

# How it works

## Solving DNA Mixtures with a Visual Calculator

### Problem: DNA mixtures can be challenging to interpret.

DNA mixtures occur when two or more individuals contribute their DNA to a biological specimen. Sexual assaults produce mixtures, as do many homicides. Mixtures can be highly probative, establishing physical contact of a perpetrator with the victim. However, mixture data can be challenging to interpret.

DNA data is produced by PCR amplifying a sample at short tandem repeat (STR) genetic loci, and separating the fragments to observe different allele lengths. At a locus, an individual inherits two (perhaps identical) alleles, forming a genotype. The quantitative STR data has an easily interpretable genotype pattern comprising one or two tall peaks, surrounded by smaller PCR artifact and background peaks (Figure 1, bottom left).

### Solution: A mixture calculator that separates quantitative data into genotypes.

Cybergenetics TrueAllele® Casework genetic calculator (TAGC™) infers genotypes from DNA mixture data, and then determines genotype match strength. The TAGC technology can solve DNA mixtures having one, two, three, or more unknown contributors. TrueAllele can analyze multiple samples jointly for greater genotype resolving power. TAGC successfully resolved the genotype of a criminal who comprised only 7% of a DNA mixture, yielding a trillion to one match rarity.

The TrueAllele computer automatically analyzes a 96-well plate of electronic data to check quality, quantify peaks, and (after a two minute visual review) upload peak height information to a database server. The forensic scientist downloads and inspects the relevant case data, and then poses questions that can help extract unknown genotypes. Using a point-and-click visual user interface (VUler™), the scientist assembles the STR data lanes/injections into extracted DNA items (Figure 1, middle). Combining these DNA items will compose interpretation questions for the genetic calculator to solve, e.g., searching for one or two unknown genotypes (Figure 1, right).

TAGC is a parallel processing machine that works on several questions simultaneously. A TrueAllele processor electronically explores thousands of parameters, reconsiders different genotype scenarios thousands of times, always staying focused on explaining the presented data. As TAGC solves each problem, it uploads genotype answers to the TrueAllele database.

The scientist visually explores TAGC answers in the VUler environment, using windows into mixture weights, genotypes, matches, and original data (Figure 2). The TrueAllele results show which data are informative, which are not, and reveal the full probative force of a genotype match to a suspect. The TrueAllele calculator is a powerful productivity tool that accelerates the DNA mixture interpretation process.

DNA mixtures add together the individual quantitative STR patterns to form a more complex pattern (Figure 1, top left). The interpretation task is to identify the perpetrator's genotype possibilities at a locus that account for the data. (The population rarity of these possibilities gives a numerical match association that can be presented in court.) This is done by reconstructing data patterns for every possible genotype combination and mixture weighting (e.g., 70% victim plus 30% perpetrator), and comparing these hypothesized quantitative patterns with the original STR data peaks. Those genotype possibilities that best fit the data have the highest probability, and are most likely to account for the perpetrator's genotype.

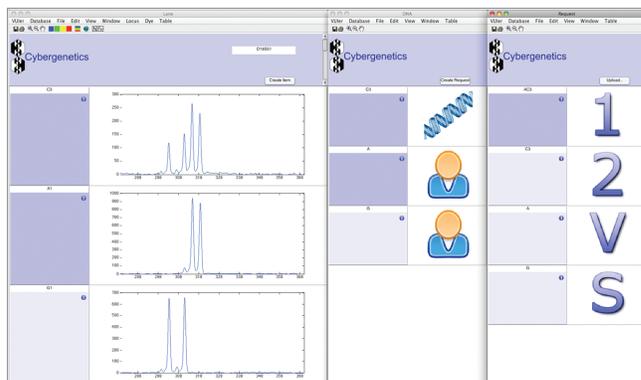


Figure 1. Visually assembling data lanes (left) into DNA specimens (middle) that request calculator questions (right).

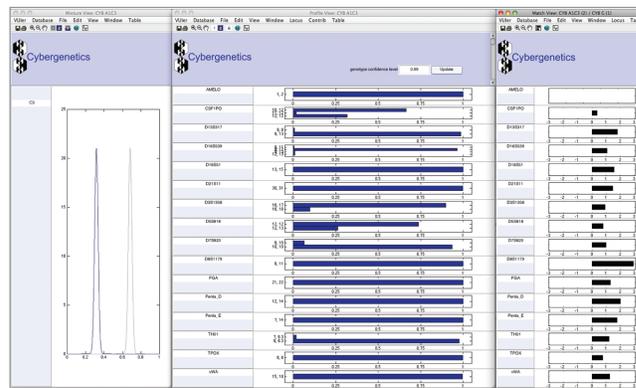


Figure 2. Visual calculator answers include DNA mixture weight (left), genotype (middle) and match strength (right).

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