how it works

DNA Information Library Service

Problem: DNA information is an important way to identify criminals. In today's forensic DNA model, biological crime scene evidence is processed by a DNA laboratory producer, which both generates and interprets electronic data. The lab then notifies the police, prosecutors, or defense.

Figure 1: The DNA library service workflow.

With the advent of lab automation, though, robots are generating ever greater quantities of more challenging DNA data. Painstaking human review of difficult data is slow and expensive, and loses considerable identification information.[1] This information loss (discarding informative data as "inconclusive," or reducing match strength a million-fold) diminishes DNA evidence.

Solution: Computer-based probabilistic genotyping can eliminate the interpretation bottleneck, providing a thorough, accurate, and objective statistical review of the DNA evidence.[1] Cybergenetics has been pioneering an on-demand approach to DNA interpretation that serves the criminal justice community. In this new processing paradigm, a public crime lab identifies challenging data and forwards it electronically to Cybergenetics for computer processing. Within days, the company sends a TrueAllele® match report to the prosecutor or other DNA information consumer. The laboratory is thus relieved of the burden of interpreting challenging DNA data, and the needs of criminal justice are met, with greater speed at lower total cost.

In a recent serial rape case, the key evidence was a DNA mixture having a minor contributor that matched the suspect with a CPI match statistic of 105 (100 thousand). More was needed that could be done. So the county lab sent their data to Cybergenetics for TrueAllele processing and within two days the prosecutor received an LR match score of 1015 (quadrillion). DNA evidence with a CPI of 106 (million) from a second victim in that crime was later sent to Cybergenetics; TrueAllele found a 1012 (trillion) LR match from a 10% minor component to the same suspect. The police and prosecutor received this second match information dispatch within two days of submission. The DNA case was then ready for trial.

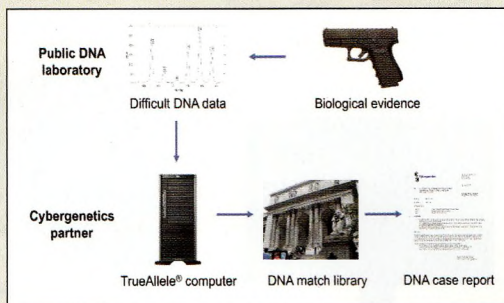The "lab generates, computer interprets" information model has also been deployed on a larger scale. A state lab had processed over a hundred cases with challenging mixture items, most containing three or four contributors, and many having little DNA. The new SWGDAM stochastic interpretation guidelines[2] affected the courtroom viability of this important DNA evidence. The lab sent their data to Cybergenetics, who built for them an on-demand DNA library containing a first round of DNA match scores for every item.

Investigators can consult TrueAllele match results to assess the strength of their DNA evidence. As these cases go to court, prosecutors or defenders "check out" cases from the pre-processed information library, requesting DNA match reports. Upon receiving a "check out" notice, Cybergenetics initiates a second round of TrueAllele computer processing, replicating all results and resolving unanswered data questions. Cybergenetics then prepares a TrueAllele DNA match report on the lab data, delivering it in time for court, and testifying if necessary.

A forensic lab can conduct routine DNA interpretation using its own in-house TrueAllele system. However, some challenging data may benefit from the experience and processing power available at Cybergenetics. Moreover, not all labs have their own TrueAllele system. In such situations, Cybergenetics can provide case and library-based TrueAllele processing that complements the laboratory's capabilities.

Totally objective and highly informative probabilistic genotyping can help solve crimes by re-examining previously "inconclusive" DNA evidence. Through an ongoing public-private partnership between forensic labs and Cybergenetics, criminal justice can be better served by empowering crime laboratories with computer interpretation capability.

For more information, visit www.cybgen.com.

References

1. Perlin MW, Legler MM, Spencer CE, Smith JL, Allan WP, Belrose JL, Duceman BW. Validating TrueAllele® DNA mixture interpretation. Journal of Forensic Sciences. 2011;56(6):1430-1447.
2. SWGDAM Interpretation guidelines for autosomal STR typing by forensic DNA testing laboratories. 2010; http://www.fbi.gov/about-us/lab/codis/swgdam-interpretation-guidelines.