MIXTURE CRISIS

Scientists and statisticians write about the DNA mixture crisis. Forensic laboratories apply “thresholds” that discard data, but the accuracy of threshold procedures has not been scientifically proven. Allowing signals before entry into statistical software can lead to inaccurate results. By omitting informative DNA data, an "inconclusive" report can deny courts evidence that could implicate the guilty or exonerate the innocent.

Adjudicating laboratory data can introduce human subjectivity. There is a danger that context bias (such as inadvertently assuming guilt) can yield a DNA analysis that is not impartial. Some mixture interpretation protocols do not use all the DNA data. Data selection can overweight the probative value of a match, which can mislead juries.

Simple software can cause DNA interpretation errors. Simple methods are appropriate for simple DNA data. Application to more challenging samples must be empirically justified. Without supporting validation data, an unvalidated software is an unknown threat DNA evidence in criminal cases.

Ten years ago NIST and others warned about misinterpretation of DNA mixture evidence. The 2010 Federal Rules of Evidence Rule 702 stipulated that expert witnesses must be qualified in the proper statistical analysis. The 2010 SWGDAM mixture guidelines were jointly developed with the NYSP DNA lab (Albany, NY). CPI can afterwards provide an impressive A 2011 TrueAllele validation study conducted jointly with the NYSP DNA lab (Albany, NY) showed that CPI vastly underreported DNA's probative value. When CPI cannot report a CPI match statistic, their number was (on average) a million times less than the true match statistic on the same data. CPI analysis removed considerable DNA information.

In 2013, NIST conducted a Mantis inter-laboratory study. The hope was that the new statistics would be more useful. The analysis found that information was incorrectly concluded that informatics were inconclusive.

In 2016, the American Academy of Forensic Science recognized the need to abandon uncorrelated threshold procedures and substituted trustworthy DNA mixture statistics.

Scientists and statisticians write about the DNA mixture crisis. Forensic laboratories apply “thresholds” that discard data, but the accuracy of threshold procedures has not been scientifically proven. Allowing signals before entry into statistical software can lead to inaccurate results. By omitting informative DNA data, an "inconclusive" report can deny courts evidence that could implicate the guilty or exonerate the innocent.

Adjudicating laboratory data can introduce human subjectivity. There is a danger that context bias (such as inadvertently assuming guilt) can yield a DNA analysis that is not impartial. Some mixture interpretation protocols do not use all the DNA data. Data selection can overweight the probative value of a match, which can mislead juries.

Simple software can cause DNA interpretation errors. Simple methods are appropriate for simple DNA data. Application to more challenging samples must be empirically justified. Without supporting validation data, an unvalidated software is an unknown threat DNA evidence in criminal cases.

Ten years ago NIST and others warned about misinterpretation of DNA mixture evidence. The 2010 Federal Rules of Evidence Rule 702 stipulated that expert witnesses must be qualified in the proper statistical analysis. The 2010 SWGDAM mixture guidelines were jointly developed with the NYSP DNA lab (Albany, NY). CPI can afterwards provide an impressive A 2011 TrueAllele validation study conducted jointly with the NYSP DNA lab (Albany, NY) showed that CPI vastly underreported DNA's probative value. When CPI cannot report a CPI match statistic, their number was (on average) a million times less than the true match statistic on the same data. CPI analysis removed considerable DNA information.

In 2013, NIST conducted a Mantis inter-laboratory study. The hope was that the new statistics would be more useful. The analysis found that information was incorrectly concluded that informatics were inconclusive.

In 2016, the American Academy of Forensic Science recognized the need to abandon uncorrelated threshold procedures and substituted trustworthy DNA mixture statistics.

SCIENCE AND THE LAW

DNA holds considerable prejudicial power over a jury. When CPI's match statistic is near zero, juries erroneously believe that the defendant is innocent.

The following recommendations may help society move beyond mixture interpretation failure, and enjoy consistently more reliable DNA evidence:

1. Open DNA data to public scrutiny.
2. The crime labs have failed to produce reliable match statistics for over fifteen years. The solution is open access to all DNA data, so that impartial scientists can publicly reassess crime lab results in every case.
3. Revisit all past DNA mixture cases.

Hundred of thousands of DNA mixture cases have been published, but many were reviewed only by not study science or mathematics. But lawyers need to understand the evidence they attack or defend. Appropriate education is needed to teach them DNA statistics.

5. Extensively validate DNA interpretation.

Most mixture statistics have not been validated for their intended use. No method, whether done by man or machine, should ever be introduced as evidence without supporting validation data.

6. Keep methods within their limits.

Defence vigilance helps ensure that crime labs stay within the bounds of their validated interpretation methods. Without this DNA pressure, false positives may falsely identify or convict innocent people.

7. Go beyond laboratory limits.

Better interpretation methods can solve DNA mixture problems that DNA mixtures can't. Independent groups should interpret these data. Otherwise false negatives may fail to identify potentially exculpatory evidence.

CONCLUSION

Unscientific, untested "statistical" analysis of DNA evidence results in incorrect results on hundreds of thousands of evidence items. When thresholds give an "inconclusive" result on mixes with data that, when analyzed correctly, are wrongly suspect. Innocent people remain in prison because informative DNA wasn't used in their defense. Defendants are wrongly convicted when misinterpreted chromosomes fail to identify the true culprit.

Perpetrators go free when DNA evidence is falsified by forensic fakery. Falsely convicted criminals cannot be released unless the false conviction is proved and the innocent person exonerated.

Modern genome-sequencing programs use probability to help interpret DNA mixtures. TrueAllele has a fully Bayesian model that considers all data and solutions. Laws threaten programs relative to probabilistic evidence.

Subjective labs require a human operator choose input data and parameters to overcome software limitations. While crime labs have started adopting better match statistic software, validation studies are needed to determine their range of applicability.

Unconstrained DNA statistics have inflicted considerable injustice on defendants, crime victims, and society. In every case that involved insufficiently validated DNA mixture statistics, victims, and society. Every case that involved insufficiently validated DNA mixture statistics, victims, and society. Every case that involved insufficiently validated DNA mixture statistics, victims, and society.

Cybergenetics © 2010-2016