, Boston University, 2016.

L.E. Alfonse, A.D. Garrett, H. Swaminathan, K.C. Peters, G. Wellner, X. Yearwood-Garcia, L.M. Taranow, J. Sheehan, S.E. Norsworthy, U. Mönich, D.S. Lun, K.R. Duffy, M. Médard, R.W. Cotton, and C.M. Grgicak. "The Development and Release of a Collection of Computational Tools and a Large-Scale Empirical Data Set for Validation: The PROVEDIt Initiative." International Symposium on Human Identification, 2016.

J.M. Butler. "Proceedings of the 2015 International Symposium on Forensic Science Error Management." International Symposium on Forensic Science Error Management; NIST Special Publication 1206, 2016.

D.J. Balding and C.D. Steele. *Weight-of-Evidence for Forensic DNA Profiles*. (2nd edition). John Wiley & Sons, 2015.

- P. Gill, H. Haned, O. Bleka, O. Hansson, G. Dorum, and T. Egeland. "Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches- Twenty years of research and development." *Forensic Science International: Genetics*, 18:100-117, 2015.
- R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.
- R. Puch-Solis and T. Clayton. "Evidential evaluation of DNA profiles using a discrete statistical model implemented in the DNA LiRa software." *Forensic Science International: Genetics*, 11:220-228, 2014.
- T. Graversen and S. Lauritzen, S. "Estimation of parameters in DNA mixture analysis." *Journal of Applied Statistics*. 40(11): 2423-2436, 2013.
- C.D. Steele and D.J. Balding. "Statistical Evaluation of Forensic DNA Profile Evidence." *Annual Review of Statistics and Its Application*, 1:361-384, 2014.
- C.C. Benschop and T. Sijen. "LoCIM-tool: An expert's assistant for inferring the major contributor's alleles in mixed consensus DNA profiles." *Forensic Science International: Genetics*, 11:154-165, 2014.
- N. Kaur, A.E. Fonneløp, and T. Egeland. "Regression Models for DNA-mixtures." *Forensic Science International: Genetics*, 11:105-110, 2014.
- V.L. Pascali and S. Merigioli. "Stochastic effects at balanced mixtures: A calibration study." *Forensic Science International: Genetics*, 8(1):113-125, 2014.
- H. Kelly. "The Application of Statistical Modelling to the Interpretation of Complex DNA Profiles." Doctoral thesis. Philosophy in Forensic Science, The University of Auckland, 2013.
- J.R. Iacona Jr. "Genomic DNA Isolation from Amplified Product for Recursive Genotyping of Low-template DNA Samples." PhD diss., Boston College, 2013.
- J.S. Dunn. "Characterization of the effects associated with amplification of degraded DNA using traditional and mini-STRs." Master's thesis. Boston University School of Medicine, 2012.
- A.A. Mitchell, J. Tamariz, K. O'Connell, N. Ducasse, Z. Budimlija, M. Prinz, and T. Caragine. "Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in." *Forensic Science International: Genetics*, 6(6):749-761, December 2012.

- V.L. Pascali and S. Merigioli. "Joint Bayesian analysis of forensic mixtures." *Forensic Science International: Genetics*, 6(6):735-748, December 2012.
- P. Gill, L. Gusmão, H. Haned, W.R. Mayr, N. Morling, W. Parson, L. Prieto, M. Prinz, H. Schneider, P.M. Schneider, and B.S. Weir. "DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods." *Forensic Science International: Genetics*, 6(6):679-688, December 2012.
- Abraham. "Remotely controlled implantable transducer and associated displays and controls." U.S. Patent # 8,235,903. August 2012.
- T. Tvedebrink, P.S. Eriksen, H.S. Mogensen, and N. Morling. "Identifying contributors of DNA mixtures by means of quantitative information of STR typing." *Journal of Computational Biology*, 19(7):887-902, July 2012.
- Wang, et al. "Least-square deconvolution (LSD): A method to resolve DNA mixtures." U.S. Patent # 8,140,271. March 2012.
- H. Kelly, J. Bright, J. Curran, and J. Buckleton. "The interpretation of low level DNA mixtures." *Forensic Science International: Genetics*, 6(2):191-197, 2012.
- T. Egeland, A.E. Fonneløp, P.R. Berg, M. Kent, and S. Lien. "Complex mixtures: A critical examination of a paper by Homer et al." *Forensic Science International: Genetics*, 6(1):64-69, January 2012.
- D. Paoletti, D. Krane, T. Doom, and M. Raymer. "Inferring the number of contributors to mixed DNA profiles." *Computational Biology and Bioinformatics*, 9(1):113-122, January 2012.
- R.G. Cowell, S.L. Lauritzen, and J. Mortera. "MAIES: A tool for DNA mixture analysis." arXiv preprint arXiv:1206.6816. 2012
- N. Masca, P.R. Burton, and N.A. Sheehan. "Participant identification in genetic association studies: improved methods and practical implications." *International Journal of Epidemiology*, 40(6):1629-1642, 2011.
- J. Perez, A.A. Mitchell, N. Ducasse, J. Tamariz, and T. Caragine. "Estimating the number of contributors to two-, three-, and four-person mixtures containing DNA in high template and low template amounts." *Croatian Medical Journal*, 52(3):314-326, 2011.
- H. Haned, L. Pène, F. Sauvage, and D. Pontier. "The predictive value of the maximum likelihood estimator of the number of contributors to a DNA mixture." *Forensic Science International: Genetics*, 5(4):281-284, August 2011.

Y. Chung and W.K. Fung. "The evidentiary values of "cold hits" in a DNA database search on two-person mixture." *Science & Justice*, 51(1):10-15, March 2011.

D. Fox. "The second generation of racial profiling." *American Journal of Criminal Law*, 38:49-79, 2010.

Wang, et al. "Least-square deconvolution (LSD): A method to resolve DNA mixtures." U.S. Patent # 7,860,661. Dec 2010.

T. Tvedebrink. "Statistical Aspects of Forensic Genetics: Models for Qualitative and Quantitative STR Data." Doctoral thesis. Department of Mathematical Sciences, Aalborg University, Denmark, 2010.

T. Tvedebrink, P.S. Eriksen, H.S. Morgensen, and N. Morling. "Evaluating the weight of evidence by using quantitative short tandem repeat data in DNA mixtures." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 59(5):855-874, November 2010.

Tvedebrink, et al. "Computer-assisted method of analyzing a DNA mixture." U.S. Patent Application Publication #2010/0198522. Aug. 2010.

Wang, et al. "Least-square deconvolution (LSD): A method to resolve DNA mixtures." U.S. Patent #7,672,789. Mar. 2010.

Birdwell, et al. "Interaction method with an expert system that utilizes stutter peak rule." U.S. Patent #7,664,719. Feb. 2010.

D.J. Balding and J. Buckleton. "Interpreting low template DNA profiles." *Forensic Science International: Genetics*, 4(1):1-10, December 2009.

Birdwell, et. al. "Method of expert system analysis of DNA electrophoresis data." U.S. Patent #7,624,087. Nov. 2009.

C.M. Hennekens. "The effects of differential extraction conditions on the premature lysis of spermatozoa." Master's thesis. Boston University School of Medicine, 2009.

J.M. Curran. Use of Knowledge-Based Systems in Forensic Science. *Wiley Encyclopedia of Forensic Science*. John Wiley & Sons. 2009.

J.S. Buckleton. "Mixture Interpretation: DNA." *Wiley Encyclopedia of Forensic Science*. John Wiley & Sons. 2009.

J.S. Buckleton. "Interpretation: Low Template DNA." In *Wiley Encyclopedia of Forensic Science*. John Wiley & Sons. 2009.

- Y. Choy. "Statistical evaluation of mixed DNA stains." Thesis. University of Hong Kong, 2009.
- R.G. Cowell. "Validation of an STR peak area model." *Forensic Science International: Genetics*, 3(3):193-199, June 2009.
- D.L. Faigman, et. al. *Modern Scientific Evidence: Forensics*. Eagan, MN. Thomson/West. 2008.
- J. Curran. "A MCMC method for resolving two person mixtures." *Science & Justice*, 48(4):168-177, December 2008.
- W.K. Fung and Y. Hu. *Statistical DNA Forensics: Theory, Methods, and Computation*. Chichester, England: John Wiley & Sons, 2008.
- J.R. Gilder. "Computational methods for the objective review of forensic DNA testing results." Wright State University, 2007.
- S.J. Walsh. Current and future trends in forensic molecular biology. *Molecular Forensics*. Chichester, England: John Wiley & Sons, 2007.
- B. Leclair and T. Scholl. Laboratory information systems for forensic analysis of DNA evidence. *Molecular Forensics*. Chichester, England: John Wiley & Sons, 2007.
- R. Rapley and D. Whitehouse, ed. *Molecular Forensics*. Chichester, England: John Wiley & Sons, 2007.
- R.G. Cowell, S.L. Lauritzen, and J. Mortera. "A gamma model for {DNA} mixture analyses." *Bayesian Analysis*, 2(2):333-348, 2007.
- R.G. Cowell, S.L. Lauritzen, and J. Mortera. "Identification and separation of DNA mixtures using peak area information." *Forensic Science International*. February 2007; 166(1): 28-34.
- Wang, et al. "Least-square deconvolution (LSD): A method to resolve DNA mixtures." U.S. Patent #7,162,372. Jan. 2007.
- T. Wang, N. Xue, and J.D. Birdwell. "Least-Square Deconvolution: A Framework for Interpreting Short Tandem Repeat Mixtures." *Journal of Forensic Sciences*, 51(6):1284-1297, November 2006.
- Wang, et al. "Least-square deconvolution (LSD): A method to resolve DNA mixtures." U.S. Patent Application Publication # 2006/0190194. Aug. 2006.

R. A. Wickenheiser. "General guidelines for categorization and Interpretation of mixed DNA profiles." *Canadian Society of Forensic Science Journal*, 39(4):179-216, 2006.

R.G. Cowell, S.L. Lauritzen, and J. Mortera. "MAIES: A Tool for DNA Mixture Analysis." *Proceedings of the 22nd Annual Conference on Uncertainty in Artificial Intelligence*. AUAI, 90-97, 2006.

P. Gill, C.H. Brenner, J.S. Buckleton, A. Carracedo, M. Krawczak, W.R. Mayr, N. Morling, M. Prinz, P.M. Schneider, and B.S. Weir. "DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures." *Forensic Science International*, 160(2-3):90-101, July 2006.

G.W. Beecham. "Statistical methods for the analysis of forensic DNA mixtures." Thesis. NC State University, July 2006.

S. Shrestha, S.A. Strathdee, K.W. Broman, and M.W. Smith. "Unknown biological mixtures evaluation using STR analytical quantification." *Electrophoresis*, 27(2):409-415, January 2006.

D.L. Faigman. *Modern Scientific Evidence: The Law and Science of Expert Testimony*. Vol. 3. Thomson/West, 2006.

J. Buckleton, C.M. Triggs, and S. J. Walsh, ed. *Forensic DNA Evidence Interpretation*. CRC Press. 2005.

G. Shutler. "An Overview of Historical Developments in Forensic DNA Analysis." in *Forensic Botany: Principles and Applications to Criminal Casework*. CRC Press. 2005.

D.R. Paoletti, T.E. Doom, C.M. Krane, M.L. Raymer, and D.E. Krane. "Empirical Analysis of the STR Profiles Resulting from Conceptual Mixtures." *Journal of Forensic Sciences*, 50(6):1-6, November 2005.

B. Leclair and T. Scholl. "Application of automation and information systems to forensic genetic specimen processing." *Expert Review of Molecular Diagnostics*, 5(2):241-250, March 2005.

M. Bill, P. Gill, J. Curran, T. Clayton, R. Pinchin, M. Healy, and J. Buckleton. "PENDULUM – a guideline-based approach to the interpretation of STR mixtures." *Forensic Science International*, 148(2-3):181-189, March 2005.

S. Shrestha, M. Smith, T. Beaty, and S. Strathdee. "Theory and methodology for utilizing genes as biomarkers to determine potential biological mixtures." *Annals of Epidemiology*, 15(1):29-38.

P. Gill, J. Curran, and K. Elliot. "A graphical simulation model of the entire DNA process associated with the analysis of short tandem repeat loci." *Nucleic Acids Research*, 33(2):632-643, 2005.

M.A. Jobling and P. Gill. "Encoded evidence: DNA in forensic analysis." *Nature Reviews Genetics*, 5:739-751, October 2004.

R. Sugita and S. Suzuki. "Forensic Geology." *14th International Forensic Science Symposium*, 125-147, 2004.

S.L. Zabell. "The Mathematics of Mixtures." Wright State University, 2003.

L.A. Foreman, C. Champod, I.W. Evett, J.A. Lambert, and S. Pope. "Interpreting DNA Evidence: A Review." *International Statistical Review*, 71(3): 473-495, December 2003.

B. Leclair, J.B. Sgueglia, P.C. Wojtowicz, A.C. Juston, C.J. Frégeau, and R.M. Fourney. "STR DNA typing: Increased sensitivity and efficient sample consumption using reduced PCR reaction volumes." *Journal of Forensic Sciences*, 48(5): 1001-1013, September 2003.

M. Sjerps and A.D. Kloosterman. "Statistical aspects of interpreting DNA profiling in legal cases." *Statistica Neerlandica*, 57(3): 368-389, August 2003.

T.A. Brettell, N. Rudin, and R. Saferstein. "Forensic Science." *Analytical Chemistry*, 75(12): 2877-2890, June 2003.

B. Simonović. "Person identification based on establishing a DNA profile." *Bezbednost, Beograd*, 44(4): 561-587, 2002.

B.B. Hellerud, S. Lien, P.R. Berg, B. Mevåg, B. Sobrino, G. Storvik, and T. Egeland. "On an experiment designed to investigate the forensic relevance of SNPs for mixture problems." Citeseer.

R.G. Cowell, S.L. Lauritzen, and J. Mortera. "Object-oriented Bayesian networks for DNA mixture analyses." Citeseer.

<http://www.cqvip.com/qk/96973x/201002/33799727.html>

<http://www.cqvip.com/qk/96140x/200605/23054550.html>

R. Potorac. "Tactica Identificării Şi Valorificării Probelor Genetice Din Scena Infraţiunilor."

http://scholar.googleusercontent.com/scholar?q=cache:GA5ARojlgBcJ:scholar.google.com/&hl=en&as_sdt=5,39&scioldt=1,39 Accessed 02 Sept 2011.

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.

P.C. Curtis, J.L. Thomas, N.R. Phillips, and R.K. Roby. "Optimization of primer-specific filter metrics for the assessment of mitochondrial DNA sequence data." *Mitochondrial DNA*, 21(6):191-197, 2010.

N.R. Phillips. "Expert Systems for High Throughput Analysis of Single Source Samples: A Comparison of GeneMarker® HID V1.71 and GeneMapper® ID V3.2 and Validation of GeneMapper® ID V3.2." Master's Thesis. University of North Texas Health Science Center, 2009.

J.H. Ryan, J.K. Barrus, B. Budowle, C.M. Shannon, V.W. Thompson, and B.E. Ward, "The application of an automated allele concordance analysis system (CompareCallsSM) to ensure the accuracy of single source STR DA profiles," *Journal of Forensic Science*, 49(3):492-499, 2004.

US Dept of Justice Federal Bureau of Investigation Laboratory Branch. "Automating the Forensic Analysis of Nuclear DNA: The FBI's Research and Development Initiative." *NCJRS*. 2004.

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.

H.M. Hakim, H.O. Khan, S.A. Ismail, N.H.M. Lazim, J. Lalung, A.E. Kofi, G.K. Chambers, and H.A. Edinur. "Assessment of QIAGEN™ Investigator® 24plex GO! kit workflow for autosomal STR profiling of forensic reference samples." *Egyptian Journal of Forensic Sciences*, 10:1-11, 2020.

Birdwell, et al. "Interaction method with an expert system that utilizes stutter peak rule." U.S. Patent #7,664,719. Feb. 2010.

Birdwell et al. "Method of organizing and presenting data in a table using stutter peak rule." U.S. Patent # 7,640,223. December 2009.

Birdwell, et. al. "Method of expert system analysis of DNA electrophoresis data." U.S. Patent #7,624,087. Nov. 2009.

J.D. Birdwell, T. Wang, D.V. Stansberry, and J. Pendleton. "Method of organizing and presenting data in a table using stutter peak rule." University of Tennessee Research Foundation. 2009.

N.R. Phillips. "Expert Systems for High Throughput Analysis of Single Source Samples: A Comparison of GeneMarker® HID V1.71 and GeneMapper® ID V3.2 and Validation of GeneMapper® ID V3.2." *Theses and Dissertations*. University of North Texas Health Science Center, 2009.

J.H. Ryan, J.K. Barrus, B. Budowle, C.M. Shannon, V.W. Thompson, and B.E. Ward, "The application of an automated allele concordance analysis system (CompareCallsSM) to ensure the accuracy of single source STR DA profiles," *Journal of Forensic Science*, 49(3):492-499, 2004.

"Automating the Forensic Analysis of Nuclear DNA: The FBI's Research and Development Initiative." *Forensic Science Communications*. Oct. 2004; 6(4).

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.

P. Chowdhury, S. Paul, P.P. Sarkar, M.D. Chando, and P. Chowdhury. "A MATHEMATICAL MODEL TO RESOLVING MIXED DNA SAMPLES BY USING LINEAR MIXTURE ANALYSIS." *Journal of Mathematical Sciences & Computational Mathematics*, 2(2):236-251. 2021.

J.H. Ryan, J.K. Barrus, B. Budowle, C.M. Shannon, V.W. Thompson, and B.E. Ward, "The application of an automated allele concordance analysis system (CompareCallsSM) to ensure the accuracy of single source STR DA profiles," *Journal of Forensic Science*, 49(3):492-499, 2004.

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.

J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.

D.O. Ojwang. "Molecular Characterization of the Wild Edible Mushrooms of the Pleurotus species in Kenya." Doctoral Dissertation, 2014.

J.K. Akhwale. "Isolation and Characterization of antibiotic and exoenzymes producing actinobacteria from guts of fungus-cultivating termites (*Macrotermes michaelseni*)." Doctoral Dissertation, 2014.

J. Bergþórsson. "Male-specific cancers in Iceland: Family history, genomic instability and genetic predisposition." Doctoral Dissertation, 2013.

- J. Gulcher. "Microsatellite markers for linkage and association studies." *Cold Spring Harbor Protocols*, 4, 2012.
- E. Guichoux, L. Lagache, S. Wagner, P. Chaumeil, P. Leger, O. Lepais, C. Lepoittevin, T. Malausa, E. Revardel, F. Salin, and R. J. Petit. "Current trends in microsatellite genotyping." *Molecular Ecology Resources*, 11(4):591-611, 2011.
- T. Matsumoto (JP), Y. Nozaki (JP), and R. Nakashige (JP). "Gene information display method and apparatus." European Patent EP 1798651, issued March 17, 2010.
- J.D. Birdwell (Oak Ridge, TN, US), T. Wang (Oak Ridge, TN, US), D. V. Stansberry (Knoxville, TN, US), and J. Pendleton (Knoxville, TN, US). "Interaction method with an expert system that utilizes stutter peak rule." U.S. Patent 7,664,719, issued February 16, 2010.
- A. Büntge. "Tracing signatures of positive selection in natural populations of the house mouse." Dissertation. Christian-Albrechts-Universität zu Kiel. 2010.
- J.D. Birdwell (Oak Ridge, TN, US), T. Wang (Oak Ridge, TN, US), D.V. Stansberry, (Knoxville, TN, US), and J. Pendleton (Knoxville, TN, US). "Method of organizing and presenting data in a table using stutter peak rule." U.S. Patent 7,640,223, issued December 29, 2009.
- J.D. Birdwell (Oak Ridge, TN, US), T. Wang (Oak Ridge, TN, US), D. V. Stansberry, (Knoxville, TN, US), and J. Pendleton (Knoxville, TN, US). "Method of expert system analysis of DNA electrophoresis data." U.S. Patent 7,624,087, issued November 24, 2009.
- J. Thompson and S. Salipante. "PeakSeeker: a program for interpreting genotypes of mononucleotide repeats." *BMC Research Notes*, 2(1):17, 2009.
- A. Palsdottir, A. Helgason, S. Palsson, H. T. Bjornsson, B. T. Bragason, S. Gretarsdottir, U. Thorsteinsdottir, E. Olafsson, and K. Stefansson. "A drastic reduction in the life span of Cystatin C L6eQ carriers due to life-style changes during the last two centuries." *PLoS Genetics*, 4(6), 2008.
- L. Hu, Q. Qiu, S. Fu, D. Sun, K. Magnusson, B. He, A. Lindblom, and I. Ernberg. "A genome-wide scan suggests a susceptibility locus on 5p13 for nasopharyngeal carcinoma." *European Journal of Human Genetics*, 16(3):343-349, 2008.
- D.C. Woo (Foster City, CA, US) and Y. Subramaniam (Belmont, CA, US). "Automated quality control method and system for genetic analysis." U.S. Patent 7,398,171, issued July 8, 2008.

Q. Qiao, A. Osterholm, B. He, J. Pitkaniemi, H. Cordell, C. Sarti, L. Kinnunen, E. Tuomilehto-Wolf, K. Tryggvason, and J. Tuomilehto. "A genome-wide scan for type 1 diabetes susceptibility genes in nuclear families with multiple affected siblings in Finland." *BMC Genetics*, 8, 2007.

A. Martinez-Mir, A. Zlotogorski, D. Gordon, L. Petukhova, J. Mo, T.C. Gilliam, D. Londono, C. Haynes, J. Ott, M. Hordinsky, K. Nanova, D. Norris, V. Price, M. Duvic, and A.M. Christiano. "Genomewide scan for evidence of several susceptibility loci for alopecia areata." *The American Journal of Human Genetics*, 80(2):316-328, 2007.

H. Hakonarson (Grjotasel 3, 109 Reykjavik, IS), M. Gurney (910 Rosewood Ave, East Grand Rapids, MI, 49506, US), and E. Halapi (Skrioustekk 16, 109 Reykjavik, IS). "Methods of diagnosis and treatment for asthma, allergic rhinitis and other respiratory diseases based on haplotype association." U.S. Patent Application 11/881,406, filed July 26, 2007.

A.M. Osterholm, B. He, J. Pitkaniemi, L. Albinsson, T. Berg, C. Sarti, J. Tuomilehto, and K. Tryggvason. "Genome-wide scan for type 1 diabetic nephropathy in the Finnish population reveals suggestive linkage to a single locus on chromosome 3q." *Kidney International*, 71:140-145, 2007.

M. Olejniczak and W. J. Krzyzosiak. "Genotyping of simple sequence repeat factors implicated in shadow band generation revisited." *Electrophoresis*, 27(19):3724-3734, 2006.

G.T. Skalski, C.R. Couch, A.F. Garber, B.S. Weir, and C.V. Sullivan. "Evaluation of DNA Pooling for the Estimation of Microsatellite Allele Frequencies: A Case Study Using Striped Bass (*Morone saxatilis*)." *Genetics*, 173(2):863-875, 2006.

S. Lindström, S.L. Zheng, F. Wiklund, B. Jonsson, H. Adami, K. A. Bälter, A.J. Brookes, J. Sun, B. Chang, W. Liu, G. Li, W. B. Isaacs, J. Adolfsson, H. Grönberg, and J. Xu. "Systematic replication study of reported genetic associations in prostate cancer: Strong support for genetic variation in the androgen pathway." *The Prostate*, 66(16): 1729-1743, 2006.

J. DeWoody, J.D. Nason, and V.D. Hipkins. "Mitigating scoring errors in microsatellite data from wild populations." *Molecular Ecology Resources*, 6(4):951-957, 2006.

H. Hakonarson (Reykjavik, IS), M.E. Gurney (East Grand Rapids, MI, US), and E. Halapi (Reykjavik, IS). "Methods of diagnosis and treatment for asthma and other respiratory diseases based on haplotype association." U.S. Patent Application 11/043,752, filed January 26, 2005.

- A. Bjornsson, G. Gudmundsson, E. Gudfinnsson, M. Hrafnisdottir, J. Benedikz, S. Skuladottir, K. Kristjansson, M.L. Frigge, A. Kong, K. Stefansson, and J.R. Gulcher. "Localization of a gene for migraine without aura to chromosome 4q21." *The American Journal of Human Genetics*, 76(4):986-993, 2005.
- T. Matsumoto and R. Nakashige. "Evaluating Robustness of Algorithm for Microsatellite Marker Genotyping," in the Proceedings of the *IEEE Symposium*. Oakland, CA, 2005.
- E. Akesson. "Genetic mapping and association analysis in multiple sclerosis." Thesis. Karolinska Institutet, Sweden, 2005.
- T. Foltynie, A. Hicks, S. Sawcer, A. Jonasdottir, E. Setakis, M. Maranian, T. Yeo, S. Lewis, C. Brayne, K. Stefansson, A. Compston, J. Gulcher, and R. A. Barker. "A genome wide linkage disequilibrium screen in Parkinson's disease." *Journal of Neurology*, 252(5):597-602, 2005.
- H. Hakonarsson and K. Stefansson. "Role of pharmacogenomics in drug development." *Drug Development Research*, 62(2): 86-96, 2004.
- R. Fossdal, F. Jonasson, G.T. Kristjansdottir, A. Kong, H. Stefansson, S. Gosh, J. R. Gulcher, and K. Stefansson. "A novel TEAD1 mutation is the causative allele in Sveinsson's chorioretinal atrophy (helicoid peripapillary chorioretinal degeneration)." *Human Molecular Genetics*, 13(9):975-981, 2004.
- T. Matsumoto, W. Yukawa, Y. Nozaki, R. Nakashige, M. Shinya, S. Makino, M. Yagura, T. Ikuta, T. Imanishi, H. Inoko, G. Tamiya, and T. Gojobori. "Novel algorithm for automated genotyping of microsatellites." *Nucleic Acids Research*, 32(20):6069-6077, 2004.
- I. Reynisdottir, G. Thorleifsson, R. Benediktsson, G. Sigurdsson, V. Emilsson, A. S. Einarsdottir, E.E. Hjorleifsdottir, G.T. Orlygsdottir, G.T. Bjornsdottir, J. Saemundsdottir, S. Halldorsson, S. Hrafnkelsdottir, S.B. Sigurjonsdottir, S. Steinsdottir, M. Martin, J.P. Kochan, B.K. Rhees, S.F.A. Grant, M.L. Frigge, A. Kong, V. Gudnason, K. Stefansson, and J.R. Gulcher. "Localization of a susceptibility gene for type 2 diabetes to chromosome 5q34-q35.2." *The American Journal of Human Genetics*, 73(2):323-335, 2003.
- Å. Johansson, P. Karlsson, and U. Gyllensten. "A novel method for automatic genotyping of microsatellite markers based on parametric pattern recognition." *Human Genetics*, 113(4):316-324, 2003.
- T.E. Thorgeirsson, H. Oskarsson, N. Desnica, J.P. Kostic, J.G. Stefansson, H. Kolbeinsson, E. Lindal, N. Gagunashvili, M.L. Frigge, A. Kong, K. Stefansson, and J.R. Gulcher. "Anxiety with panic disorder linked to chromosome 9q in Iceland." *The American Journal of Human Genetics*, 72(5):1221-1230, 2003.

H. Modin, T. Masterman, T. Thorlaciuss, M. Stefansson, A. Jonasdottir, K. Stefansson, J. Hillert, and J. Gulcher. "Genome-wide linkage screen of a consanguineous multiple sclerosis kinship." *Multiple Sclerosis*, 9(2):128-134, 2003.

S.E. Stefansson, H. Jonsson, T. Ingvarsson, I. Manolescu, H.H. Jonsson, G. Olafsdottir, E. Palsdottir, G. Stefansdottir, G. Sveinbjornsdottir, M.L. Frigge, A. Kong, J.R. Gulcher, and K. Stefansson. "Genomewide scan for hand osteoarthritis: A novel mutation in matrilin-3." *The American Journal of Human Genetics*, 72(6):1448-1459, 2003.

H. Hakonarson, U.S. Bjornsdottir, E. Halapi, S. Palsson, E. Adalsteinsdottir, D. Gislason, G. Finnbogason, T. Gislason, K. Kristjansson, T. Arnason, I. Biriksson, M.L. Frigge, A. Kong, J.R. Gulcher and K. Stefansson. "A major susceptibility gene for asthma maps to chromosome 14q24." *The American Journal of Human Genetics*, 71(3):483-491, 2002.

G. Gudmundsson, S.E. Matthiasson, H. Arason, H. Johannsson, F. Runarsson, H. Bjarnason, K. Helgadottir, S. Thorisdottir, G. Ingadottir, K. Lindpaintner, J. Sainz, V. Gudnason, M.L. Frigge, A. Kong, J.R. Gulcher, and K. Stefansson. "Localization of a gene for peripheral arterial occlusive disease to chromosome 1p31." *The American Journal of Human Genetics*, 70(3):586-592, 2002.

S. Gretarsdottir, S. Sveinbjornsdottir, H.H. Jonsson, F. Jakobsson, E. Einarsdottir, U. Agnarsson, D. Shkolny, G. Einarsson, H.M. Gudjonsdottir, E.M. Valdimarsson, O.B. Einarsson, G. Thorgeirsson, R. Hadzic, S. Jonsdottir, S.T. Reynisdottir, S.M. Bjarnadottir, T. Gudmundsdottir, G.J. Gudlaugsdottir, R. Gill, K. Lindpaintner, J. Sainz, H.H. Hannesson, G.T. Sigurdsson, M.L. Frigge, A. Kong, V. Gudnason, K. Stefansson, and J.R. Gulcher. "Localization of a susceptibility gene for common forms of stroke to 5q12." *The American Journal of Human Genetics*, 70(3):593-603, 2002.

H. Stefansson, A. Einarsdottir, R.T. Geirsson, K. Jonsdottir, G. Sverrisdottir, V.G. Gudnadottir, S. Gunnarsdottir, A. Manolescu, J. Gulcher, and K. Stefansson. "Endometriosis is not associated with or linked to the GALT gene." *Fertility and Sterility*, 76(5):1019-1022, 2001.

J.L. Li, H. Deng, D.B. Lai, F. Xu, J. Chen, G. Gao, R.R. Recker, and H.W. Deng. "Toward high throughput genotyping dynamic and automatic software for manipulating large-scale genotype data using fluorescently labeled dinucleotide markers," *Genome Research*, 11:1304-1314, 2001.

S. Rodriguez, G. Visedo, and C. Zapata. "Detection of errors in dinucleotide repeat typing by nondenaturing electrophoresis." *Electrophoresis*, 22(13):2656-2664, 2001.

T. Ingvarsson, S.E. Stefánsson, J. R. Gulcher, H.H. Jónsson, H. Jónsson, M.L. Frigge, E. Pálsdóttir, G. Ólafsdóttir, Þ. Jónsdóttir, G.B. Walters, L.S. Lohmander, and K. Stefánsson. "A large Icelandic family with early osteoarthritis of the hip associated with a susceptibility locus on chromosome 16p." *Arthritis & Rheumatism*, 44(11):2548-2555, 2001.

T.J. Puolakka, H.J. Laine, T.P. Moilanen, A.M. Koivisto, and K.J. Pajamaki. "Alarming wear of the first-generation polyethylene liner of the cementless porous-coated Biomet Universal cup: 107 hips followed for mean 6 years." *Acta Orthopaedica Scandinavica*. 72(1):1-7, 2001.

B.R. Olafsdottir, D.B. Rye, T. Scammell, J.K. Matheson, K. Stefansson, and J.R. Gulcher. "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy." *Neurology*, 57(10):1896-1899, 2001.

T. Ingvarsson. "Prevalence and inheritance of hip osteoarthritis in Iceland." *Acta Orthop Scand Suppl*, 298:1-46, 2001.

K. Avela. "Positional Cloning of the Mulibrey Nanism Gene (*MUL*)." Academic Dissertation. University of Helsinki, 2000.

A. Helgason, S. Siguroardottir, J. Nicholson, B. Sykes, E.W. Hill, D.G. Bradley, V. Bosnes, J.R. Gulcher, R. Ward, and K. Stefansson. "Estimating Scandinavian and Gaelic ancestry in the male settlers of Iceland." *The American Journal of Human Genetics*, 67(3):697-717, 2000.

K.R. Ewen, M. Bahlo, S.A. Treloar, D.F. Levinson, B. Mowry, J.W. Barlow, and S.J. Foote. "Identification and analysis of error types in high-throughput genotyping." *The American Journal of Human Genetics*, 67(3):727-736, 2000.

G. Lancia and M. Perlin, "Genotyping of pooled microsatellite markers by combinatorial optimization techniques," *Discrete Applied Math.*, 88(1-3):291-314, 1998.

P. Blain, C. Davis, J. Silva, C. Vinzant, S. Bulenko, W.A. Chaovalitwongse, and P.M. Pardalos. "Diversity Graphs." In *Clustering Challenges in Biological Networks*. World Scientific Publishing. 129-150. 2009.

Z. Li, W. Zhou, Z.S. Zhang, and L. Chen. "A parsimonious tree-grow method for haplotype inference." *Bioinformatics*, 21(17):2475-3481, 2005.

Y. Lai. (2003). "Branching processes and microsatellite evolution." (Doctoral dissertation), University of Southern California. 2003.

Y. Lai, D. Shinde, N. Arnheim, and F. Sun. "The mutation process of microsatellites during the polymerase chain reaction." *Journal of Computational Biology*, 10(2):143-155, April 2003.

Y. Lai and F. Sun. "Microsatellite mutations during the polymerase chain reaction: mean field approximations and their applications." *Journal of Theoretical Biology*, 244(1):127-137, 2003.

C. Davis and A.G. Holder, "Haplotyping and Minimu Diversity Graphs." *Mathematics Faculty Research at Trinity University*. Paper 48. 2003.

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.

J.D. Aronson. Genetic Witness: Science, Law, and Controversy in the Making of DNA Profiling. New Brunswick: Rutgers University, 2007.

S. Ng and J.H. Morris. "Automating computational molecular genetics: Solving the microsatellite genotyping problem." Doctoral thesis. School of Computer Science, Carnegie Mellon University, 1998.

G. Lancia. "Optimization problems in computational molecular biology." Dissertation. Carnegie Mellon University. 1997.

M.W. Perlin, G. Lancia, and S.K. Ng, "Toward fully automated genotyping: genotyping microsatellite markers by deconvolution," *Am. J. Hum. Genet.*, 57(5):1199-1210, 1995.

T. Ishige, M. Kikuchi, H. Kakoi, K. Hirota, A. Ohnuma, T. Tozaki, Y. Hirosawa, S. Tanaka, and S. Nagata. "Evaluation of parentage testing using single nucleotide polymorphism markers for draft horses in Japan." *Animal Science Journal*, 94(1):e13854, 2023.

S.N. Mandape, U. Smart, J.L. King, M. Muenzler, K.B. Kapema, B. Budowle, and A.E. Woerner. "MMDIT: A tool for the deconvolution and interpretation of mitochondrial DNA mixtures." *Forensic Science International: Genetics*, 55:102568, 2021.

Y.A. Liu, "Development of Bioinformatic Methods for Data-Driven Forensic Short Tandem Repeat Analyses." (Doctoral Dissertation). ResearchSpace@ Auckland, 2021.

- M. Arca, T. Mary-Huard, B. Gouesnard, A. Bérard, C. Bauland, V. Combes, D. Madur, A. Charcosset, and S.D. Nicolas. "Deciphering the genetic diversity of landraces with high-throughput SNP genotyping of DNA bulks: methodology and application to the maize 50k array." *Frontiers in Plant Science*, 11:568699, 2021.
- P. Chowdhury, S. Paul, P.P. Sarkar, M.D. Chando, and P. Chowdhury. "A MATHEMATICAL MODEL TO RESOLVING MIXED DNA SAMPLES BY USING LINEAR MIXTURE ANALYSIS." *Journal of Mathematical Sciences & Computational Mathematics*, 2(2):236-251. 2021.
- K.J. Livak, J. Stevens, M. Francisco, M. Rhodes, L.R. Bellon, Dawn Madden et al. "Methods for placing, accepting, and filling orders for products and services." U.S. Patent 10,689,692, issued June 23, 2020.
- L. Malek. "Stabilizing information content in DNA evidence to improve lab-to-lab inference." (Doctoral dissertation). Rutgers University-Camden Graduate School, 2019.
- J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.
- Q. Liu, F. Liu, X. Zhang, N. Yang, and J. Ran. "Characterization of 22 New Polymorphic Microsatellite Loci from the Endangered Buff-Throated Partridge (*Tetraophaps szechenyii*) by using Next-Generation Sequencing." *Pakistan J. Zool*, 50(2):795-797, 2018.
- M.A.C.S.S. Fernando. "Bayesian Models for PCR Stutter." Doctoral Thesis. The University of Auckland, 2017.
- H.M. Holl, J. Vanhnasy, R.E. Everts, K. Hoefs-Martin, D. Cook, S.A. Brooks, M.L. Carpenter, C.D. Bustamante, and C. Lafayette. "Single nucleotide polymorphisms for DNA typing in the domestic horse." *Animal Genetics*, 48(6):669-676, 2017.
- R.T. Koehler, K.J. Livak, J. Stevens, M. Francisco, M. Rhodes, L.R. Bellon, J. Williams, et al. "Methods for placing, accepting, and filling orders for products and services." U.S. Patent 9,464,320, issued October 11, 2016.
- R.G. Cowell, T. Graversen, S.L. Lauritzen, and J. Mortera. "Analysis of forensic DNA mixtures with artefacts." *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 64(1):1-48, 2015.
- J. Bright. "Informing biological models for probabilistic methods of DNA profile interpretation." Doctoral Dissertation. The University of Auckland, 2015.

U.J. Monich, K. Duffy, M. Medard, V. Cadambe, L.E. Alfonse, and C. Grgicak. "Probabilistic characterisation of baseline noise in STR profiles." *Forensic Science International: Genetics*, 19:107-122, 2015.

J.A. Bright, J. Curran, and J. Buckleton. "Modelling PowerPlex® Y stutter and artefacts." *Forensic Science International: Genetics*, 11:126-136, 2014.

Q. Jia, Y. Wu, N. He, and Y. Deng. "Bioinformatics tools for genome-wide single nucleotide polymorphisms management and analyses: a review." *International Journal of Bio-Inspired Computation*, 6(3):205-227, 2014.

S.R. Coticone and W. Bloch. "Methods for the reduction of stutter in microsatellite amplification." *U.S. Patent No. 8,785,126*. Washington, DC: U.S. Patent and Trademark Office, 2014.

U.J. Monich, C. Grgicak, V. Cadambe, J.Y. Wu, G. Wellner, K. Duffy, and M. Médard. "A Signal Model for Forensic DNA Mixtures." In: *Asilomar Conference on Signals, Systems & Computers*, 2-5 November 2014, Pacific Grove, California.

J.D. Oduro. "Morphological and genetic diversity of persea americana mill.(avocado) using microsatellites in the Ashanti and Central regions of Ghana.", 2014.

I. Lee-Montero, A. Navarro, Y. Borrell, M. García-Celdrán, N. Martín, D. Negrín-Báez, and J.M. Afonso. "Development of the first standardised panel of two new microsatellite multiplex PCRs for gilthead seabream (*Sparus aurata* L.)." *Animal genetics*. Published online 10 April 2013.

J.N. Cobb, G. DeClerck, A. Greenberg, R. Clark, and S. McCouch. "Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement." *Theoretical and Applied Genetics*, 126(4):867-887, April 2013.

J.A. Bright, D. Taylor, J.M. Curran, and J.S. Buckleton. "Developing allelic and stutter peak height models for a continuous method of DNA interpretation." *Forensic Science International: Genetics*, 7(2), 296-304, February 2013.

S.K. Wasala and B. M. Prasanna. "Microsatellite marker-based diversity and population genetic analysis of selected lowland and mid-altitude maize landrace accessions of India." *Journal of Plant Biochemistry and Biotechnology*, 22(4):392-400, 2013.

C. Alexander, R. Ryan, N. Hasan, D. Bailey, H. Chen, B. Milligan, and P. Houde. "HighSSR: High throughput SSR characterization and locus development from next gen sequencing data." *Bioinformatics*. 2012.

- S.T. Dammannagoda, V. Chand, and P.B. Mather. "Development and characterisation of tri- and tetra-nucleotide polymorphic microsatellite markers for skipjack tuna (*Katsuwonus pelamis*)." *Ceylon Journal of Science*, 41(1):11-17, 2012.
- J.D. Oduro. "Morphological and genetic diversity of *Persea americana* Mill. (avocado) using microsatellites in the Ashanti and Central regions of Ghana." Thesis. University of Cape Coast, 2012.
- S.J. Overturf and M.A. Overturf. "A genetic form of distal myopathy within descendants." *Manuscript*.
http://scholar.googleusercontent.com/scholar?q=cache:A-a8c096veUJ:scholar.google.com/&hl=en&as_sdt=5,39&scioldt=0,39
- H. Kelly, J. Bright, J. Curran, and J. Buckleton. "The interpretation of low level DNA mixtures." *Forensic Science International: Genetics*, 6(2):191-197, 2012.
- A.J. Fazekas, R. Steeves, and S.G. Newmaster. "Improving sequencing quality from PCR products containing long mononucleotide repeats." *Biotechniques*, 48(4):277-285, 2010.
- W. Deng, B.S. Maust, D.C. Nickle, G.H. Learn, Y. Liu, L. Heath, S.L. Kosakovsky Pond, and J.I. Mullins. "DIVEIN: a web server to analyze phylogenies, sequence divergence, diversity, and informative sites." *Biotechniques*, 48(5):405-408, 2010.
- L. Sharma, B. Prasanna, and B. Ramesh. "Analysis of phenotypic and microsatellite-based diversity of maize landraces in India, especially from the North East Himalayan region." *Genetica*, 138(6):619-631, 2010.
- B. Hanelt, M.L. Steinauer, I.N. Mwangi, G.M. Maina, L.E. Agola, G.M. Mkoji, and E.S. Loker. "A new approach to characterize populations of *Schistosoma mansoni* from humans: development and assessment of microsatellite analysis of pooled miracidia." *Tropical Medicine & International Health*, 14(3):322-331, 2009.
- S.Y. Hill, E.K. Hoffman, N. Zezza, A. Thalamuthu, D.E. Weeks, A.G. Matthews, and I. Mukhopadhyay. "Dopaminergic mutations: within-family association and linkage in multiplex alcohol dependence families." *American Journal of Medical Genetics*, 147B(4):517-526, 2008.
- B. Hadj Kacem, J. Gargouri, and A. Gargouri. "In Vitro Direct Repeats-mediated Deletion During PCR Amplification." *Molecular Biotechnology*, 40(1):39-45, 2008.
- G.M. Makrigiorgos. "Amplification of DNA in a hairpin structure, and applications." U.S. Patent 7,452,699, issued November 18, 2008.

M.E. Samuels, B. Higgins, S. Provost, J. Marcadier, C. Blouin, S. Bowman, and M. Dube. "New technologies in human genetic analysis." *American Biotechnology Laboratory*, 25(5):22, 2007.

E.A.M. Graham. "An evaluation of forensic DNA profiling techniques currently used in the United Kingdom." Thesis. University of Leicester, 2007.

J. Oksenberg, D. Brassat, S. Schmidt, and L.F. Barcellos. "Genomic Variation and Autoimmune Disease." *Immunogenetics of Autoimmune Disease*, pp. 13-27, 2006.

G.T. Skalski, C.R. Cough, A.F. Garber, B.S. Weir, and C.V Sullivan. "Evaluation of DNA pooling for the Estimation of Microsatellite Allele Frequencies: A Case Study Using Striped Bass (*Morone saxatilis*)." *Genetics*, 173(2): 863-875, 2006.

G.W. Beecham Jr. "Statistical Methods for the Analysis of Forensic DNA Mixtures." Dissertation. NC State University. 2006.

M. Olejniczak and W.J. Krzyzosiak. "Genotyping of simple sequence repeat factors implicated in shadow band generation revisited." *Electrophoresis*, 27(19):3724-3734, 2006.

P. Dubreuil, M. Warburton, M. Chastanet, D. Hoisington, and A. Charcosset. "More on the Introduction of Temperate Maize into Europe: Large Scale Bulk SSR Genotyping and New Historical Elements." *Maydica*, 51:281-291, 2006.

C.A. Parsons, H.J. Mroczkowski, F.E.A. McGuigan, O.M.E. Albagha, S. Manlagas, D.M. Reid, S.H. Ralston, and R.J. Schmoekler Reis. "Interspecies synteny mapping identifies a quantitative trait locus for bone mineral density on human chromosome Xp22." *Human Molecular Genetics*, 14(21):3141-3148, 2005.

F. Pompanon, A. Bonin, E. Bellemain, and P. Taberlet. "Genotyping errors: causes, consequences and solutions." *Nature Reviews Genetics*, 6:847-846, 2005.

D.C. Stahl. "Genotype pattern recognition and classification." U.S. Patent 6,950,755, issued September 27, 2005.

E. Graham. "Automated DNA profile analysis." *Forensic Science, Medicine, and Pathology*, 1(4):285-288, 2005.

S. Quade, R. Elston, and K. Goddard. "Estimating haplotype frequencies in pooled DNA samples when there is genotyping error." *BMC Genetics*, 6(1):25, 2005.

- J. Brohede, R. Dunne, J.D. McKay, and G.N. Hannan. "PPC: an algorithm for accurate estimation of SNP allele frequencies in small equimolar pools of DNA using data from high density microarrays." *Nucleic Acids Research*, 33(17):e142, 2005.
- Y. Lai and F. Sun. "Sampling distribution for microsatellites amplified by PCR: mean field approximation and its applications to genotyping." *Journal of Theoretical Biology*, 228(2):185-194, 2004.
- G.M. Makrigiorgos, "PCR-Based detection of minority point mutations," *Human Mutation*, 23(5):406-412, 2004.
- I.R. Konig and A. Ziegler. "Analysis of SNPs in pooled DNA: A decision theoretic model." *Genetic Epidemiology*, 26(1):31-43, 2004.
- H.G. Schnack, S.C. Bakker, R. van't Slot, B.M. Groot, R.J. Sinke, R.S. Kahn, and P.L. Pearson. "Accurate determination of microsatellite allele frequencies in pooled DNA samples." *European Journal of Human Genetics*, 12(11):925-934, 2004.
- Y. Lai, D. Shinde, N. Arnheim and F. Sun. "The mutation process of microsatellites during the polymerase chain reaction." *Journal of Computational Biology*, 10(2):143-155, April 2003.
- G.D. Esselink, M.J.M. Smulders, and B. Vosman. "Identification of cut rose (*Rosa hybrida*) and rootstock varieties using robust sequence tagged microsatellite site markers." *Theoretical and Applied Genetics*, 106:277-286, 2003.
- Å. Johansson, P. Karlsson, and U. Gyllensten. "A novel method for automatic genotyping of microsatellite markers based on parametric pattern recognition." *Human Genetics*, 113(4):316-324, 2003.
- L.F. Barcellos and G. Thomson. "Genetic analysis of multiple sclerosis in Europeans." *Journal of Neuroimmunology*, 143(1):1-6, 2003.
- Y. Lai and F. Sun. "Microsatellite mutations during the polymerase chain reaction: mean field approximations and their applications." *Journal of Theoretical Biology*, 244(1):127-137, 2003.
- M. Kaur and G.M. Makrigiorgos. "Novel Amplification of DNA in a hairpin structure: towards a radical elimination of PCR errors from amplified DNA." *Nucleic Acids Research*, 31(6):e26, 2003.
- Y.B. Fu. "Applications of bulking in molecular characterization of plant germplasm: a critical review." *Plant Genetic Resources*, 1:161-168, 2003.

D. Kube, M. Mörmann, J. Tomiuk, H. Rieth, T.D. Hua, P.G. Kremsner, and M. Vockerodt. "Simultaneous analysis of interleukin-10 gene microsatellites and single-nucleotide polymorphisms in parallel with tumour necrosis factor and interferon-gamma short tandem repeats by fluorescence-based polymerase chain reaction." *Genes and Immunity*, 4(7):459-468, 2003.

M.M. Manolaraki, D.A. Arvanitis, G. Sourvinos, S. Sifakis, E. Koumantakis, and D.A. Spandidos. "Frequent loss of heterozygosity in chromosomal region 9pter-p13 in tumor biopsies and cytological material of uterine cervical cancer." *Cancer Letters*, 176(2):175-181, 2002.

P.S. Umesh Adiga, P. Jeavons, and J. Flint. "Automation of agarose gel image analysis." Dissertation. University of Oxford. 2002.

C.S. Pareek, R.S. Pareek, and K. Walawski. "Novel linkage mapping approach using DNA pooling in human and animal genetics. I. Detection of complex disease loci." *Journal of Applied Genetics*, 43(2):175-192, 2002.

S. Sawcer, M. Maranian, E. Setakis, V. Curwen, E. Akesson, A. Hensiek, F. Coraddu, R. Roxburgh, D. Sawcer, J. Gray, J. Deans, P.N. Goodfellow, N. Walker, D. Clayton, and A. Compston. "A whole genome screen for linkage disequilibrium in multiple sclerosis confirms disease associations with regions previously linked to susceptibility." *Brain*, 125(6):1337-1347, 2002.

E. Lipkin, J. Fulton, H. Cheng, N. Yonash, and M. Soller. "Quantitative trait locus mapping in chickens by selective DNA pooling with dinucleotide microsatellite markers by using purified DNA and fresh or frozen red blood cells as applied to marker-assisted selection." *Poultry Science*, 81(3):283-292, 2002.

C. Kwok and K. Schmitt. "Microsatellite Genotyping." *Molecular Genetic Epidemiology – A Laboratory Perspective*, 55-85, 2002.

D.A. Arvanitis, E. Angelakis, E.E. Koumantakis, and D.A. Spandidos. "Allelic imbalance in hMLH1 or BRCA2 loci associated with response of cervical and endometrial cancer to radiotherapy." *International Journal of Molecular Medicine*, 10:55-63, 2002.

J. Heil, S. Glanowski, J. Scott, E. Winn-Deen, I. McMullen, L. Wu, C. Gire, and A. Sprague. An automated computer system to support ultra high throughput SNP genotyping." In *Pacific Symposium on Biocomputing 2002: Kauai, Hawaii, 3-7 January 2002*. p. 30. World Scientific Publishing Company Incorporated, 2001.

- R. Plomin, L. Hill, I.W. Craig, P. McGuffin, S. Purcell, P. Sham, D. Lubinski, L.A. Thompson, P.J. Fisher, D. Turic, and M.J. Owen. "A genome-wide scan of 1842 DNA markers for allelic associations with general cognitive ability: a five-stage design using DNA pooling and extreme selected groups." *Behavior Genetics*, 31(6):497-509, 2001.
- P.S. Umesh Adiga, A. Bhomra, M.G. Turri, A. Nicod, S.R. Datta, P. Jeavons, R. Mott, and J. Flint. "Automatic analysis of agarose gel images." *Bioinformatics*, 17(11):1084-1089, 2001.
- L.F. Barcellos, S. Germer, and W. Klitz. "DNA pooling methods for the association mapping of complex disease loci." *Molecular Epidemiology* (ed. by M. Carrington, A.R. Hoelzel), Oxford University Press, Oxford, UK. 251. 2001.
- D. Kube, D. Schmidt, M. Mörmann, A.C. Uhlemann, J. Tomiuk, H. Tesch, and P.G. Kremsner. "Semiautomated and simultaneous analysis of the interleukin-10 gene microsatellites IL-10G and IL-10R by fluorescence-based polymerase chain reaction reveals significant differences in allele distributions between Caucasians (Germany) and Africans (Gabon)." *European Cytokine Network*, 12(3):537-544, 2001.
- J.Á. Baro, C. Carleos, N. Corral, T López, and J. Cañón. "Power analysis of QTL detection in half-sib families using selective DNA pooling," *Genetics Selection Evolution*, 33:231-247, 2001.
- J.L. Li, H. Deng, D.B. Lai, F. Xu, J. Chen, G. Gao, R.R. Recker, and H.W. Deng. "Toward high throughput genotyping dynamic and automatic software for manipulating large-scale genotype data using fluorescently labeled dinucleotide markers," *Genome Research*, 11:1304-1314, 2001.
- R. Plomin and I. Craig. "Genetics, environment and cognitive abilities: review and work in progress towards a genome scan for quantitative trait locus associations using DNA pooling." *British Journal of Psychiatry*, 178:s41-s8, 2001.
- H.E. Collins, H. Li, S.E., Inda, J. Anderson, K. Laiho, J. Tuomilehto, and M.F. Seldin. "A simple and accurate method for determination of microsatellite total allele content differences between DNA pools." *Human Genetics*, 106(2):218-226, 2000.
- A.M. Isaacs, K.E. Davies, A.J. Hunter, P.M. Nolan, L. Vizer, J. Peters, D.G. Gale, D.P. Kelsell, I.D. Latham, J.M. Chase, E. Fisher, M.M. Bouzyk, A. Potter, M. Masih, F.S. Walsh, M.A. Sims, K.E. Doncaster, C.A. Parsons, J. Martin, S.D.M. Brown, S. Rastan, N.K. Spurr, and I.C. Gray. "Identification of two new Pmp22 mouse mutants using large-scale mutagenesis and a novel rapid mapping strategy." *Human Molecular Genetics*, 9(12):1865-1871, 2000.

- P.T. O'Reilly, M.F. Canino, K.M. Bailey, and P. Bentzen. "Isolation of twenty low stutter di- and tetranucleotide microsatellites for population analyses of walleye Pollock and other gadoids." *Journal of Fish Biology*, 56(5):1074-1086, 2000.
- G. Kirov, N. Williams, P. Sham, N. Craddock, and M.J. Owen. "Pooled Genotyping of Microsatellite Markers in Parent-Offspring Trios." *Genome Research*, 10:105-115, 2000.
- K. Avela. "Positional Cloning of the Mulibrey Nanism Gene (MUL)." Dissertation. Department of Medical Genetics Haartman Institute University of Helsinki. 2000.
- C. Phillips. "Methods for Accurately Determining Allele Content in DNA Pools." *Prized Writing*. UC Davis University of California. 1999-2000.
- B. Degen, R. Streiff, and B. Ziegenhagen. "Comparative study of genetic variation and differentiation of two pedunculate oak (*Quercus robur*) stands using microsatellite and allozyme loci." *Heredity*, 83(5):597-603, 1999.
- L. Moreau, S. Lemarle, A. Charcosset, and A. Gallais. "Economic Efficiency of One Cycle of Marker-Assisted Selection." *Crop Science*, 40(2):329-337, 1999.
- L. Hill, I.W. Craig, P. Asherson, D. Ball, T. Eley, T. Ninomiya, P.J. Fisher, D. Turic, P. McGuffin, M.J. Owen, K. Chorney, M.J. Chorney, C.P. Benbow D. Lubinski, L.A. Thompson, and R. Plomin. "DNA pooling and dense marker maps: a systematic search for genes for cognitive ability." *Cognitive Neuroscience*, 10(4):843-848, 1999.
- V.P. Kozobolis, E.T. Detorakis, G. Sourvinos, I.G. Pallikaris, and D.A. Spandidos. "Loss of heterozygosity in pseudoexfoliation syndrome." *Investigative Ophthalmology & Visual Science*, 40(6):1255-1260, 1999.
- N.M. Williams and M.J. Owen. "DNA pooling in allelic association studies." *Techniques in the Behavioral and Neural Sciences*, 13:122-131, 1999.
- M.M. Shi, M.R. Bleavins, and F.A. de la Iglesia. "Technologies for detecting genetic polymorphisms in pharmacogenomics." *Molecular Diagnosis*, 4(4):343-351, 1999.
- E.T. Detorakis, G. Sourvinos, J. Tsamparlakis, and D.A. Spandidos. "Evaluation of loss of heterozygosity and microsatellite instability in human pterygium: clinical correlations." *British Journal of Ophthalmology*, 82(11):1324-1328, 1998.

H. Feit, A. Silbergleit, L.B. Schneider, J.A. Gutierrez, R.P. Fitoussi, C. Reyes, G.A. Rouleau, B. Brais, C.E. Jackson, J.S. Beckmann, and E. Seboun. "Vocal Cord and Pharyngeal Weakness with Autosomal Dominant Distal Myopathy: Clinical Description and Gene Localization to 5q31." *American Journal of Human Genetics*, 63(6):1732-1742, 1998.

V. Hongtrakul, M.B. Slabaugh, and S.J. Knapp. "DFLP, SSCP, and SSR markers for $\Delta 9$ -stearoyl-acyl carrier protein desaturases strongly expressed in developing seeds of sunflower: intron lengths are polymorphic among elite inbred lines." *Molecular Breeding*, 4(3):195-203, 1998.

E. Lipkin, M.O. Mosig, A. Darvasi, E. Ezra, A. Shalom, A. Friedmann, and M. Soller. "Quantitative Trait Locus Mapping in Dairy Cattle by Means of Selective Milk DNA Pooling Using Dinucleotide Microsatellite Markers: Analysis of Milk Protein Percentage." *Genetics*, 149(3):1557-1567, 1998.

T. Ooasa, H. Karasaki, H. Kanda, K. Nomura, T. Kitagawa, and K. Ogawa. "Loss of imprinting of the insulin-like growth factor II gene in mouse hepatocellular carcinoma cell lines." *Molecular Carcinogenesis*, 23(4):248-253, 1998.

H. Khatib, N. Sagiv, and Y. Gruenbaum. "Research notes: Fresh and frozen pools of chicken red blood cells as substrates for direct polymerase chain reaction." *Poultry Science*, 77(6):902-904, 1998.

K.F. Damji, C.J. Gallione, R.R. Allingham, B. Slotterbeck, A.E. Guttmacher, K.A. Pasyk, J.M. Vance, M.A. Pericak-Vance, M.C. Speer, and D.A. Marchuk. "Quantitative DNA pooling to increase the efficiency of linkage analysis in autosomal dominant disease." *Human Genetics*, 102(2):207-212, 1998.

J. Daniels, P. Holmans, N. Williams, D. Turic, P. McGuffin, R. Plomin, and M.J. Owen. "A simple method for analyzing microsatellite allele image patterns generated from DNA pools and its application to allelic association studies." *The American Journal of Human Genetics*, 62(5):1189-1197, 1998.

L.F. Barcellos, W. Klitz, L.L. Field, R. Tobias, A.M. Bowcock, R. Wilson, M.P. Nelson, J. Nagatomi, and G. Thomson. "Association Mapping of Disease Loci, by Use of a Pooled DNA Genomic Screen." *The American Journal of Human Genetics*, 61(3):734-747, 1997.

L.W. Ballard. "High-Throughput Genetic Analysis in the Core Facility." *Association of Biomolecular Resource Facilities News*, 8:22-28, 1997.

G. Lancia. "Optimization problems in computational molecular biology." Dissertation. Carnegie Mellon University. 1997.

S. Ghosh, Z.E. Karanjawala, E.R. Hauser, D. Ally, J.I. Knapp, J.B. Rayman, A. Musick, J. Tannenbaum, C. Te, S. Shapiro, W. Eldridge, T. Musick, C. Martin, J.R. Smith, J.D. Carpten, M.J. Brownstein, J.I. Powell, R. Whiten, P. Chines, S.J. Nylund, V.L. Magnuson, M. Boehnke, and F.S. Collins. "Methods for precise sizing, automated binning of alleles, and reduction of error rates in large-scale genotyping using fluorescently labeled dinucleotide markers. FUSION (Finland-U.S. Investigation of NIDDM Genetics) Study Group." *Genome Research*, 7:165-178, 1997.

M.J. Miller and B. Yuan. "Semiautomated resolution of overlapping stutter patterns in genomic microsatellite analysis." *Analytical Biochemistry*, 251(1):50-56, 1997.

R.M. Idury and L.R. Cardon. "A simple method for automated allele binning in microsatellite markers." *Genome Research*, 7:1104-1109, 1997.

J.S.C. Smith, E.C.L. Chin, H. Shu, O.S. Smith, S.J. Wall, M.L. Senior, S.E. Mitchell, S. Kresovich, and J. Ziegler. "An evaluation of the utility of SSR loci as molecular markers in maize (*Zea mays L.*): comparisons with data from RFLPS and pedigree." *Theoretical Applied Genetics*, 95:163-173, 1997.

J.M. Hall, C.A. LeDuc, A.R. Watson, and A.H. Roter. "An approach to high-throughput genotyping." *Genome Research*, 6(9):781-790, 1996.

C. Delahunty, W. Ankener, Q. Deng, J. Eng, and D.A. Nickerson. "Testing the feasibility of DNA typing for human identification by PCR and an oligonucleotide ligation assay." *American Journal of Human Genetics*, 58(6):1239-1246, 1996.

C. Mir. "Introduction to the Bulk DNA Method of Analysis,"
http://www.generationcp.org/capcorner/gcp_training_april_india/file/lectures/lecture_2.doc

N. Herbon. "SNP Assoziationsstudien multifaktorieller Erkrankungen auf Chromosom 6p"
http://scholar.googleusercontent.com/scholar?q=cache:Bdb4s17E2kMJ:scholar.google.com/&hl=en&as_sdt=5,39&scioldt=0,39

A. Kiewert. "Empfehlungen zur Qualitätssicherung von Genotypisierungsdaten bei familienbasierten Studien mit Mikrosatelliten"
http://scholar.googleusercontent.com/scholar?q=cache:eK_sH2nXC3QJ:scholar.google.com/&hl=en&as_sdt=5,39&scioldt=0,39

M.W. Perlin, M.B. Burks, R.C. Hoop, and E.P. Hoffman, "Toward fully automated genotyping: allele assignment, pedigree construction, phase determination, and recombination detection in Duchenne muscular dystrophy," *Am. J. Hum. Genet.*, 55(4):777-787, 1994.

J.S. Buckleton, J. Bright, S. Gittelsohn, T.R. Moretti, A.J. Onorato, F.R. Bieber, B. Budowle, and D.A. Taylor. "The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity." *Journal of Forensic Sciences*, 64(2):393-405, 2019.

C. Schafer, A.H. Schmidt, and J. Sauter. "Hapl-o-Mat: open-source software for HLA haplotype frequency estimation from ambiguous and heterogeneous data." *BMC Bioinformatics*, 18:284, 2018.

J.A. Bright, J. Curran, and J. Buckleton. "Modelling PowerPlex® Y stutter and artefacts." *Forensic Science International: Genetics*, 11:126-136, 2014.

S.K. Wasala and B. M. Prasanna. "Microsatellite marker-based diversity and population genetic analysis of selected lowland and mid-altitude maize landrace accessions of India." *Journal of Plant Biochemistry and Biotechnology*, 22(4):392-400, 2013.

I. Lee-Montero, A. Navarro, Y. Borrell, M. García-Celdrán, N. Martín, D. Negrín-Báez, and J.M. Afonso. "Development of the first standardised panel of two new microsatellite multiplex PCRs for gilthead seabream (*Sparus aurata* L.)." *Animal genetics*, 44(5):533-546, 2013.

J.A. Bright, D. Taylor, J. Curran, and J. Buckleton. "Developing allelic and stutter peak height models for a continuous method of DNA interpretation." *Forensic Science International: Genetics*, 7(2): 296-304, 2013.

J.N. Cobb, G. DeClerck, A. Greenberg, R. Clark, and S. McCouch. "Next-generation phenotyping: requirements and strategies for enhancing our understanding of genotype–phenotype relationships and its relevance to crop improvement." *Theoretical and Applied Genetics*, 126(4):867-887, 2013.

J.D. Oduro. "Morphological and genetic diversity of *Persea americana* mill.(avocado) using microsatellites in the Ashanti and Central regions of Ghana." 2012.

D. Acharige, S. Terrence, V. Chand, and P.B. Mather. "Development and characterisation of tri- and tetra-nucleotide polymorphic microsatellite markers for skipjack tuna (*Katsuwonus pelamis*)." *Ceylon Journal of Science (Bio. Sci)*, 41(1):11-17, 2012.

- A. Churbanov, R. Ryan, N. Hasan, D. Bailey, H. Chen, B. Milligan, and P. Houde. "HighSSR: high-throughput SSR characterization and locus development from next-gen sequencing data." *Bioinformatics*, 28(21):2797-2803, 2012.
- H. Kelly, J. Bright, J. Curran, and J. Buckleton. "The interpretation of low level DNA mixtures." *Forensic Science International: Genetics*, 6(2):191-197, 2012.
- A.J. Fazekas, R. Steeves, and S.G. Newmaster. "Improving sequencing quality from PCR products containing long mononucleotide repeats." *Biotechniques*, 48(4): 277-285, 2010
- L. Sharma, B. M. Prasanna, and B. Ramesh. "Analysis of phenotypic and microsatellite-based diversity of maize landraces in India, especially from the North East Himalayan region." *Genetica*, 138(6)619-631, 2010.
- W. Sung. Algorithms in Bioinformatics: A Practical Introduction. Boca Raton: Chapman & Hill/CRC Press, 2009.
- Z. Babio, et al. "Gedap method (genotyping based on diagnostic amplification products) for detecting and/or preventing genotyping errors from amplification products of a polymorphic focus." U.S. Patent #7,402,382. Jul 2008.
- E.A.M. Graham. "An evaluation of forensic DNA profiling techniques currently used in the United Kingdom." Thesis. University of Leicester, 2007.
- Z. Yu. "Haplotype block and genetic association." Doctoral thesis. Rice University, 2006.
- R.R. Denton, R.S. Judson, G. Rúaño, J.C. Stephens, A.K. Widemuth, and C. Xu. "Methods for obtaining and using haplotype data." *U.S. Patent No. 7,058,517*, issued June 6, 2006.
- R. Guerra and Z. Yu. "Single Nucleotide Polymorphisms and Their Applications." Computational and Statistical Approaches to Genomics. Springer US. 311-349, 2006.
- E. Graham. "Automated DNA profile analysis." Forensic Science, Medicine, and Pathology, 1(4):285-288, 2005.
- T. Matsumoto and R. Nakashige. "Evaluating Robustness of Algorithm for Microsatellite Marker Genotyping," in the Proceedings of the *IEEE Symposium*. Oakland, CA, 2005.
- C.G.T. Quiñones. "Análisis de tres polimorfismos del gen DMD/DMB en familias Mexicanas." Thesis. División de Ciencias Biológicas y de la Salud. Universidad Autónoma Metropolitana, 2004.

- Z. Babio, et al. "GEDAP method (genotyping based on diagnostic amplification products) for detecting and/or preventing genotyping errors from amplification products of a polymorphic locus." U.S. Patent Application Publication. #2004/0219550. Nov 2004.
- T. Matsumoto, W. Yukawa, Y. Nozaki, R. Nakashige, M. Shinya, S. Makino, M. Yagura, T. Ikuta, T. Imanishi, H. Inoko, G. Tamiya, and T. Gojobori. "Novel algorithm for automated genotyping of microsatellites." *Nucleic Acids Research*, 32(20):6069-6077, 2004.
- Y. Lai and F. Sun. "Sampling distribution for microsatellites amplified by PCR: mean field approximation and its applications to genotyping." *Journal of Theoretical Biology*, 228(2):185-194, 2004.
- Z. Babío, et al. "Método GEDAP (Genotyping Based on Diagnostic Amplification Products) para detectar y/o prevenir errores de genotipado a partir de los productos de amplification de un locus polimórfico." Oficina Española de Patentes y Marcas, # 2 190 877. Aug 2003.
- Y. Lai, D. Shinde, N. Arnheim, and F. Sun. "The mutation process of microsatellites during the polymerase chain reaction." *Journal of Computational Biology*, 10(2):143-155, April 2003.
- Å. Johansson, P. Karlsson, and U. Gyllensten. "A novel method for automatic genotyping of microsatellite markers based on parametric pattern recognition." *Human Genetics*, 113(4):316-324, 2003.
- Y. Lai and F. Sun. "Microsatellite mutations during the polymerase chain reaction: mean field approximations and their applications." *Journal of Theoretical Biology*, 244(1):127-137, 2003.
- P.S. Umesh Adiga, P. Jeavons, and J. Flint. "Automation of agarose gel image analysis." Dissertation. University of Oxford. 2002.
- J.L. Li, H. Deng, D.B. Lai, F. Xu, J. Chen, G. Gao, R.R. Recker, and H.W. Deng. "Toward high throughput genotyping dynamic and automatic software for manipulating large-scale genotype data using fluorescently labeled dinucleotide markers," *Genome Research*, 11:1304-1314, 2001.
- P.S. Umesh Adiga, A. Bhomra, M.G. Turri, A. Nicod, S.R. Datta, P. Jeavons, R. Mott, and J. Flint. "Automatic analysis of agarose gel images." *Bioinformatics*, 17(11):1084-1089, 2001.

M.A. Alcántara, R. Carcia-Cavazos, E. Hernández-U, A. González-del Angel, A. Carnevale, and L. Orozco. "Carrier detection and prenatal molecular diagnosis in a Duchenne muscular dystrophy family without any affected relative available." *Annales de Génétique*, 44(3):149-153, 2001.

M.J. Miller and B. Yuan. "Semiautomated resolution of overlapping stutter patterns in genomic microsatellite analysis." *Analytical Biochemistry*, 251(1):50-56, 1997.

R.M. Idury and L.R. Cardon. "A simple method for automated allele binning in microsatellite markers." *Genome Research*, 7:1104-1109, 1997.

R. Stoughton, R. Bumgarner, W.J. Frederick III, and R.A. McIndoe. "Data-adaptive algorithms for calling alleles in repeat polymorphisms." *Electrophoresis*, 18(1):1-5, 1997.

G. Lancia. "Optimization problems in computational molecular biology." Dissertation. Carnegie Mellon University. 1997.

L.W. Ballard. "High-Throughput Genetic Analysis in the Core Facility." *Association of Biomolecular Resource Facilities News*, 8:22-28, 1997.

L. Excoffier and M. Slatkin. "Maximum-likelihood estimation of molecular haplotype frequencies in a diploid population." *Molecular Biology and Evolution*, 12(5):921-927, 1995.

J.R. Smith, J.D. Carpten, M.J. Brownstein, S. Ghosh, V.L. Magnuson, D.A. Gilbert, J.M. Trent, and F.S. Collins. "Approach to genotyping errors caused by nontemplated nucleotide addition by Taq DNA polymerase." *Genome Research*, 5:312-317, 1995.

M.W. Perlin. "Transforming conjunctive match into RETE: a call-graph caching approach." *International Journal of Software Engineering and Knowledge Engineering*, 1(4):373:408, 1991.

G. Varró and F. Deckwerth. "A Rete Network Construction Algorithm for Incremental Pattern Matching." In: K. Duddy, and G. Kappel (eds) *Theory and Practice of Model Transformations*. ICMT 2013. Lecture Notes in Computer Science, vol 7909. Springer, Berlin, Heidelberg, 2013