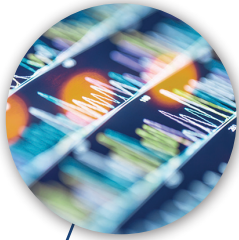


The TrueAllele Difference

Improve DNA interpretation in five areas



1. Mixtures

- ✓ TrueAllele computing is a complete statistical model that produces accurate answers on all mixture data.
- ✓ It separates DNA data into genotypes (genotype probability distributions).
- ✓ All contributors are resolved, including minor contributors. TrueAllele has no artificial limits, and handles any number of contributors.



2. Capabilities

- ✓ TrueAllele interprets mixtures without references. It produces investigative information for no-suspect cases.
- ✓ DNA from family members is reliably separated into genotypes.
- ✓ An internal database compares evidence to evidence. It identifies genotypes that appear on multiple items, and calculates match statistics.



3. Data

- ✓ TrueAllele requires no thresholds. The system accounts for all data, and models for PCR artifacts.
- ✓ With low level data, the computer determines variation from evidence.
- ✓ TrueAllele learns from the data. No calibration is required.



4. System

- ✓ The powerful but simple VUIer™ interface shows results as images and tables. Analysts can visually verify data, and export as tab text.
- ✓ The client-server configuration puts the computing on the server. Individual computers are freed for other tasks.
- ✓ TrueAllele produces exportable files that can be taken with you or shared.



5. Results

- ✓ TrueAllele produces easily-understood ratios of match probabilities.
- ✓ For non-contributors, the computer can calculate exclusionary statistics.
- ✓ TrueAllele reports a false match probability (match statistic error rate).