

# New York State Police Validation of TrueAllele: a Statistical Tool for Genotype Inference and Match that Solves Casework Mixtures Problems

Presented by: Jamie L. Belrose  
NYS DNA Sub-committee Meeting; New York, NY  
March 5, 2010

---

---

---

---

---

---

---

---

## Why?

- Increased Automation
- Increased Sample Processing
- Bottleneck at Data Interpretation & Peer Review
- Despite sample automation – limited increase in throughput.

---

---

---

---

---

---

---

---

## Outline of Validation

- 41-Adjudicated cases
- A variety of case types
- Varying degrees of complexity
- Original raw data files

---

---

---

---

---

---

---

---

## Range of Evidence Items

- 368 total evidence items (Epi & Spm = 2 items)
  - 97 Reference Samples
  - 25 Vaginal, Anal, or Penile Swabs
  - 39 Semen Stains
  - 13 Clothing or Bedding
  - 11 Weapons
  - 69 Bloodstains
  - 9 Fingernail Scrapings
  - 8 Dried Secretions
  - 32 Misc (cigarette, condom, hair, bite marks, etc.)

---

---

---

---

---

---

---

---

## Single-source Profiles

- 202 Single-Source Profiles in study
  - 4958 concordant allele calls
  - All profiles were concordant
- NYSP has had TrueAllele online in their Databank section since 2007.
  - To date, processed more than one hundred thousand sample successfully.

---

---

---

---

---

---

---

---

## Case Classifications

- Cases assigned a degree of difficulty
  - Simple: 2-person mixtures with known victim
  - Moderate: 2-unknown mixture samples
  - Complex: partial profiles, 3 or more unknown contributors to mixtures

---

---

---

---

---

---

---

---



## Mixing Weight

- There were 88 mixture samples in the study.
- The mixing weight is modeled for mixture samples, with an associated probability distribution.
- As the uncertainty of the data increases, the probability distribution increases.

---

---

---

---

---

---

---

---

## Statistical Strength

- As the data interpretation difficulty increases, the statistical strength decreases – for both human and computer-based methods.
- However, the computer-based method is still able to preserve more identification information with every sample.

---

---

---

---

---

---

---

---

## Conclusions

- TrueAllele is capable of:
- Unattended quality checks and data review
  - Standardization of mixture interpretation
  - Unbiased approach to data interpretation
  - Increased sample processing capabilities

---

---

---

---

---

---

---

---

## NYSP Looks to Achieve

- Analyst assistance with difficult mixtures
- Reduced peer review case file bottleneck
- And thus, increased throughput

---

---

---

---

---

---

---

---

## Aknowledgements

- NYSP:
  - Dr. Barry Duceman
  - Dr. Russ Gettig
  - Shannon Morris
  - Melissa Lee
  - Elizabeth Staude
  - Dan Meyers
  - Urfan Muktar
- Cybergenetics:
  - Dr. Mark Perlin
  - Matthew Ledger
  - Erin Turo
  - William Allen
  - Cara Spencer
  - Jessica Staab

---

---

---

---

---

---

---

---

## Questions?

- Technical or software specific, please contact Dr. Mark Perlin: [perlin@cybgen.com](mailto:perlin@cybgen.com)
- NYSP validation specific, please contact Dr. Barry Duceman: [BDuceman@troopers.state.ny.us](mailto:BDuceman@troopers.state.ny.us)
- Regarding this presentation, Jamie L. Belrose: [Jamie.Belrose@gmail.com](mailto:Jamie.Belrose@gmail.com)

---

---

---

---

---

---

---

---