

Additional Training Resources

Forensic STR Data Interpretation (on-line training): <http://www.forensic-training-network.com>

STR Data Analysis and Interpretation (on-line training): <http://www.nij.gov/training/courses/analyst-str-data.htm>

Boston University DNA Mixture Training: <http://www.bu.edu/dnamixtures/>

NIST DNA Analyst Training on Mixture Interpretation: <http://www.nist.gov/oles/forensics/dna-analyst-training-on-mixture-interpretation.cfm>

NIST 2013 webcast: <http://www.nist.gov/oles/forensics/dna-analyst-training-on-mixture-interpretation-webcast.cfm>

NIST STRBase Mixture Information: <http://www.cstl.nist.gov/strbase/mixture.htm>

Guidance for DNA Interpretation

Butler, J.M. (2013). Forensic DNA advisory groups: DAB, SWGDAM, ENFSI, and BSAG. *Encyclopedia of Forensic Sciences, 2nd Edition*. Elsevier Academic Press: New York.

DNA Commission of the ISFG: <http://www.isfg.org/Publications/DNA+Commission>

European Network of Forensic Science Institutes (ENFSI) DNA Working Group: <http://www.enfsi.eu/about-enfsi/structure/working-groups/dna?uid=98>

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.

Gill, P., Guinness, J., Iveson, S. (2012). The interpretation of DNA evidence (including low-template DNA). Available at <http://www.homeoffice.gov.uk/publications/agencies-public-bodies/fsr/interpretation-of-dna-evidence>

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, 6*, 679-688.

Hobson, D., et al. (1999). STR analysis by capillary electrophoresis: development of interpretation guidelines for the Profiler Plus and COfiler systems for use in forensic science. *Proceedings of the 10th International Symposium on Human Identification*. Available at <http://www.promega.com/products/pm/genetic-identity/ishi-conference-proceedings/10th-ishi-oral-presentations/>.

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>.

QAS (2011). Quality Assurance Standards for Forensic DNA Testing Laboratories effective 9-1-2011. See <http://www.fbi.gov/about-us/lab/codis/qas-standards-for-forensic-dna-testing-laboratories-effective-9-1-2011>.

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).

Scientific Working Group on DNA Analysis Methods (SWGDAM): <http://www.swgdam.org>

SWGDAM (2010). SWGDAM Interpretation Guidelines for Autosomal STR Typing by Forensic DNA Testing Laboratories. Available at http://www.swgdam.org/Interpretation_Guidelines_January_2010.pdf

SWGDAM (2012). Validation Guidelines for DNA Analysis Methods. Available at http://swgdam.org/SWGDAM_Validation_Guidelines_APPROVED_Dec_2012.pdf.

Software for DNA Analysis and Interpretation

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

BatchExtract: <ftp://ftp.ncbi.nih.gov/pub/forensics/BATCHEXTRACT>

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

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

EPG Maker program (Steven Myers): [http://www.cstl.nist.gov/strbase/tools/EPG-Maker\(SPMv.3,Dec2-2011\).xlt](http://www.cstl.nist.gov/strbase/tools/EPG-Maker(SPMv.3,Dec2-2011).xlt)
(13 Mb Excel file)

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

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

GeneMapper/D-X (from Applied Biosystems): <http://www.lifetechnologies.com/us/en/home/technical-resources/software-downloads/genemapper-id-x-software.html>

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

Genetic Analysis Data File Format, Sept 2009. Available at
<http://www.appliedbiosystems.com/absite/us/en/home/support/software-community/tools-for-accessing-files.html>

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

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

Lab Retriever (Scientific Collaboration, Innovation & Education Group): http://www.scieg.org/lab_retriever.html

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

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

OSIRIS (Open Source Independent Review and Interpretation System):
<http://www.ncbi.nlm.nih.gov/projects/SNP/osiris/>

STRmix (Ducan Taylor, Jo-Anne Bright, John Buckleton): <http://strmix.com/>

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

STR Kits, Loci, and Population Data

Butler, J.M. & Hill, C.R. (2013). Biology and genetics of new autosomal STR loci useful for forensic DNA analysis. Chapter 9 in Shewale, J. (ed.), *Forensic DNA Analysis: Current Practices and Emerging Technologies*. Taylor & Francis/CRC Press: Boca Raton. pp. 181-198.

FBI (2012). Planned process and timeline for implementation of additional CODIS core loci. Available at
<http://www.fbi.gov/about-us/lab/codis/planned-process-and-timeline-for-implementation-of-additional-codis-core-loci>.

GlobalFiler information: <http://www.invitrogen.com/site/us/en/home/industrial/human-identification/globalfiler-str-kit/resources.html>

NIST U.S. Population Data: <http://www.cstl.nist.gov/strbase/NISTpop.htm>.

PowerPlex Fusion System. <http://www.promega.com/products/pm/genetic-identity/powerplex-fusion>.

STRBase: <http://www.cstl.nist.gov/strbase>.

Setting Thresholds

- Bregu, J., et al. (2013). Analytical thresholds and sensitivity: establishing RFU thresholds for forensic DNA analysis. *Journal of Forensic Sciences*, 58, 120-129.
- 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.
- 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*, 6, 723-728.

Statistical Approaches

- Curran, J.M., et al. (1999). Interpreting DNA mixtures in structured populations. *Journal of Forensic Sciences*, 44, 987-995.
- 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.
- Curran, J.M., & Buckleton, J. (2010). Inclusion probabilities and dropout. *Journal of Forensic Science*, 55, 1171-1173.
- Evetts, 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.
- Evetts, I.W., & Weir, B.S. (1998). *Interpreting DNA Evidence: Statistical Genetics for Forensic Scientists*. Sunderland, MA: Sinauer Associates.
- 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.
- Pascali, V.L., & Merigioli, S. (2012). Joint Bayesian analysis of forensic mixtures. *Forensic Science International: Genetics*, 6, 735-748.
- 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.
- Weir, B.S., et al. (1997). Interpreting DNA mixtures. *Journal of Forensic Sciences* 42, 213-222.

Stutter Products & Peak Height Ratios

- 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.
- Bright, J.-A., Curran, J.M., Buckleton, J.S. (2013). Investigation into the performance of different models for predicting stutter. *Forensic Science International: Genetics*, 7(4), 422-427.
- Bright, J.-A., et al. (2013). Developing allelic and stutter peak height models for a continuous method of DNA interpretation. *Forensic Science International: Genetics*, 7(2), 296-304.
- Brookes, C., Bright, J.A., Harbison, S., Buckleton, J. (2012). Characterising stutter in forensic STR multiplexes. *Forensic Science International: Genetics*, 6(1), 58-63.
- 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*, 6, 729-734.
- Kirkham, A., et al. (2013). High-throughput analysis using AmpFISTR Identifiler with the Applied Biosystems 3500xl Genetic Analyzer. *Forensic Science International: Genetics*, 7, 92-97.
- 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.
- Manabe, S., et al. (2013). Mixture interpretation: experimental and simulated reevaluation of qualitative analysis. *Legal Medicine*, 15, 66-71.
- 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.
- Moretti, T.R., et al. (2001). Validation of STR typing by capillary electrophoresis. *Journal of Forensic Sciences*, 46, 661-676.
- 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.

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*, 6, 689-696.
- 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. (2007). Towards understanding the effect of uncertainty in the number of contributors to DNA stains. *Forensic Science International: Genetics*, 1, 20-28.
- Egeland, T., et al. (2003). Estimating the number of contributors to a DNA profile. *International Journal of Legal Medicine*, 117, 271-275.
- 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.

Mixture Ratios & Deconvolution

- 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.
- Evet, I.W., et al. (1998). Taking account of peak areas when interpreting mixed DNA profiles. *Journal of Forensic Sciences*, 43, 62-69.
- 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. (2012). Identifying contributors of DNA mixtures by means of quantitative information of STR typing. *Journal of Computational Biology*, 19(7), 887-902.
- Wang, T., et al. (2006). Least-squares deconvolution: a framework for interpreting short tandem repeat mixtures. *Journal of Forensic Sciences*, 51, 1284-1297.

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.
- Gill, P., & Haned, H. (2013). A new methodological framework to interpret complex DNA profiles using likelihood ratios. *Forensic Science International: Genetics*, 7, 251-263.
- 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.
- Puch-Solis, R., et al. (2013). Evaluating forensic DNA profiles using peak heights, allowing for multiple donors, allelic dropout and stutters. *Forensic Science International: Genetics*, 7, 555-563.
- 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.
- 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.

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*, 6, 697-707.

Benschop, C.C.G., et al. (2013). Consensus and pool profiles to assist in the analysis and interpretation of complex low template DNA mixtures. *International Journal of Legal Medicine*, 127, 11-23.

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.

Haned, H., et al. (2012). Exploratory data analysis for the interpretation of low template DNA mixtures. *Forensic Science International: Genetics*, 6, 762-774.

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.

Mitchell, A.A., et al. (2012). Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in. *Forensic Science International: Genetics*, 6, 749-761.

Pfeifer, C., et al. (2012). Comparison of different interpretation strategies for low template DNA mixtures. *Forensic Science International: Genetics*, 6, 716-722.

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*, 6, 708-715.

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.

Probabilistic Genotyping

Cowell, R.G., et al. (2008). Probabilistic modeling 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.

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.

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

Perlin, M.W., et al. (2011). Validating TrueAllele DNA mixture interpretation. *Journal of Forensic Sciences*, 56(6), 1430-1447.

Taylor, D., Bright, J.-A., Buckleton, J. (2013). The interpretation of single source and mixed DNA profiles. *Forensic Science International: Genetics*, 7(5), 516-528.