Core Principles and Literature

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Acknowledgment and Disclaimers

Meaningful discussions with Catherine Grgicak, Robin Cotton, and Charlotte Word

I appreciate input on our NIST scientific foundation review project from **Rich Cavanagh, Mike Coble, Hari Iyer, John Paul Jones, Willie May, Rich Press, Melissa Taylor, Pete Vallone, and Sheila Willis – *and a 13-member DNA Mixtures Resource Group***

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Greg Matheson on
Forensic Science Philosophy

The CAC News – 2nd Quarter 2012 – p. 6
"Generalist vs. Specialist: a Philosophical Approach"
http://www.cacnews.org/news/2ndq12.pdf

"If you want to be a technician, performing tests on requests, then just focus on the policies and procedures of your laboratory. If you want to be a scientist and a professional, learn the policies and procedures, but go much further and learn the philosophy of your profession. **Understand the importance of why things are done** the way they are done, the scientific method, the viewpoint of the critiques, the issues of bias and the importance of ethics."

Critical Challenges Faced Today

- **Success of DNA testing** → significant growth in sample submissions → sample backlogs
  - Laboratory automation and expert system data review
  - Restrictive case acceptance policies to avoid law enforcement investigator 'swab-athons' at crime scenes

- **Greater detection sensitivity** → more complex DNA mixtures and low-template DNA with 'touch' evidence
  - Probabilistic genotyping to cope with increase in data interpretation uncertainty
  - Use of a complexity threshold to avoid "skating on thin ice"

Butler, J.M. (2015) The future of forensic DNA analysis. *Phil. Trans. R. Soc.* B 370: 20140252

Reflections on the NIST Scientific Foundation Review of DNA Mixture Interpretation

- Discussions with our Resource Group have been valuable in illustrating common challenges across laboratories
- We do not always use terminology the same and as a community we can **benefit from having a more uniform language and terminology** (standardized definitions that are used and understood)
- In some cases, we need to **consider what questions we are addressing** when we are working with small amounts of material that can be transferred
- Looking more towards **performance based testing** (what do my validation data actually demonstrate?) instead of task-driven efforts (did I follow the check list of studies?) – see ASB Standard 20
- The community will benefit from developing a **comprehensive, curated reference list** of foundational publications
- Spelling out **key principles** that we need to understand will help with training more consistently across laboratories and analysts

Robin Cotton's recent work

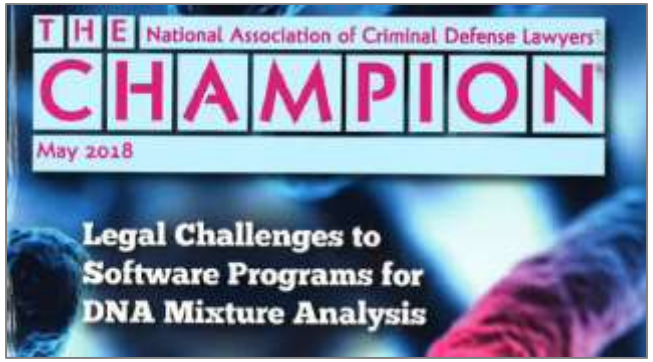
Number of Alleles (L)

Number of Contributors (N)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	Total Genotype Combinations
1	1	1															2
2	1	4	6	3													14
3	1	8	29	52	45	15											150
4	1	13	84	297	600	690	420	105									2,120
5	1	19	192	1, 116	3, 933	8, 661	11, 970	10, 080	4, 725	945							41,642
6	1	26	381	3, 321	18, 080	63, 919	150, 332	236, 978	247, 275	163, 800	62, 370	10, 395					956,878
7	1	34	687	8, 484	66, 645	346, 644	1, 231, 857	3, 052, 008	5, 316, 885	6, 483, 330	5, 415, 795	2, 952, 180	945, 945	135, 135			25, 955,630
8	1	43	1, 155	19, 428	210, 645	1, 529, 064	7, 687, 512	27, 472, 653	71, 004, 690	133, 874, 415	184, 033, 080	182, 338, 695	126, 756, 630	58, 648, 590	16, 216, 200	2, 027, 025	811, 819,826

Lynch & Cotton (2018) Determination of the possible number of genotypes which can contribute to DNA mixtures… *FSI Genetics* 37:235-240

15+ Published Perspectives on Probabilistic Genotyping System (PGS) Validation

1. Perlin (2011, 2013, 2014) – validating TrueAllele
2. Bright (2015) – a series of recommended tests when validating PGS
3. Taylor (2015) – testing LRs produced from complex DNA profiles
4. Greenspoon (2015) – establishing limits of TrueAllele
5. **SWGDAM (2015) – guidelines for PGS validation**
6. Inman (2015) – Lab Retriever capabilities and limitations
7. Haned (2016) – validation of PGS for use in casework
8. Bright (2016) – STRmix developmental validation
9. **Coble (2016) – ISFG DNA Commission recommendations**
10. ENFSI (2017) – best practice manual for PGS internal validation
11. Moretti (2017) – FBI validation of STRmix
12. PCAST (2016) – supports single-source DNA and 2p mixtures with some cautions towards more complex mixtures involving ≥3p mixtures
13. Bright (2018) – PCAST response of 31 labs with 2825 mixtures
14. Adams (2018) – JFS letter to editor on IEEE standards for software verification
15. UK FSR (2018) – software validation for DNA mixture interpretation
16. OSAC/ASB (forthcoming) – standards for PGS validation



May 2018 Issue of *The Champion*

published by the National Association for Criminal Defense Lawyers (NACDL)

Probabilistic genotyping software programs analyze complex DNA mixtures. Are these programs accurate? Does the defense have the right to see the software source code?

Article Title	Author(s)
Mixing It Up: Legal Challenges to Probabilistic Genotyping Programs for DNA Mixture Analysis	Jessica Goldthwaite, Clinton Hughes, and Richard Torres
Opening the Black Box: Defendants' Rights to Confront Forensic Software	Stephanie J. Lacambra, Jeanna Matthews, and Kit Walsh
The Dawning of a New Era in DNA Profiling	Simon Ford and Dan Krane
When DNA Is Not a Gold Standard: Failing to Interpret Mixture Evidence	Mark W. Perlin, Ph.D., M.D., Ph.D.
What Does Software Engineering Have to Do with DNA?	Nathaniel Adams

The Legal Aid Society (NYC)

Electronic Frontier Foundation (CA)

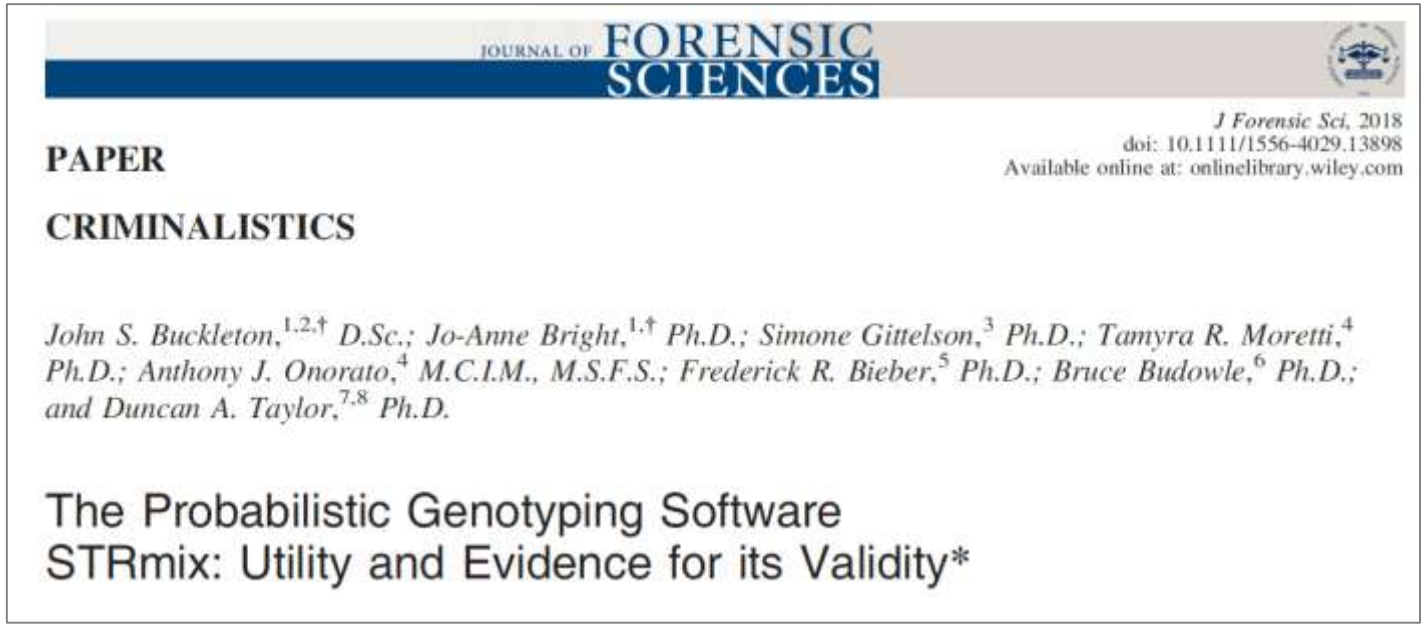
Forensic Bioinformatics (OH)

Cybergenetics – TrueAllele (PA)

Forensic Bioinformatics (OH)

STRmix "Court-Challenges Response" Article

in press **(on-line August 21, 2018)**



JOURNAL OF FORENSIC SCIENCES

J Forensic Sci, 2018
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Available online at: onlinelibrary.wiley.com

PAPER

CRIMINALISTICS

John S. Buckleton,[1,2,†] D.Sc.; Jo-Anne Bright,[1,†] Ph.D.; Simone Gittelson,[3] Ph.D.; Tamyra R. Moretti,[4] Ph.D.; Anthony J. Onorato,[4] M.C.I.M., M.S.F.S.; Frederick R. Bieber,[5] Ph.D.; Bruce Budowle,[6] Ph.D.; and Duncan A. Taylor,[7,8] Ph.D.

The Probabilistic Genotyping Software STRmix: Utility and Evidence for its Validity*

This article examines issues seen in recent STRmix admissibility hearings

Topics Covered

Introduction to Prob Gen
Introduction to LRs
Naming the Propositions
Transfer and Persistence of DNA
Effects of Different Propositions
Assumed Contributors
Dealing with Multiple POIs
Evidential Items Not Associated with POI

The General Acceptance Test
Peer-review and independent testing
PCAST Report
Disclosure of the Algorithms
Error Rate
Coding Standards and Miscodes
Precision of the Output
Reliability of PG at Low Template
Number of Contributors (constrained and unconstrained)
Subjectivity
GHEP-ISFG LRmix interlaboratory result

Sobering Thoughts from a 2014 Article

"There has been very little work published on the **variation of reporting practices of mixtures between laboratories**, but it has been previously demonstrated that **there is little consistency**. **This is because there is no current uniformity of practice, so different laboratories will operate using different rules**. The interpretation of mixtures is not solely a matter of using some software to provide 'an answer.'…"

"We show that **by introducing a structured training [program]**, it is possible to demonstrate, for the first time, that a high degree of standardization, leading to **uniformity of results can be achieved by participating laboratories**."

Prieto et al. (2014) Euroforgen-NoE collaborative exercise on LRmix to demonstrate standardization of the interpretation of complex DNA profiles. *FSI Genetics* 9: 47-54

Perspective on Requirements for Being a Forensic Science Expert

“It is a clear expectation of the courts that expert evidence is presented by people who are indeed experts in their field. This necessitates **an up to date knowledge of developments in the relevant field**, which in turn necessitates **access to scientific literature** and **sufficient time** to ensure that each expert has the current relevant knowledge that they need.”

- **Dr. Gillian Tully,** UK Forensic Science Regulator (*Annual Report 2017*, p. 10; published 19 Jan 2018)

https://www.gov.uk/government/publications/forensic-science-regulator-annual-report-2017

Forthcoming FBI Quality Assurance Standards (2019)
Professional Development Standard 16 Summarized

STANDARD 16.1 Maintain technical qualifications through **participation in continuing education**

16.1.1 **Stay abreast of topics relevant** to the field of forensic DNA analysis **by attending seminars**, etc. for **at least 8 hours per year**

16.1.1.1 Document continuing education; regional, national, or international conferences meet 8 hour requirement

16.1.1.2 Document attendance through certificates, etc.

16.1.1.3 Maintain record of presentation content and qualifications of presenter

16.1.1.4 **May use multimedia or internet delivery with technical leader approval**

16.1.2 **Need ongoing reading of the scientific literature** (approved by technical leader and documented)

16.1.2.1 **Have access to a collection of current books, reviewed journals, or other literature** applicable to DNA analysis

STANDARD 16.2 Define and follow a program to **review the testimony of each analyst**

16.2.1 Define elements and mechanisms for testimony review

16.2.2 Document the testimony review and provide it to the testifying individual

16.2.2.1 Document any deficiency and subsequent corrective actions, as applicable

Future QAS (2019) – available on SWGDAM website (approved January 11, 2018):
https://docs.wixstatic.com/ugd/4344b0_cb582ec38a7d4aeabb5f5e749be111bf.pdf

Does the Community Know the Literature and Are We Learning from It?

- **There are numerous published articles on forensic DNA, and it is difficult to keep up-to-date and to absorb the implications**

- For example, in July 2006, the International Society for Forensic Genetics DNA Commission published nine recommendations for interpreting DNA mixtures
  - Recommendation 1: The likelihood ratio is the preferred approach to mixture interpretation. **The RMNE [CPI: combined probability of inclusion] approach is restricted to DNA profiles where the profiles are unambiguous [i.e., where allele drop-out is not expected].** If the DNA crime stain profile is low level and some minor alleles are the same size as stutters of major alleles, and/or if drop-out is possible, then the RMNE method may not be conservative.
  - Recommendation 9: In relation to low copy number, stochastic effects limit the usefulness of heterozygous balance and mixture proportion estimates. In addition, allelic drop-out and allelic drop-in (contamination) should be taken into consideration of any assessment. [addressed in ISFG 2012 recommendations]

Challenges the Forensic DNA Community Faces with Continuing Education

- **QAS requirement for continuing education are only a start**
  - Minimum of eight (8) hours per year for seminars and one (1) or more articles to read will not cover much ground
  - **How does anyone know if you learned anything since there is no assessment of what was learned?**
  - **Which articles are essential for you to understand to be an expert in DNA mixture interpretation?**

- **Rapid and continuous evolution of the field**
  - New STR kits, new CE instruments, new software, new potential approaches for analysis (e.g., NGS) and interpretation (e.g., probabilistic genotyping software)
  - **There are lots of articles to chose from based on interest or need…**

- **Numerous articles are being published each year**
  - **Which articles should you choose to study?**

Some Recent PubMed Searches

https://www.ncbi.nlm.nih.gov/pubmed (3 December 2018)

- **[BROAD TOPIC] "Forensic DNA": 10,943**
- **[JOURNAL] "Forensic Sci Int Genet": 1767**
- **[LAST YEAR] "Forensic DNA" and "2017": 860**

[FOCUSED TOPICS]

- **"Forensic DNA mixture interpretation": 131**
- **"Probabilistic genotyping": 105**
- **"TrueAllele" or "STRmix": 23**

These lists do not contain all pertinent papers

19 TrueAllele journal articles listed on their website:
https://www.cybgen.com/

22 STRmix journal articles listed on their website:
https://strmix.esr.cri.nz/

Some Issues the Community Faces

- Simple searches may not reveal all useful information (we may miss valuable articles)
- Too much information is available in some cases, which can be overwhelming
- Not all information is of equal value
  - We should seek out the best available information if possible
- Little-to-no assessment of what we learn and understand from reviewing the literature or other sources of information

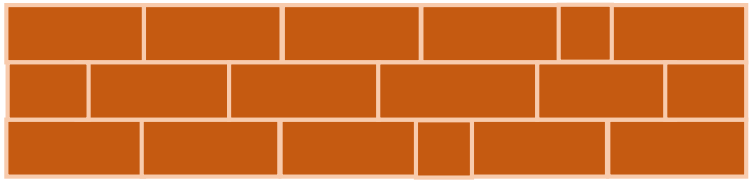
Underlying Principles should be Published (and Understood)

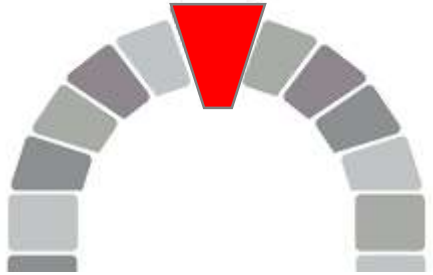
- **FBI QAS (2011, 2019) requires (8.2.2) peer-reviewed publication of underlying scientific principles** of a technology
  - Defined by the QAS as "a rule concerning a natural phenomenon or function that is a part of the basis used to proceed to more detailed scientific functions"

- **Can we define underlying (foundational) principles that govern DNA mixture interpretation** to help us understand "why" something is important and what we should do in specific situations?

What is a “Foundational” Principle?

- It is relied upon as being **solid** (i.e., it can be trusted as tried and true)
- It is **established** (i.e., it has been around a while and demonstrated to be trustworthy through repeated studies)
- **The field is built upon it** (i.e., it serves as a center piece – a keystone – to support and underpin other parts of the structure or enterprise)





Retrievable **Respected** **Reliable**

Most Important Articles to Read and Understand Regarding DNA Mixture Interpretation Principles

Thoughts from our Resource Group on June 13, 2018 and JMB discussions with colleagues:

- ISFG DNA Commission 2006, 2012, 2018
- Gill 2000 LCN and introduction of probabilistic genotyping theory
- Gill 2015 review of 20 years in advancements
- Moretti et al. 2017 STRmix internal validation paper
- Bieber 2016 correct use of CPI
- Grgicak articles on setting analytical thresholds
- Cook 1998 CAI and hierarchy of propositions
- Buckleton 2007 & Coble 2015 number of contributor estimation
- Benschop NFI mixture articles
- Cowell 2018 on math and theory
- Gill 2005 simulations of PCR and other processes

Taroni, F., Biedermann, A., Vuille, J., and Morling, N. (2013). Whose DNA is this? How relevant a question? (a note for forensic scientists). *Forensic Sci. Int. Genet*. 7: 467-470.

- **Brief summary:** [building on a meeting held in Rome in April 2012] Considers source-level and activity-level propositions and notes that there sometimes can be a gap between the information offered by scientists' reports and what is needed by report users
  - "laboratories [can] devote substantial instrumental and human resources to the analysis of single cells while remaining fundamentally incapable of addressing questions of the following kind: 'What is the probative value of a DNA profile of a single cell found to correspond with the profile of a named individual?'"

- **Key principles taught**: Analysts need to consider sample relevance and context and what question(s) they are attempting to answer with a DNA result

- Citations (Google Scholar as of 15 Aug 2018): **18 times**

Walsh, P.S., Erlich, H.A. and Higuchi, R. (1992) Preferential PCR amplification of alleles: mechanisms and solutions. *PCR Methods Appl.* 1(4): 241-250.

- **Brief summary:** [using HLA-DQα and early VNTRs] Discusses stochastic (random) variation in producing an incorrect or ambiguous genetic typing of a heterozygous sample and offers a potential solution
  - "Preferential amplification due to stochastic fluctuation can occur when amplifying very low amounts of target DNA molecules; the possibility of an unequal sampling of the two alleles of a heterozygote…is increased when only a few DNA molecules are used to initiate PCR. **This problem can be avoided by adjusting the cycle number** such that approximately 20 or more copies of target DNA [~125 pg] are required to give a typing result for that PCR system."

- **Key principles taught**: Stochastic effects are expected in PCR when amplifying ~125 pg or less of a target DNA molecule (i.e., minor components in most mixtures)

- Citations (Google Scholar as of 15 Aug 2018): **346 times**

Clayton, T.M., Whitaker, J.P., Sparkes, R. and Gill, P. (1998) Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci. Int.* 91(1): 55-70.

- **Brief summary:** [using early FSS Quad or SGM assay and ABI 373 gels] Introduces five steps for mixture interpretation: (1) identify the presence of a mixture and designate alleles versus artefacts, (2) identify the number of potential contributors, (3) estimate the relative ratio of the contributor components, (4) determine the possible pairwise combinations (i.e., potential genotypes) for the components, and (5) compare the resultant profiles for the possible components of the mixture with those from the reference samples
  - "This approach requires a detailed knowledge—gained through a mixture of experiments and validation studies—of the behavior of each locus within the multiplex…" [you need to understand and test your system]

- **Key principles taught**: Relative peak heights are a "measure of the amount of amplified DNA" and can be used to consider possible genotypes (with 2-person mixtures existing at the time)

- Citations (Google Scholar as of 15 Aug 2018): **267 times**

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

- **Brief summary:** Discusses **nine best practice recommendations** that "can be universally applied to assist with mixture interpretation" and recognizes that "scientists should be trained to a level appropriate to carry out the necessary calculations" and that future approaches will involve "using a probabilistic weighting for each possible genotype"
  - "The operational definition of low copy number PCR [usually "less than 200 pg"] is the manifestation of stochastic effects leading to allelic imbalance, drop-out, and increased prevalence of laboratory-based contamination … the effects may occur at 28 PCR cycles…LCN mixture analysis will have to allow for stochastic events (drop-out, heterozygous imbalance and contamination)…allelic drop-out and allelic drop-in (contamination) should be taken into consideration of any assessment."

- **Key principles taught**: A random man not excluded (RMNE or CPI) approach only works when the mixture profiles are "unambiguous" (i.e., no allele drop-out in the crime scene profile) and therefore "the likelihood ratio is the preferred approach to mixture interpretation" (recommendation #1); peaks in the stutter position that are similar heights to minor alleles need to be considered in the assessment (recommendation #6)

- Citations (Google Scholar as of 15 Aug 2018): **276 times**

Butler, J.M., Kline, M.C. and Coble, M.D. (2018) NIST interlaboratory studies involving DNA mixtures (MIX05 and MIX13): Variation observed and lessons learned. *Forensic Sci. Int. Genet.* 37: 81-94.

- **Brief summary:** Provides a snapshot of DNA mixture interpretation as practiced by 69 and 108 participating laboratories in 2005 and 2013 when examining data files from two, three, or four person mixtures
  - "This study highlights the difference in agreement when dealing with simple [2-person] mixtures, or instances when the genotype of interest is [from] the major profile, compared with complex mixtures and situations where the genotype of interest is [part of] a minor profile. In addition, limitations in the use of CPI for complex mixtures were highlighted in several of the MIX13 cases."

- **Key principles taught**: When interpretation principles are not applied uniformly, extensive variation can exist among analysts and laboratories

- Citations (Google Scholar as of 15 Aug 2018): **0 times**
  - Published too recently to be cited yet in the literature, but 20 citations were found to NIST talks on MIX05 and MIX13

Gill, P., Gusmao, L., Haned, H., Mayr, W.R., Morling, N., Parson, W., Prieto, L., Prinz, M., Schneider, H., Schneider, P.M. and Weir, B.S. (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.

- **Brief summary:** Provides four recommendations to explain how probabilistic approaches and LR principles can be applied to partial DNA profiles using simple scenarios to demonstrate underlying principles
  - "The combined efforts of the scientific community should be focused at taking into account the stochastic phenomena that we have all been aware of for many years, and to develop interpretation tools that will become generally accepted and used. We do not advocate a 'black-box' approach."

- **Key principles taught**: "Estimates of drop-out and drop-in probabilities should be based on **validation studies that are representative of the method used**" and "software tools used for casework implementation must be **evaluated with known samples**"

- Citations (Google Scholar as of 15 Aug 2018): **79 times**

Gill, P. and Haned, H. (2013) A new methodological framework to interpret complex DNA profiles using likelihood ratios. *Forensic Sci. Int. Genet.* 7(2): 251-263.

- **Brief summary:** Explores analysis of complex propositions with concurrent examination of casework mixture and reference profiles using three examples and discusses use of performance tests to measure effectiveness of case-specific models as well as the value of a joint pre-trial review of the evidence by scientists working for the defense and the prosecution
  - **"**Whereas the complexity of applying consensus and composite methods restricted their use to profiles categorized as non-mixtures and simple mixtures, probabilistic methods are not restricted by the number of replicates, or the number of contributors. This leads to the necessity to move the focus of the discussion to the formulation of propositions."

- **Key principles taught**: "Because they are based on different assumptions, it is expected that different models [e.g., LRmix and STRmix] will produce different LRs for a given case, for a given set of propositions"; frequency of allele drop-in increases with higher sensitivity of detection; non-contributor performance tests ["Hd true sample profiles"] can assess the performance of a model

- Citations (Google Scholar as of 15 Aug 2018): **75 times**

Steele, C.D. and Balding, D.J. (2014) Statistical evaluation of forensic DNA profile evidence. *Annu. Rev. Stat. Appl.* 1: 361-384.

- **Brief summary:** Reviews aspects of standard DNA profiles, difficulties with statistical evaluation of low-template DNA samples, the development of likelihood ratio approaches using discrete and continuous models, and describes six probabilistic genotyping programs (Forensim LRmix, FST, likeLTD, TrueAllele, DNAmixtures, STRmix)
  - "Owing to the recent emergence of new programs and updates to existing programs, few systematic comparisons of the performance of the programs described above have been published. Such comparisons are a high priority now that the field is beginning to mature."

- **Key principles taught**: Weight-of-evidence is "specific to the stated pair of hypotheses" and "it is fruitless to insist on very precise likelihood calculations under any specific model…[results] should be reported to at most one decimal place."

- Citations (Google Scholar as of 15 Aug 2018): **49 times**

Gill, P., Hicks, T., Butler, J.M., Connolly, E., Gusmão, L., Kokshoorn, B., Morling, N., van Oorschot, R.A.H., Parson, W., Prinz, M., Schneider, P.M., Sijen, T. and Taylor, D. (2018) DNA Commission of the International Society for Forensic Genetics: Assessing the value of forensic biological evidence – guidelines highlighting the importance of propositions. Part I: Evaluations of DNA profiling comparisons given (sub-) source propositions. *Forensic Sci. Int. Genet.* 36: 189-202.

- **Brief summary:** Recognizes that "interpretation of evidence continues to be one of the biggest challenges facing the forensic community" and offers nine recommendations and six considerations to assist in this effort
  - "The scientist works in an investigative mode if there is no person of interest in the case. If a suspect is identified, then generally the scientist switches to evaluative mode with respect to this suspect and needs to assign the value of their results in the context of the case."
  - "It is important to ensure that methods of evaluation are as robust as methods of analysis."

- **Key principles taught**: "There are no true likelihood ratios, just like there are no true models" and LR values depend on assumptions, case circumstances, results assessed, and the probabilistic model and propositions used. "Assumptions regarding the model and the background information (i.e., case information and data) used should be disclosed."

- Citations (Google Scholar as of 15 Aug 2018): **0 times**
  - Cited by UK Forensic Science Regulator (July 2018); too soon to be cited yet in the literature

Gill, P., Haned, H., Bleka, O., Hansson, O., Dorum, G. and Egeland, T. (2015) Genotyping and interpretation of STR-DNA: Low-template, mixtures and database matches-Twenty years of research and development. *Forensic Sci. Int. Genet.* 18: 100-117.

- **Brief summary: Reviews the development of probabilistic genotyping**
  - "A key goal of the continuous approach is to describe a DNA profile by modelling all sources of variation and to encapsulate evidence into a single likelihood ratio…No statistical methods can capture all of the uncertainty that is inherent to casework analysis of complex DNA profiles….Software is used as *part* of the overall evaluation of the evidence." (emphasis in the original)
  - "Does the questioned profile fall within the scope of the software validation"… "within the limited defined by validation"?
  - "There is no agreement within the forensic community on the best approach, and it is unrealistic to suppose that any single method will be universally adopted. This means that in practice a diversity of methods will be used for the foreseeable future. In principle, there is nothing wrong with this."

- **Key principles taught**: "It is desirable to use as much of the relevant information [from a crime scene mixture profile] as possible…[but] **the incorporation of more data into the model leads to more complexity and more assumptions**" and "**a computer program does not replace the need to think carefully about the case**." "All laboratories are currently analyzing low-template DNA" and it is important to keep in mind that "**the lower the amount of DNA present in a sample, the greater the chance that it may not be associated with a crime-event**" [due to the possibility of transfer]

- Citations (Google Scholar as of 15 Aug 2018): **44 times**

Summary of Points in Papers Examined

- Are we addressing the right question(s) with our results?
- Are we aware of possible stochastic effects?
- Are we able to deconvolute the mixture into component genotypes?
- Are we recognizing peaks in stutter positions as potential minor alleles?
- Are we aware of variation in how others may approach a mixture?

Probabilistic Genotyping

- Are we performing validation studies to estimate drop-out and drop-in probabilities with known samples?
- Are we assessing performance with potential non-contributors?
- Are we reporting results with clear propositions and limited sig. figs.?
- Are we disclosing assumptions made and contextual information used?
- Are we thinking carefully about the case data and context and not just feeding information into a computer program?

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FREE

All articles in this issue are currently available for free download

Forensic Science International: Genetics 38 (2019) 140–166

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen

Review article

DNA transfer in forensic science: A review

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Probabilistic genotyping software: An overview

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International Society for Forensic Genetics (ISFG)

https://www.isfg.org/

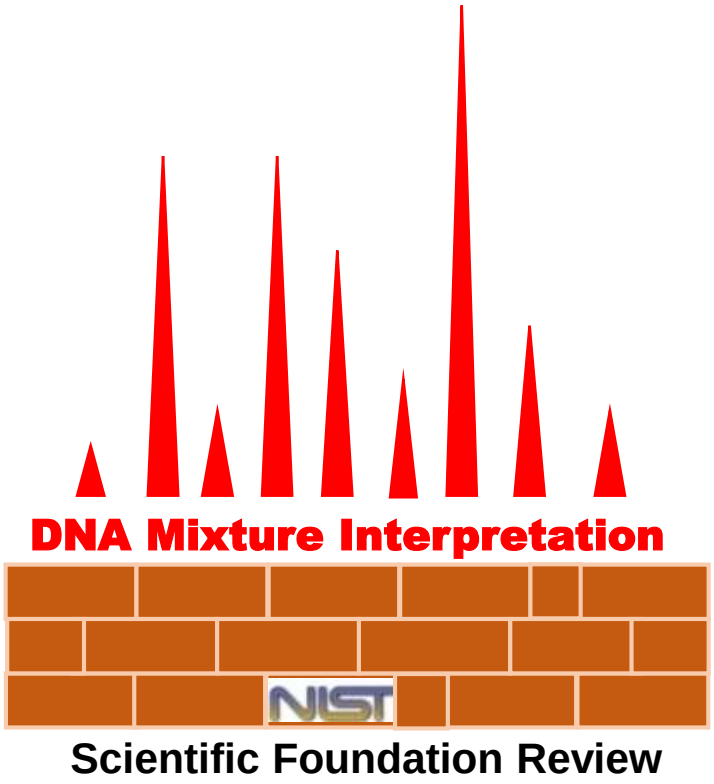
- Membership **provides access to *FSI Genetics*** and reduced meeting registration costs

ISFG DNA Commission articles are freely-available:
https://www.isfg.org/Publications/DNA+Commission

- ISFG meeting **coming to Washington DC in 2021**
  - August 30 to September 4, 2021
  - See http://www.isfg2021.org/ when the time gets closer

Next meeting (http://www.isfg2019.org/)

Thank you for your attention!



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