



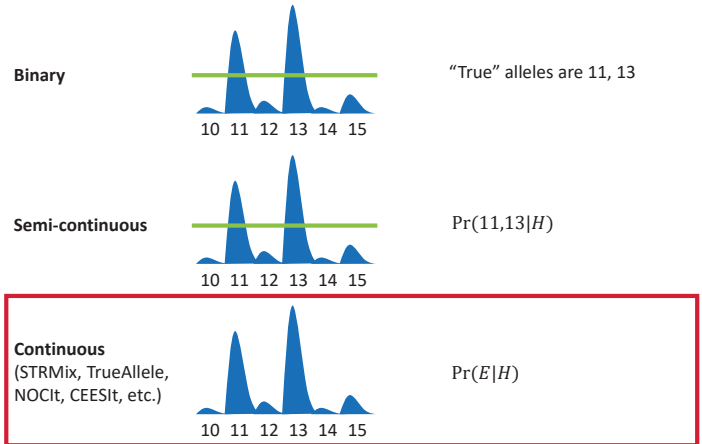
The Impact of Continuous DNA Mixture Interpretation Methods on Evidential Inference

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Green Mountain DNA Conference
July 25, 2017

Continuous DNA mixture interpretation methods are becoming dominant



But what probabilistic model to use?

$$LR = \frac{\Pr(E|n_p, H_p)}{\Pr(E|n_d, H_d)}$$

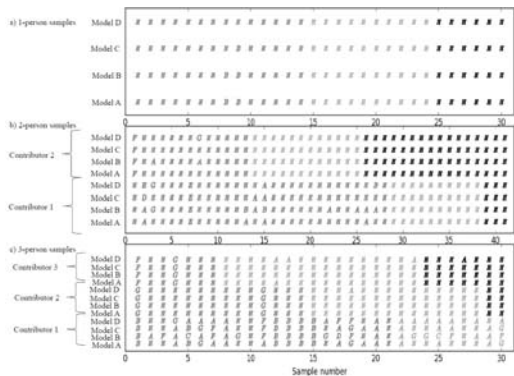
- E : Evidence
 - H_p : Prosecution's hypothesis (suspect contributed to the sample)
 - H_d : Defense's hypothesis (suspect did not contribute to the sample)
 - n_p : Number of contributors specified by the prosecution
 - n_d : Number of contributors specified by the defense
- $LR > 1$: Evidence has more support for prosecution's hypothesis
- $LR < 1$: Evidence has more support for defense's hypothesis

Do minor changes in model lead to major changes in LR?

Numerical value	Verbal expression
1 - 10	Weak
10 - 100	Moderate
100 - 1,000	Moderately strong
1,000 - 10,000	Strong
10,000 - 1,000,000	Very strong
> 1,000,000	Extremely strong

Standards for verbal expression of Likelihood Ratio from
Association of Forensic Science Providers

Yes: models matter



In 17 of 195 LRs (8.7%), verbal classification changed from one model to another

We constructed a comprehensive experimental dataset

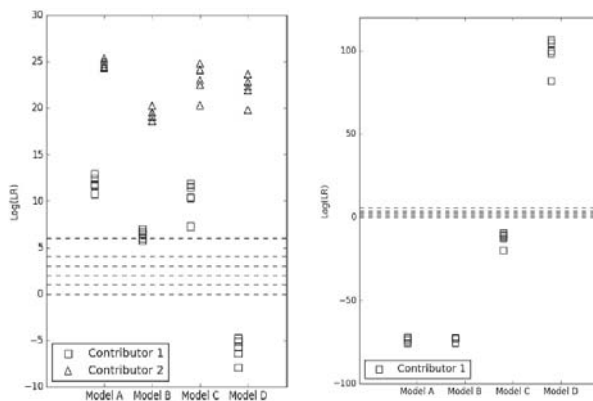
- 313 single-person samples used for calibration (model construction)
- 101 1-, 2-, and 3-person mixtures used for testing
- 0.008 ng to 1.0 ng DNA
- Mixture ratios (largest:smallest) of 1:1 to 1:19
- Identifiler Plus kit
- 3130 Genetic Analyzer

We considered four common model variations

LRs computed using CEESIt (Swaminathan et al., *Forensic Sci. Int. Genet.*, 2016)

Parameter	Model A	Model B	Model C	Model D
Mixture ratio	Constant across markers	Can vary across markers	Constant across markers	Constant across markers
Noise peak height distribution	Normal	Normal	Lognormal	Lognormal
Forward stutter	Included	Included	Included	Not included

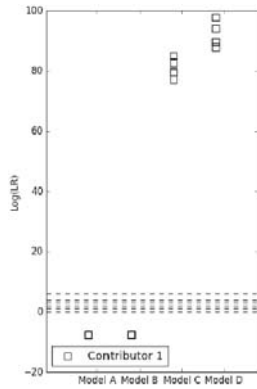
The forward stutter model can significantly affect LRs



1.0 ng 1:19 2-person mixture

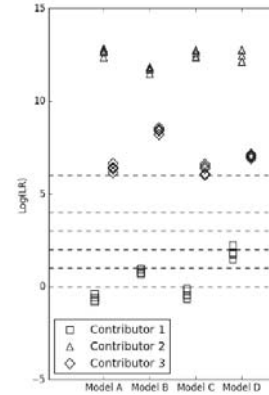
0.03 ng 1-person mixture

The noise model can significantly affect LRs



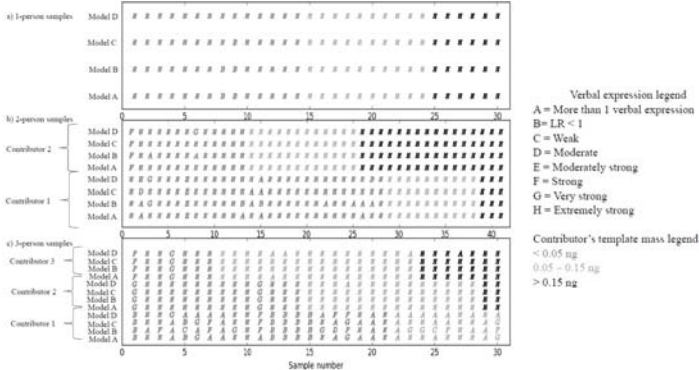
0.03 ng 1-person mixture

The assumption of constant mixture ratios across markers can significantly affect LRs



0.047 ng 1:1:1 3-person mixture

Overall results show significant variation in LRs, especially when DNA contribution is small



In 17 of 195 LRs (8.7%), verbal classification changed from one model to another

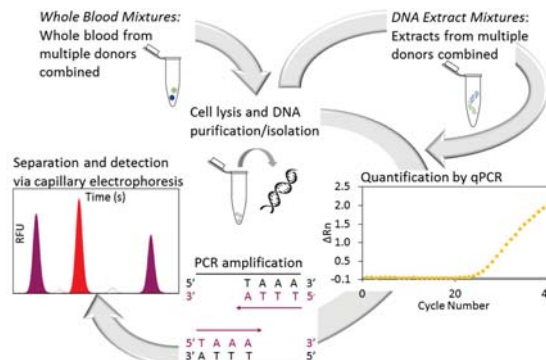
What are the implications?

- Models matter, yet all models are wrong
- Need: Empirical assessment of models and interpretation methods

PROVEDIt is a database of STR profiles and tools for their analysis

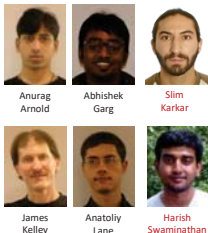
- Over 25,000 profiles
- One to five person mixtures
- Different laboratory conditions
 - Untreated
 - UV-damaged
 - Enzymatically-degraded
 - Sonically-degraded
 - Inhibited DNA
- CE instruments: 3130 and 3500 Genetic Analyzers
- Amplification kits: PowerPlex 16HS, Identifiler Plus, GlobalFiler

PROVEDIt is a database of STR profiles and tools for their analysis



Acknowledgments

Lab members



Boston University

Catherine Grgicak
Lauren Alfonse
Amanda Garrett
Sarah Norsworthy
Genevieve Wellner

MIT

Muriel Médard
Viveck Cadambe
Ullrich Mönich

Maynooth University

Ken Duffy

Engine Room Technology Co.

Dennis Egen
Rob Carpenter

Funding Support



Data and tools available at sites.bu.edu/grgicak/provedit

