

# DNA Mixtures Reference List

## Background on Elements of Mixture Interpretation and Resources for Further Learning

### Mixture Principles & Recommendations

Buckleton, J.S., & Curran, J.M. (2008). A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Science International: Genetics*, 2, 343-348.

Budowle, B., et al. (2009). Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. *Journal of Forensic Sciences*, 54, 810-821.

DNA Advisory Board (2000) Statistical and population genetic issues affecting the evaluation of the frequency of occurrence of DNA profiles calculated from pertinent population database(s) (approved 23 February 2000). Forensic Science Communications, July 2000. Available at: <http://www.fbi.gov/about-us/lab/forensic-science-communications/fsc/july2000/dnastat.htm>.

Gill, P., et al. (2006). DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Science International*, 160, 90-101.

Gill, P., et al. (2008). National recommendations of the technical UK DNA working group on mixture interpretation for the NDNAD and for court going purposes. *Forensic Science International: Genetics*, 2, 76-82.

Morling, N., et al. (2007). Interpretation of DNA mixtures – European consensus on principles. *Forensic Science International: Genetics*, 1, 291-292.

Puch-Solis, R., Roberts, P., Pope, S., Aitken, C. (2012). Assessing the probative value of DNA evidence: *Guidance for judges, lawyers, forensic scientists and expert witnesses*. Available at <http://www.maths.ed.ac.uk/~cgga/Guide-2-WEB.pdf>.

Rudin, N. & Inman, K. (2012). [The discomfort of thought - a discussion with John Butler](#). *The CACNews*. 1st Quarter 2012, pp. 8-11.

Schneider, P.M., et al. (2006). Editorial on the recommendations of the DNA commission of the ISFG on the interpretation of mixtures. *Forensic Science International*, 160, 89-89.

Schneider, P.M., et al. (2009). The German Stain Commission: recommendations for the interpretation of mixed stains. *International Journal of Legal Medicine*, 123, 1-5. (originally published in German in 2006 -- *Rechtsmedizin* 16:401-404).

Stringer, P., et al. (2009). Interpretation of DNA mixtures—Australian and New Zealand consensus on principles. *Forensic Science International: Genetics*, 3, 144-145.

SWGDM (2010). SWGDM interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories. Available at <http://www.fbi.gov/about-us/lab/codis/swgdam.pdf>.

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

### Setting Thresholds

Currie, L. (1999). Detection and quantification limits: origin and historical overview. *Analytica Chimica Acta*, 391, 127–134.

Gilder, J.R., et al. (2007). Run-specific limits of detection and quantitation for STR-based DNA testing. *Journal of Forensic Sciences*, 52, 97-101.

Gill, P., et al. (2009). The *low-template-DNA* (stochastic) threshold -- its determination relative to risk analysis for national DNA databases. *Forensic Science International: Genetics*, 3, 104-111.

Gill, P. and Buckleton, J. (2010). A universal strategy to interpret DNA profiles that does not require a definition of *low-copy-number*. *Forensic Science International: Genetics*, 4, 221-227.

Kaiser, H. (1970). Report for analytical chemists: part II. Quantitation in elemental analysis. *Analytical Chemistry*, 42, 26A-59A.

Long, G.L., & Winefordner, J.D. (1983). Limit of detection: a closer look at the IUPAC definition. *Analytical Chemistry*, 55, 712A-724A.

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### Background on Elements of Mixture Interpretation and Resources for Further Learning

Miller J.C., & Miller J.N. (2005). Errors in instrumental analysis; regression and correlation in *Statistics for Analytical Chemistry*, Ellis Horwood and Prentice Hall, pp. 101-137.

Mocak, J., Bond, A.M., Mitchell, S., & Scollary, G. (1997). A statistical overview of standard (IUPAC and ACS) and new procedures for determining the limits of detection and quantification: application to voltammetric and stripping techniques. *Pure and Applied Chemistry*, 69, 297-328.

Puch-Solis, R., et al. (2011). Practical determination of the low template DNA threshold. *Forensic Science International: Genetics*, 5(5), 422-427.

Rakay, C.A., et al. (2012). Maximizing allele detection: effects of analytical threshold and DNA levels on rates of allele and locus drop-out. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.06.012>

Rubinson, K.A., & Rubinson, J.F. (2000). Sample size and major, minor, trace, and ultratrace components. *Contemporary Instrumental Analysis*. Upper Saddle River: Prentice Hall, pp. 150–158.

### Stutter Products & Peak Height Ratios

Blackmore, V.L., et al. (2000). Preferential amplification and stutter observed in population database samples using the AmpFISTR Profiler multiplex system. *Canadian Society of Forensic Sciences Journal*, 33, 23-32.

Bright, J.-A., et al. (2010). Examination of the variability in mixed DNA profile parameters for the Identifiler multiplex. *Forensic Science International: Genetics*, 4, 111-114.

Bright, J.-A., et al. (2011). Determination of the variables affecting mixed MiniFiler™ DNA profiles. *Forensic Science International: Genetics*, 5(5), 381-385.

Brookes, C., Bright, J.A., Harbison, S., Buckleton, J. (2012). Characterising stutter in forensic STR multiplexes. *Forensic Science International: Genetics*, 6(1), 58-63.

Buckleton, J. (2009). Validation issues around DNA typing of low level DNA. *Forensic Science International: Genetics*, 3, 255-260.

Buse, E.L., et al. (2003). Performance evaluation of two multiplexes used in fluorescent short tandem repeat DNA analysis. *Journal of Forensic Sciences*, 48, 348-357.

Debernardi, A., et al. (2011). One year variability of peak heights, heterozygous balance and inter-locus balance for the DNA positive control of AmpFISTR Identifiler STR kit. *Forensic Science International: Genetics*, 5(1), 43-49.

Gibb, A.J., et al. (2009). Characterisation of forward stutter in the AmpFISTR SGM Plus PCR. *Science & Justice*, 49, 24-31.

Gilder, J.R., et al. (2011). Magnitude-dependent variation in peak height balance at heterozygous STR loci. *International Journal of Legal Medicine*, 125, 87-94.

Gill, P., et al. (1997). Development of guidelines to designate alleles using an STR multiplex system. *Forensic Science International*, 89, 185-197.

Gill, P., et al. (1998). Interpretation of simple mixtures when artifacts such as stutters are present—with special reference to multiplex STRs used by the Forensic Science Service. *Forensic Science International*, 95, 213-224.

Hill, C.R., et al. (2011). Concordance and population studies along with stutter and peak height ratio analysis for the PowerPlex® ESX 17 and ESI 17 Systems. *Forensic Science International: Genetics*, 5, 269-275.

Kelly, H., et al. (2012). Modelling heterozygote balance in forensic DNA profiles. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.08.002>

Leclair, B., et al. (2004). Systematic analysis of stutter percentages and allele peak height and peak area ratios at heterozygous STR loci for forensic casework and database samples. *Journal of Forensic Sciences*, 49, 968-980.

Moretti, T.R., et al. (2001). Validation of short tandem repeats (STRs) for forensic usage: performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. *Journal of Forensic Sciences*, 46, 647-660.

## **DNA Mixtures Reference List**

### Background on Elements of Mixture Interpretation and Resources for Further Learning

- Moretti, T.R., et al. (2001). Validation of STR typing by capillary electrophoresis. *Journal of Forensic Sciences*, 46, 661-676.
- Mulero, J.J., et al. (2006). Characterization of the N+3 stutter product in the trinucleotide repeat locus DYS392. *Journal of Forensic Sciences*, 51, 1069-1073.
- Wallin, J.M., et al. (1998). TWGDAM validation of the AmpFISTR Blue PCR amplification kit for forensic casework analysis. *Journal of Forensic Sciences*, 43, 854-870.
- Walsh, P.S., et al. (1996). Sequence analysis and characterization of stutter products at the tetranucleotide repeat locus vWA. *Nucleic Acids Research*, 24, 2807-2812.

### **Stochastic Effects & Allele Dropout**

- Balding, D.J., & Buckleton, J. (2009). Interpreting low template DNA profiles. *Forensic Science International: Genetics*, 4: 1-10.
- Benschop, C.C.G., et al. (2011). Low template STR typing: effect of replicate number and consensus method on genotyping reliability and DNA database search results. *Forensic Science International: Genetics*, 5, 316-328.
- Bright, J.-A., et al. (2012). A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. *Forensic Science International: Genetics*, 6(2), 180-184.
- Bright, J.-A., et al. (2012). Composite profiles in DNA analysis. *Forensic Science International: Genetics*, 6(3), 317-321.
- Gill, P., et al. (2005). A graphical simulation model of the entire DNA process associated with the analysis of short tandem repeat loci. *Nucleic Acids Research*, 33, 632-643.
- Gill, P., et al. (2008). Interpretation of complex DNA profiles using empirical models and a method to measure their robustness. *Forensic Science International: Genetics*, 2, 91-103.
- Gill, P., et al. (2008). Interpretation of complex DNA profiles using Tippett plots. *Forensic Science International: Genetics Supplement Series*, 1, 646-648.
- Haned, H., et al. (2011). Estimating drop-out probabilities in forensic DNA samples: a simulation approach to evaluate different models. *Forensic Science International: Genetics*, 5, 525-531.
- Kelly, H., et al. (2012). The interpretation of low level DNA mixtures. *Forensic Science International: Genetics*, 6(2), 191-197.
- Puch-Solis, R., et al. (2009). Assigning weight of DNA evidence using a continuous model that takes into account stutter and dropout. *Forensic Science International: Genetics Supplement Series*, 2, 460-461.
- Stenman, J., & Orpana, A. (2001). Accuracy in amplification. *Nature Biotechnology*, 19, 1011-1012.
- Taberlet, P., et al. (1996). Reliable genotyping of samples with very low DNA quantities using PCR. *Nucleic Acids Research*, 24, 3189-3194.
- Tvedebrink, T., et al. (2008). Amplification of DNA mixtures—missing data approach. *Forensic Science International: Genetics Supplement Series*, 1, 664-666.
- Tvedebrink, T., et al. (2009). Estimating the probability of allelic drop-out of STR alleles in forensic genetics. *Forensic Science International: Genetics*, 3, 222-226.
- Tvedebrink, T., et al. (2012). Statistical model for degraded DNA samples and adjusted probabilities for allelic drop-out. *Forensic Science International: Genetics*, 6(1), 97-101.
- Tvedebrink, T., et al. (2012). Allelic drop-out probabilities estimated by logistic regression – further considerations and practical implementation. *Forensic Science International: Genetics*, 6(2), 263-267.
- Walsh, P.S., et al. (1992). Preferential PCR amplification of alleles: Mechanisms and solutions. *PCR Methods and Applications*, 1, 241-250.

## **DNA Mixtures Reference List**

### Background on Elements of Mixture Interpretation and Resources for Further Learning

Weiler, N.E.C., et al. (2012). Extending PCR conditions to reduce drop-out frequencies in low template STR typing including unequal mixtures. *Forensic Science International: Genetics*, 6(1), 102-107.

### **Estimating the Number of Contributors**

Biedermann, A., et al. (2012). Inference about the number of contributors to a DNA mixture: comparative analyses of a Bayesian network approach and the maximum allele count method. *Forensic Science International: Genetics*, (in press).  
<http://dx.doi.org/10.1016/j.fsigen.2012.03.006>

Brenner, C.H., et al. (1996). Likelihood ratios for mixed stains when the number of donors cannot be agreed. *International Journal of Legal Medicine* 109, 218-219.

Buckleton, J.S., et al. (1998). Setting bounds for the likelihood ratio when multiple hypotheses are postulated. *Science & Justice* 38, 23-26.

Buckleton, J.S., et al. (2007). Towards understanding the effect of uncertainty in the number of contributors to DNA stains. *Forensic Science International: Genetics*, 1, 20-28.

Clayton, T.M., et al. (2004). A genetic basis for anomalous band patterns encountered during DNA STR profiling. *Journal of Forensic Sciences*, 49, 1207-1214.

Egeland, T., et al. (2003). Estimating the number of contributors to a DNA profile. *International Journal of Legal Medicine*, 117, 271-275.

Ge, J., et al. (2011). Comparisons of familial DNA database searching strategies. *Journal of Forensic Sciences*, 56(6), 1448-1456.

Haned, H., et al. (2011). The predictive value of the maximum likelihood estimator of the number of contributors to a DNA mixture. *Forensic Science International: Genetics*, 5(5), 281-284.

Haned, H., et al. (2011). Estimating the number of contributors to forensic DNA mixtures: does maximum likelihood perform better than maximum allele count? *Journal of Forensic Sciences*, 56(1), 23-28.

Lauritzen, S.L., & Mortera, J. (2002). Bounding the number of contributors to mixed DNA stains. *Forensic Science International* 130, 125-126.

Paoletti, D.R., et al. (2005). Empirical analysis of the STR profiles resulting from conceptual mixtures. *Journal of Forensic Sciences*, 50, 1361-1366.

Paoletti, D.R., et al. (2012). Inferring the number of contributors to mixed DNA profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 9(1), 113-122.

Perez, J., et al. (2011). 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.

Presciuttini, S., et al. (2003) Allele sharing in first-degree and unrelated pairs of individuals in the Ge. F.I. AmpFISTR Profiler Plus database. *Forensic Science International*, 131, 85-89.

Tvedebrink, T., et al. (2012). Identifying contributors of DNA mixtures by means of quantitative information of STR typing. *Journal of Computational Biology*, 19(7), 887-902.

### **Mixture Ratios**

Clayton, T.M., et al. (1998). Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Science International*, 91, 55-70.

Cowell, R.G., et al. (2007). Identification and separation of DNA mixtures using peak area information. *Forensic Science International*, 166, 28-34.

Cowell, R.G. (2009). Validation of an STR peak area model. *Forensic Science International: Genetics*, 3(3), 193-199.

## **DNA Mixtures Reference List**

### Background on Elements of Mixture Interpretation and Resources for Further Learning

- Evett, I.W., et al. (1998). Taking account of peak areas when interpreting mixed DNA profiles. *Journal of Forensic Sciences*, 43, 62-69.
- Frégeau, C.J., et al. (2003). AmpFISTR Profiler Plus short tandem repeat DNA analysis of casework samples, mixture samples, and nonhuman DNA samples amplified under reduced PCR volume conditions (25 microL). *Journal of Forensic Sciences*, 48, 1014-1034.
- Gill, P., et al. (1998). Interpreting simple STR mixtures using allelic peak areas. *Forensic Science International*, 91, 41-53.
- Perlin, M.W., & Szabady, B. (2001). Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *Journal of Forensic Sciences*, 46, 1372-1378.
- Tvedebrink, T., et al. (2010). Evaluating the weight of evidence by using quantitative short tandem repeat data in DNA mixtures. *Journal of Royal Statistical Society: Series C (Applied Statistics)*, 59(5), 855-874.
- Wang, T., et al. (2006). Least-squares deconvolution: a framework for interpreting short tandem repeat mixtures. *Journal of Forensic Sciences*, 51, 1284-1297.

### **Statistical Approaches**

- Balding, D.J. (2005) *Weight-of-evidence for Forensic DNA Profiles*. John Wiley & Sons; see mixture section on pp. 101-110.
- Chung, Y.K., et al. (2010). Evaluation of DNA mixtures from database search. *Biometrics*, 66, 233-238.
- Chung, Y.K., & Fung, W.K. (2011). The evidentiary values of "cold hits" in a DNA database search on two-person mixture. *Science & Justice*, 51(1), 10-15.
- Cowell, R.G., et al. (2007). A gamma model for DNA mixture analyses. *Bayesian Analysis*, 2(2), 333-348.
- Curran, J.M., et al. (1999). Interpreting DNA mixtures in structured populations. *Journal of Forensic Sciences*, 44, 987-995.
- Curran, J.M., & Buckleton, J. (2010). Inclusion probabilities and dropout. *Journal of Forensic Science*, 55, 1171-1173.
- Devlin, B. (1993). Forensic inference from genetic markers. *Statistical Methods in Medical Research*, 2, 241-262.
- Evett, I.W., et al. (1991). A guide to interpreting single locus profiles of DNA mixtures in forensic cases. *Journal of Forensic Science Society*, 31, 41-47.
- Evett, I.W., & Weir, B.S. (1998). *Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists*. Sunderland, MA: Sinauer Associates.
- Fung, W.K., & Hu, Y.-Q. (2001). The evaluation of mixed stains from different ethnic origins: general result and common cases. *International Journal of Legal Medicine*, 115, 48-53.
- Fung, W.K., & Hu, Y.-Q. (2002). The statistical evaluation of DNA mixtures with contributors from different ethnic groups. *International Journal of Legal Medicine*, 116, 79-86.
- Fung, W.K., & Hu, Y.-Q. (2002). Evaluating mixed stains with contributors of different ethnic groups under the NRC-II Recommendation 4.1. *Statistics in Medicine*, 21, 3583-3593.
- Fung, W.K., & Hu, Y.-Q. (2008). *Statistical DNA Forensics: Theory, Methods and Computation*. Wiley: Hoboken, NJ.
- Hu, Y.-Q., & Fung, W.K. (2003). Interpreting DNA mixtures with the presence of relatives. *International Journal of Legal Medicine*, 117, 39-45.
- Hu, Y.-Q., & Fung, W.K. (2003). Evaluating forensic DNA mixtures with contributors of different structured ethnic origins: a computer software. *International Journal of Legal Medicine*, 117, 248-249.

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### Background on Elements of Mixture Interpretation and Resources for Further Learning

Hu, Y.-Q., & Fung, W.K. (2005). Evaluation of DNA mixtures involving two pairs of relatives. *International Journal of Legal Medicine*, 119(5), 251-259.

Ladd, C., et al. (2001). Interpretation of complex forensic DNA mixtures. *Croatian Medical Journal*, 42, 244-246.

Pascali, V.L., & Meriglioli, S. (2012). Joint Bayesian analysis of forensic mixtures. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.08.005>

Perlin, M.W. (2010). Explaining the likelihood ratio in DNA mixture interpretation. *Proceedings of the 21<sup>st</sup> International Symposium on Human Identification (Promega Corporation)*. Available at <http://www.cybgcn.com/information/publication/page.shtml>.

Puch-Solis, R., et al. (2010). Calculating likelihood ratios for a mixed DNA profile when a contribution from a genetic relative of a suspect is proposed. *Science & Justice*, 50(4), 205-209.

van Nieuwerburgh, F., et al. (2009). Impact of allelic dropout on evidential value of forensic DNA profiles using RMNE. *Bioinformatics* 25, 225-229.

van Nieuwerburgh, F., et al. (2009). RMNE probability of forensic DNA profiles with allelic drop-out. *Forensic Science International: Genetics Supplement Series*, 2, 462-463.

Weir, B.S., et al. (1997). Interpreting DNA mixtures. *Journal of Forensic Sciences* 42, 213-222.

### **Low Template DNA Mixtures**

Bekaert, B., et al. (2012). Automating a combined composite-consensus method to generate DNA profiles from low and high template mixture samples. *Forensic Science International: Genetics*, 6(5), 588-593.

Benschop, C.C.G., et al. (2012). Assessment of mock cases involving complex low template DNA mixtures: a descriptive study. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.04.007>

Benschop, C.C.G., et al. (2012). Consensus and pool profiles to assist in the analysis and interpretation of complex low template DNA mixtures. *International Journal of Legal Medicine*, (in press). doi:10.1007/s00414-011-0647-5

Budimilija, Z.M., & Caragine, T.A. (2012). Interpretation guidelines for multilocus STR forensic profiles from low template DNA samples. *DNA Electrophoresis Protocols for Forensic Genetics (Methods in Molecular Biology, volume 830)*, pp. 199-211.

Caragine, T., et al. (2009). Validation of testing and interpretation protocols for low template DNA samples using AmpFISTR Identifier. *Croatian Medical Journal*, 50(3), 250-267.

Mitchell, A.A., et al. (2011). Likelihood ratio statistics for DNA mixtures allowing for drop-out and drop-in. *Forensic Science International: Genetics Supplement Series*, 3, e240-e241.

Pfeifer, C., et al. (2012). Comparison of different interpretation strategies for low template DNA mixtures. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.06.006>

Westen, A.A., et al. (2012). Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.05.001>

### **Separating Cells to Avoid Mixtures**

Li, C.-X., et al. (2011). New cell separation technique for the isolation and analysis of cells from biological mixtures in forensic caseworks. *Croatian Medical Journal*, 52(3), 293-298.

Rothe, J., et al. (2011). Individual specific extraction of DNA from male mixtures--First evaluation studies. *Forensic Science International: Genetics*, 5(2), 117-121.

Schneider, H., et al. (2011). Hot flakes in cold cases. *International Journal of Legal Medicine*, 125, 543-548.

## DNA Mixtures Reference List

### Background on Elements of Mixture Interpretation and Resources for Further Learning

#### Software

Bill, M., et al. (2005). PENDULUM-a guideline-based approach to the interpretation of STR mixtures. *Forensic Science International*, 148, 181-189.

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

Haned, H., & Gill, P. (2011). Analysis of complex DNA mixtures using the Forensim package. *Forensic Science International: Genetics Supplement Series*, 3, e79-e80.

Hansson, O., & Gill, P. (2011). Evaluation of GeneMapper ID-X mixture analysis tool. *Forensic Science International: Genetics Supplement Series*, 3, e11-e12.

Mortera, J., et al. (2003). Probabilistic expert system for DNA mixture profiling. *Theoretical and Population Biology*, 63, 191-205.

Oldroyd, N., & Shade, L.L. (2008) Expert assistant software enables forensic DNA analysts to confidently process more samples. *Forensic Magazine Dec 2008/Jan 2009*, 25-28; available at <http://www.forensicmag.com/articles.asp?pid=240>.

Perlin, M.W. (2006). Scientific validation of mixture interpretation methods. *Proceedings of Promega's Seventeenth International Symposium on Human Identification*. Available at <http://www.promega.com/geneticidproc/ussymp17proc/oralpresentations/Perlin.pdf>.

ISFG Software Resources Page: <http://www.isfg.org/software>

Forensic DNA Statistics (Peter Gill): <https://sites.google.com/site/forensicdnastatistics/>

DNAMIX (Bruce Weir): <http://www.biostat.washington.edu/~bsweir/DNAMIX3/webpage/>

LRmix (Hinda Haned): <https://sites.google.com/site/forensicdnastatistics/PCR-simulation/Lrmix>

Forensim (Hinda Haned): <http://forensim.r-forge.r-project.org/>

DNA Mixture Separator (Torben Tvedebrink): <http://people.math.aau.dk/~tvede/mixsep/>

likeLTD (David Balding): <https://sites.google.com/site/baldingstatisticalgenetics/software/likeltd-r-forensic-dna-r-code>

Armed Xpert (NicheVision): <http://www.armedxpert.com/>

GeneMapperID-X (Life Technologies/Applied Biosystems): <http://idx.appliedbiosystems.com>

GeneMarker HID (Soft Genetics): <http://www.softgenetics.com/GeneMarkerHID.html>

GenoProof Mixture (Qualitytype): <http://www.qualitytype.de/en/qualitytype/genoproof-mixture>

TrueAllele Casework (Cybergenetics): <http://www.cybgen.com/systems/casework.shtml>

#### Probabilistic Genotyping Approach

Ballantyne, J., Hanson, E.K., Perlin, M.W. (2012). DNA mixture genotyping by probabilistic computer interpretation of binomially-sampled laser captured cell populations: combining quantitative data for greater identification information. *Science & Justice*, (in press) DOI 10.1016/j.scijus.2012.04.004.

Cowell, R.G., et al. (2008). Probabilistic modelling for DNA mixture analysis. *Forensic Science International: Genetics Supplement Series*, 1, 640-642.

Cowell, R.G., et al. (2011). Probabilistic expert systems for handling artifacts in complex DNA mixtures. *Forensic Science International: Genetics*, 5(3), 202-209.

Curran, J.M. (2008). A MCMC method for resolving two person mixtures. *Science & Justice*, 48, 168-177.

## **DNA Mixtures Reference List**

### Background on Elements of Mixture Interpretation and Resources for Further Learning

- Gill, P., & Buckleton, J. (2010). Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL. Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. *J Forensic Sci* 2009;54(4):810-21. *Journal of Forensic Sciences*, 55(1), 265-268.
- Gill, P., et al. (2012). 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*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.06.002>
- Perlin, M.W. (2006). Scientific validation of mixture interpretation methods. *Proceedings of the 17<sup>th</sup> International Symposium on Human Identification (Promega Corporation)*. Available at <http://www.cybgen.com/information/publication/page.shtml>.
- Perlin, M.W., & Sinelnikov, A. (2009). An information gap in DNA evidence interpretation. *PLoS ONE*, 4(12), e8327.
- Perlin, M.W., et al. (2009). Match likelihood ratio for uncertain genotypes. *Law, Probability and Risk*, 8, 289-302.
- Perlin, M.W., et al. (2011). Validating TrueAllele DNA mixture interpretation. *Journal of Forensic Sciences*, 56(6), 1430-1447.
- Perlin, M.W. (2012). Easy reporting of hard DNA: computer comfort in the courtroom. *Forensic Magazine*, 9(4), 32-37. Available at <http://www.cybgen.com/information/publication/page.shtml>.

### **General Information on Mixtures**

- Clayton, T., & Buckleton, J. (2005). Mixtures. Chapter 7 in *Forensic DNA Evidence Interpretation* (Eds.: Buckleton, J., Triggs, C.M., Walsh, S.J.), CRC Press, pp. 217-274.
- Dror, I.E., & Hampikian, G. (2011). Subjectivity and bias in forensic DNA mixture interpretation. *Science & Justice*, 51(4), 204-208.
- Kamodyova, N., et al. (2012). Prevalance and persistence of male DNA identified in mixed saliva samples after intense kissing. *Forensic Science International: Genetics*, (in press). <http://dx.doi.org/10.1016/j.fsigen.2012.07.007>
- Nurit, B., et al. (2011). Evaluating the prevalence of DNA mixtures found in fingernail samples from victims and suspects in homicide cases. *Forensic Science International: Genetics*, 5, 532-537.
- Tomsey, C.S., et al. (2001). Case work guidelines and interpretation of short tandem repeat complex mixture analysis. *Croatian Medical Journal*, 42, 276-280.
- Torres, Y., et al. (2003). DNA mixtures in forensic casework: a 4-year retrospective study. *Forensic Science International*, 134, 180-186.
- Wetton, J.H., et al. (2011). Analysis and interpretation of mixed profiles generated by 34 cycle SGM Plus amplification. *Forensic Science International: Genetics*, 5(5), 376-380.