2012 Mixture Interpretation Workshop: <u>Mixtures Using SOUND Statistics</u>, Interpretation, & Conclusions



Different Assumptions-Different Interpretations

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October 15, 2012 Nashville, TN





Single Source Sample



High Certainty Leads to High Confidence

- High peaks above stochastic threshold
 - True alleles easy to distinguish from stutter & other artifacts
 - >All alleles present with high confidence
- >1 or 2 alleles at all loci
- Balanced peak heights (inter- & intra-locus)
 - Number of Contributors easily assumed
 - ≻Single source
 - Genotypes easy to determine





Two-Person Mixtures

High Certainty Leads to High Confidence

- High peaks above stochastic threshold
 - True alleles easy to distinguish from stutter & other artifacts
 - >All alleles present with high confidence
- ➤ ≤ 4 alleles at all loci
 - Number of Contributors reasonably assumed as 2
 - Peak heights consistent with 2 person mixture

Two-Person Mixtures



High Certainty Leads to High Confidence

- Genotypes and Genotype combinations
 - Limited number of possible genotypes present
 - ➢ Easy to determine

> May increase certainty of genotypes by:

- >Assessing mixture ratio
- Determining if distinguishable/major:minor or indistinguishable mixture
- Deducing second contributor if one contributor is known

REAL Casework



Increased uncertainty and decreased confidence for some profiles

- With that comes increased chance/risk that different interpretations may come from:
- Other analysts in your lab
- Other experts outside of lab

Change in assumptions regarding data affects the interpretation

REAL Casework Experience



Situations with increased uncertainty, and therefore decreased confidence:

- >Alleles vs. artifacts? (LT or high level DNA)
- Stochastic effects possible? (Low peak heights; all or some below stochastic threshold)
 - Sure all alleles are present (drop-out)?
 - Elevated stutter & drop-in present?
- >Number of contributors? 1, 2, 3 or more?
- Inability to confidently associate all alleles into reasonable genotypes

When there are different opinions for reporting a profile, our lab reports...

- 1. Inconclusive
- 2. Conclusion most favorable to client
- 3. Conclusion most agree on
- 4. Single consensus agreement
- 5. What the technical reviewer/leader says
- 6. All conclusions with different assumptions





What do you do when...

You have increased uncertainty, and therefore decreased confidence?

Options for interpreting and reporting:

- Do not interpret the data → report inconclusive
 - When uncertainty is too high
- 2. Pick one interpretation to report
 - When have minimal uncertainty
- 3. Interpret and report the data under two or more different assumptions
 - When certainty is medium-to-high but possible scientifically sound alternatives exist

When to Consider Different Assumptions



May need to consider multiple assumptions for data interpretation when:

- Possible LT DNA profile
 - Stochastic effects (allelic drop-in, allelic drop-out, elevated stutter)
- Possible minor contributor in mixed DNA profile
- Possible known contributor(s) and deducing
- ➢ More than 2 contributors (later today)



I would report the previous profile as:

- 1. Single source
- 2. Mixture
- 3. Inconclusive
- 4. Single source and mixture
- 5. Not sure

Correct answer is a single-source sample from ~62 pg DNA template with drop-in at D18 (allele 20) Data from 104 responses





I am confident that the number of contributors in the previous profile is...

Data from 108 responses

- 1. 1
- 2. 2
- 3. 3
- 4. >3
- 5. At least 2
- 6. Not sure

Correct answer is 2 contributors; but "at least 2" is very appropriate





The known individual is:

- 1. Included
- 2. Excluded
- 3. Inconclusive
- 4. Not sure
- Included and excluded using different assumptions
- Whatever my technical reviewer says!

Data from 106 responses





EXCLUDED as major & minor if assume only 2 contributors:

Must have 1 major and 1 minor contributor due to peak height ratio and mixture ratio calculations.

Major *must* have genotype of 13,16 and 28,28 and minor *must* have genotype of 14,15 and 30,32.2.

Genotypes NOT included even if alleles are!



NOT EXCLUDED based on alleles being present if assume >2 contributors

Assuming >2 contributors (≥ 2 minor) is reasonable due to the possibly of alleles missing since low peak heights (i.e., LT DNA) for alleles are observed at each locus

All alleles and genotypes represented?

Report: Inclusion (Stats??) INCONCLUSIVE (insufficient data for minors)



Indistinguishable Mixture Profile





Reporting Multiple Conclusions

Different conclusions may result from using different assumptions.

If 2 contributors:



EXCLUDED

BUT

If 3 contributors:



INCLUDED INCONCLUSIVE

REPORT ALL CONCLUSIONS!









Mark Sample for Deleti







8,11 = true minorcontributor 8 allele filtered

out by software

Stutter or true allele? All alleles present? If assume 8 is a stutter peak and assume all peaks are present, would exclude the true contributor!

Uncertainty in evaluating the presence or absence of alleles leads to false inclusions and exclusions

Indistinguishable? Major vs.







3 vs. 4 vs. 5 or more Contributors

Stay tuned for talk this afternoon

If a sample has more than one possible conclusion using different assumptions, then...

- 1. The best one for the client should be reported.
- 2. Some should be saved for court testimony.
- 3. Some should be ignored.
- 4. All should be reported.

Data from 92 responses







The results (all alleles and genotypes) are consistent with a mixture of DNA from the two individuals.



Two Inclusions



The results are NOT consistent with both of the individuals being contributors together in the sample.

This is important to report because....

Two Inclusions – Total of Four Possibilities



Reporting

- Report all opinions, assumptions and conclusions
 - Single source or mixture
 - Number of contributors if mixture
 - Gender of contributor(s)
 - Partial profile (inconclusive loci)
 - Inclusions, Exclusions and Inconclusives
 - Statistics for all Inclusions
 - Explanations for Inconclusives
- Report results and conclusions for all data obtained for all samples

Reporting

- Consider the data from several scientific perspectives – for conclusions and statistical calculations
- Report all appropriate scientific conclusions and opinions in the laboratory report
- ESPECIALLY if the conclusions differ under different reasonable assumptions

Why Report?

- Opinions may be important to different individuals reading the report (e.g., law enforcement, prosecutor, defense attorney, client, judge, jury)
- Reports should be neutral to the case yet address the question(s) asked by the client

Why Report?

• Not all cases (<10%) make it to court

 Critical decisions often based on report and (mis)understandings alone

• If not provided in advance to all parties, opinions may not be admissible in court

THANK YOU!!