"Using Computer Technology to Overcome Bottlenecks in the Forensic DNA Testing Process and Improve Data Recovery from Complex Samples"

2018 AAFS Annual Scientific Meeting
February 22, 2018

How Many DNA Profiles?

• 96-well plate
• 6 to 8 allelic ladders
• At least two PCR controls
• Several DNA extraction blanks

Typical plate could contain 80 to 84 DNA profiles

Interpretation Bottleneck

Eight hour workday
• 8 hours x 60 minutes = 480 minutes
• 480 minutes / 84 DNA profiles =

5 minutes, 42 seconds per DNA profile

Interpretation Bottleneck

- Volume of data

- Complexity

- Thresholds

"Thresholds? Where we're going, we don't need thresholds."

Automate DNA Interpretation with TrueAllele®

ViewStation
User Client

Database
Server

Interpret/Match
Expansion

Visual User Interface
VUIer™ Software

Parallel Processing Computers
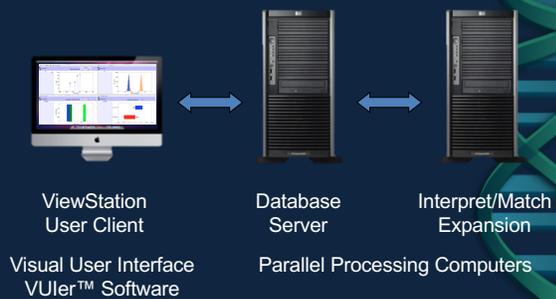
Automated Process

1. Upload entire plate to server
2. Computer interprets the mixtures
3. Automated matching
4. Operator checks results
5. Perform detailed processing on probative matches

Benefits of Automated DNA Interpretation

1. No thresholds, all data examined, nothing discarded

2. Speed
   - One plate in ~6 hours

Benefits of Automated DNA Interpretation

3. All data compared:
   - Evidence, references, lab staff, crime scene investigators, controls
   - Identify more case-to-case matches and potential contamination

4. CODIS specimen and candidate match assessment

CODIS Match Evaluation Example #1

Offender	Human Review, 30 minutes	TrueAllele, 5 minutes	LR	CPI (1 in)
#1	Uncertain	Eliminated	1.5	39,000
#2	Not eliminated	Eliminated	2.7	39,000
#3	Not eliminated	Match	73 billion	39,000

CODIS Match Evaluation Example #2

Offender	MME	CPI (1 in)	LR
#1	1.728×10^4	65	158 trillion

Improved Data Recovery

Uploaded 7 years of data to TrueAllele®

- >7,500 DNA profiles (Q and K)
- ~ 15,000 inferred genotypes
- Compared all data

Previously Unidentified Matches

2014: Burglary case, uploaded to SDIS
- Offender hit
- Match confirmed in laboratory

2017: Process old data, upload to TrueAllele®
- 3 additional cases from 2012 - 2014
- Never entered into CODIS

Sample	Minimum # Contributors	Major?	4x4 Rule?	CPI (1 in)	LR
2012	3	No	No	28,000	6 quintillion
2013	3	No	No	920	27 trillion
2014	3	No	No	760	9 trillion

Can we use the automated process for CODIS screening?

CODIS Screening

1. KL computed by TrueAllele®
   - Measures information value of inferred genotype
2. MME calculated by CODIS
   - Predicts matches at moderate stringency

Compare MME, KL, and LR for CODIS profile assessment

Information Value, MME vs. KL vs. LR
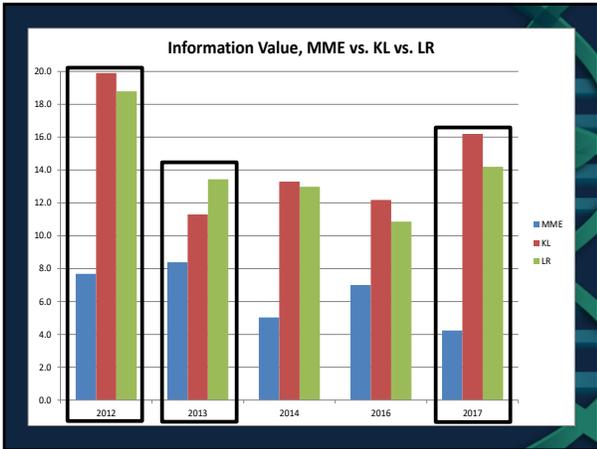
What We Are Implementing

1. Use KL to predict quality of match

2. Use MME to filter adventitious matches

   - High KL – build MME, search CODIS
   - Low KL – do not upload

Summary

- DNA interpretation is automatable
- Reduce/eliminate interpretation bottlenecks
- Output searched internally and screened for suitable CODIS profiles
- More information recovered from same amount of data

Thank you!