Communicating Forensic Findings Workshop: Current Practices and Future Directions

Session 2: Communicating Results in Forensic Reports and Testimony

Clinton Hughes – Brooklyn Defender Services

Question 1 – **Fantasy Island**

If we took all your advice and suggestions today on how to communicate results effectively – what would that look like tomorrow in lab reports or in court testimony?

Question 4 – **Culture Club**

Can you discuss more of the *cultural divide* between scientists and their use of language vs. what those reading the reports or hearing the testimony want/need? (*scientific language and precision vs layman's terminology*)

Fantasy Island – Example

Assumption – the greatest danger of assigning false support for a non-contributor in Forensic DNA Mixture Analysis occurs when relative(s) of the person mixture are contributors to a crime scene sample.

NISTIR 8503

May 2024

Forensic DNA Interpretation and Human Factors: Improving Practice Through a Systems Approach

Report of the Expert Working Group on Human Factors in Forensic DNA Interpretation

This publication is available free of charge from: https://doi.org/10.6028/NIST.IR.8503

HUMAN FACTORS in Forensic DNA Interpretation
NIST NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY U.S. DEPARTMENT OF COMMERCE
NIJ NATIONAL INSTITUTE OF JUSTICE ADVANCING JUSTICE THROUGH SCIENCE

“**Likelihood Ratio** (LR): A measure of the relative strength of support that particular findings give to one proposition against a stated alternative. . .” (xix)

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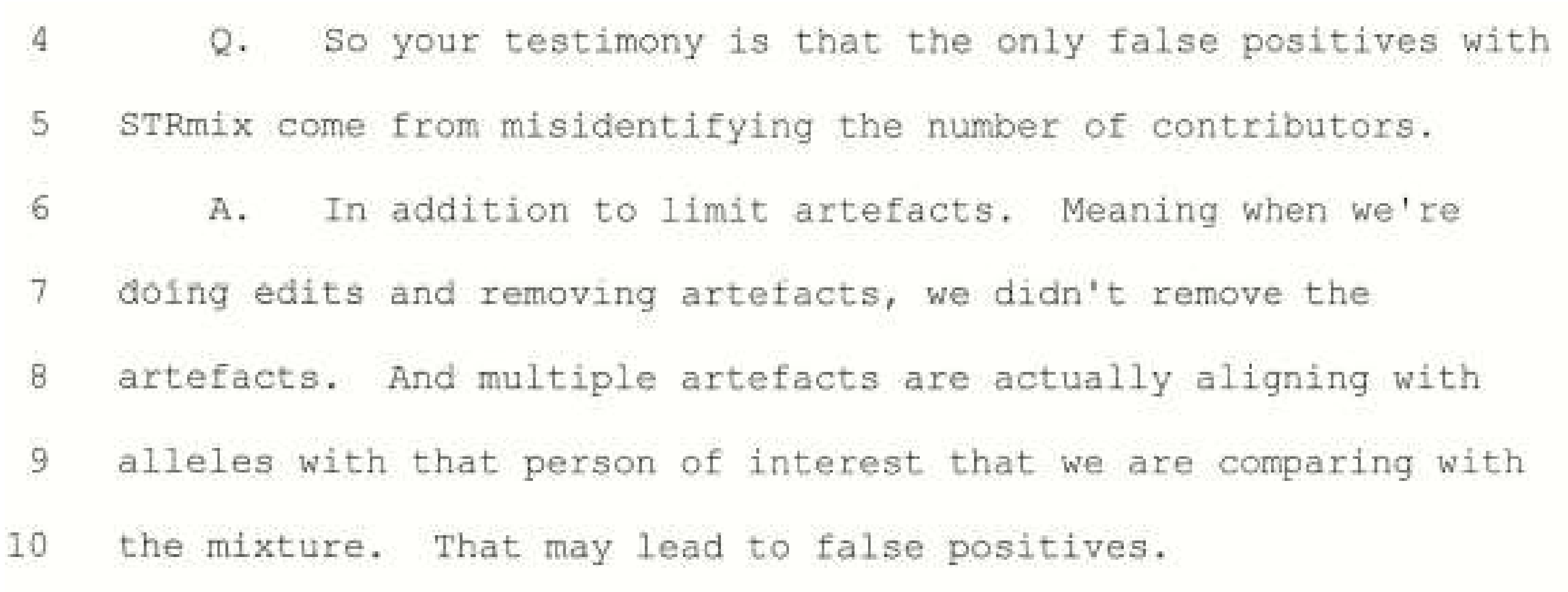
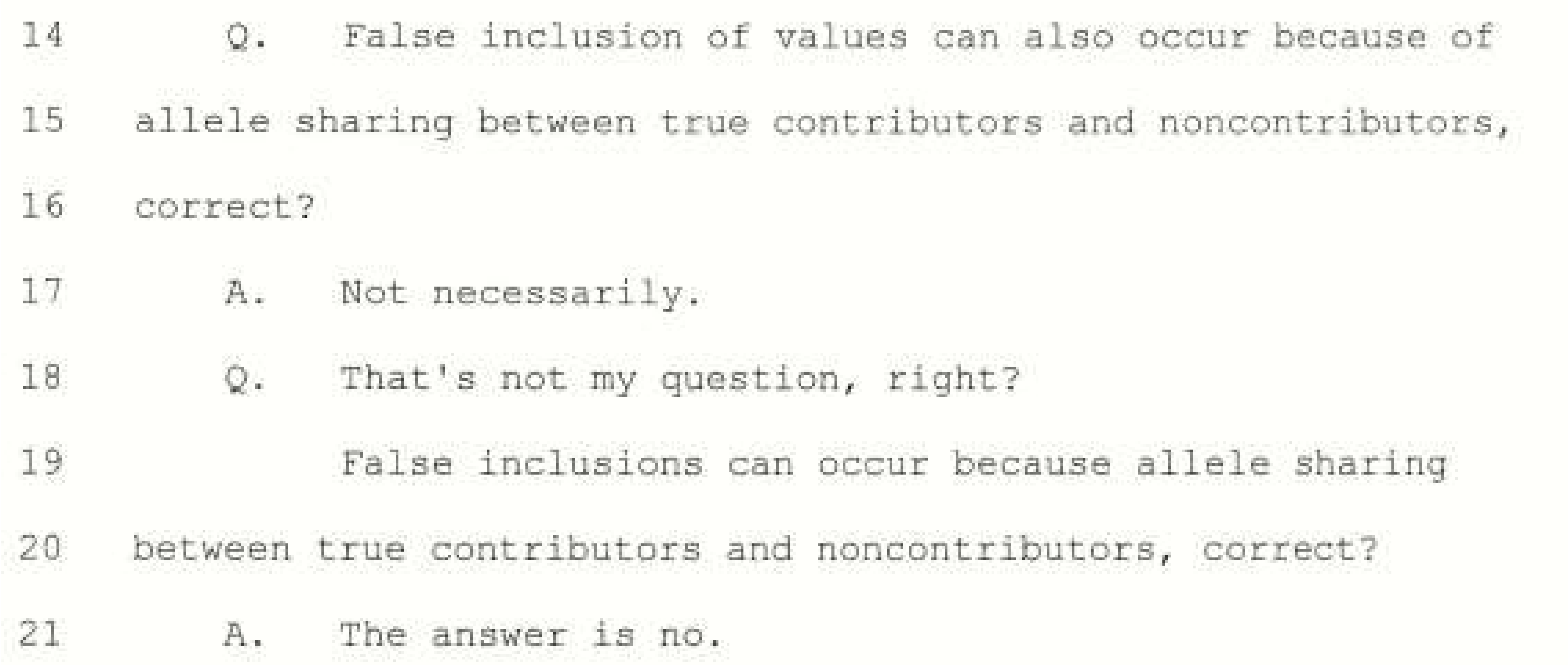
“We define **error** as the failure of a system to achieve its intended goal or outcome.” (16)

“**Outcome Error:** An error in the final opinion or result.” (xix)



Q. So your testimony is that the only false positives with STRmix come from misidentifying the number of contributors.

A. In addition to limit artefacts. Meaning when we're doing edits and removing artefacts, we didn't remove the artefacts. And multiple artefacts are actually aligning with alleles with that person of interest that we are comparing with the mixture. That may lead to false positives.



Q. False inclusion of values can also occur because of allele sharing between true contributors and noncontributors, correct?

A. Not necessarily.

Q. That's not my question, right?

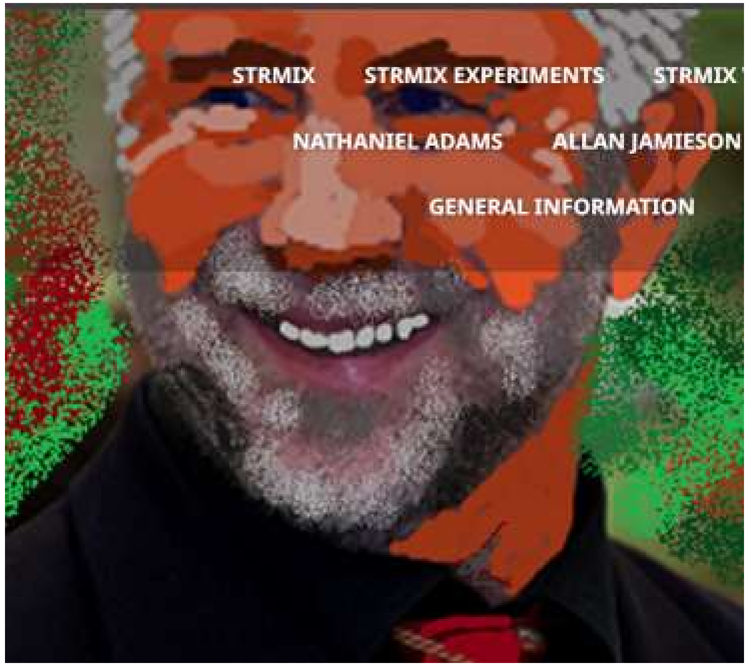
False inclusions can occur because allele sharing between true contributors and noncontributors, correct?

A. The answer is no.

Workshop Description – Day 1

"From the presentations and discussions, we are looking to examine . . . *any knowledge gaps that may impact an end user's understanding of the findings*."


MY THREE SONS


STRMIX
STRMIX EXPERIMENTS
STRMIX
NATHANIEL ADAMS
ALLAN JAMIESON
GENERAL INFORMATION

February 2021

AMERICAN ACADEMY OF FORENSIC SCIENCES

73RD AAFS ANNUAL SCIENTIFIC MEETING

ONE ACADEMY

PURSUING JUSTICE THROUGH TRUTH IN EVIDENCE

2021 AAFS
VIRTUAL
MEETING

CRIMINALISTICS

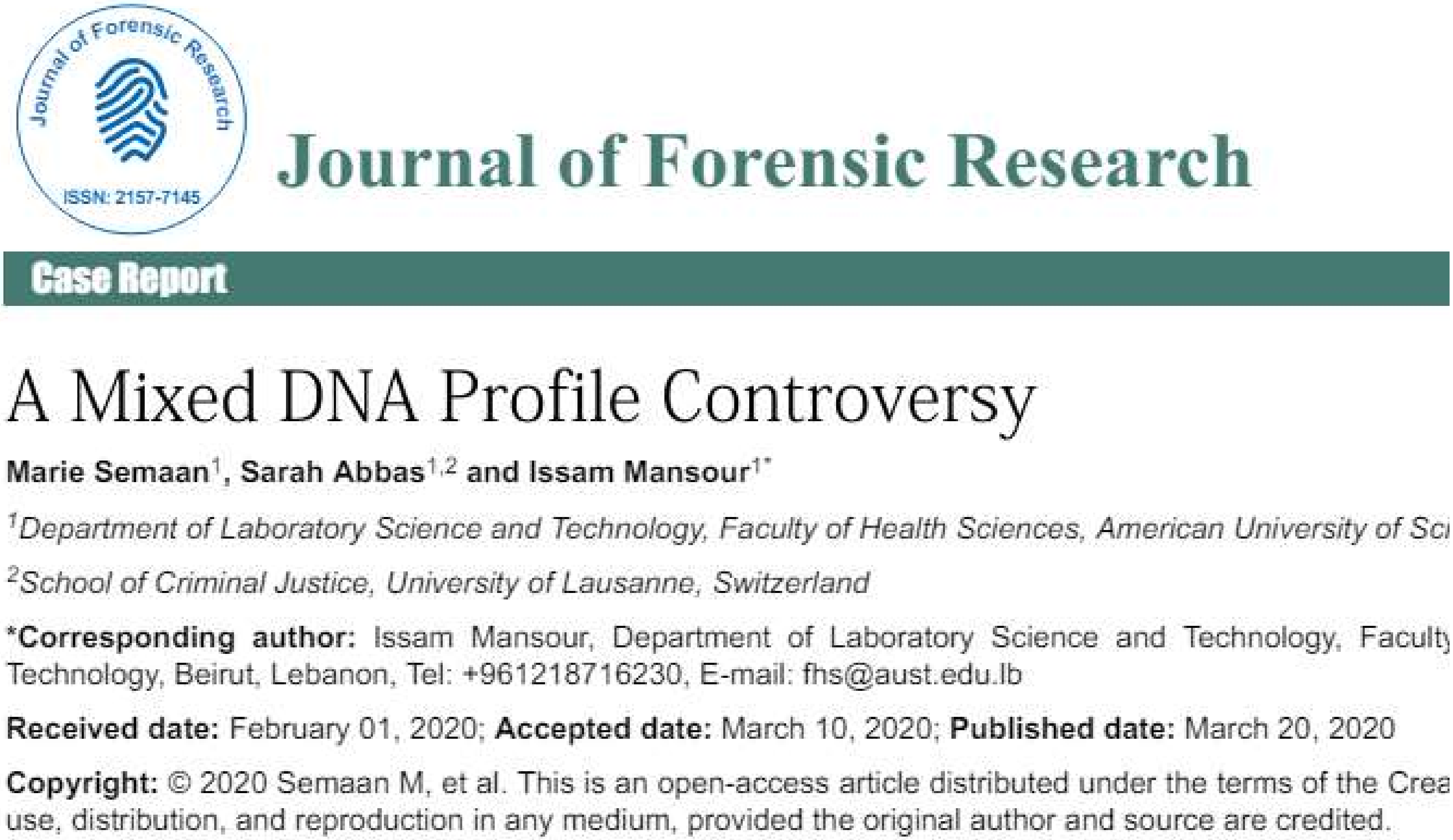
The False Inclusion of Non-Contributors in DNA Mixtures Cases

Marie Semaan, MS; Sarah Abbas, MS; Issam Mansour, PhD*

(FSF Emerging Forensic Scientist Award Oral Presentation)

AUST - American University of Science and Technology is with **Marie S. Semaan** and **Sarah Abbas**.
September 18, 2017 ·

The American University of Science and Technology attended the 21st triennial meeting of the International Association of Forensic Sciences IAFS 2017 that was held in Toronto, Canada; on August 21-25 2017.
Two graduate students from the Faculty of Health Sciences, Ms. Marie Semaan and Mrs. Sarah Abbas, presented part of the research work conducted at AUST in the field of Forensic Science (DNA Analysis), under the supervision of Dr. Issam Mansour.
Ms. Semaan presented her Master's research in an oral presentation entitled "DNA Mixture Analysis in inbred Lebanese communities. Assessment of expert DNA mixture software". Whereas, Mrs. Abbas' communication entitled "Inbreeding effect on forensic investigations involving DNA mixtures: The Lebanese population case" was presented as part of her PhD research work conducted in collaboration with the University of Lausanne - Switzerland.
Forensic Science experts, professional organizations and delegates from around the world were available in this meeting to share information, new practices and advancements in the field.
Among the audience were Professor Frederick Bieber, Professor Pierre Margot, Dr. Michael Pollanen, world leaders in the field of Forensic Science and decision makers in forensic investigative strategies.
The meeting served as a unique opportunity for the AUST community to reassure their pivotal role in the advancement of forensic sciences in the Middle-East and North Africa region, introduce themselves to



Journal of Forensic Research

ISSN: 2157-7145

Case Report

A Mixed DNA Profile Controversy

Marie Semaan[1], **Sarah Abbas**[1,2] **and Issam Mansour**[1*]

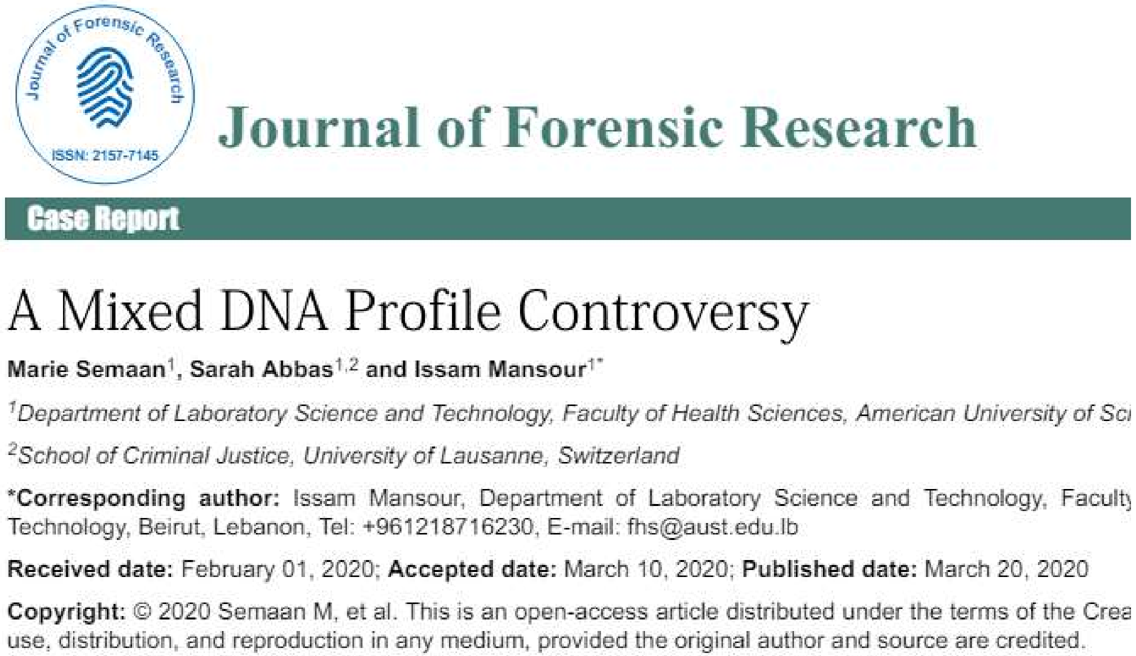
[1]*Department of Laboratory Science and Technology, Faculty of Health Sciences, American University of Sci*

[2]*School of Criminal Justice, University of Lausanne, Switzerland*

***Corresponding author:** Issam Mansour, Department of Laboratory Science and Technology, Facult
Technology, Beirut, Lebanon, Tel: +961218716230, E-mail: fhs@aust.edu.lb

Received date: February 01, 2020; **Accepted date:** March 10, 2020; **Published date:** March 20, 2020

9.5 Novemvigintillion (9.50E+90)



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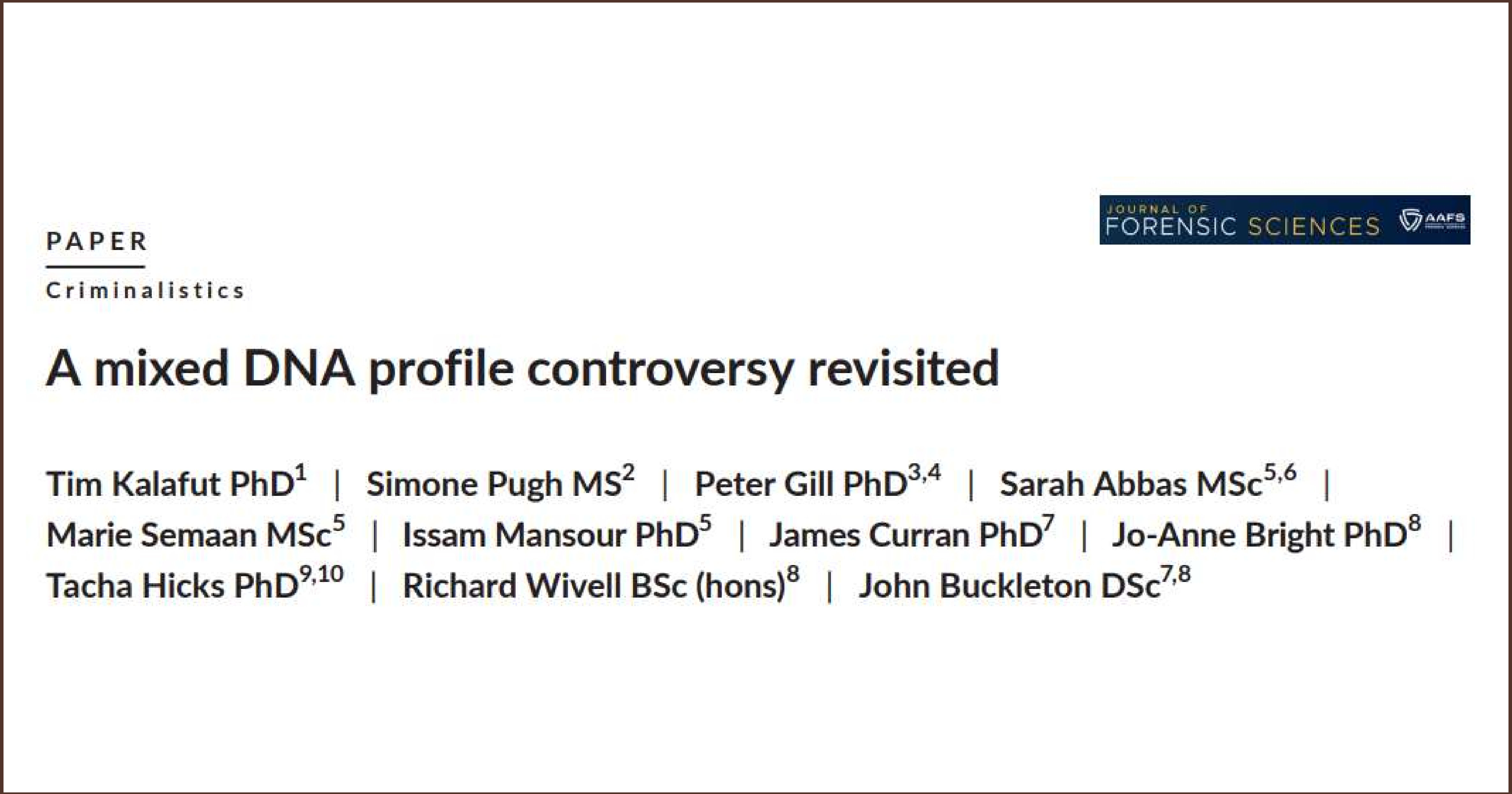

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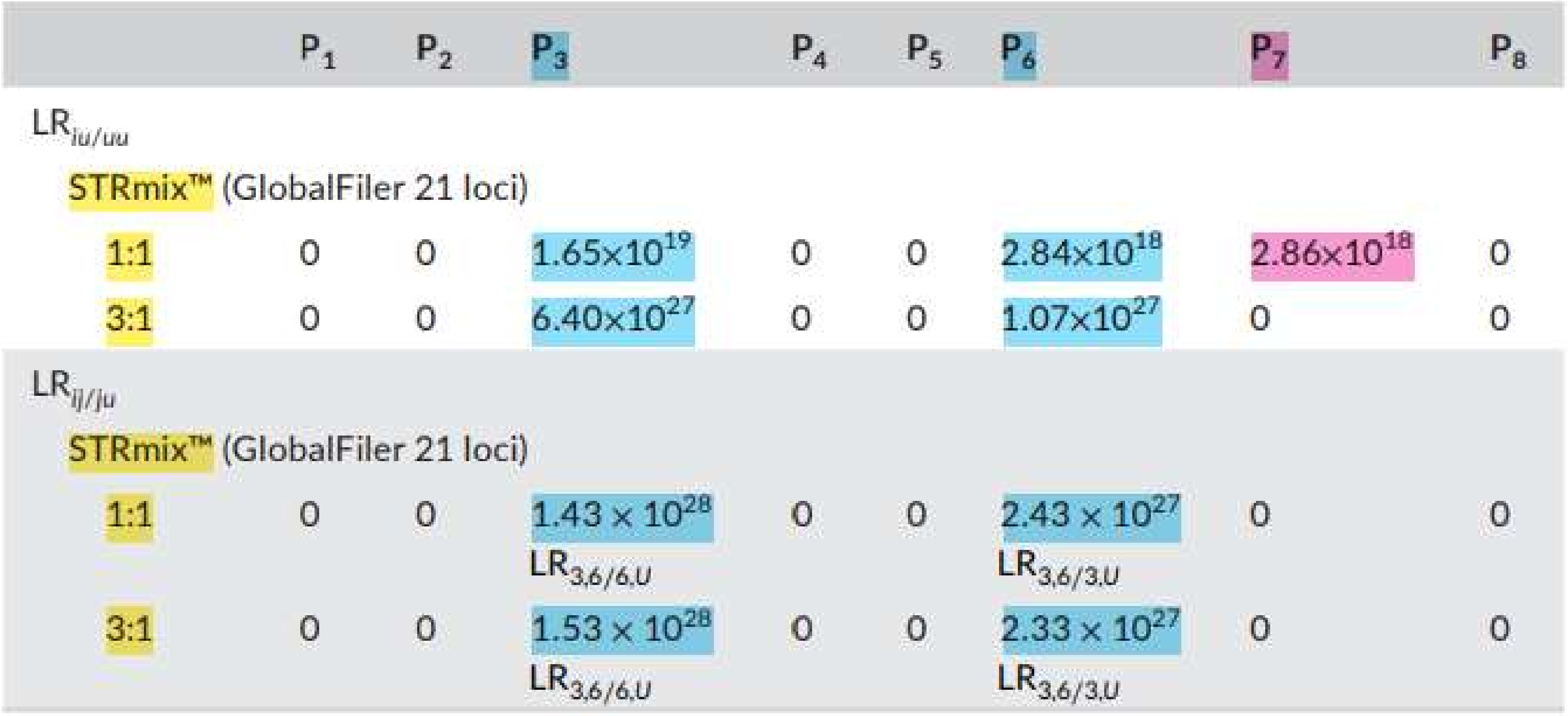
2.86 Quintillion
(2.86E+18)



	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8
$LR_{iu/uu}$								
STRmix™ (GlobalFiler 21 loci)								
1:1	0	0	1.65×10^{19}	0	0	2.84×10^{18}	2.86×10^{18}	0
3:1	0	0	6.40×10^{27}	0	0	1.07×10^{27}	0	0
$LR_{ij/ju}$								
STRmix™ (GlobalFiler 21 loci)								
1:1	0	0	1.43×10^{28} $LR_{3,6/6,U}$	0	0	2.43×10^{27} $LR_{3,6/3,U}$	0	0
3:1	0	0	1.53×10^{28} $LR_{3,6/6,U}$	0	0	2.33×10^{27} $LR_{3,6/3,U}$	0	0

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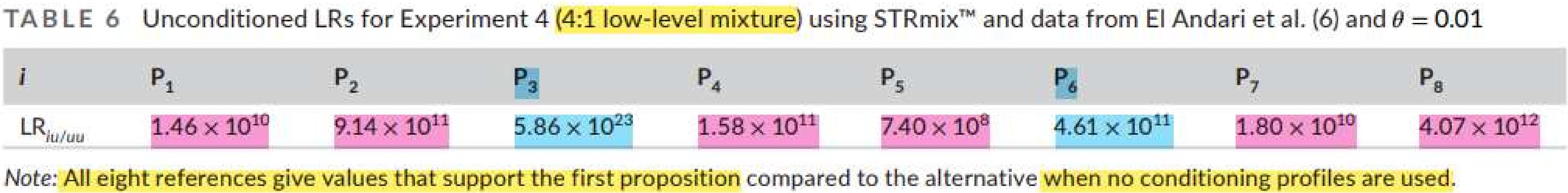

TABLE 6 Unconditioned LRs for Experiment 4 (4:1 low-level mixture) using STRmix™ and data from El Andari et al. (6) and $\theta = 0.01$

i	P_1	P_2	P_3	P_4	P_5	P_6	P_7	P_8
$LR_{iu/uu}$	1.46×10^{10}	9.14×10^{11}	5.86×10^{23}	1.58×10^{11}	7.40×10^{8}	4.61×10^{11}	1.80×10^{10}	4.07×10^{12}

Note: All eight references give values that support the first proposition compared to the alternative when no conditioning profiles are used.

4.07 Trillion
(2.86E+12)

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“Most software deal with dyadic relationships, that is relationships between two individuals. . .”

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"*Neither* STRmix™ *nor* LRmix deal with *triadic situations* or higher, although DBLR™ does [22]."

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“Neither LRmix *nor any other software* or interpretation method can claim that the rate of false support is *zero*.”

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"...there will always be uncertainty about the source of the DNA, as we cannot know who left the DNA trace."

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"... this explains why DNA (or any evidence) should not be solely relied upon to reach a conclusion, but instead must be considered in combination with the other elements of the case."

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"Empirical work has previously been reported assessing the risk of false support to a non-donor who is related to the true donor(s) **(see for example [4])**."


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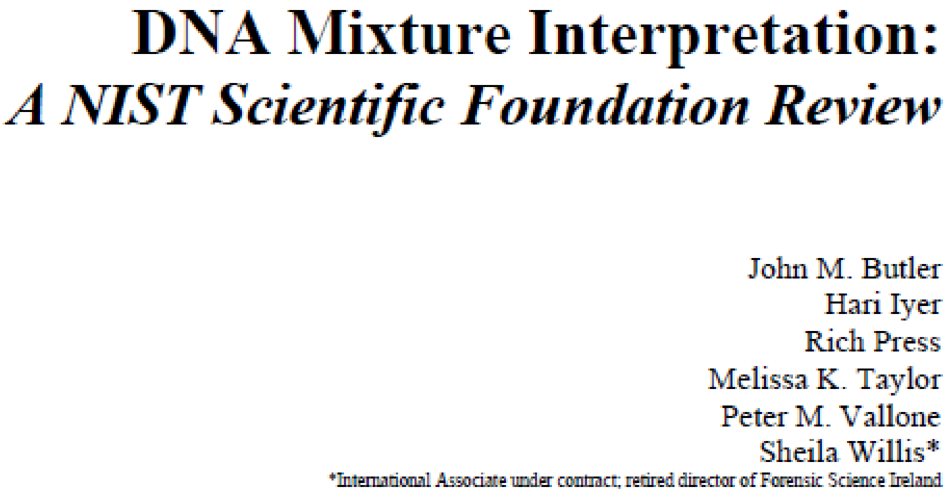
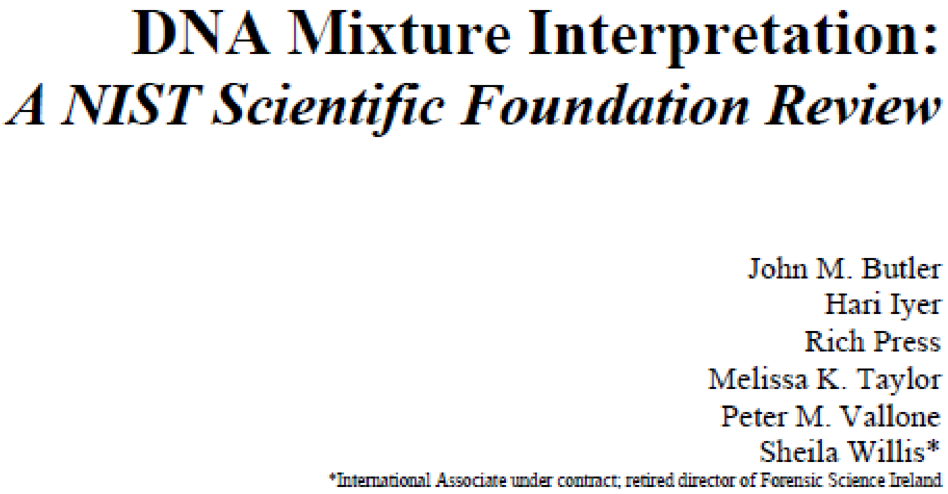
Colorado-Bureau-Investigation-2018-STRmix-Validation_ Summary.pdf. 2018. **https://indefenseof.us/uploads/ColoradoBureau-Investigation-2018-STRmix-Validation_Summary.pdf.** Accessed 30 Jul 2021.



DNA Mixture Interpretation:
A NIST Scientific Foundation Review

John M. Butler
Hari Iyer
Rich Press
Melissa K. Taylor
Peter M. Vallone
Sheila Willis*
*International Associate under contract; retired director of Forensic Science Ireland

"An important **missing element** from many validation studies is the **degree of allele** sharing that has been tested." (86)



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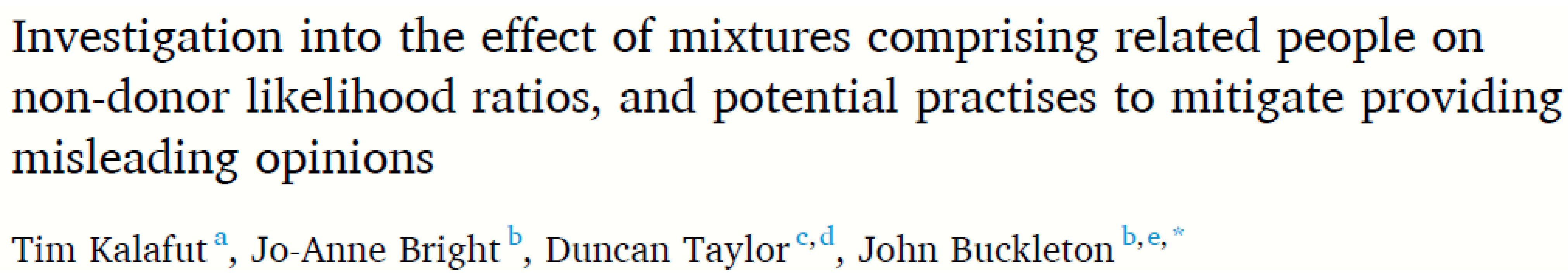
“If validation studies are conducted using mixtures that do not explore the complexity induced by allele sharing, **the user may inadvertently extrapolate validation results** and **apply methods beyond the limits of the validation studies** conducted.” (89)



Investigation into the effect of mixtures comprising related people on non-donor likelihood ratios, and potential practises to mitigate providing misleading opinions

Tim Kalafut[a], Jo-Anne Bright[b], Duncan Taylor[c,d], John Buckleton[b,e,*]

> **“The analysis of the in vitro and in silico mixtures assuming NoC = 3 with no use of a conditioning profile or *with the use of a conditioning profile* but without informed priors on the mixture proportions (Mx priors) was *ineffective*.”**

Workshop Description – Day 1

“From the presentations and discussions, we are looking to examine . . . *any knowledge gaps that may impact an end user’s understanding of the findings*.”

Thank you –
Dr. Sandra Koch,
Donna Ramkissoon,
and all the other folks at NIST!