



ANEXO I: Bibliografía

Interpretación y tratamiento estadístico

- Bill M, Gill P, Curran J, Clayton T, Pinchin R, Healy M, Buckleton J (2004). PENDULUM—a guideline based approach to the interpretation of STR mixtures. *Forensic Sci Int* 148: 181–189.
- Brenner CH, Fimmers R, Baur MP (1996). Likelihood ratios for mixed stains when the number of donors cannot be agreed. *Int J Legal Med* 109, pp. 218–219.
- Chung YK, Hu YQ, Fung WK (2009). Evaluation of DNA mixtures from database search. *Biometrics* 66: 233-238.
- Chung YK, Hu YQ, Fung WK (2010). Familial database search on two-person mixture. *Computational Statistics and Data Analysis* 54: 2046-2051.
- Chung YK, Hu YQ, Fung WK (2011). The evidentiary values of “cold hits” in a DNA database search on two-person mixture. *Science and Justice* 51: 10-15.
- Chung YK and Fung WK. Identifying contributors of two-person DNA mixtures by familial database search. *Int J Legal Med*, 2012 Jan 22. [Epub ahead of print].
- Coletti A, Meriglioli S, Severini S, Lancia M, Massetti S, Suadoni F, Carnevali E (2009). Statistical analysis of DNA mixtures using peak area information and allelic drop out. *Forensic Sci Int: Genet Supplement Series* 2: 202-203.
- Cowell RG, Lauritzen SL, Mortera J (2004). Identification and separation of DNA mixtures using peak area information. Statistical Research Paper 25, Sir John Cass Business School, City University, London.
- Cowell RG, Lauritzen SL, Mortera J (2006). A conditional-gamma Bayesian network for DNA mixture analyses. *Bayesian Analysis* 2: 212-239.
- Cowell RG, Lauritzen SL, Mortera J (2007). A gamma model for DNA mixture analyses. *Bayesian Analysis* 2: 333-348.
- Cowell RG, Lauritzen SL, Mortera J (2007). Identification and separation of DNA mixtures using peak area information. *Forensic Sci Int* 166: 28-34.
- Cowell RG, Lauritzen SL, Mortera J (2008). Probabilistic modelling for DNA mixture analysis. *Forensic Sci Int: Genet Supplement Series* 1: 640-642.
- Cowell RG, Lauritzen SL, Mortera J (2011). Probabilistic expert systems for handling artefacts in complex DNA mixtures. *Forensic Sci Int Genet* 5: 202-209.
- Curran JM, Triggs CM, Buckleton J, Weir BS (1999). Interpreting DNA mixtures in structured populations. *J Forensic Sci* 44: 987–995.
- Curran JM (2008). A MCMC method for resolving two person mixtures. *Science and Justice* 48: 168-177.
- Dror IE, Hampikian G (2011). Subjectivity and bias in forensic DNA mixture interpretation. *Science & Justice*, 51(4):204-208.
- Evett IW, Buffery C, Willott G, Stoney D (1991). A guide to interpreting single locus profiles of DNA mixtures in forensic cases. *J Forensic Sci Soc* 31: 41-47.
- Evet IW, Gill P, Lambert J (1998). Taking account of peak areas when interpreting mixed DNA profiles. *J Forensic Sci* 43: 62–69.
- Fukshansky N and Bär W (1999). Biostatistical evaluation of mixed stains with contributors of different ethnic origin. *Int J Legal Med* 112: 383-387
- Fukshansky N and Bär W (2000). Biostatistics for mixed stain: the case of tested relatives of a non-tested suspect. *Int J Legal Med* 114: 78–82.



- Fukshansky N and Bär W (2005). DNA mixtures: biostatistics for mixed stains with haplotypic genetic markers. *Int J Legal Med* 119: 285-290.
- Fung WK and Hu YQ (2000). Interpreting forensic DNA mixtures: allowing for uncertainty in population substructure and dependence. *Journal of the Royal Statistical Society, Series A* 163: 241–254.
- Fung WK and Hu YQ (2000). Interpreting DNA mixtures based on the NRC-II Recommendation 4.1. *Forensic Science Communications* 2.
- Fung WK and Hu YQ (2002). The statistical evaluation of DNA mixtures with contributors from different ethnic groups. *Int J Legal Med* 116: 79–86.
- Fung WK and Hu YQ (2002). Evaluating mixed stains with contributions of different ethnic groups under the NRC-II Recommendation 4.1. *Statistics in Medicine* 21: 3583-3593.
- Fung WK and Hu YQ (2004). Interpreting DNA mixtures with related contributors in subdivided populations. *Scandinavian Journal of Statistics* 31: 115-130.
- Gill P, Whitaker J, Flaxman C, Brown N, Buckleton J. An investigation of the rigor of interpretation rules for STRs derived from less than 100 pg of DNA, *Forensic Sci. Int.* 112 (2000) 17–40.
- Gill P and Buckleton J (2010). A universal strategy to interpret DNA profiles that does not require a definition of *low-copy-number*. *Forensic Sci Int Genet* 4: 221-227.
- Gill P, Puch-Solis R, Curran J (2009). The low - template (stochastic) threshold - Its determination relative to risk analysis for national DNA databases. *Forensic Sci Int Genet* 3(2): 104-11.
- Gill P, Sparkes R, Pinchin R, Clayton T, Whitaker J, Buckleton J (1998). Interpreting simple STR mixtures using allele peak areas. *Forensic Sci Int* 91: 41–53.
- Gill P, Buckleton J (2010). Commentary on: Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttmann 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. *J Forensic Sci* 55(1): 265-8.
- Gill P and Haned H. A new methodological framework to interpret complex DNA profiles using likelihood ratios. *Forensic Sci. Int. Genet.* 7 (2013) 251-63.
- Haned H, Pène L, Sauvage F, Pontier D (2011). The predictive value of the maximum likelihood estimator of the number of contributors to a DNA mixture. *Forensic Sci Int Genet* 5: 281-284.
- Haned H, Pène I, Lobry JR, Dufour AB, Pontier D (2011). Estimating the number of contributors to forensic DNA mixtures: does maximum likelihood perform better than maximum allele count? *J Forensic Sci* 56: 23-28.
- Haned H, Slooten K, Gill P. Exploratory data analysis for the interpretation of low template DNA mixtures. *Forensic Sci. Int. Genet.* 6 (2012) 762-74.
- Hu YQ and Fung WK (2003). Interpreting DNA mixtures with the presence of relatives. *Int J Legal Med* 117: 39–45.
- Hu YQ and Fung WK (2003). Evaluating forensic DNA mixtures with contributors of different structured ethnic origins: A computer software. *Int J Legal Med* 117: 248-249.
- Hu YQ and Fung WK (2005). Evaluation of DNA mixtures involving two pairs of relatives. *Int J Legal Med* 119: 251–259.
- Hu YQ, Fung WK, Lu J (2005). Evaluating mixed DNA profiles with the presence of relatives: Theory, method and computer software. *Forensic Science Communications* 7.



- Kelly H, Bright JA, Curran J, Buckleton J (2012). The interpretation of low level DNA mixtures. *Forensic Sci Int Genet* 6: 191-197.
- Ladd C, Lee HC, Yang N, Bieber FR (2001). Interpretation of complex forensic DNA mixtures. *Croatian Medical Journal* 4: 244-246.
- Lauritzen SL and Mortera J (2002). Bounding the number of contributors to mixed DNA stains. *Forensic Sci Int* 130: 125-126.
- Leclair B, Frégeau CJ, Bowen KL, Fourney RM (2004). Systematic analysis of stutter percentages and allele peak height and peak area ratios at heterozygous STR loci for forensic casework and database samples. *J Forensic Sci* 49(5): 968-980.
- Mortera J, Dawid AP, Lauritzen SL (2003). Probabilistic expert systems for DNA mixture profiling. *Theoretical Population Biology* 63: 191–205.
- Mortera J (2003). Analysis of DNA mixtures using probabilistic expert systems. In: PJ Green, NL Hjort, S Richardson (Eds.), *Highly Structured Stochastic Systems*. Oxford University Press.
- Nurit B, Anat G, Michal S, Lilach F, Maya F (2011). Evaluating the prevalence of DNA mixtures found in fingernail samples from victims and suspects in homicide cases. *Forensic Sci Int Genet* 5(5): 532-537.
- Paoletti DR, Krane DE, Doom TE, Raymer M (2011). Inferring the number of contributors to mixed DNA profiles. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. Disponible en <http://www.personal.psu.edu/dr15/publications/TCBB-2008-11-0196-Final.pdf>.
- Pérez J, Mitchell AA, Ducasse N, Tamariz J, Caragine T (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: 314-326.
- Perlin MW and Szabady B (2001). Linear mixture analysis: a mathematical approach to resolving mixed DNA samples. *J Forensic Sci* 46: 1372–1378.
- Puch-Solis R, Pope S, Evett IW (2010). Calculating likelihood ratios for a mixed DNA profile when a contribution from a genetic relative of a suspect is proposed. *Science and Justice* 50: 205-209.
- Tomsey CS, Kurtz M, Flowers B, Fumea J, Giles B, Kucherer S (2001). Case work guidelines and interpretation of short tandem repeat complex mixture analysis. *Croatian Medical Journal*, 42: 276-280.
- Tvedebrink T, Eriksen PS, Mogensen HS, Morling N (2008). Amplification of DNA mixtures-missing data approach. *Forensic Sci Int Genet Supplement Series* 1: 664-666.
- Tvedebrink T, Eriksen PS, Mogensen HS, Morling N (2012). Identifying contributors of DNA mixtures by means of quantitative information of STR typing. *Journal of Computational Biology* 19(7): 887-902.
- Wang T, Xue N, Wickenheiser R (2002). Least square deconvolution (LSD): a new way of resolving STR/DNA mixture samples. *Proceedings of the 13th International Symposium on Human Identification October 7–10, Phoenix, AZ*.
- Wang T, Xue N, Birdwell JD (2006). Least-Square Deconvolution: A framework for interpreting short tandem repeat mixtures. *J Forensic Sci* 51: 1284-1297.
- Weir BS, Triggs CM, Starling L, Stowell KAJ, Buckleton J (1997). Interpreting DNA mixtures. *J Forensic Sci* 42: 213-222.



Validación

- Bright JA, Turkington J, Buckleton J (2010). Examination of the variability in mixed DNA profile parameters for the Identifiler multiplex. *Forensic Sci Int Genet* 4: 111-114.
- Bright JA, Huizing E, Melia L, Buckleton J (2011). Determination of the variables affecting mixed MiniFiler™ DNA profiles. *Forensic Sci Int Genet* 5: 381-385.
- Bright JA, McManus K, Harbison S, Gill P, Buckleton J (2012). A comparison of stochastic variation in mixed and unmixed casework and synthetic samples. *Forensic Sci Int Genet* 6: 180-184.
- Butler JM, Tomsey CS, Kline MC (2004). Can the Validation Process in Forensic DNA Typing Be Standardized?. 15th International Symposium on Human Identification.
- Butler JM (2006). Validation: Debunking some urban legends surrounding validation within the forensic community. *Profiles in DNA* 9(2): 3-6.
- Ensenberger MG, Thompson J, Hill B, Homick K, Kearney V, Mayntz-Press KA, Mazur P, McGuckian A, Myers J, Raley K, Raley SG, Rothove R, Wilson J, Wieczorek D, Fulmer PM, Storts DR, Krenke BE (2010). Developmental validation of the PowerPlex 16 HS System: an improved 16-locus fluorescent STR multiplex. *Forensic Sci Int Genet* 4(4): 257-264.
- Greenspoon SA, Ban JD, Pablo L, Crouse CA, Kist FG, Tomsey CS, Glessner AL, Mihalacki LR, Long TM, Heidebrecht BJ, Braunstein CA, Freeman DA, Soberalski C, Nathan B, Amin AS, Douglas EK, Schumm JW (2004). Validation and implementation of the PowerPlex 16 BIO System STR multiplex for forensic casework. *J Forensic Sci* 49(1): 71-80.
- Hill CR, Duewer DL, Kline MC, Sprecher CJ, McLaren RS, Rabbach DR, Krenke BE, Ensenberger MG, Fulmer PM, Storts DR, Butler JM (2011). Concordance and population studies along with stutter and peak height ratio analysis for the PowerPlex® ESX 17 and ESI 17 Systems. *Forensic Sci Int Genet* 5(4): 269-275.
- Krenke BE, Tereba A, Anderson SJ, Buel E, Culhane S, Finis CJ, Tomsey CS, Zachetti JM, Masibay A, Rabbach DR, Amiott EA, Sprecher CJ (2002). Validation of a 16-locus fluorescent multiplex system. *J Forensic Sci* 47(4): 773-785.
- Moretti TR, Baumstark AL, Defenbaugh DA, Keys KM, Brown AL, Budowle B (2001a). Validation of STR typing by capillary electrophoresis. *J Forensic Sci* 46(3): 661-676.
- Moretti TR, Baumstark AL, Defenbaugh DA, Keys KM, Smerick JB, Budowle B (2001b). Validation of short tandem repeats (STRs) for forensic usage: performance testing of fluorescent multiplex STR systems and analysis of authentic and simulated forensic samples. *J Forensic Sci* 46(3): 647-660.
- Mulero JJ, Chang CW, Lagacé RE, Wang DY, Bas JL, McMahon TP, Hennessy LK (2008). Development and validation of the AmpFISTR MiniFiler PCR Amplification Kit: a MiniSTR multiplex for the analysis of degraded and/or PCR inhibited DNA. *J Forensic Sci* 53(4): 838-852.
- Perlin MW, Legler MM, Spencer CE, Smith JI, Allan WP, Belrose JL, Duceman BW (2011). Validating TrueAllele DNA mixture interpretation. *J Forensic Sci* 56:1430-1447.



- Weiler NEC, Matai AS, Sijen T (2012). Extending PCR conditions to reduce drop-out frequencies in low template STR typing including unequal mixtures. *Forensic Sci Int Genet* 6: 102-107.
- Wetton JH, Lee-Edghill J, Archer E, Tucker VC, Hopwood AJ, Whitaker J, Tully G (2011). Analysis and interpretation of mixed profiles generated by 34 cycle SGM Plus amplification. *Forensic Sci Int Genet*, 5(5): 376-380.

Guías y recomendaciones

- Budowle B, Onorato AJ, Callaghan TF, Della Manna A, Gross AM, Guerrieri RA, Luttman JC, McClure DL (2009). Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. *J Forensic Sci*.54(4): 810-821.
- Clayton TM, Whitaker JP, Sparkes R, Gill P (1998). Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci Int* 91(1):55-70.
- DNA Advisory Board (DAB) (2000). Quality Assurance Standards for Forensic DNA Testing Laboratories. URL: <http://www.fbi.gov/hq/lab/fsc/backissu/july2000/codis2a.htm> / <http://www.fbi.gov/hq/lab/fsc/backissu/july2000/codis1a.htm>
- ENFSI DNA WORKING GROUP (2010). Recommended Minimum Criteria for the Validation of Various Aspects of the DNA Profiling Process (approved November 2010). URL: <http://www.enfsi.eu>
- Gill P, Brenner CH, Buckleton JS, Carracedo A, Krawczak M, Mayr WR, Morling N, Prinz M, Schneider PM, Weir BS (2006). DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Sci Int* 160: 90–101.
- Gill P, Brown RM, Fairley M, Lee L, Smyth M, Simpson N, Irwin B, Dunlop J, Greenhalgh M, Way K, Westacott EJ, Ferguson SJ, Ford LS, Clayton T, Guinness J, (2008). National recommendations of the Technical UK DNA working group on mixture interpretation for the NDNAD and for court going purposes. *Forensic Sci Int Genet* 2(1): 76–82.
- Gill P, Gusmão L, Haned H, Mayr WR, Morling N, Parson W, Prieto L, Prinz M, Schneider H, Schneider PM, Weir BS. (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 Sci Int Genet* 6(6): 679-688.
- Morling N, Bastisch I, Gill P, Schneider PM (2007). Interpretation of DNA mixtures—European consensus on principles. *Forensic Sci Int Genet* 1: 291–292.
- Schneider PM, Fimmers R, Keil W, Molsberger G, Patzelt D, Pflug W, Rothämel T, Schmitter H, Schneider H, Brinkmann B (2009). The German Stain Commission: recommendations for the interpretation of mixed stains. *Int J Legal Med* 123: 1–5.
- Stringer P, Scheffer JW, Scott P, Lee J, Goetz R, Lentile V, Eckhoff C, Turbett G, Carroll D, Harbison S (2009). Interpretation of DNA mixtures—Australian and New Zealand consensus on principles. *Forensic Sci Int Genet* 3(2): 144-145.
- Scientific Working Group on DNA Analysis Methods (SWGDAM) (2003). Revised validation guidelines (approved December 2012) http://swgdam.org/SWGDAM_Validation_Guidelines_APPROVED_Dec_2012.pdf



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

Presentaciones

- Butler JM (2005a). Developmental Validation. Validation Workshop, Aug. 24, 2005 at NFSTC.
URL:
<http://www.cstl.nist.gov/strbase/validation/DevelopmentalValidation.pdf>
- Butler JM (2006b). Validation Workshop. HID University/Future Trends in Forensic DNA Technology, May 10, 2006. URL:
http://www.cstl.nist.gov/strbase/pub_pres/ValidationWorkshop_May2006.pdf
- Butler JM (2010a). SWGDAM Autosomal STR Interpretation Guidelines. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/NISTpub.htm>
- Butler JM (2010b). Introduction to the SWGDAM Guidelines and the Mixture Literature. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Butler JM (2010c). Number of Contributors. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Butler JM (2010d). Mixture Ratios. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Coble MD (2010a). Sttuter. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Coble MD (2010b). Statistical Approaches (CPI, LR, RMP). ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Cotton RW (2010). Amplification Variation and Stochastic Effects. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL: <http://www.cstl.nist.gov/biotech/strbase/training.htm>
- DNA MIXTURE INTERPRETATION WORKSHOP & WEBCAST. Workshop celebrado en el National Institute of Standards and Technology
<http://www.cstl.nist.gov/strbase/training/NIST-MixtureWebcast-Apr2013.htm>
- Grgicak CM (2010). Analytical Thresholds: Determination of Minimum Distinguishable Signals. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>
- Word CJ (2010a). Peak Height Ratios. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL:
<http://www.cstl.nist.gov/biotech/strbase/training.htm>



MINISTERIO
DE JUSTICIA

Word CJ (2010b). Mixture Principles & Reporting Basics. ISHI 2010 Mixture Interpretation Workshop: Principles, Protocols, and Practice. San Antonio, TX. October 14, 2010. URL: <http://www.cstl.nist.gov/biotech/strbase/training.htm>