

# On the threshold of injustice: manipulating DNA evidence

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Jurisprudence Section  
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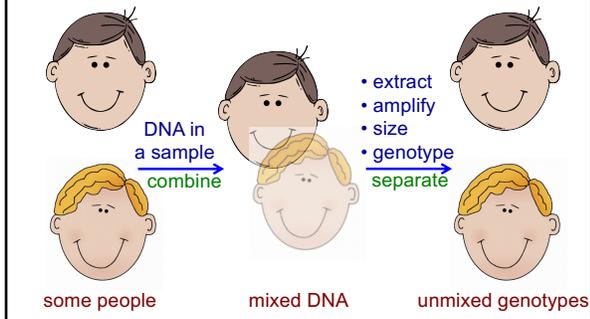
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## DNA mixing and unmixing



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## Probabilistic genotyping

### Bayesian

- Noise      Model baseline
- Much data      Use all peaks
- Low data      All genotypes
- Stutter      Mine the data
- Variation      More variables

Objective computer operation

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## Less math, less capability

	Bayesian	Incomplete
Noise	Model baseline	Thresholds
Much data	Use all peaks	Discard peaks
Low data	All genotypes	Set dropout
Stutter	Mine the data	Calibrate lab
Variation	More variables	Give up

Subjective human operator

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## Choices and consequences

Objective probability can be fair



Gambling with justice

Human choices  
introduce bias

Subjectivity leads to  
unfair outcomes

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## DNA evidence and results

Death by strangulation of 12 year old boy

150 biological **evidence** items,  
with focus on DNA under victim's **fingernails**

**Software** finds match statistic of **ten million**,  
connecting fingernails to defendant DNA

Unknown **minor** contributor is **0.4%** or **1:250**

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## Rule 702

- a. Sufficient data
- b. Reliable method
- c. Reliably apply method to data

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## Sufficient data

### Mixture

- ratio is 1:250
- less than 1 cell

Fingernail data show  
low mixture amount  
& low peak heights  
for minor contributor

### Peak height

- 30 to 70 rfu

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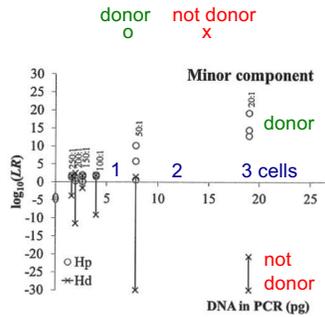
## Reliable method

### Mixture (validation)

- ratio of 1:25
- many cells

### Peak threshold

- 30 rfu in study



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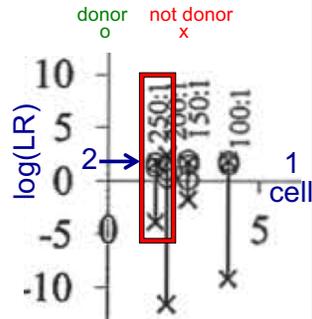
## Reliably apply method to data

### Mixture (case)

- ratio is 1:250
- less than 1 cell

### Peak threshold

- 30 rfu in study
- 50 rfu in case




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## Applying thresholds

RFU	Data choices	LR	All stutters
80	0	0	9
70	30	30	51
60	250	250	1,660
50	15,500,000	15,500,000	69,200 include
40	0	0	0 exclude
30	0	0	0

Different choices, different answers  
Software does not agree with itself

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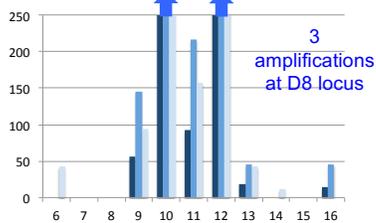
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## Choosing data



Victim V V  
 Foreign  
 Defendant D  
 Exculpatory X X X X X } expert report  
 other choices

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## Double dropout

	Allele	Amp 1	Amp 2	Amp 3
Peak height data at the D18 locus	9	55	80	97
	10	1,315	2,009	2,653
	11		95	121
	12	969	1,757	2,368

"Q" means **not** 9, 10, 11 or 12 data allele  
Defendant's **17,17** is **not in the data**

Hp weight for Q,Q genotype = 15%  
Hd weight for Q,Q genotype = 14%  
Likelihood ratio is 15%/14% = **1.05 > 1**  
Non-data Q,Q matches defendant 17,17  
**Excluded from data, but inclusionary LR**

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## Judge's ruling

The Expert conceded at the hearing that **no internal validation studies were performed** by the State crime lab for the use of the Software on casework samples developed at the lab.

As a result the Expert was forced to **pick and choose data** from different "reliable sources" and **input parameters** into the program in such a way that he believed the system would tolerate.

**ORDERED** that the **defendant's motion to preclude** the prosecution from calling an expert witness to testify on their direct case regarding any conclusion reached by the use of the Software is **granted** as the prosecution cannot lay a foundation for the introduction of evidence that had not been internally validated.

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## Rule 403

**Probative value**  
unreliably applied method  
on insufficient DNA data



**Danger of**  
unfair DNA prejudice,  
confusing the issues,  
misleading the jury

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## Recommendations

### Discovery for Software

- validation studies (internal & other)
- user, procedure and training manuals
- papers, reports, math description
- data choices, parameter settings
  
- all electronic DNA Data in the case
- demand working Software program
- run Software on Data to replicate results
- run different Software on Data to confirm

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## More information

<http://www.cybgen.com/information>



- Courses
- Newsletters
- Newsroom
- Presentations
- Publications
- Webinars

<http://www.youtube.com/user/TrueAllele>  
TrueAllele YouTube channel



Cybergenetics



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