Transcript of Dr. Mark Perlin's presentation on "The Science of Quantitative DNA Mixture Interpretation" delivered on 11 January 2011 in Fredericksburg, VA at Scientific Working Group on DNA Analysis Methods (SWGDAM).

Dr. Perlin: Thank you for inviting me. Today, I will be talking for about a half an hour on the Science of Quantitative DNA Mixture Interpretation. In particular, I was asked to speak about the TrueAllele® Casework system.

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The TrueAllele Casework system has been around for around ten years. It performs quantitative interpretation of STR evidence through a statistical search using a probability model. The key concept is to preserve all of the identification information that is present in the data. After collecting biological evidence, forensic scientists run it through their laboratory to produce highly quantitative STR data. Our goal is retain all the identification information in that data.

TrueAllele objectively infers genotypes without ever seeing suspects. Only afterward inferring a genotype is it ever matched against a suspect, or a whole CODIS database of suspects. TrueAllele can assume any number of mixture contributors, and its mathematics models PCR stutter, peak imbalance, degraded DNA, and other laboratory variables. Importantly, the system calculates the uncertainty of every peak. The first TrueAllele was built over 10 years ago, and

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the system is now in its 25th version. TrueAllele has been used on over 100,000 evidence samples. The technology is available as a product for use inside of a laboratory, or as a forensic interpretation service provided by Cybergenetics. Some labs like both the product and service models, and find them to be complementary.

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This talk is structured to answer the five questions that Heather had posed to Cybergenetics, as well as answer a few additional questions. The first question we were asked is: "What advancements have been made in the casework software that would make the software eligible to be a casework expert system?"

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Let us go back ten or fifteen years to the beginning of informative DNA mixture interpretation. Even back then, the concept was to model the quantitative STR data. In green, we see data that is from a two-person mixture that has a major and minor component. Our goal is to come up with explanatory peak height patterns, which can be seen as gray triangles underneath.

In looking at and explaining the data (green), we see a certain quantity of DNA, along with a stutter peak and other quantities. The interpretation concept is that

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the proposed explanation pattern (gray) fits (or matches, or explains) the data EPG signal (green).

(Note that most of the pictures in this talk were taken directly from the TrueAllele VUIer™ interface.) We have now reviewed visually the old concept of "modeling" quantitative data, explaining the observed peak pattern with a predicted pattern. Something newer that I have lectured about over the last year is the modeling of "peak uncertainty."

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If we observe a peak in STR data, then it is not really a definite peak with an absolute unchanging value. Instead, the observed value is a sample from a population of possible peak height values. Suppose we kept repeating the same STR experiment over and over again, re-amplifying the DNA, and running it out on our sequencer. We would then observe a set of peak height results that reflected an underlying probability distribution of different peak possibilities.

Taller peaks have a higher spread of possibilities, but also a smaller coefficient of variation (the "CV" is the average height, divided by the standard deviation). Shorter peaks have a smaller absolute spread, but a greater relative spread (i.e., CV).

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We must model the peak uncertainty in order to understand how data varies. Both the average and the variation (of peak height) are needed to tell us about what the peak data means. We must model the peak uncertainty to do quantitative mixture interpretation, since we need to know the distribution of probable events based on the observed peak data. Knowing the uncertainty is required to know to what extent the observed peaks represent the underlying chemical DNA mass that is present at an allele.

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The computer infers an accurate genotype by repeated sampling from the joint probability distribution of model and data. (Note that references are given across the top of the slides. At the end of the talk there is a website that has most of the material referenced here available on-line at no cost for download, including articles and presentations.)

In the background, we see the data uncertainty, a probability distribution of possible peak heights based on the one we measured. We see tall peaks and short peaks. The computer proposes genotype values (say) for one individual who is a minor contributor with two different alleles (shown in blue), along with a major contributor from some other individual who is homozygote with the same two alleles (in orange). With this amount and proportion of alleles, we see a visual explanation of the data (not yet accounting for stutter, relative

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amplification, and so on). If the heights of the predicted bars (in color) lie in the region of the observed data (gray scale), then the predicted genotype and mixture weight values provide a reasonable explanation of the data.

The computer tries out all possible patterns like this. It varies all quantities, such as alleles and mixture proportions; this exhaustive search is something that computers are good at. By trying out every possibility of every variable, it can work out how well different values explain the data. This is done mathematically using a likelihood function. The better the likelihood function explains the data, the higher the probability of the underlying values (genotypes, etc.). After the computer has tried out all values (or, at least the more probable ones), it ends up forming a probability distribution of the possible values that can explain the observed data.

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From the inferred genotype probability distribution, we can then immediately report out a likelihood ratio (LR). The LR is a match statistic that tells us how much more a suspect matches the evidence than some random person. In the referenced Promega 2010 talk, I showed four (there are many more) equivalent ways of expressing a likelihood ratio, some in more human friendly language than others.

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This form is particularly human friendly. Note that conditional probability is not used here, hence there is no possibility of "transposing the conditional". These different LR forms are all mathematically equivalent, but they say different things. For example, it is easier to say in court that "a match between the suspect and the evidence is a billion times more probable than a coincidence." That sounds better to some ears (and juries) than describing a ratio of the probability of the evidence. The point of this paper is to get the forensic DNA community more comfortable with expressing DNA match information using likelihood ratios, since LRs can preserve more of the information in the data.

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Question two: "Are there issues that are still being addressed prior to releasing to laboratories for this consideration?" The answer is no, there are no issues.

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This what the TrueAllele system looks like. From the user side, all we see is a large screen computer, which can be Macintosh or Windows, running a visual user-interface VUIer™ program. We will be seeing some of the VUIer interfaces throughout this talk. There is a separate database server computer that runs four to eight parallel TrueAllele interpretation processes.

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The reason for a parallel system is that the computer has to work on thousands of variables. These random variables include all the peak uncertainties, as well as more routine variables such as genotype, mixture weight or stutter. This degree of modeling is necessary in order to work out the uncertainty of every peak in the data. Cybergenetics can provide a lab with expansion modules that have another 8 parallel processes.

Regardless, until the computer has modeled all the peak uncertainty, and has determined the spread around every peak, it really cannot make valid genotype inferences. TrueAllele's peak uncertainty modeling is like thresholds on steroids, done at every peak to form a probability distribution.

All that computation takes a lot of computer time. If someone says, “I can solve a mixture in one second,” well, that was done that 10 years ago by us and others. This is unworkable because the genotype answers can be quite incorrect on occasion if the certainty of our data at every peak has not been modeled. Therefore, the computer spends a lot of time computing peak uncertainty, and that is why we use a parallel system. In our office, we have 36 parallel processors. Letting the computer take an hour or two to solve each mixture problem, every few minutes another answer comes off the production line.

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In any TrueAllele roll-out, Cybergenetics provides a lot of support. That is where we spend most of our time. We perform an initial process planning to design the lab's deployment. We provide considerable science education because most forensic practitioners are not yet entirely familiar with quantitative mixture interpretation using probabilistic genotypes. We provide a week of software training, along with user documentation. Cybergenetics reviews all the validation data ahead of time in TrueAllele to assist the laboratory in their studies. We have regular ongoing user meetings, and provide project management to help bring a TrueAllele workflow into the laboratory. We also provide testifying support.

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Question three: "Why can TrueAllele® be relied upon as an expert system?" There are two answers.

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The first answer is that TrueAllele has been extensively validated over the last 10 years, and these studies have been published. The slide cites a paper that will be coming out in the *Journal of Forensic Sciences* (JFS) in November 2011, done in collaboration with the New York State DNA lab. The NYS validation looked at two metrics that are most important for demonstrating reliability in court. The first is the amount of *information* that TrueAllele can preserve from

the DNA evidence, and second metric is how *reproducible* the results are.

We first address *information*. In this study axis, we looked at 8 different mixture items from cases, show the likelihood ratio on a log scale. The logarithm of the likelihood ratio is a standard measure of information. In the same way that we can multiply probabilities, we can similarly add probability logarithms (that's what logs do, they transform multiplication into addition). Here are the additive units 5, 10, 15 (which is a quadrillion to one LR). These are two-person mixtures, and in this axis, we assume that the victim genotype was unknown or unused.

For these two unknown contributor cases, 10^{13} (or 10 trillion) was the average amount of information preserved. With manual use of the CPI inclusion method on the identical data, the lab reported an average LR of 10^7 (or 10 million). The ratio of 10 trillion to 10 million is 10^6 (or one million). So the answer is that, yes TrueAllele® *preserves information*, generally about a million times more than human review with these sort of DNA mixture items. (In another axis of this study that compared TrueAllele with CLR manual interpretation, with a known contributing victim genotype, the computer similarly preserved more information.)

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We also assessed *reproducibility* in our validation study. In his 2005 inter-laboratory DNA mixture study, John Butler found 10 orders of magnitude

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variation in human review on the same DNA mixture sample, with match statistics spanning 10^4 to 10^{14}. The reproducibility of the TrueAllele statistical program is about 10% of a log unit, which is 100 times less than the 10 orders of magnitude variation found with human review. Therefore, TrueAllele is quite reproducible. We can measure reproducibility, and that is part of our validation study. The paper shows that TrueAllele's results are efficacious and reproducible.

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Here are results from another TrueAllele information comparison study. Dr. Duceman and I presented this slide at the 2010 ANZFSS Australia meeting. We examined all 86 mixture items of evidence from criminal cases, and ranked them by how much information was preserved by the computer. (The y-axis shows the likelihood ratio on a logarithmic scale, 10^5, 10^{10}, 10^{15}, 10^{20}, etc.)

The vast blue background shows how much information TrueAllele reported, computed in duplicate. Of these 86 informative items, only 30% of them were assigned a match score when using manual review. The other items were not reported. Several different human review methods were used, depending on whether a mixture was treated as a single source sample (gray), a victim reference was used (green) or not (orange).

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We see that quantitative interpretation preserved the information all of the time, and was able to produce a match statistic. But human review using a threshold could not. The peak threshold methods discarded useful identification information 70% of the time. Each item of evidence may be used to convict or find a criminal, possibly preventing further crimes. A large false negative rate of unreported informative DNA evidence (i.e., 70%) can have major adverse impact on society and public safety.

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TrueAllele evidence has been presented in court, and there are publications describing its use. The newsletter cited here is probably the easiest introduction to what happened in the Foley case (*Commonwealth of Pennsylvania v. Foley*). The case is a fascinating tale of murder, sex and DNA. If you are interested in the details, you can visit our website and see the on-line CLE lectures.

The FBI was able to extract DNA from under the victim's fingernails. In this two person mixture, the 6.7% minor contributor matched the suspect. Their (human threshold review) inclusion method produced a match score of 13,000. An outside DNA expert reviewed the same STR data, and used an obligate allele method to report a stat of 23 million. The TrueAllele computer ran the data, objectively producing a genotype; subsequent comparison with the suspect genotype yielded a 189 billion match score. As predicted, TrueAllele preserved

about a million times more information than human review. In this and other cases, we consistently see that probability modeling preserves information, whereas applying thresholds to peaks discards information.

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TrueAllele has been used to provide a reliable weight of evidence. When a DNA laboratory cannot report a match score, they often ask Cybergenetics to run TrueAllele® on their data. Then, Cybergenetics can infer genotypes and provide a report. If necessary, we can testify on the DNA likelihood ratio match statistic found, which may be required in many jurisdictions.

Groups usually send us their more challenging cases. Many times they could not produce a match score. We often process a lab's case data as part of a free trial examination. In some instances, the lab shared our preliminary match report with their police, who then used the TrueAllele statistics to obtain a confession. That is a fundamental role of TrueAllele – reducing court costs through better science.

We have also work on cases with foreign labs overseas, and testify in their cases as necessary. In the remainder of this talk, I will be using a case example with a degraded two-person mixture DNA. The data illustrate some of the questions we were asked to address today. The Pennsylvania homicide case is

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Commonwealth v. Glenn Lyons.

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The fourth question we were asked was: "Specifically, how are mixtures addressed?"

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We begin with data (shown in green). The figure shown is from the TrueAllele VUIer™ Explain interface. Overlain on top of the data, we see (in gray) the victim's allele pair. Since this is a two-contributor mixture, and the victim genotype is known, the task is to solve for the one unknown genotype.

The computer tries out all possible allele pairs at every locus, in different mixing proportions. The figure shows a (13,14) allele pair candidate, at locus D8. For each genotype possibility, the computer generates a proposed peak height pattern. TrueAllele compares its proposed pattern with the observed peak height data pattern.

The proposed quantitative pattern in the upper figure explains the observed DNA data shown in green. The pattern combines one quantity of victim genotype (14,15) shown in gray, with a smaller amount of unknown second genotype

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(13,14) shown in blue. The combination of allele pairs in mixture proportion shown explains the data very well.

The computer puts all the alleles together into one pattern, as shown in the lower figure. The proposed peak pattern (gray bars) explain the data (shown in green) very well. However, the computer must try every possible solution, in order to follow the laws of probability.

When TrueAllele is finished, it forms a probability distribution at every locus. Since it has tried out all possible allele pairs, including alleles that are rare or not seen in the data, at each locus it has looked at thousands of possible allele pairs, very few of which are probable.

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The genotype probability distribution for locus D8 shows that allele pair (13,14) was given virtually all of the probability. There are also a few other allele pair possibilities that the computer found to be feasible. This is a *posterior* probability distribution, because it was found after examining the data. The genotype was inferred objectively, without any reference to a suspect genotype.

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TrueAllele then compares the inferred genotype probability distribution with the suspect genotype in order to calculate a likelihood ratio (LR) DNA match statistic, as described in the cited conference paper. In blue, we see again the locus D8 genotype allele pair probabilities for the unknown contributor, the posterior distribution *after* it has examined the data. In brown, we see the prior genotype probability at this locus for a human population. The population distribution describes our prior belief about the genotype distribution for a person, *before* the computer has examined the phenotypic data from STRs.

There are many ways to formulate a likelihood ratio. After we infer an evidence genotype, we then compare its distribution with the suspect genotype. We see that there is a loss in probability at some allele pairs, while there is a gain at others. The DNA LR asks, “At the suspect's allele pair, what is the ratio of the genotype probability after we have seen the data, divided by the probability before?” Here the D8 locus ratio is a factor of about 6.

This genotype probability ratio approach offers an intuitive and visual way to explain the likelihood ratio. We can express the LR as a logarithmic factor (right figure), to count the number of zeros in the order of magnitude. The LR reports a ratio of match probabilities, comparing a match to evidence with a coincidental match. The match probability after examining the data, relative to the population probability before seeing the data, quantifies how much information the evidence data contains for identifying the suspect.

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Prosecutors find this visual approach understandable. I recall before a trial explaining the LR to a prosecutor at one locus using the TrueAllele VUIer visual interface. He then continued on by himself at the remaining loci, using TrueAllele to explain the LR to other prosecutors and police. He found it exciting to easily explain likelihood ratios to his peers using pictures, without needing a scientist to do it for him.

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Going on to question five, we were asked: "How are the peak height differences addressed in terms of degradation versus mixture?" The answer is that degradation is just another variable in our mathematical model.

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In this evidence mixture item, we look at all the data, with base pair size on the x-axis and rfu peak height on the y-axis. There is not much degradation of the known victim profile (shown in gray), but there is considerable degradation of the unknown second contributor (shown in blue), whose genotype turns out to match the suspect. TrueAllele computes the extent of degraded DNA, up to some uncertainty, as just one more statistical parameter to be considered. The computer can consider degraded DNA for any number of contributors (e.g., two,

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three or four), examining the degradation separately for every contributor in the mixture.

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TrueAllele also considers the mixture weight of the template as a random variable of interest. The victim mixture weight is seen in the gray histogram to be a major contributor, with mean of about 70%. The distribution has a broad standard deviation of around 10%, expressing the allele (peak height) variation in the data.

The blue histogram shows the mixture weight posterior probability distribution for the unknown minor contributor, the probative component of interest. The mean is centered at 30%, again with a dispersion of 10%. While TrueAllele determines the mixture weight at each locus, these histograms show the average mixture weight of the underlying DNA template. This template variable tells us about the DNA composition, measuring the different proportions of contributors in the sample.

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With the time remaining, let's address two further questions. The first of these is: "Why don't thresholds work?" This question is on the mind of many forensic DNA

practitioners, so let's take a look now and see why. The answers are interrelated.

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A first answer is that when using thresholds, we are looking at the wrong DNA data using the wrong mathematical model. We are presented with quantitative data having real peaks that are trying to tell us how much of the genotypes are there. When someone applies a threshold, they are ignoring the quantitative information present in the data.

The classification is all or none. Over the threshold, peaks are treated as if they were allele events. Under the threshold, peaks are considered to not exist. The result is that informative quantitative data is truncated down to an absolute (though arbitrary) all or none decision – the peak is either there or it is not.

Of course, that "threshold decision" is not what the DNA chemistry is telling us. There are certain amounts of DNA genotype alleles that are truly in the data. Statistical inference does not permit us to modify our data, say by cutting off the tops of the peaks. If the data arrive in quantitative form, we are supposed to model them quantitatively. So a real problem here is that the threshold procedure uses an all-or-none binary model, whereas our data is continuous. That is one place where human mixture interpretation starts going wrong.

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A second reason why thresholds cannot work is that they model uncertainty in the wrong way.

In some situations, there is a certain amount of background noise that has constant variation, and we can legitimately ask, “Are we seeing events over a background, like a baseline in signal detection. Is there something that is noise or not noise?” We could then construct a single fixed bell curve (normal distribution), and check to see what lies far away from the center. Modern statistics has better methods, since computers can work out the actual probability distribution from the data, but it could make sense.

However, the most interesting peak height variation comes from the stochastic effects arising the PCR amplification or allele dropout. There is a different amount of variation at each STR peak, depending on how much DNA is present. With more DNA, there is more variation. Less DNA gives less variation.

When attempting to draw a single line through all the peaks and their variation, the threshold assumption that there is one fixed variation amount around a peak is wrong. We are working with chemistry, not Photoshop. When the peak height doubles, then so does the variance. When the peak height quadruples, then the

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variance quadruples as well. Since the standard deviation is the square root of the variance, quadrupling peak height doubles the standard deviation.

Think about that the current threshold contradiction. Thresholds use a model that assumes a fixed variance, but nature tells us otherwise. When we look at the data from repeated PCR experiments, we see that peak variation changes with peak height. Therefore, any model (whether calculated by computer, hand or eye) that assumes a fixed variation is wrong. Such DNA misinterpretation loses information because it uses the wrong model.

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A bad DNA model fails to concentrate probability onto allele pairs that better explain the quantitative data. The CPI method ignores both peak height and victim genotype. CPI spreads its genotype distribution over many allele pair candidates, many of which are not feasible.

In this Pennsylvania case, Commonwealth v. Lyons, any mixture interpretation would produce a genotype probability distribution at locus D8. That follows naturally from the mathematics of genotype inference and match, whether or not forensic practitioners are aware of the details. The original laboratory's CPI interpretation corresponded to a genotype probability distribution (light blue) that comes from considering thresholded data using an inclusion likelihood function.

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CPI diffused the probability over the genotype possibilities, asking only ‘are alleles present or not’, rather than looking at the actual quantitative peak heights. Diffusing probability over all many impossible events that the quantitative data does not support reduces the probability at the correct allele pair. By reducing genotype probability, thresholds and CPI reduce the likelihood ratio. Probability diffusion is the mechanism by which thresholds reduces the match statistic and lose identification information.

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The VUIer figure shows the LR results at every STR locus, on a linear scale. We see the TrueAllele Casework LR (top blue bars), and the lab's match scores (bottom blue bars). The red circles indicate loci where the lab reported nothing at all, because the data (with thresholds applied) did not match the suspect. In human review, evidence that does not support the prosecution's case is not used.

It is clear that there is a lot of information being thrown out (locus LRs of 50, 35, 40, and), with highly informative data being ignored. Thus, instead of reporting a match statistic number close to the computer's 10 trillion, human review reports out a number of only 43,000 on the same evidence data. This failure to preserve information is why the prosecutor contacted Cybergenetics for expert DNA

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interpretation in this murder case. It can be helpful to go to court with a more accurate match statistic.

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The human match results are actually quite worse. Considering co-ancestry, what is the probability of seeing another genotype allele pair given we have already seen it in the population? Suddenly, the allele is not so rare. A scientifically reasonable co-ancestry is about 1% in a Western population. However, if the prosecution does not account for co-ancestry, the defense can counter with unrealistic co-ancestries of 3%, and artificially (and incorrectly) reduce the DNA match statistic.

We can also compute confidence intervals around the likelihood ratio. This is due to the fact that our population databases have only 100 alleles or in them, not 30,000 alleles enjoyed by databases in other countries, such as Australia.

By increasing the co-ancestry theta value, and broadening the LR range with confidence intervals, the TrueAllele result drops down to 13 billion. However, the human review CPI threshold result is now down near a thousand, which is not highly compelling to a jury. With a competent defense opposition employing experts who consider co-ancestry and confidence intervals, CPI inclusion methods with thresholds can drop their match scores down into the hundreds or

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thousands for many DNA items of evidence.

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Thresholds can introduce a high false negative error, as we presented at the December Canada meeting. In this study, we looked at known mixture proportions of different DNA concentrations. The x-axis shows the mixture weights 50-50, 30-70 and 10-90, ordered from most to least DNA in the minor contributor. The y-axis gives the false negative rate as the number of missed alleles per locus. Each cluster of bars indicates the DNA template amount by descending DNA amount, as 1, 1/2, 1/4 and 1/8 nanogram. We had examined thresholds set at 50, 100, and 200 rfu. Here we show the results for 200 rfu, since that is most relevant for the higher stochastic thresholds now in use.

We see that, overall, a DNA mixture interpreted with thresholds loses information at a rate of around one allele per locus. Consider an imbalanced mixture. As we draw a threshold, manual interpretation with CPI begins to lose the minor contributor. Quantifying the false negatives, we observe an error rate of missed alleles per locus of over one hundred percent. An error rate exceeding 100% is highly unusual in science. Imagine a diagnostic medical procedure that was wrong that often.

When DNA labs report a match, they are usually correct. However, thresholds

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miscall true matches as nonmatches. Missing the DNA identifications that are really there in the evidence needlessly frees criminals to inflict preventable harm on society.

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The CODIS national DNA database suffers from a high false negative information loss because its forensic component is largely based on CPI mixture interpretation. CODIS represents genotypes as watered down allele lists, instead of as allele pairs. The database therefore loses a CPI factor of one million, when it is even capable of representing an evidence genotype. CODIS also discards highly informative evidence as “inconclusive”, when most of the time the mixture is not inconclusive at all, just as we saw earlier in the 70% evidence loss in our mixture study.

The TrueAllele database stores and matches probabilistic genotypes, and uses likelihood ratios to preserve identification information. Usually, if a person can see it, our computer can extract it. A probabilistic genotype DNA database is useful in casework for identifying convicted offenders from mixture evidence.

A probabilistic genotype database that matches DNA can identify missing people. Cybergenetics used a TrueAllele database approach when re-analyzing the World Trade Center data. TrueAllele DNA database matching can perform

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kinship calculations, using probability distributions and likelihood ratios.

When TrueAllele does familial search, it does so fully automatically, without requiring a user to enter different alternatives. The database matcher works the same way as it does when checking against convicted offenders, automatically comparing with the genotypes of the family members of interest. TrueAllele lets us know when it finds a match between evidence and suspect. As with CODIS, Cybergenetics can customize the system's match rules to each state or country's particular regulations and statutes.

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There is an ongoing controversy about low template DNA interpretation. In a fascinating closed session conference meeting in September in Sydney, Drs. Bruce Budowle, John Buckleton, Peter Gill and Andrea van Daal debated the issues. After some passionate discussion, I was asked to find some consensus between the panelists.

These are the principles that they unanimously agreed with: (1) DNA data is continuous and has random variation. Bruce preferred the phrase "stochastic effects" to "random variation", which means the same thing to me. (2) Thresholds do not work for low template DNA. (3) Mathematical models can account for random variation. They also agreed to my summation statement that

(4) objective computer interpretation that can infer genotypes up to probability is the way to move forward in the twenty first century.

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We come to our final question, Question B: "How can I learn more about scientific DNA mixture interpretation that uses all the quantitative data?"

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There is a great deal of public information available on Cybergenetics website. We have been preparing many resources for the community, including online courses and conference presentations. We have been writing papers, validation studies, newsletters, and so on. We have posted over a dozen course lectures that we use in our own scientific teaching, both basic and advanced, for both scientists and lawyers.

We post all our scientific presentations, and make narrated movies from the PowerPoint slides. For each lecture, we provide handouts, slides and transcripts. Similarly, we share our manuscripts for submitted and accepted publications. While we take time for quality control, the material eventually ends up on our website.

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For anyone is interested in the science of quantitative DNA mixture interpretation, our website “Information” page is a great place to start. We provide links to many courses, presentations, and publications. For example, I received an email from a teacher in England this morning who asked if she could use the Oxford Broughton case to illustrate a joint DNA mixture interpretation in her course. I immediately replied "yes", but she needn't have asked; all the material there is freely available for everyone to use.

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Cybergenetics also provides TrueAllele DNA interpretation services. Many crime labs are quite comfortable with their current interpretation methods. Why should they change everything overnight and give up thresholds, and move to examining all the quantitative data? Obviously better science can extract more identification information, and can help prevent letting guilty criminals go free. However, a lab may not be comfortable with rapid technological change.

The TrueAllele service allows a lab (or prosecutor or police) to test out the system, and see how it works in practice. We have a standing invitation to any crime lab – send us a few test cases or items, and we will have TrueAllele look at your data and show you what the computer finds. If you can see it, we can solve it™.

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Is there an important case that needs a DNA answer? If you ask your police or prosecutors to send us your data, Cybergenetics can take care of it, without cost or involvement by the lab. Many groups have learned a lot about probabilistic genotype interpretation by seeing sending us their data, and seeing how TrueAllele works.

Many labs are not yet ready to replace or augment human review with computer interpretation. In that situation, Cybergenetics can complement the lab's current capability with more powerful computer interpretation of their existing STR data. Cybergenetics can take care of the interpretation problem for the lab, and the case is still solved. Moreover, the reporting and testifying obligations then become Cybergenetics responsibility, not the lab's. Visit our web site to see how to send us DNA data.

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In conclusion, quantitative DNA mixture interpretation preserves identification information. Thresholds discard considerable information, as shown in repeated studies. As an international commission on forensic genetics said, "it does not make as much use of the data as what is possible." TrueAllele® is a validated, courtroom-tested DNA interpretation system. The technology is available today, whether for use in your own DNA laboratory, or as a complementing forensic DNA interpretation service. Thank you.

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