

Selected Forensic Statistic References
September 2015

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

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

Buckleton, J.S., Curran, J.M., Gill, P., Towards understanding the effect of uncertainty in the number of contributors to DNA stains, *Forensic Science International: Genetics* 1 (2007) 20–28.

Gill, P., Kirkham, A., Curran, J., LoComatioN: A software tool for the analysis of low copy number DNA profiles, *Forensic Science International* 166 (2007) 128–13.

Balding, D.J., Buckleton J., Interpreting low template DNA profile, *Forensic Science International: Genetics* 4 (2009) 1–10.

Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N., Estimating the probability of allelic drop-out of STR alleles in forensic genetics. *Forensic Science International: Genetics* 3 (2009) 222–226.

Perlin, M.W., Sineelnikov, A., An Information Gap in DNA Evidence Interpretation, *PLOS one*, (2009), 4(12)

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

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

Perlin, M.W., et al., Validating TrueAllele DNA Mixture Interpretation, *J Forensic Sci*, (2011), Vol. 56, No. 6

Haned, H., Egeland, T., Pontier, D., Pene, L., Gill, P., Estimating drop-out probabilities in forensic DNA samples: A simulation approach to evaluate different model, *Forensic Science International: Genetics* 5 (2011) 525–531.

Tvedebrink, T., Eriksen, P.S., Mogensen, H.S., Morling, N., Statistical model for degraded DNA samples and adjusted probabilities for allelic drop-out, *Forensic Science International: Genetics* 6 (2012) 97–101.

Carracedo, A., Schneider, P.M., Butler, J., Prinz, M., Focus issue—Analysis and biostatistical interpretation of complex and low template DNA samples, *Forensic Science International: Genetics* 6 (2012) 677–678.

Gill et al., 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 (2012) 679–688.

Benschop, C.C.G., Assessment of mock cases involving complex low template DNA mixtures: A descriptive study, *Forensic Science International: Genetics* 6 (2012) 697–707.

Biedermann, A., Bozza, S., Konis, K., Taroni, F., 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 (2012) 689–696.

Haned, H., Slooten, K., Gill, P., Exploratory data analysis for the interpretation of low template DNA mixtures, *Forensic Science International: Genetics* 6 (2012) 762–774.



- Bright, J-A., McManus, K., Harbison, S., Gill, P., Buckleton., A comparison of stochastic variation in mixed and unmixed casework and synthetic samples., *Forensic Science International: Genetics* 6 (2012) 180–184.
- Kelly, H., Bright, J-A., Curran, J., Buckleton, J., The interpretation of low level DNA mixtures, *Forensic Science International: Genetics* 6 (2012) 191–197.
- Mitchell, A. et al., Validation of a DNA mixture statistics tool incorporating allelic drop-out and drop-in, *Forensic Science International: Genetics* 6 (2012) 749–76.
- Pfeifer, C.M., et al., Comparison of different interpretation strategies for low template DNA mixture, *Forensic Science International: Genetics* 6 (2012) 716–722
- Rakay, C.A., Bregu, J., Gricak, C.M., Maximizing allele detection: Effects of analytical threshold and DNA levels on rates of allele and locus drop-out, *Forensic Science International: Genetics* 6 (2012) 723–728
- Tvedebrink, T., et al., Allelic drop-out probabilities estimated by logistic regression—Further considerations and practical implementation, *Forensic Science International: Genetics* 6 (2012) 263–267
- Lohmueller, K.E., Rudin, N., Calculating the Weight of Evidence in Low-Template Forensic DNA Casework, *J Forensic Sci*, 2012
- Westen, A.A., et al., Assessment of the stochastic threshold, back- and forward stutter filters and low template techniques for NGM, *Forensic Science International: Genetics* 6 (2012) 708-715
- Bright, J-A, Taylor, D., Curran, J.M., Buckleton, J.S., Developing allelic and stutter peak height models for a continuous method of DNA interpretation, *Forensic Science International: Genetics* 7 (2013) 296-304
- Taylor, D., Bright, J-A., Buckleton, J., The interpretation of single source and mixed DNA profiles, *Forensic Science International: Genetics* 7 (2013) 516-528
- Gill, P., Haned, H., A new methodological framework to interpret complex DNA profiles using likelihood ratios, *Forensic Science International: Genetics* 7 (2013) 251-263
- Balding, D.J., Evaluation of mixed-source, low-template DNA profiles in forensic science, *PNAS early edition* (2013)
- Balding, D., likeLTD (likelihoods for low-template DNA profiles)
<https://sites.google.com/site/baldingstatisticalgenetics/software/likeltd-r-forensic-dna-r-code>
- Lohmueller, K.E., Rudin, N., Inman, K., Analysis of allelic drop-out using the Identifiler and PowerPlex 16 forensic STR typing systems, *Forensic Science International: Genetics* 12 (2014) 1-11
- Kelly, H., Bright, J-A, Buckleton, J.S., Curran, J.M., A comparison of statistical models for the analysis of complex forensic DNA profiles, *Science and Justice* 54 (2014) 66-70
- Steele, C.D., and Balding, D.J., Statistical Evaluation of Forensic DNA Profile Evidence in *Annu. Rev Stat. Appl.* 2014. 1:361-84
- Steele, C.D., et al., Verifying likelihoods for low template DNA profiles using multiple replicates, *Forensic Science International: Genetics* 13 (2014) 82-89
- Timken, M.D., Klein, S.B., Buoncristiani, M.R., Stochastic sampling effects in STR typing; Implications for analysis and interpretation, *Forensic Science International: Genetics* 11 (2014) 195-204
- Hedell, R., et al., Enhanced low-template DNA analysis conditions and investigation of allele dropout patterns, *Forensic Science International: Genetics* 14 (2015) 61-75
- Haned, H., et al., Complex DNA mixture analysis in a forensic context: Evaluating the probative value using a likelihood ratio model, *Forensic Science International: Genetics* 16 (2015) 17-25



Bright et al.; A series of recommended tests when validating probabilistic DNA profile interpretation software, *Forensic Science International: Genetics* 16 (2015) 13-16

Swaminathan, H., et al., A computational method to infer number of contributors to DNA samples analyzed by STR genotyping, *Forensic Science International: Genetics* 16 (2015) 172-180

Inman, K., Rudin, N., Cheng, K., Robinson, C., Kirschner, A., Inman-Semeran, L., and Lohmueller, K.E., Lab Retriever: a software tool for calculating likelihood ratios incorporating a probability of drop-out for forensic DNA profiles, *BMC Bioinformatics* 2015, 16:298 <<http://www.biomedcentral.com/1471-2105/16/298>>

Haned, H., Gill, P., Lohmueller, K., Inman, K., Rudin, N.; Validation of probabilistic genotyping software for use in forensic DNA casework: Definitions and illustrations, *Science and Justice* 56 (2016) 104–108

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

π