

September Newsletter

Better Justice Through Better Science [™]

Cybergenetics continues to pioneer forensic DNA computation

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- <u>Cybergenetics awarded another US patent for error rate</u> <u>determination</u>
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TrueAllele supports NGS technology with SNP, Indel and STR markers

Next-generation Sequencing (NGS) is an advanced DNA sequencing technology for forensic science identification. Cybergenetics TrueAllele[®] software can input and process NGS data. This pathway brings Verogen MiSeq FGx autosomal STR data into the TrueAllele Casework process.

Once NGS data is imported, downstream processing integrates seamlessly into the lab's existing TrueAllele workflow. TrueAllele can use NGS data for DNA mixture interpretation and matching, just like any other STR data source.

The Single Nucleotide Polymorphism (SNP) is a ubiquitous source of genetic variation. SNPs have been widely used in medicine for diagnosis and treatment. They were introduced into forensics for human identification and ancestry.

Newer forensic NGS kits combine SNP and STR markers. Cybergenetics can use SNPs to analyze DNA mixtures. SNP data can enhance mixture separation, identifying DNA contributors through their SNP genotypes. Cybergenetics continually adds NGS, SNP and Indel markers to the TrueAllele Casework engine.

Please contact Cybergenetics for more details about NGS technology or SNP markers for your TrueAllele forensic process.

Cybergenetics launches new website for better user

experience

Cybergenetics is pleased to announce the creation and launch of its <u>new</u> <u>website</u>. The website showcases the company's <u>products and services</u>, adding new user-friendly features. Enhanced user capability and navigation ensures an engaging visitor experience. We encourage you to stop by: explore our new <u>products and services</u>, sign up for our newsletter, or visit our <u>Trials page</u> to see cases we've worked on.

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Cybergenetics awarded another US patent for error rate

determination

Cybergenetics was awarded a second patent for its ground-breaking <u>innovations</u> on finding error rates for match statistics. This United States <u>patent</u>, granted July 12, 2022, is on their "Method, apparatus and computer software program for determining probability of error in identifying evidence" invention. Scientists generally report error rates in their studies. Under *Daubert v. Merrell Dow*, judges must consider error rate determination as a factor for reliable scientific evidence that can be used in court. Yet most forensic DNA labs still cannot report error rates for their likelihood ratio (LR) match statistics.

TrueAllele[®] software can always rapidly (1/100 second) and exactly (1/1000 information unit) report error rates for DNA evidence. This method is described in Cybergenetics' 2018 landmark <u>Heliyon paper</u> on "Efficient construction of match strength distributions for uncertain multi-locus genotypes." Convolving independent loci thoroughly considers a trillion-trillion DNA profiles. Older sampling methods – slower and less precise – are limited to just thousands.

The <u>latest TrueAllele version</u> includes a new Distribution module. This visual genotype interface can essentially compare DNA evidence with the profiles of everyone on Earth. The resulting match strength distribution curve fully reveals the genotype's LR behavior. TrueAllele's VUIer[™] software then instantly delivers accurate error rates for any match statistic – whether inclusionary or exclusionary.

View the patent here

Why error rates are needed for reliable DNA evidence

A match statistic measures the strength of DNA evidence. Evidence can change our belief in whether someone was at a crime scene; the match strength quantifies that change. Positive (logarithmic) numbers support the belief, negative ones militate against it, while values near zero give little information either way.

An error rate provides a frequency context for LR match information. Suppose the LR is 100. What is the chance that someone who *didn't leave their DNA* matches as strongly? Is it one in a thousand? Or is it one in a million? That probability – the false positive error rate – informs a juror. It tells them, "How often might this DNA match evidence falsely implicate me?" Without an error rate, there is no frequency context to tell us how often a DNA match may be false. An "inconclusive" statement means no reported DNA result. Unethical trial lawyers sometimes try to twist this non-result into fake "evidence" of guilt.

Santa Clara County Judge Kelley Paul and Cybergenetics CEO Dr. Mark Perlin exposed this illogical ploy at the February American Academy of Forensic Sciences conference. You can watch their <u>myth-busting presentation</u> "Making something out of nothing: the inconclusive fallacy" on YouTube.

Cybergenetics' accurate match statistics and error rates overcome the "inconclusive" fallacy. In criminal cases from California to New York, TrueAllele analyst testimony helps block unscientific injustice.

Making something out of nothing

Upcoming conference appearances

Every year, Cybergenetics participates in several conferences. This is Cybergenetics first time attending the <u>Illinois Homicide Investigators</u> <u>Association (ILHIA)</u> Conference in Itasca, Illinois, on October 11-13, 2022. Per the conferences website, the primary goal of the Illinois Homicide Investigators Association is to support law enforcement officers, prosecutors, and coroners by providing professional training, leadership, and resources essential to the solving of homicide cases and other criminal investigations.

We are also returning to the <u>Southeastern Homicide Investigators</u> <u>Association (SEHIA)</u> in Gulf Shores, Alabama, from November 14-18, 2022. The goal of the SEHIA conference is to enhance the dialogue between members of law enforcement tasked with investigating the most heinous and impactful life events faced by members of society. Cybergenetics is excited to attend both conferences within the next few months.







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