What We Have Learned & Where We Need to Go

John M. Butler
NIST

NIJ Conference Mixture Workshop
June 20, 2012

My Presentation Outline

- Review recent mixture workshops
- Some responses from clicker questions
- Valuable mixture literature and how to obtain it
- Important lessons & common misunderstandings
- Thoughts on where we need to go as a community to improve mixture interpretation

Thanks to NIJ for Support of BU and NIST

- NIJ Forensic Science Training Development and Delivery Program Grant # 2008-DN-BX-K158, awarded to Biomedical Forensic Science Program at Boston University School of Medicine

- NIJ has an Interagency Agreement (IAA) with the NIST Office of Law Enforcement Standards (OLES)

The NIJ grant to BU funded…

- Free ISHI 2010 and 2011 workshop registration for state and local forensic DNA analysts (**~360 total**)

- Visits to four regions to conduct four 8-hour workshops
  - FL (Apr 2011), TX (May 2011), MI (May 2011), AZ (June 2011)
  - About 50 attended each workshop (**~200 total**)

- Creation of STR profiles with 2, 3, and 4 person mixtures at various mixture ratios, DNA amounts, and CE injection
  - PP 16 HS, Identifiler, Yfiler, and MiniFiler (amplified in quadruplicate)
  - Over 2000 profiles available for download on BU website

- Development of **a web site for training** in mixture analysis
  - STR mixtures profiles can be downloaded and used for training

Mixture Workshop Presenters

Robin Cotton
Boston University

617-638-1952
rwcotton@bu.edu

John Butler
NIST

301-975-4049
john.butler@nist.gov

Catherine Grgicak
Boston University

617-638- 1968
cgrgicak@bu.edu

Mike Coble
NIST

301-975-4330
michael.coble@nist.gov

Charlotte Word
Consultant

301-527-1350
cjword@comcast.net

Our presentations handouts are available on the NIST STRBase website

http://www.cstl.nist.gov/strbase/mixture.htm

Use of Audience Response Systems (the TurningPoint Clickers)

Used in ISHI 2011 workshop and FL, TX, MI, and AZ regional workshops

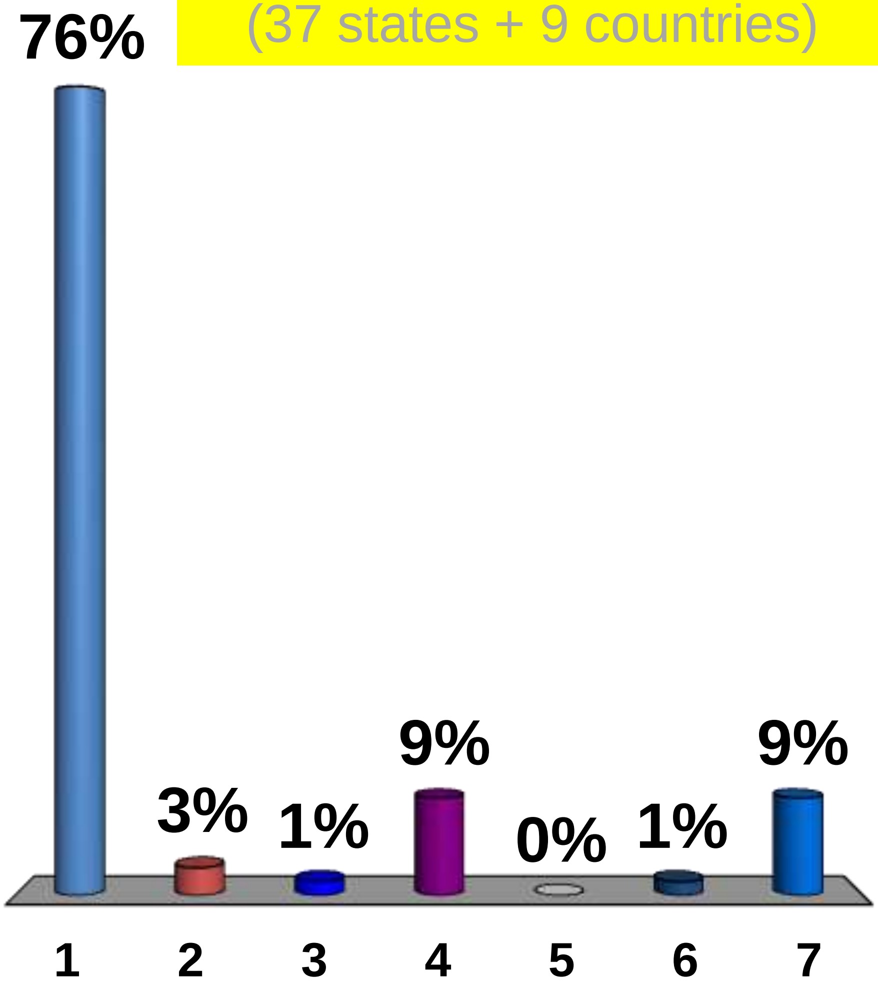
- **Kept the audience engaged** with the opportunity to participate and offer their opinions with anonymity
- **Provided real-time results** so the audience could enjoy learning how everyone responded to the question
- **Enabled us to gather information** from audience members
  - answers can be tracked across the questions to the specific clicker used

A question asked at the ISHI 2011 workshop in Washington, DC (Oct 3, 2011)…

What is your role in the laboratory?

Total responses = 152
(37 states + 9 countries)

1. **DNA analyst**
2. DNA technician
3. Database analyst
4. DNA technical leader
5. QA Manager
6. Attorney
7. Other



BU Grant Supported Mixture Workshops

Meeting	**Date**	**Location**	**# Attendees** (approximate)	**Clickers Used**
ISHI 2010	Oct 11, 2010	San Antonio, TX	200	N
FL	Apr 2011	Palm Beach, FL	50	**Y**
TX	May 2011	Houston, TX	50	**Y**
MI	May 2011	Lansing, MI	50	**Y**
AZ	June 2011	Mesa, AZ	50	**Y**
ISHI 2011	Oct 3, 2011	Washington, DC	160	**Y**

~600 people reached through these workshops

Additional NIST Mixture Workshops

Meeting/ Location	**Date**	**#Attended** (approximate)	**Who Presented**	**Clickers Used**
AAFS	Feb 2011	220	JB & MC (and 6 others)	N
NFTSC	Mar 2011	120	MC (and 5 others)	Y
Indiana	Mar 2011	65	JB	N
Maryland	Apr 2011	60	JB (and 2 others)	N
Hawaii	Aug 2011	10	MC	N
NYC OCME	**Apr 2012**	**150**	**JB & MC**	**Y**
Canada (CSFS)	May 2012	40	MC	Y
Taiwan	Jun 2012	60	JB	N

>700 additional people reached with these workshops

ISHI 2010
ISHI 2011
AAFS 2011

Mixture Workshop Attendees

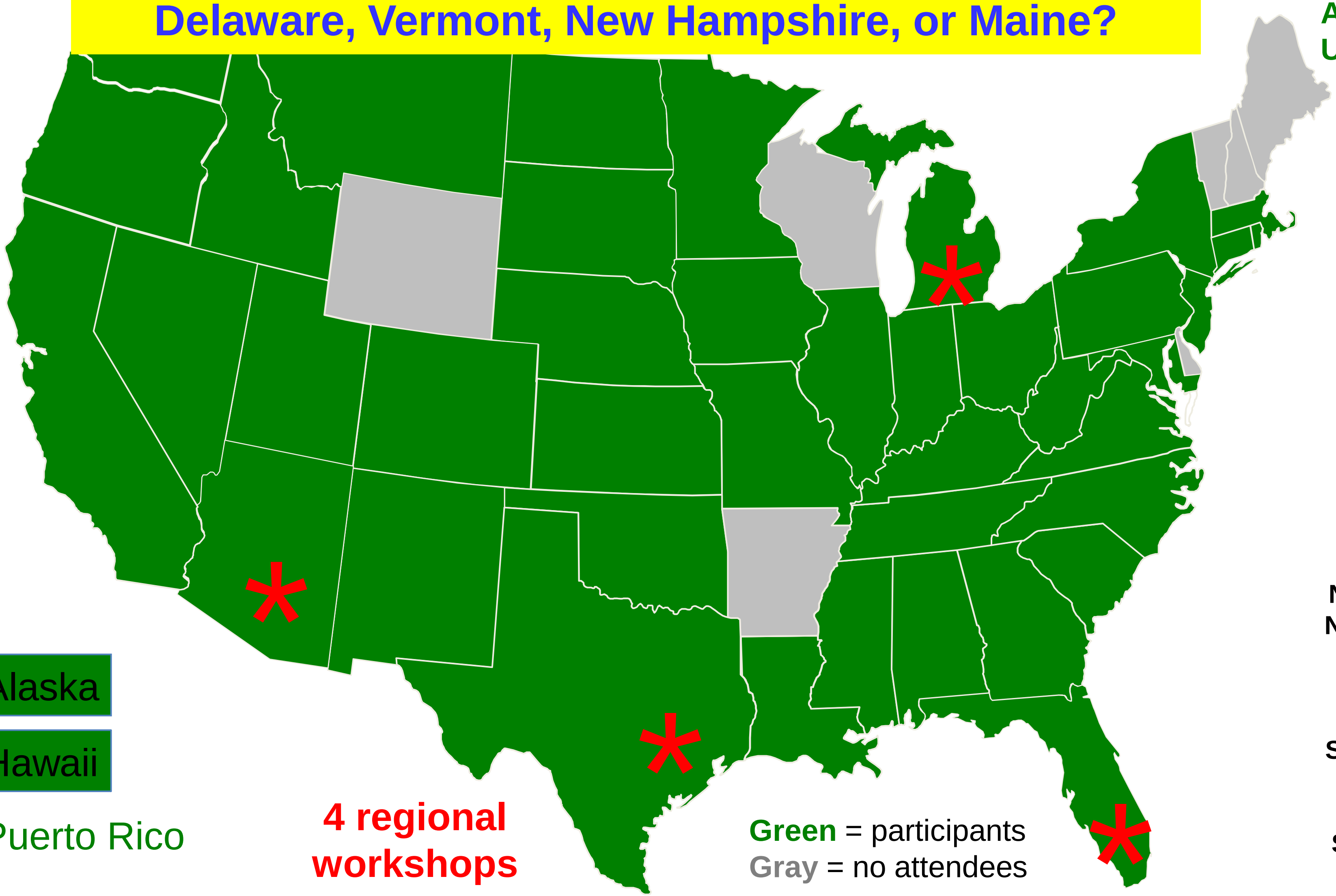
43 states and 25 other countries

Anyone here from Wyoming, Arkansas, Wisconsin, Delaware, Vermont, New Hampshire, or Maine?

Federal Labs

FBI
ATF
AFDIL
USACIL

Algeria
Argentina
Bahamas
Belgium
Brazil
Canada
Croatia
Finland
France
Israel
Italy
Jamaica
Japan
Korea
Mexico
Netherlands
New Zealand
Panama
Peru
Russia
Saudi Arabia
Singapore
Spain
Switzerland
UK



🟩 Alaska

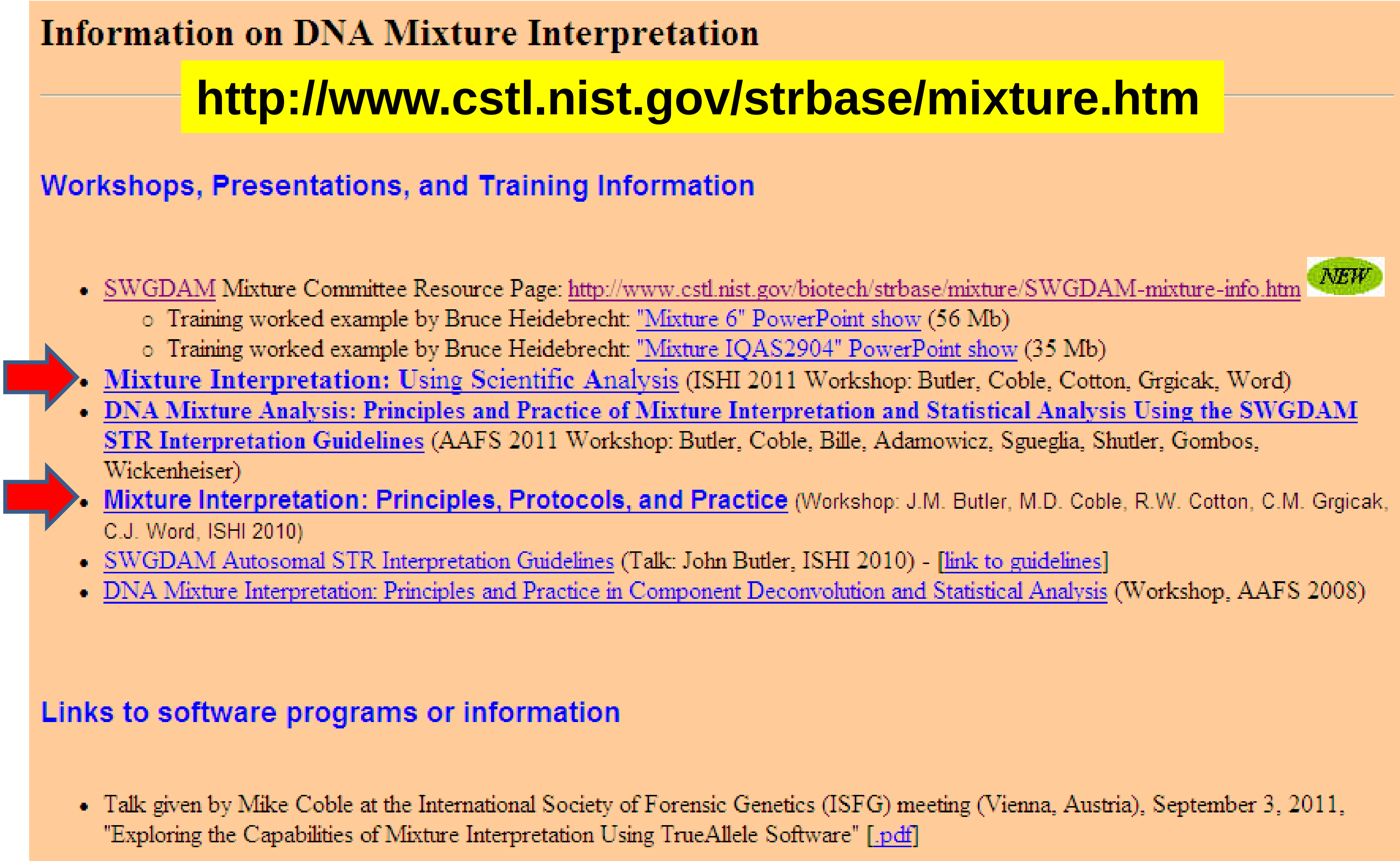
🟩 Hawaii

Puerto Rico

4 regional workshops

Green = participants
Gray = no attendees

Mixture Section of STRBase website



Information on DNA Mixture Interpretation

http://www.cstl.nist.gov/strbase/mixture.htm

Workshops, Presentations, and Training Information

- SWGDAM Mixture Committee Resource Page: http://www.cstl.nist.gov/biotech/strbase/mixture/SWGDAM-mixture-info.htm NEW
    - Training worked example by Bruce Heidebrecht: "Mixture 6" PowerPoint show (56 Mb)
    - Training worked example by Bruce Heidebrecht: "Mixture IQAS2904" PowerPoint show (35 Mb)
- **Mixture Interpretation: Using Scientific Analysis** (ISHI 2011 Workshop: Butler, Coble, Cotton, Grgicak, Word)
- **DNA Mixture Analysis: Principles and Practice of Mixture Interpretation and Statistical Analysis Using the SWGDAM STR Interpretation Guidelines** (AAFS 2011 Workshop: Butler, Coble, Bille, Adamowicz, Sgueglia, Shutler, Gombos, Wickenheiser)
- **Mixture Interpretation: Principles, Protocols, and Practice** (Workshop: J.M. Butler, M.D. Coble, R.W. Cotton, C.M. Grgicak, C.J. Word, ISHI 2010)
- SWGDAM Autosomal STR Interpretation Guidelines (Talk: John Butler, ISHI 2010) - [link to guidelines]
- DNA Mixture Interpretation: Principles and Practice in Component Deconvolution and Statistical Analysis (Workshop, AAFS 2008)

Links to software programs or information

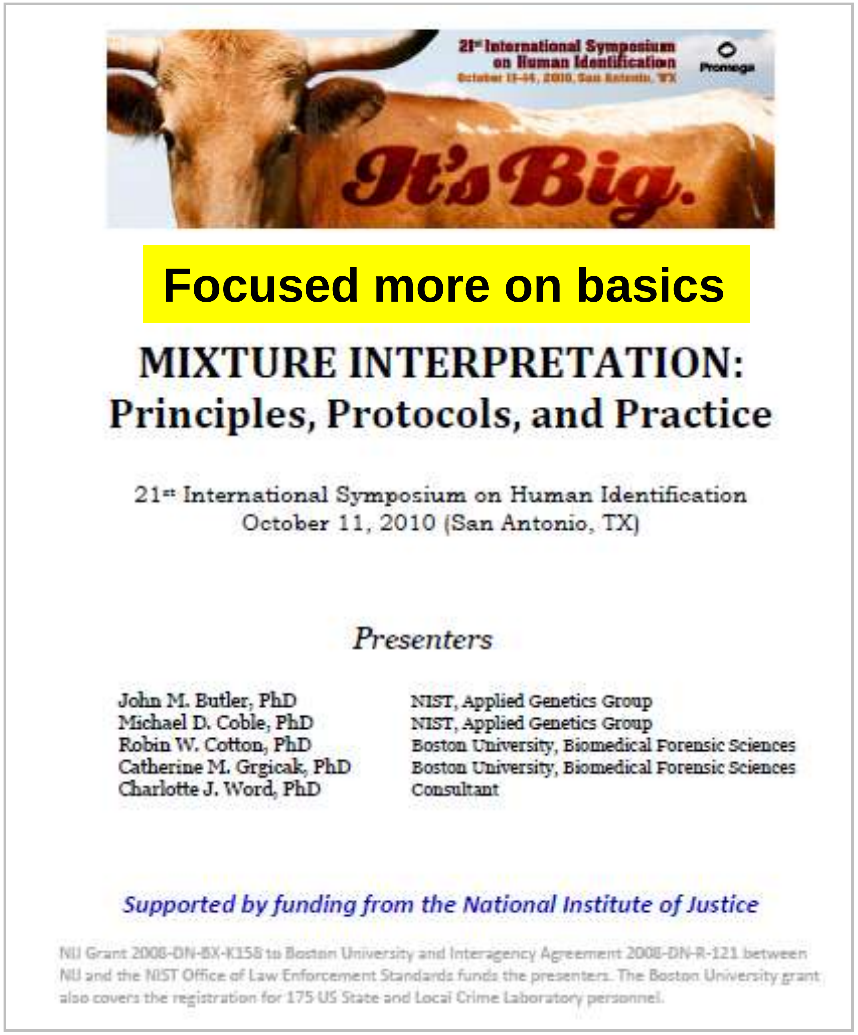
- Talk given by Mike Coble at the International Society of Forensic Genetics (ISFG) meeting (Vienna, Austria), September 3, 2011, "Exploring the Capabilities of Mixture Interpretation Using TrueAllele Software" [.pdf]

Website also lists >100 helpful references on DNA mixture interpretation…

Mixture Workshop Handouts

Available at http://www.cstl.nist.gov/strbase/mixture.htm

ISHI 2010 Mixture Workshop



Focused more on basics

MIXTURE INTERPRETATION:
Principles, Protocols, and Practice

21st International Symposium on Human Identification
October 11, 2010 (San Antonio, TX)

Presenters

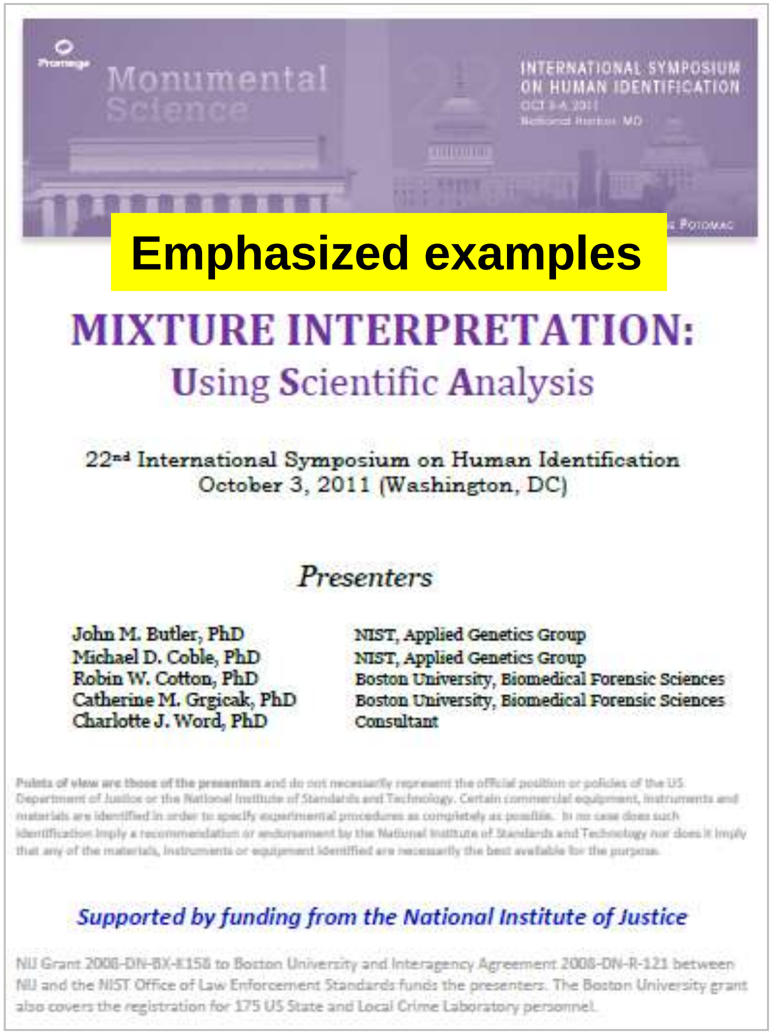
John M. Butler, PhD	NIST, Applied Genetics Group
Michael D. Coble, PhD	NIST, Applied Genetics Group
Robin W. Cotton, PhD	Boston University, Biomedical Forensic Sciences
Catherine M. Grgicak, PhD	Boston University, Biomedical Forensic Sciences
Charlotte J. Word, PhD	Consultant

Supported by funding from the National Institute of Justice

NIJ Grant 2008-DN-BX-K158 to Boston University and Interagency Agreement 2008-DN-R-121 between NIJ and the NIST Office of Law Enforcement Standards funds the presenters. The Boston University grant also covers the registration for 175 US State and Local Crime Laboratory personnel.

198 pages (60 pages of literature)

ISHI 2011 Mixture Workshop



Emphasized examples

MIXTURE INTERPRETATION:
Using Scientific Analysis

22nd International Symposium on Human Identification
October 3, 2011 (Washington, DC)

Presenters

John M. Butler, PhD	NIST, Applied Genetics Group
Michael D. Coble, PhD	NIST, Applied Genetics Group
Robin W. Cotton, PhD	Boston University, Biomedical Forensic Sciences
Catherine M. Grgicak, PhD	Boston University, Biomedical Forensic Sciences
Charlotte J. Word, PhD	Consultant

Points of view are those of the presenters and do not necessarily represent the official position or policies of the US Department of Justice or the National Institute of Standards and Technology. Certain commercial equipment, instruments and materials are identified in order to specify experimental procedures as completely as possible. In no case does such identification imply a recommendation or endorsement by the National Institute of Standards and Technology nor does it imply that any of the materials, instruments or equipment identified are necessarily the best available for the purpose.

Supported by funding from the National Institute of Justice

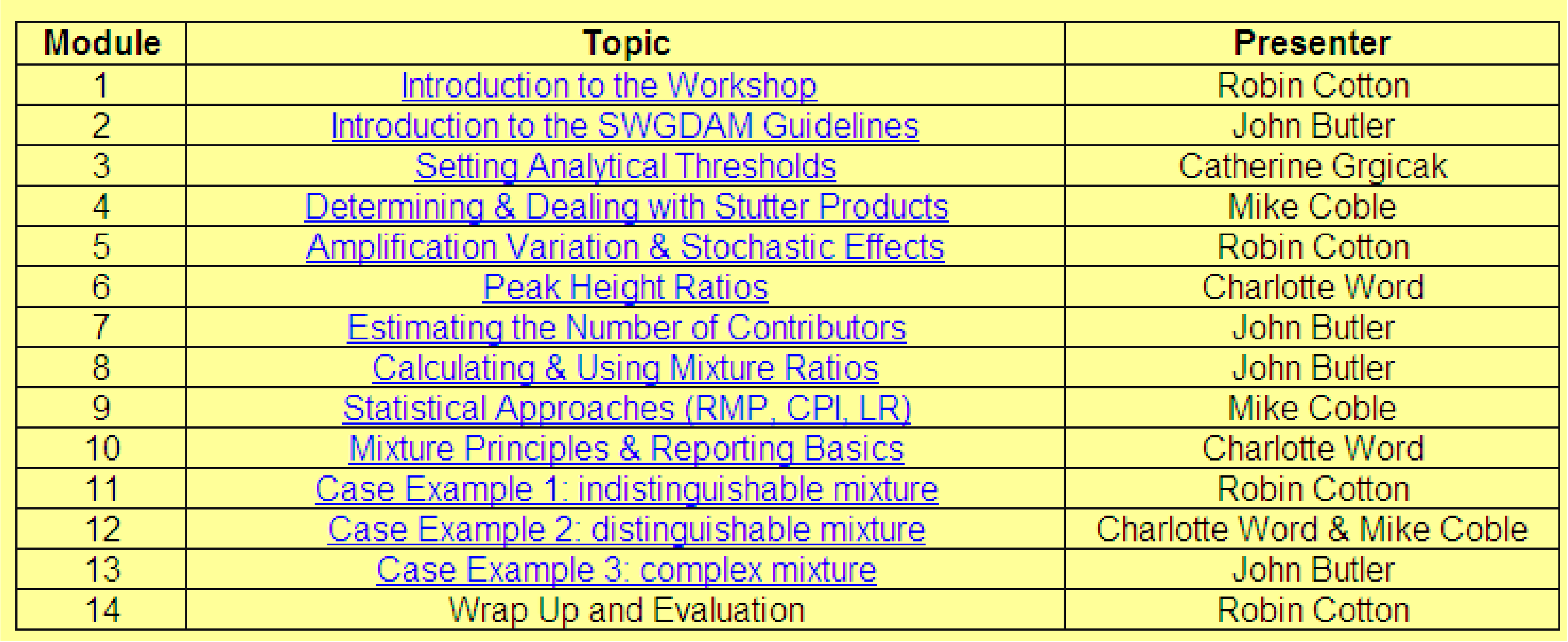
NIJ Grant 2008-DN-BX-K158 to Boston University and Interagency Agreement 2008-DN-R-121 between NIJ and the NIST Office of Law Enforcement Standards funds the presenters. The Boston University grant also covers the registration for 175 US State and Local Crime Laboratory personnel.

154 pages (literature not included)

Handouts Available on STRBase

ISHI 2010 Mixture Workshop

MIXTURE INTERPRETATION:
Principles, Protocols, and Practice



Module	Topic	Presenter
1	Introduction to the Workshop	Robin Cotton
2	Introduction to the SWGDAM Guidelines	John Butler
3	Setting Analytical Thresholds	Catherine Grgicak
4	Determining & Dealing with Stutter Products	Mike Coble
5	Amplification Variation & Stochastic Effects	Robin Cotton
6	Peak Height Ratios	Charlotte Word
7	Estimating the Number of Contributors	John Butler
8	Calculating & Using Mixture Ratios	John Butler
9	Statistical Approaches (RMP, CPI, LR)	Mike Coble
10	Mixture Principles & Reporting Basics	Charlotte Word
11	Case Example 1: indistinguishable mixture	Robin Cotton
12	Case Example 2: distinguishable mixture	Charlotte Word & Mike Coble
13	Case Example 3: complex mixture	John Butler
14	Wrap Up and Evaluation	Robin Cotton

Comments on Mixture Training We Have Conducted These Past Two Years

- Trying to help analysts better understand the SWGDAM 2010 Interpretation Guidelines
  - It is important to note that **the 2010 SWGDAM Guidelines were written primarily for 2-person mixtures situations**

- However, **many labs are doing or attempting more complex mixtures often without appropriate underlying validation support** or consideration of complicating factors

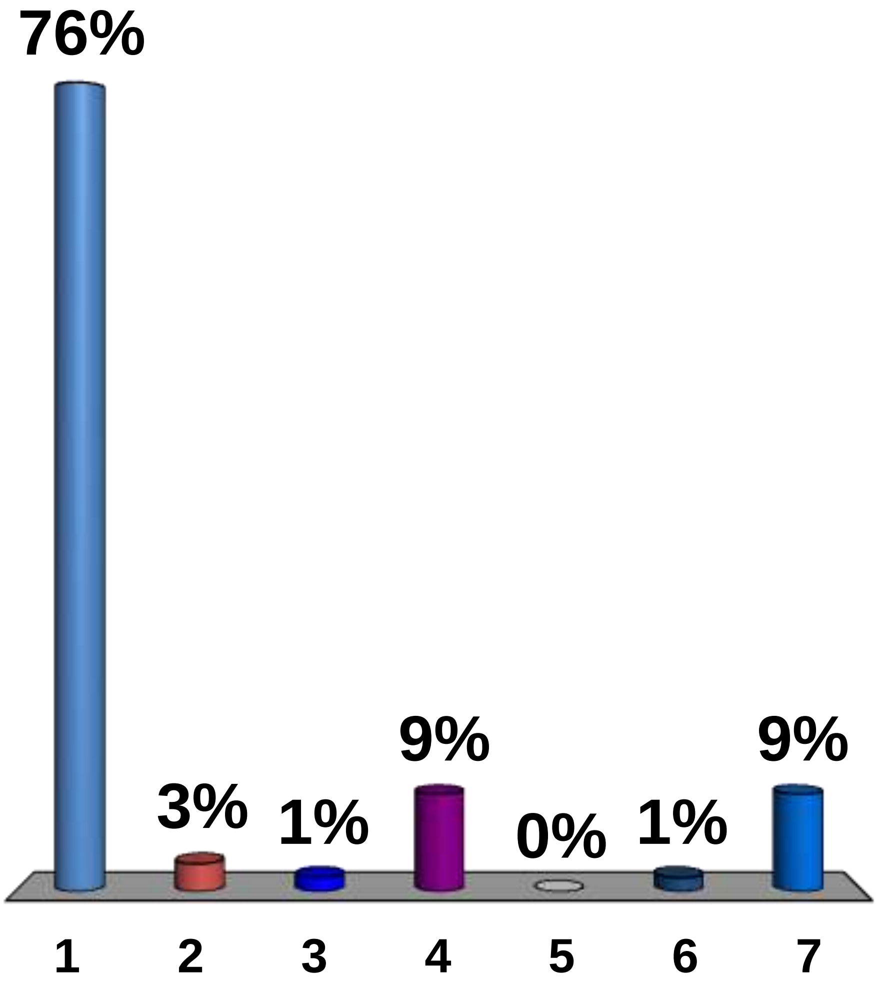
- **The information content in our workshops has continued to evolve to include the latest published articles…**

Some of the Data Collected
Using Audience Response “Clickers”

What is your role in the laboratory?

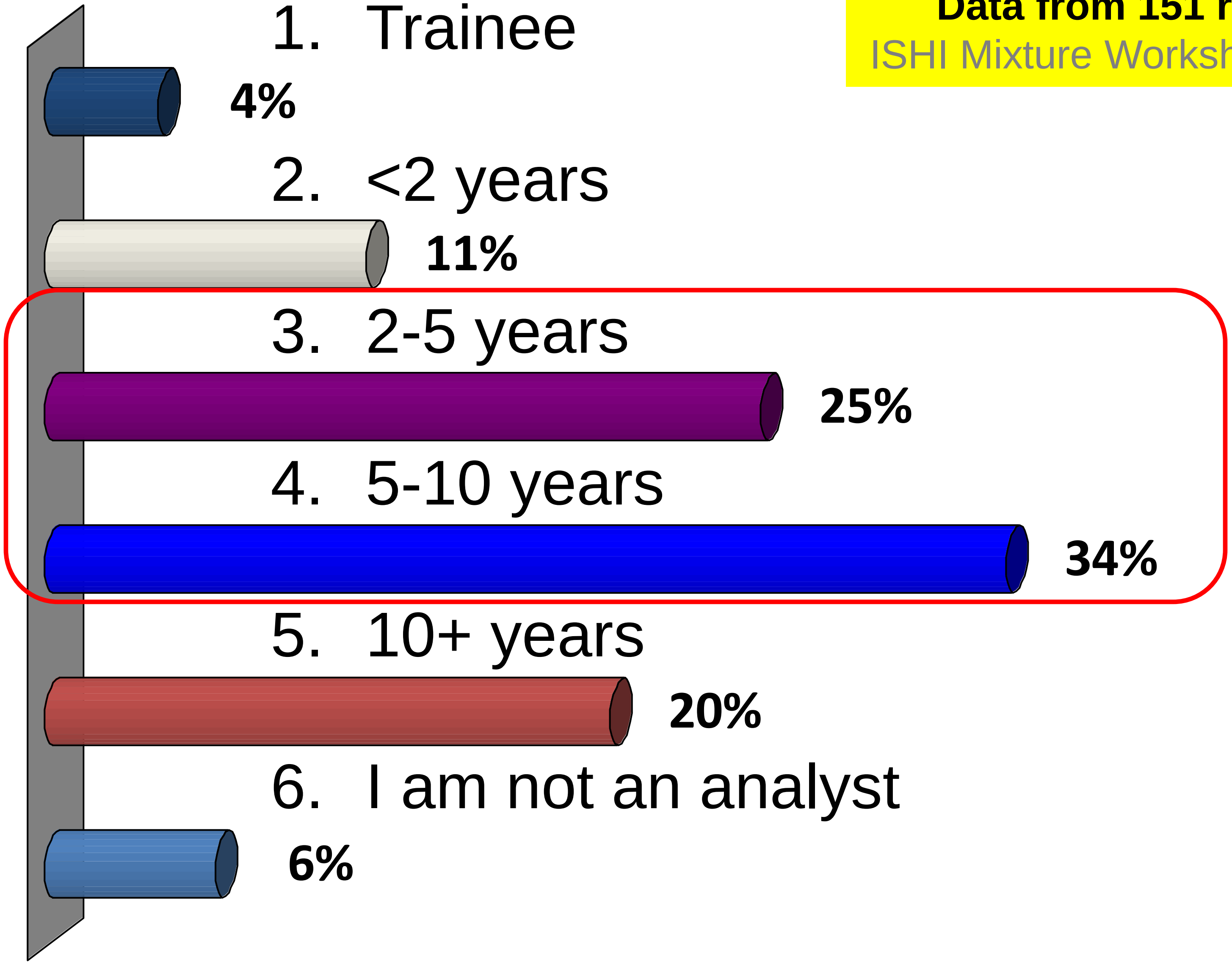
Data from 152 responses
ISHI Mixture Workshop (Oct 2011)

1. **DNA analyst**
2. DNA technician
3. Database analyst
4. **DNA technical leader**
5. QA Manager
6. Attorney
7. Other



Your Experience Level as a DNA Analyst

Data from 151 responses
ISHI Mixture Workshop (Oct 2011)

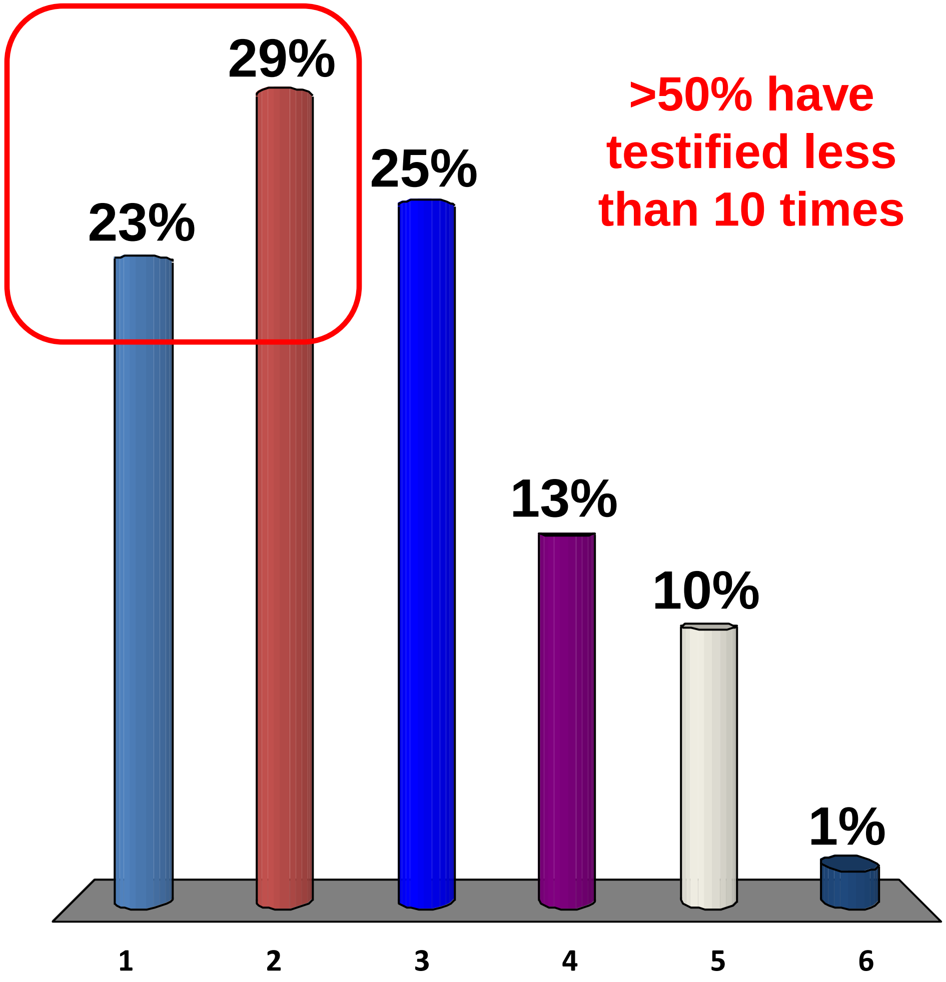


2-10 years experience = 59%

How much DNA court testimony experience do you have?

Data from 154 responses
ISHI Mixture Workshop (Oct 2011)

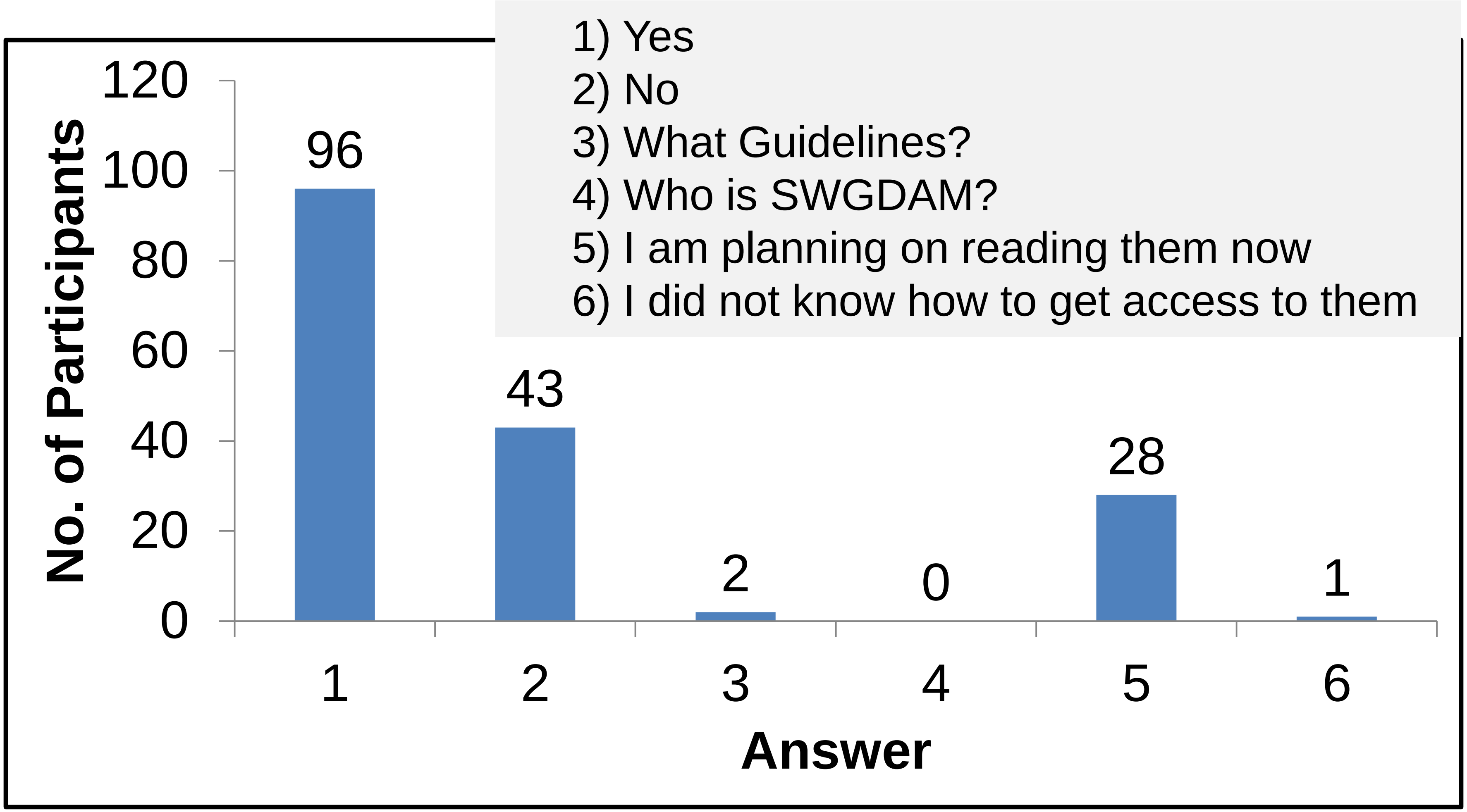
1. Have not testified yet
2. 1 to 10 times
3. 11 to 25 times
4. 25 to 50 times
5. > 50 times
6. One more time and I will need a good shrink.



>50% have testified less than 10 times

Have you read the 2010 SWGDAM Interpretation Guidelines? **Yes = 56%**

N = 170 from 4 regional groups (16 different labs)



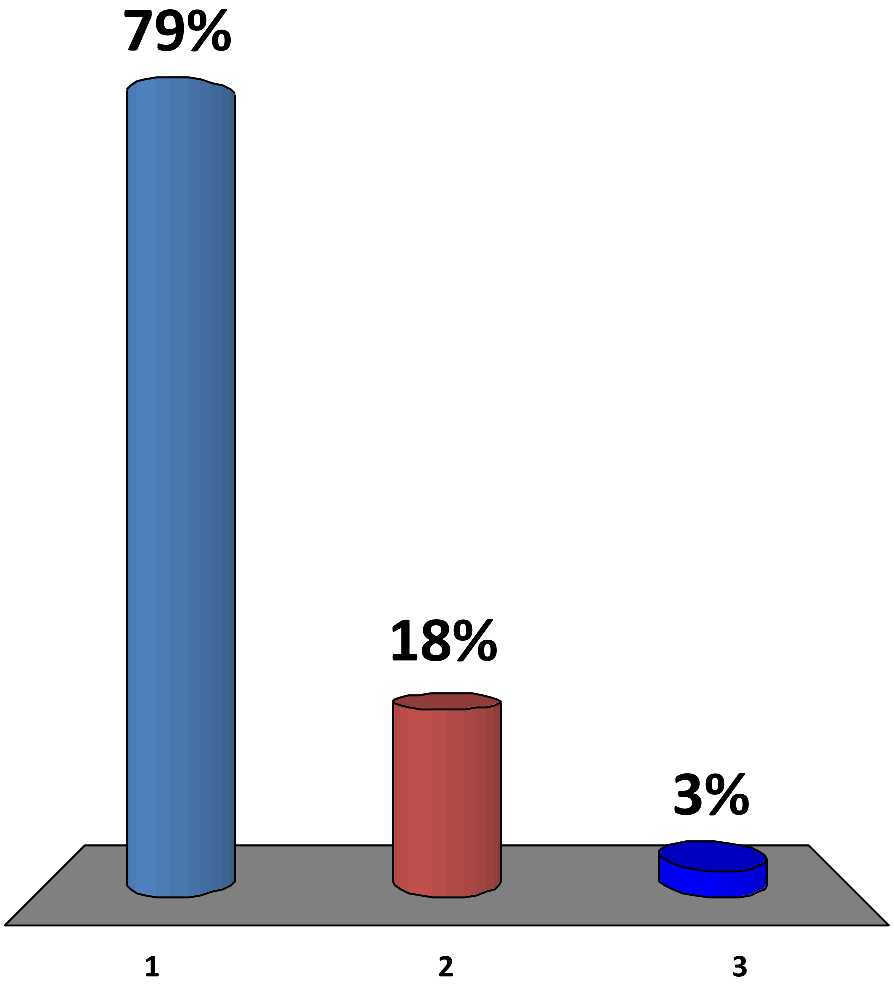
1) Yes
2) No
3) What Guidelines?
4) Who is SWGDAM?
5) I am planning on reading them now
6) I did not know how to get access to them

From ISHI 2011 poster "Impact of the SWGDAM Mixture Interpretation Guidelines: Successes, Issues and Suggested Future Directions"

Have you read the 2010 SWGDAM STR Interpretation Guidelines? **Yes = 79%**

1. Yes
2. No
3. Never heard of them before!

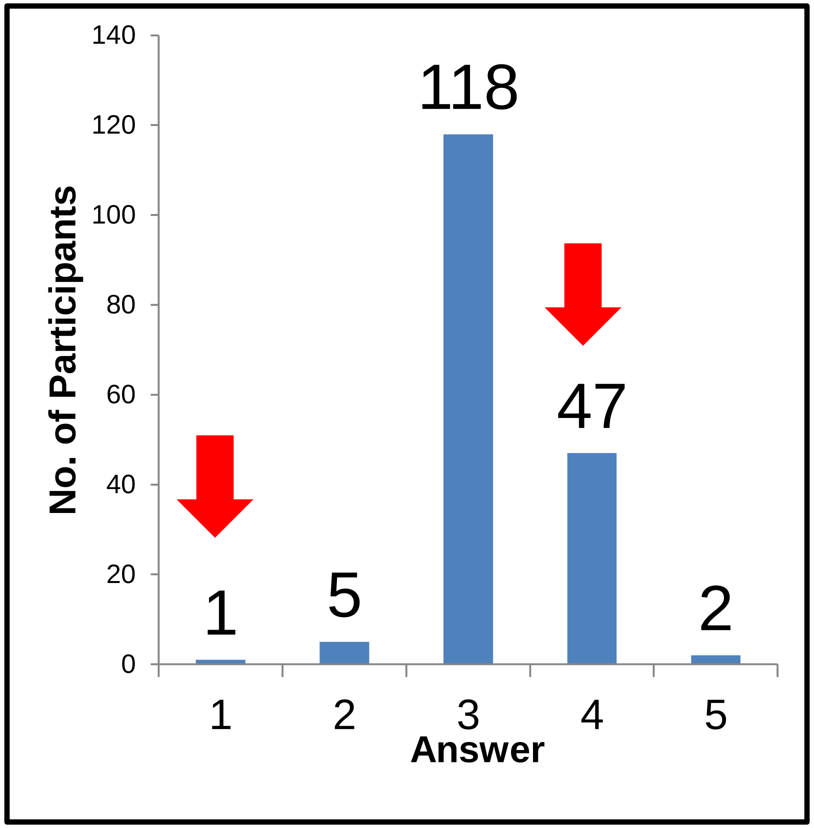
Data from 149 responses
ISHI Mixture Workshop (Oct 2011)



If you asked 10 analysts in your laboratory to interpret a complex mixture you would get:

N=174
Regional mixture workshops
(Apr – June 2011)

1. 100% consensus
2. 100% non-consensus
3. **Mostly consensus**
4. **A large range of answers**
5. We don't interpret complex mixtures

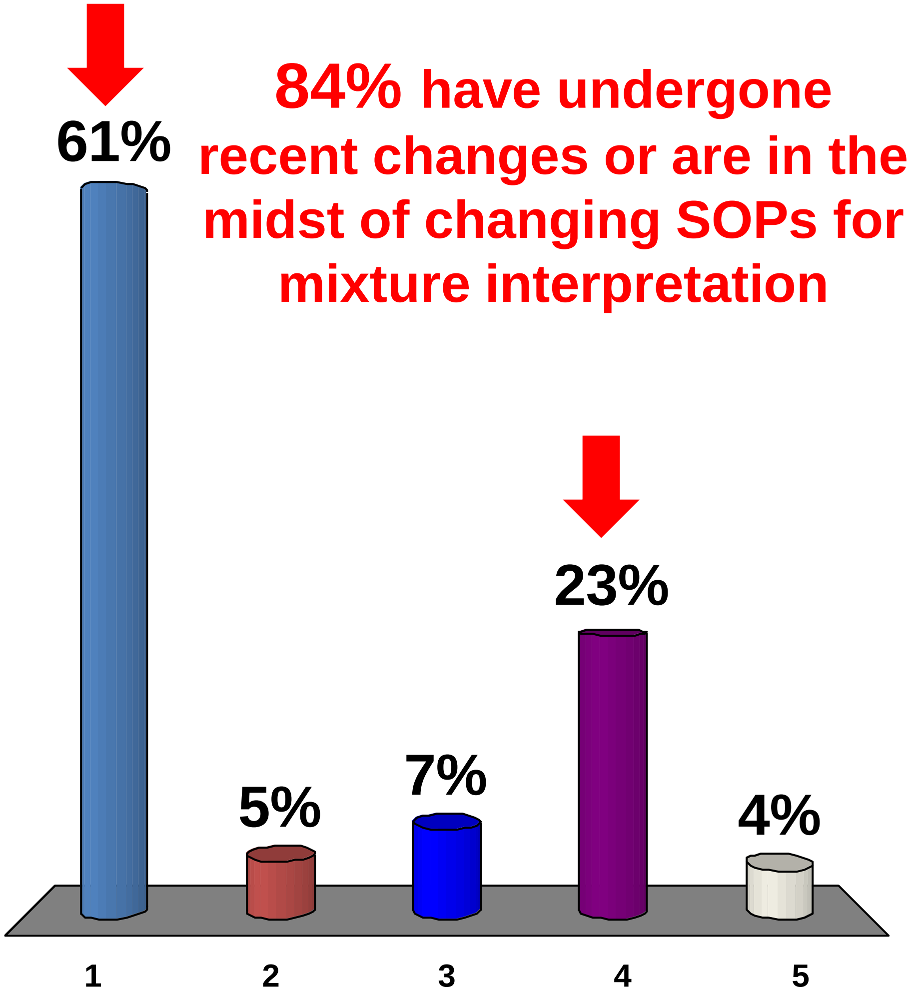


There is a recognition of the variation that exists with how analysts interpret complex mixtures.

From ISHI 2011 poster "Impact of the SWGDAM Mixture Interpretation Guidelines: Successes, Issues and Suggested Future Directions"

Has your lab implemented changes to your SOPs based on the new guidelines?

1. Yes
2. No
3. Reviewed SOPs but no changes needed
4. Working on it
5. Not applicable (I do not work in a forensic lab)



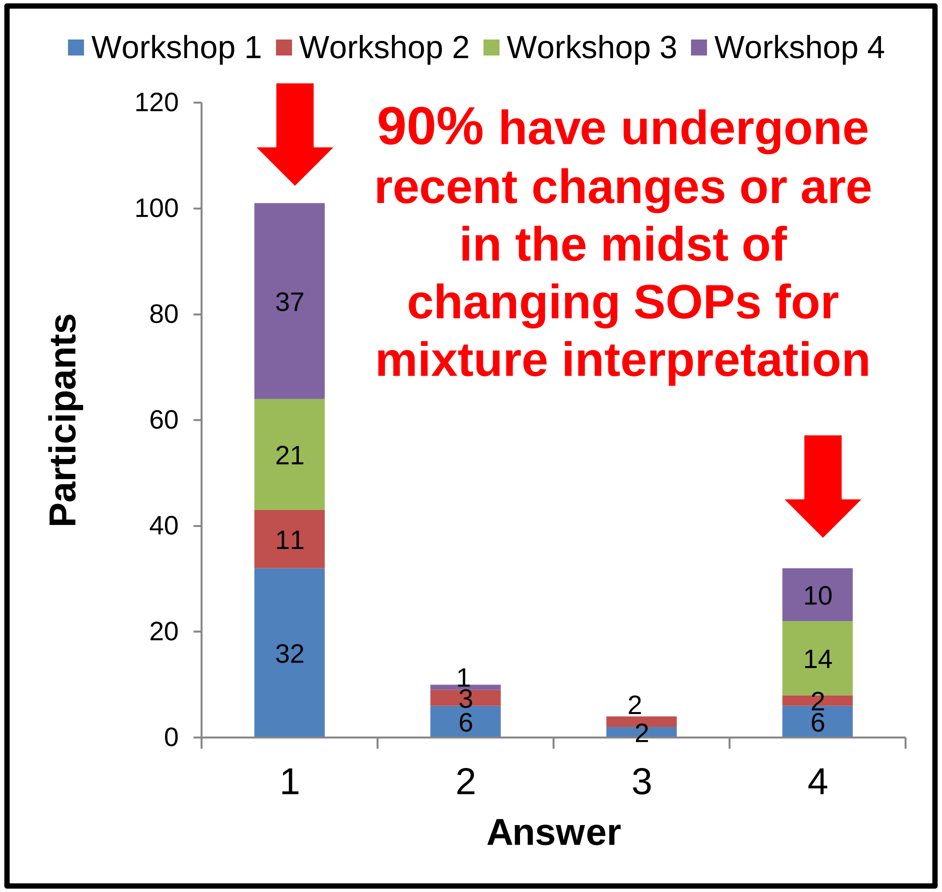
84% have undergone recent changes or are in the midst of changing SOPs for mixture interpretation

Data from 150 responses
ISHI Mixture Workshop (Oct 2011)

Has your lab implemented changes to your SOPs based on the new guidelines?

1. Yes
2. No
3. Reviewed SOPs but no changes needed
4. Working on it

N=147
Regional mixture workshops
(Apr – June 2011)



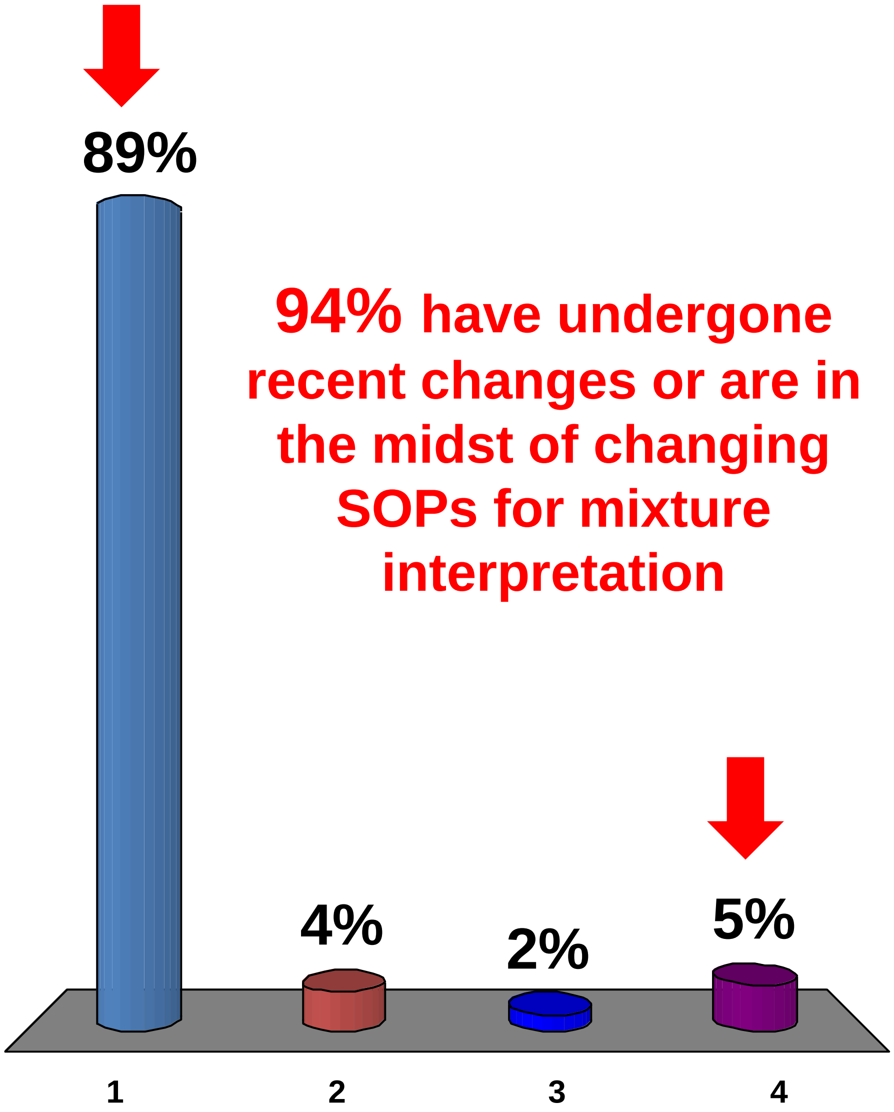
90% have undergone recent changes or are in the midst of changing SOPs for mixture interpretation

From ISHI 2011 poster “Impact of the SWGDAM Mixture Interpretation Guidelines: Successes, Issues and Suggested Future Directions”

Has your lab implemented changes to your SOPs based on the new guidelines?

1. Yes
2. No
3. Reviewed SOPs but no changes needed
4. Working on it

N=121 from 7 different labs
NYC Apr 2012



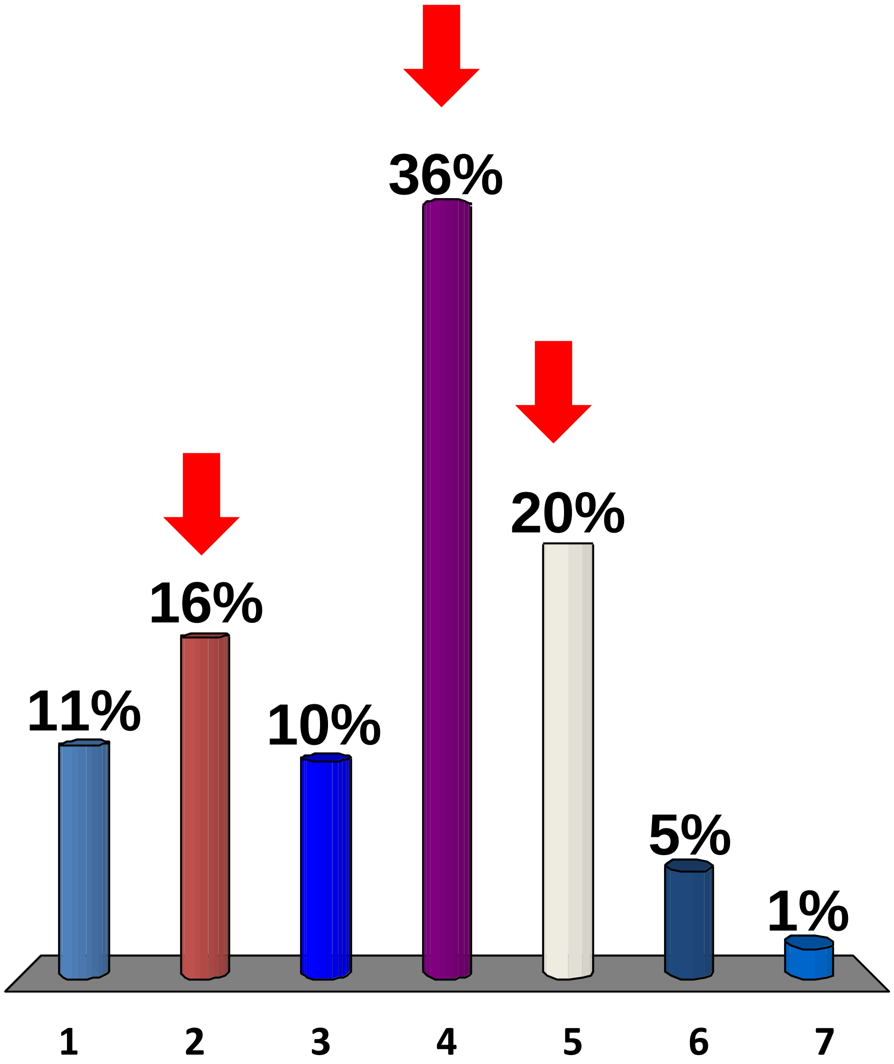
94% have undergone recent changes or are in the midst of changing SOPs for mixture interpretation

What kind of mixture statistic does your lab use?

1. LR
2. CPE (RMNE, CPI)
3. RMP
4. CPE or RMP
5. Other combinations
6. Probabilistic modeling (e.g., TrueAllele)
7. We don’t use stats (contradicting the new guidelines – section 4.1)

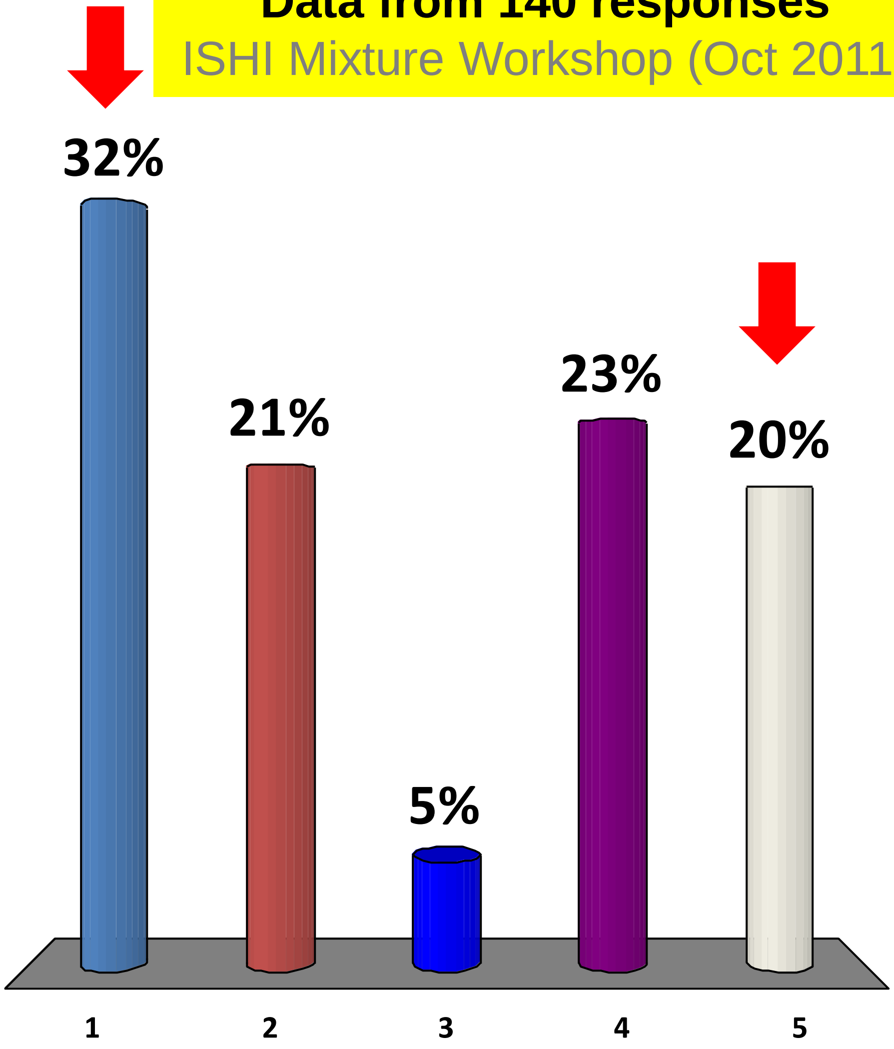
Data from 138 responses
ISHI Mixture Workshop (Oct 2011)

72% using CPI



If your laboratory uses a stochastic threshold (ST), it is:

1. Same value as our analytical threshold (**we don't use a ST**)
2. About twice as high as our AT (e.g., AT = 50 and ST = 100 RFU)
3. Less than twice as high as our AT
4. Greater than twice as high as our AT
5. I don't know!

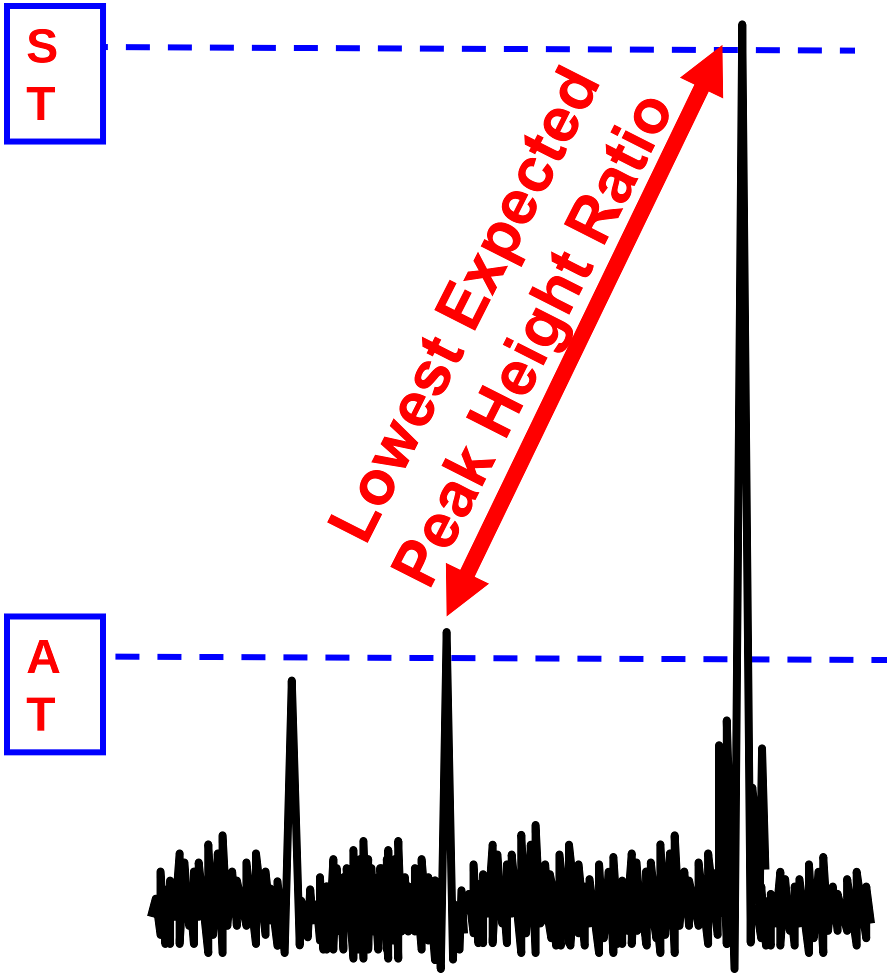


Data from 140 responses

ISHI Mixture Workshop (Oct 2011)

Stochastic and Analytical Thresholds

Impact Lowest Expected Peak Height Ratio



The lower you go trying to analyze low-level data… (i.e., more sensitive STR kits)

the worse your expected peak height ratios for single-source samples

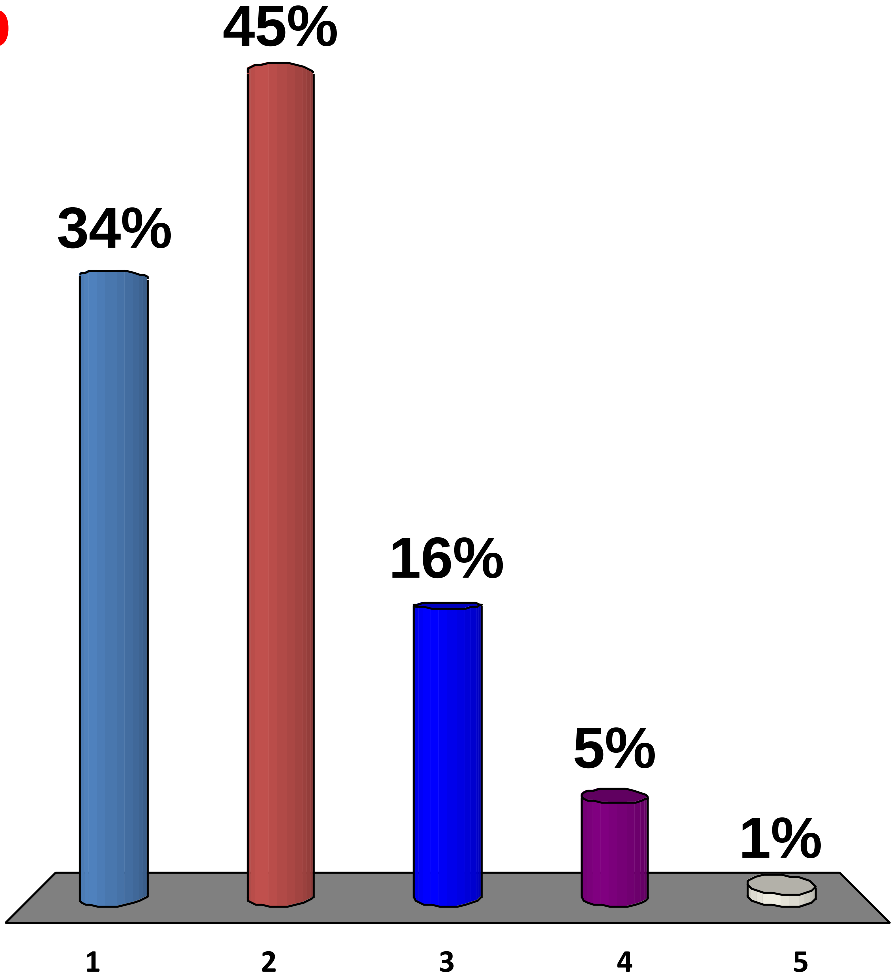
Therefore, there is greater uncertainty with associating genotypes of contributors in mixtures

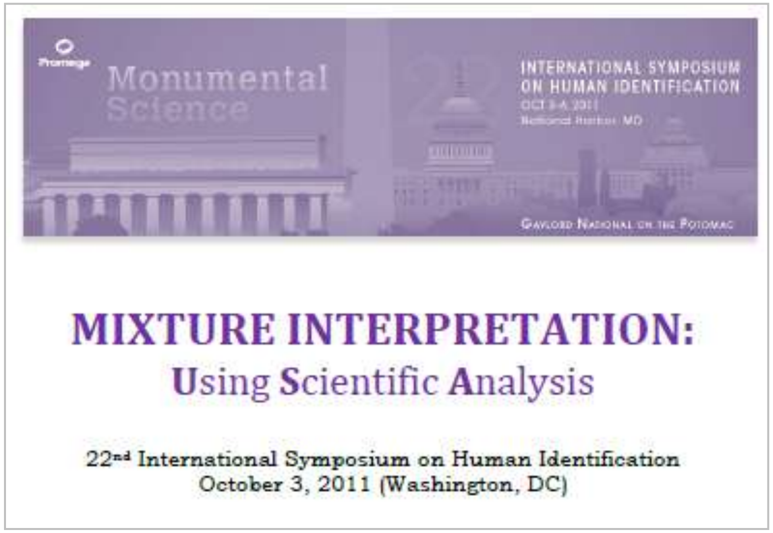
Overall the workshop was:

Data from 146 responses
ISHI Mixture Workshop (Oct 2011)

1. **Excellent**
2. **Very good**
3. Good
4. Fair
5. Poor

~80%




Monumental Science

INTERNATIONAL SYMPOSIUM ON HUMAN IDENTIFICATION
OCT 3-6, 2011
National Harbor, MD

Gaylord National on the Potomac

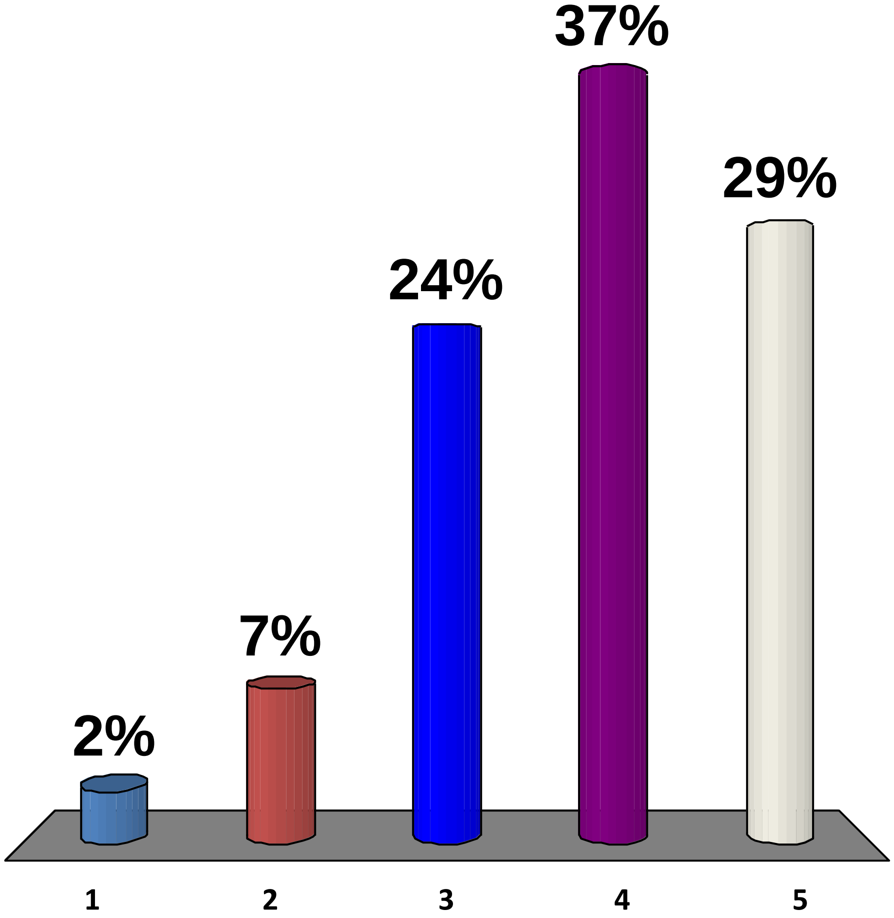
MIXTURE INTERPRETATION:
Using Scientific Analysis

22nd International Symposium on Human Identification
October 3, 2011 (Washington, DC)

Which of the topics below would be your first choice for additional training?

1. Relevant literature
2. How to validate thresholds
3. How to develop relevant SOPs
4. **Interpretation of low level mixtures**
5. **Statistics**

From one of the regional mixture workshops (Apr – June 2011)

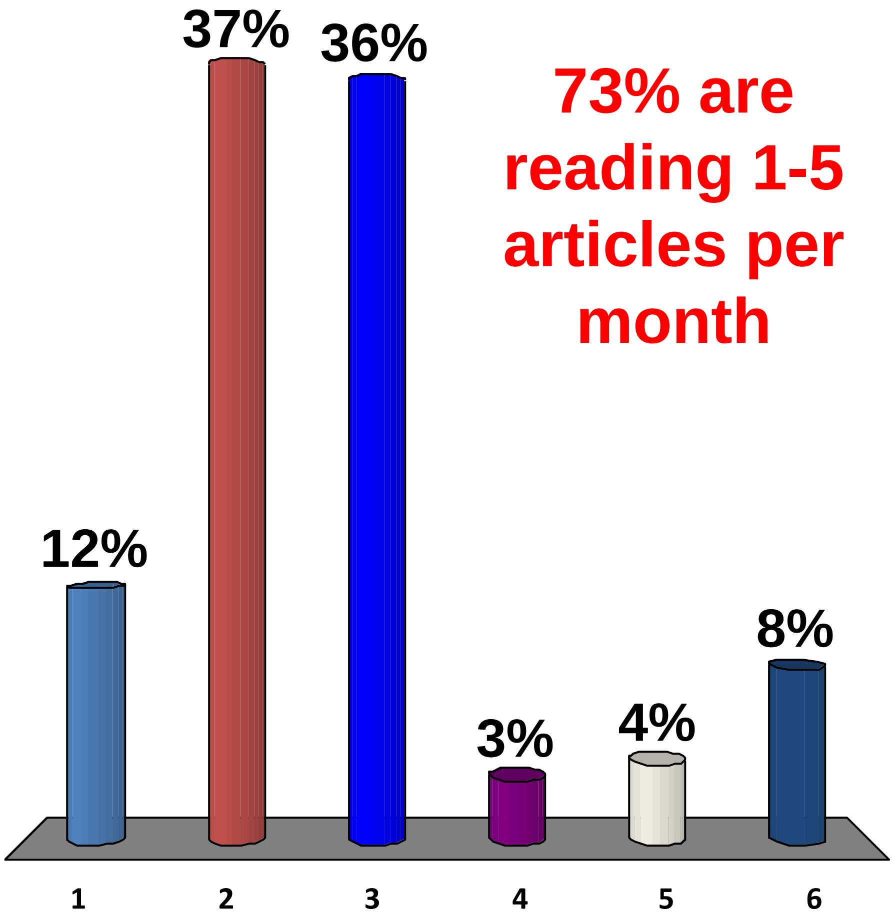


Mixture Literature
you should be reading…

How many DNA-related articles would you estimate that you read in a typical month?

1. None
2. 1 article
3. 2 to 5 articles
4. More than 5 articles
5. None, I only read the abstracts
6. I don’t make time to read!

Data from 133 responses
ISHI Mixture Workshop (Oct 2011)



73% are reading 1-5 articles per month

Useful Articles on DNA Mixture Interpretation

- **Buckleton, J.S. and Curran, J.M. (2008) A discussion of the merits of random man not excluded and likelihood ratios. *Forensic Sci. Int. Genet.* 2: 343-348.**
- Budowle, B., *et al.* (2009) Mixture interpretation: defining the relevant features for guidelines for the assessment of mixed DNA profiles in forensic casework. *J. Forensic Sci.* 54: 810-821.
- Clayton, T.M., *et al.* (1998) Analysis and interpretation of mixed forensic stains using DNA STR profiling. *Forensic Sci. Int.* 91: 55-70.
- **Gill, P., *et al.* (2006) DNA commission of the International Society of Forensic Genetics: Recommendations on the interpretation of mixtures. *Forensic Sci. Int.* 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. *FSI Genetics* 2(1): 76–82.
- Schneider, P.M., *et al.* (2009) The German Stain Commission: recommendations for the interpretation of mixed stains. *Int. J. Legal Med.* 123: 1-5.

Read to Maintain a Big Picture View!

If you are not following the recent literature, you would have missed:

  - Software applications & implementation
  - Impact of allele dropout on stats
  - Studies on number of contributors

- The literature is changing very fast
  - Read more than *Journal of Forensic Sciences* to stay caught up
- Make time in your schedule to read and ask critical questions

STRBase Mixture Reference List

http://www.cstl.nist.gov/strbase/mixture.htm

Topic category	# References
Mixture Principles & Recommendations	12
Setting Thresholds	10
Stutter Products & Peak Height Ratios	18
Stochastic Effects & Allele Dropout	14
Estimating the Number of Contributors	14
Mixture Ratios	7
Statistical Approaches	20
Separating Cells to Avoid Mixtures	3
Software	4
Probabilistic Genotyping Approach	6
General Information on Mixtures	6
TOTAL	**114**

Recent articles on mixtures not found in JFS…


Forensic Science International: Genetics 6 (2012) 191–197

Contents lists available at ScienceDirect

Forensic Science International: Genetics

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

The interpretation of low level DNA mixtures

Hannah Kelly[a,*], Jo-Anne Bright[a], James Curran[b], John Buckleton[a]

[a] ESR, PB 92021 Auckland, New Zealand
[b] Department of Statistics, University of Auckland, PB 92019 Auckland, New Zealand


Forensic Science International: Genetics 6 (2012) 102–107

Contents lists available at ScienceDirect

Forensic Science International: Genetics

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

Extended PCR conditions to reduce drop-out frequencies in low template STR typing including unequal mixtures

Natalie E.C. Weiler[1], Anuska S. Matai[1], Titia Sijen[*]

Netherlands Forensic Institute, Laan van Ypenburg 6, The Hague 2497GB, The Netherlands


Forensic Science International: Genetics 6 (2012) 180–184

Contents lists available at ScienceDirect

Forensic Science International: Genetics

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

A comparison of stochastic variation in mixed and unmixed casework and synthetic samples

Jo-Anne Bright[a,*], Kurt McManus[a], SallyAnn Harbison[a], Peter Gill[b,c], John Buckleton[a]

[a] ESR, Private Bag 92021, Auckland, New Zealand
[b] Institute of Forensic Medicine, Oslo University, Norway
[c] Centre for Forensic Science, University of Strathclyde, Glasgow, UK


Contents lists available at SciVerse ScienceDirect

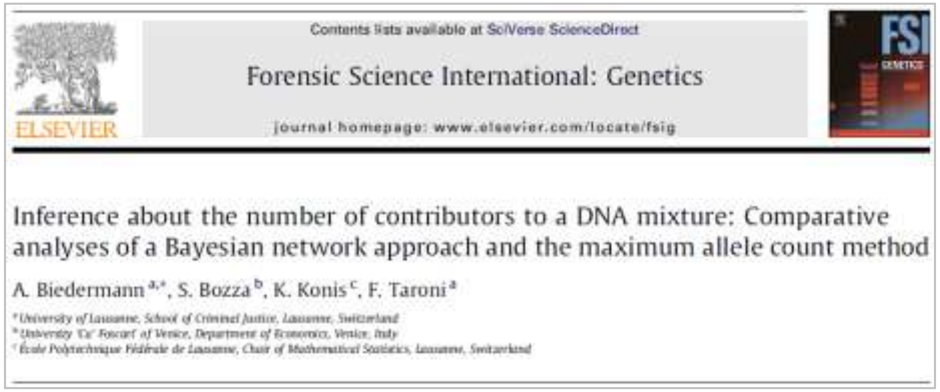
Forensic Science International: Genetics

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

Assessment of mock cases involving complex low template DNA mixtures: A descriptive study

Corina C.G. Benschop, Hinda Haned, Tanja J.P. de Blaeij, Alexander J. Meulenbroek, Titia Sijen[*]

Department of Human Biological Traces, Netherlands Forensic Institute, P.O. Box 24044, 2490 AA The Hague, The Netherlands


Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

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

Inference about the number of contributors to a DNA mixture: Comparative analyses of a Bayesian network approach and the maximum allele count method

A. Biedermann[a,*], S. Bozza[b], K. Konis[c], F. Taroni[a]

[a] University of Lausanne, School of Criminal Justice, Lausanne, Switzerland
[b] University 'Ca' Foscari' of Venice, Department of Economics, Venice, Italy
[c] École Polytechnique Fédérale de Lausanne, Chair of Mathematical Statistics, Lausanne, Switzerland


Contents lists available at SciVerse ScienceDirect

Forensic Science International: Genetics

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

Automating a combined composite–consensus method to generate DNA profiles from low and high template mixture samples

Bram Bekaert[a,1,*], Anneleen Van Geystelen[b,c,1], Nancy Vanderheyden[a], Maarten H.D. Larmuseau[a,d,e], Ronny Decorte[a,e]

[a] UZ Leuven, Laboratory of Forensic Genetics and Molecular Archaeology, UZ Leuven, Leuven, Belgium
[b] Applied Molecular Genomics Group, Department of Molecular Genetics, Flanders Institute for Biotechnology (VIB), Flanders, Belgium
[c] University of Antwerp (UA), Antwerp, Belgium
[d] K.U. Leuven, Laboratory of Animal Diversity and Systematics, Leuven, Belgium
[e] K.U. Leuven, Department of Human Genetics, Campus Gasthuisberg, Leuven, Belgium

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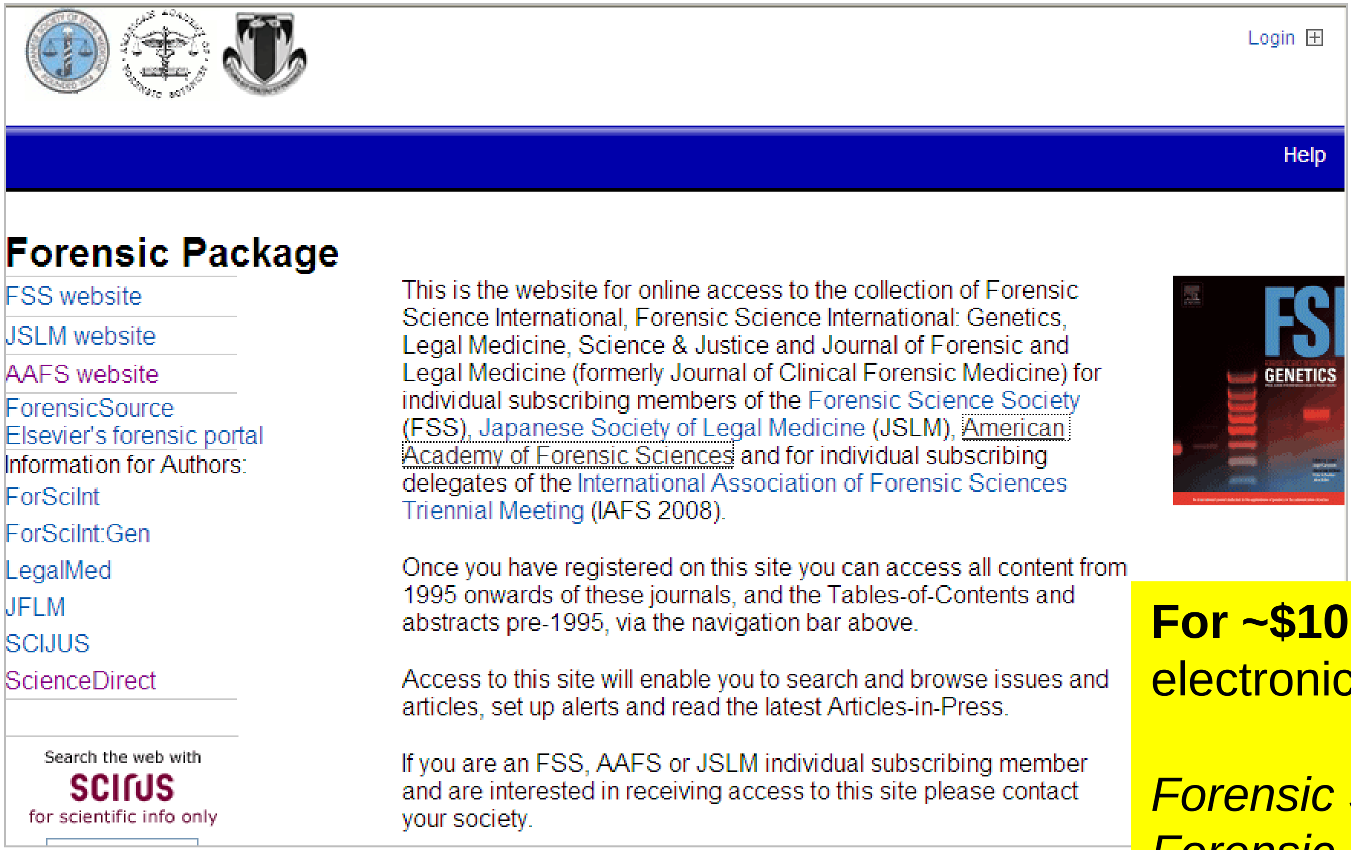

Forensic Package

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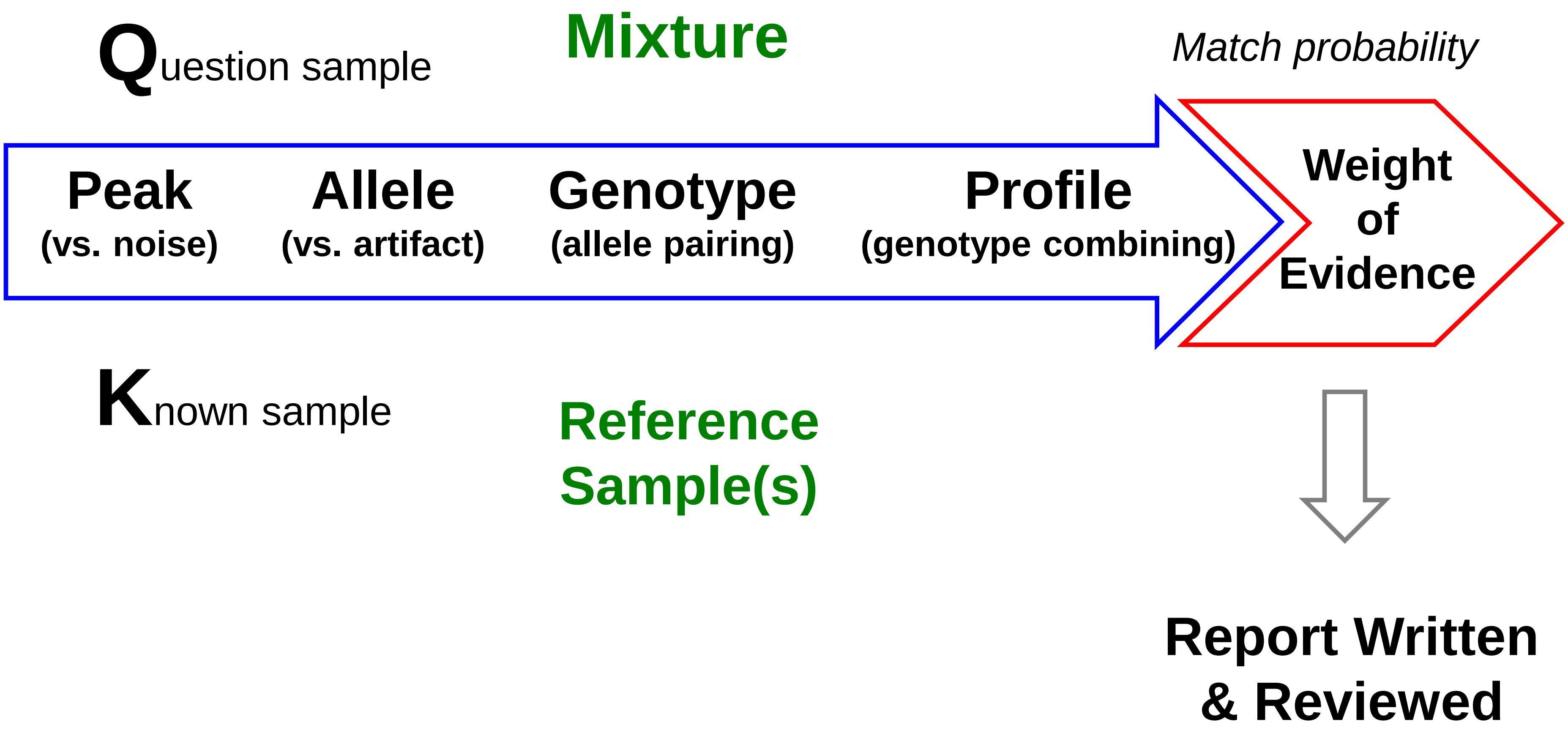
Important lessons and common misunderstandings

Steps in DNA Interpretation



Question sample

Mixture

Match probability

Peak
(vs. noise)

Allele
(vs. artifact)

Genotype
(allele pairing)

Profile
(genotype combining)

Weight of Evidence

Known sample

Reference Sample(s)

Report Written & Reviewed

Important Lessons

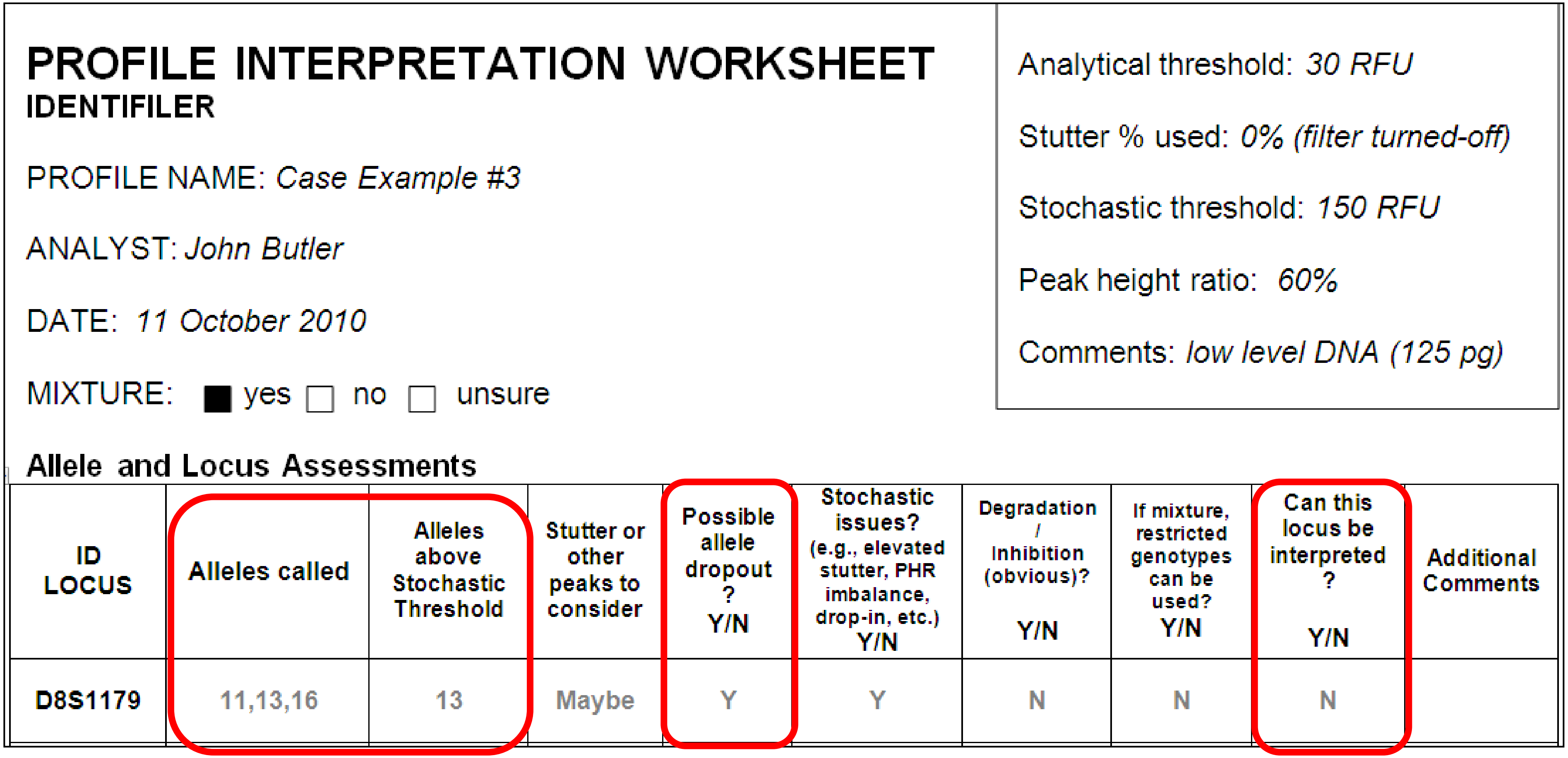
- People think they understand the basics of interpretation better than they actually do – this is what leads to observed variation in interpreting mixtures…

- Increased complexity of mixtures (with more allele sharing) leads to higher uncertainty which leads to lack of confidence in potential contributor genotypes

- Worked examples are beneficial in training (participants need to work through the examples themselves)

- There is value in using a profile interpretation worksheet to document assumptions and decisions made

Value of Using a Profile Interpretation Worksheet



PROFILE INTERPRETATION WORKSHEET

IDENTIFILER

PROFILE NAME: *Case Example #3*

ANALYST: *John Butler*

DATE: *11 October 2010*

MIXTURE: ■ yes ☐ no ☐ unsure

Analytical threshold: *30 RFU*

Stutter % used: *0% (filter turned-off)*

Stochastic threshold: *150 RFU*

Peak height ratio: *60%*

Comments: *low level DNA (125 pg)*

Allele and Locus Assessments

ID LOCUS	Alleles called	Alleles above Stochastic Threshold	Stutter or other peaks to consider	Possible allele dropout ? Y/N	Stochastic issues? (e.g., elevated stutter, PHR imbalance, drop-in, etc.) Y/N	Degradation / Inhibition (obvious)? Y/N	If mixture, restricted genotypes can be used? Y/N	Can this locus be interpreted ? Y/N	Additional Comments
D8S1179	11,13,16	13	Maybe	Y	Y	N	N	N	

Make decisions on the evidentiary sample and document them prior to looking at the known(s) for comparison purposes

Common Misunderstandings

- Using CPI stats is conservative to the defendant
  - The numerical stat is low but by throwing out information the ability to EXCLUDE innocent people is reduced

- Using CPI stats means that the potential number of contributors is not important
  - Higher numbers of contributors dilutes out the amount of DNA for each contributor which leads to more stochastic effects and the possibility of allele dropout (more uncertainty)
  - The CPI stat cannot handle allele dropout!

Handling Complex Mixtures

- Stochastic thresholds work in combination with CPI statistics but may not apply for >2 person mixtures (due to potential allele shares)

- Most labs are not adequately equipped to cope with complex mixtures
  - Extrapolating validation studies from simple mixtures will not be enough to create appropriate interpretation SOPs

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.

Thoughts on Where We Need to Go

- Away from CPI and towards likelihood ratio approaches
  - As noted in the Gill et al. (2006) ISFG DNA Commission recommendation #2
- This will require software to perform the calculations
  - This software will need to be validated
  - Peter Gill and others in Europe are pushing freeware solutions
- Still will require analysts to understand what is going on in the computer calculations!
  - Will require more significant engagement in mixture training
- The U.S. will be moving to more STR loci in the near future (from 13 to ~20 core STRs)
  - Using loci with better powers of discrimination will be helpful

ISHI 2010 Mixture Workshop

October 11, 2010

Catherine Grgicak
Boston U.

Mike Coble
NIST

Robin Cotton
Boston U.

John Butler
NIST

Charlotte Word
Consultant

Promega ISHI 2012 Mixture Workshop


Monday, October 15, 2012

Mixtures
Using
Sound statistical analysis
Interpretation &
Conclusions

- **John Butler,** Ph.D., NIST, Gaithersburg, MD
- **Michael Coble**, Ph.D., NIST, Gaithersburg, MD
- **Robin Cotton**, Ph.D., Boston University, Boston, MA
- **Catherine Grgicak**, Ph.D., Boston University, Boston, MA
- **Charlotte J. Word**, Ph.D., Gaithersburg, MD

This workshop is for analysts, technical reviewers and technical leaders performing and interpreting validation studies and/or interpreting and reviewing STR data, particularly more difficult mixtures. Various DNA profiles will be analyzed and interpreted using selected analytical thresholds and stochastic thresholds to demonstrate the impact of those values on the profiles amplified with low-template DNA vs. higher amounts of DNA. Different statistical approaches and conclusions suitable for the profiles will be presented.