TrueAllele SPEED FOR GRAND JURY NEED: SAME DAY REPORTING OF COMPLEX MIXTURES

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Current DNA mixture interpretation is plagued by a lack of speed and accuracy. Crime laboratory match statistics can vary a billion-fold on an uncomplicated two-person mixture, with many mixtures never reported. Months may pass between generating electronic DNA data and producing a report. Yet there is a clear societal need for more speed and information when reporting mixtures in important cases.

Fast, parallel computing by a validated genotype probability modeling system can overcome this mixture interpretation bottleneck, providing rapid turnaround time and preserving identification information. Cybergenetics TrueAllele® Casework is regularly used to rapidly solve DNA mixtures have three, four or more unknown contributors. By successively "peeling" away genotype layers, TrueAllele can dissect complex mixtures, often of related individuals. Out of twenty TrueAllele validation studies, five are published peer-reviewed papers.

At 2 pm on Wednesday, December 11, 2013, a New York State district attorney contacted Cybergenetics. His rape case was going to a Grand Jury the next day. The crime lab had done STR analysis on the inside of a glove. One swab was reported as "consistent with" the victim (major) and two male donors (minors), but excluded the suspect. Another swab contained at least three contributors, but due to "the complexity of the genetic information" no comparisons were made. New DNA results by morning could postpone the case a week.

At 4:30 pm, the lab emailed their .fsa data files to Cybergenetics. By 5 pm, the peak height data were analyzed and uploaded to a TrueAllele server. The computer was asked twelve separate questions: consider both evidence items, in duplicate computer runs, and assume three contributors under different scenarios – all unknown, victim known, and victim and elimination both known. At 5:30 pm, twelve computer cores set to work on their assigned mixture questions. Parallel processing of all twelve 10,000 cycle Markov chains was completed by 11 pm.

Within hours Cybergenetics emailed the DA a preliminary match report on the suspect, a 15% contributor to each three-person mixture. TrueAllele match statistics for the two evidence items were around fifty thousand and five hundred thousand, respectively. A phone call to the DA the next morning explained the results, in time for the Grand Jury.

The following Tuesday Cybergenetics received the lab's case reports, and that day completed a draft TrueAllele report, along with PowerPoint visual aids sent to the DA. On Thursday, December 19, a Cybergenetics scientist appeared in NYS before the Grand Jury to present the DNA match results. The defendant was indicted, arrested, and charged with multiple counts of burglary and rape.

Time and information are important for public safety and criminal justice. DNA delayed is DNA denied. When informative evidence is wrongly deemed "inconclusive" or exclusionary, violent criminals can remain at large. Rapid and reliable parallel computer processing can meet society's demands for timely DNA information. TrueAllele routinely provides this capability. This talk tells how.