



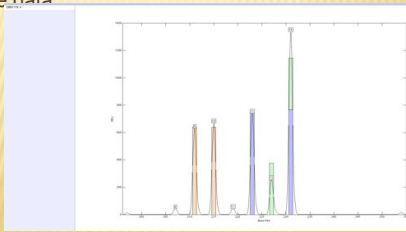
Pushing the Limits of TrueAllele® Casework

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TRUEALLELE® CASEWORK

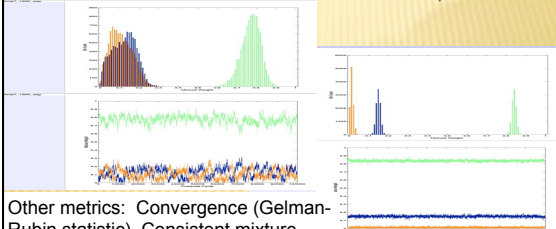
- ✘ Continuous probabilistic modeling statistical analysis software for evidence and reference sample analysis
- ✘ Uses Markov Chain Monte Carlo (MCMC) sampling of the data – searches for a best fit explanation of the data



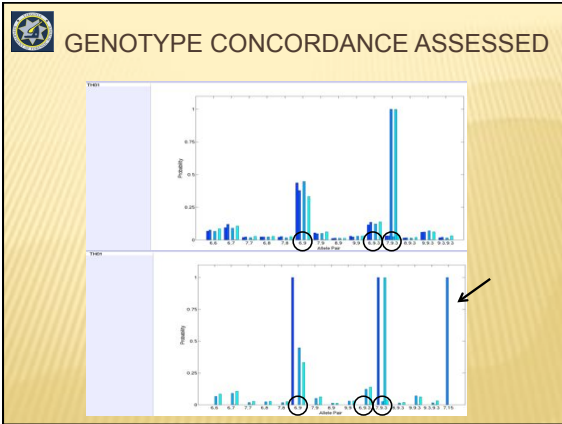


EACH TRUEALLELE ANALYSIS REVIEWED

- ✘ MCMC chain was assessed – ideal or non-ideal (only ideal analyses were used for concordance)

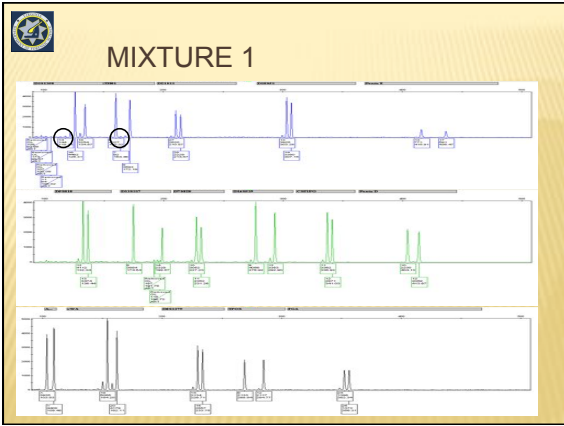


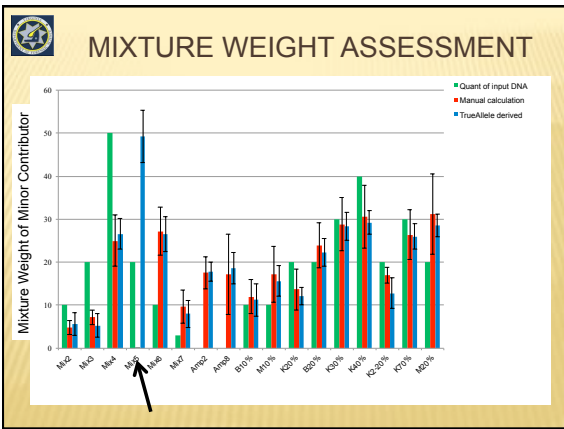
Other metrics: Convergence (Gelman-Rubin statistic), Consistent mixture weights, Match statistic concordance (within 2 log units)

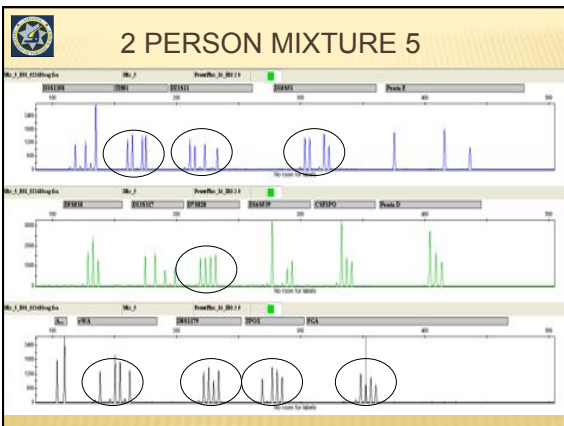


- VDFS VALIDATION STUDY**
- ✘ Used mock casework samples which included the following:
 - + 17 single source profiles (degraded and stochastic)
 - + 18 two person mixtures
 - + 14 three person mixtures
 - + 7 four person mixtures

- Tested using TrueAllele® Casework (TA):**
- + Single source samples
 - ✘ With allelic and locus drop-out
 - + Reproducibility of the process
 - + Accuracy of the TA process
 - ✘ Exclusion of non-contributors
 - ✘ Inclusion of true contributors
 - ✘ Mixture weight assessment for two-person mixtures
 - + Sensitivity of the TA process
 - ✘ Minor contributor contribution level below which results in negative log likelihood ratio {log(LR)}
 - + Specificity of the TA process
 - ✘ Elimination of non-contributors
 - ✘ Elimination of relatives of the contributors









SUMMARY OF VALIDATION WORK

- × 17 stochastic and degraded single source profiles analyzed
 - + Negative match scores may result for samples with many false homozygotes
- × 39 mixture profiles analyzed
 - + 18 two person
 - + 14 three person
 - + 7 four person
- × All non-contributors excluded except for one four person mixture (#17) where a non-reproducible log(LR) was produced for a non-contributor
 - Note: additional runs and/or for longer cycles could potentially resolve the non-contributor
- × Assumed knowns can increase the match statistic
- × First degree relatives to 2-person mixtures were excluded, small positive match score for 3 and 4-person mixtures were observed for four samples
 - × Two sons of a 3-person mixture contributor reproducible
 - × Two sons, one 3-person, one 4-person, not reproducible
 - × One brother of a 3-person mixture contributor – not reproducible
- × Specificity
 - + 214 derived contributors from ideal analyses of two, three and four contributor mixtures were compared to 100 random reference profiles
 - × for a total of 21,400 comparisons
 - + Only one small non-reproducible positive match statistic generated for a four person mixture, 2.9X more likely



CONCLUSION

- × TrueAllele Casework:
 - + is accurate
 - × Non-contributors excluded (one example of an inconclusive)
 - × Contributors included (three examples where most minor excluded)
 - + is highly specific
 - × Only one false positive out of 21,400 comparisons for the 2, 3 and 4-person mixtures tested
 - + is sensitive
 - × but when the minor contributor is 10% or below, then a negative log(LR) may be generated
 - + might produce a small positive match score for a first degree relative for 3 and 4-person mixtures
 - + might produce a higher match score if a correct assumed known is used



ADMISSIBILITY HEARING ON TRUEALLELE® CASEWORK

- × TrueAllele used for mixture analysis in a capital murder case
 - + Mixture analysis outsourced to Cybergeneics (CG)
- × Dr. Mark Perlin subpoenaed to testify on TA
- × VDFS staff subpoenaed to testify:
 - + Cathy Shannon
 - × About her DNA profiling in the case
 - + Lisa Schiermeier-Wood
 - × SWGDAM guidelines and selection of CG
 - + Brad Jenkins
 - × Financial commitment by VDFS to Cybergeneics
 - + Purchase of the software program for in-house training and use
 - + Contract for outsourcing certain cases to Cybergeneics for TA analysis
 - + Susan Greenspoon
 - × Presented on the TA validation data
 - + Validation study performed independently of Cybergeneics
 - + Results of the study testified to in detail



ADMISSIBILITY HEARING

- ✦ Lasted for an entire week
- ✦ Dr. Perlin – testified for 2 & ½ days!
- ✦ Cathy, Lisa and Brad – each testified for 1-2 hours
- ✦ Susan – testified for ½ day
- ✦ Three defense expert witnesses – one testified for ½ day (other two were present but not called by the defense)
 - + Criticized the work primarily on the grounds that CG doesn't make the source code available for the software
 - + Criticized the use of MCMC for statistical sampling
 - + Attacked validation for having many unused runs, for two four person mixtures where the most minor contributor produced a negative log(LR), that some three and four person mixtures displayed positive log(LRs) for first degree relatives (but small!) and other
- ✦ **The judge ruled TA admissible and in his ruling stated that TrueAllele® Casework was a “valuable tool”!**



ACKNOWLEDGEMENTS

- ✦ Cybergenetics
 - + Dr. Mark Perlin
 - + Matt Legler
 - + Bill Allan
- ✦ VDFS
 - + Brad Jenkins – Program Manager
 - + Lisa Shiermeier-Wood – Section supervisor (TA team)
 - + Cathy Shannon – Senior forensic scientist
 - + Angie Rainey – Senior forensic scientist (TA team)
 - + Lee Collins – Group supervisor (TA team)



QUESTIONS?
