Dr Jonathan Whitaker

Dr Peter Gill

DNA Mixture Interpretation Workshop | John Buckleton

"Few cell DNA profiling" - Gill, Whitaker, Buckleton International Patent Number WO 01/79541

The issue

- I cannot teach the drop model for complex mixtures in 2 hours.
- What is wrong with existing methods.
- The pressure for change is coming from non-concordances.
- Non-concordance POI = ab or aa
- One or both of the alleles not seen in profile
- I will try to use LCN = 34 cycles
- LtDNA any low level profile (28 or not)

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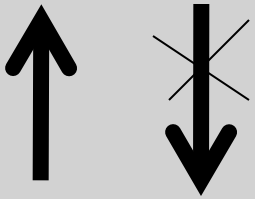
Heterozygote balance

$$Hb = \frac{H_{shorter}}{H_{taller}} \qquad 0 \le Hb \le 1$$



$$Hb = \frac{H_{hmw}}{H_{lmw}} \qquad 0 \le Hb \le \infty$$

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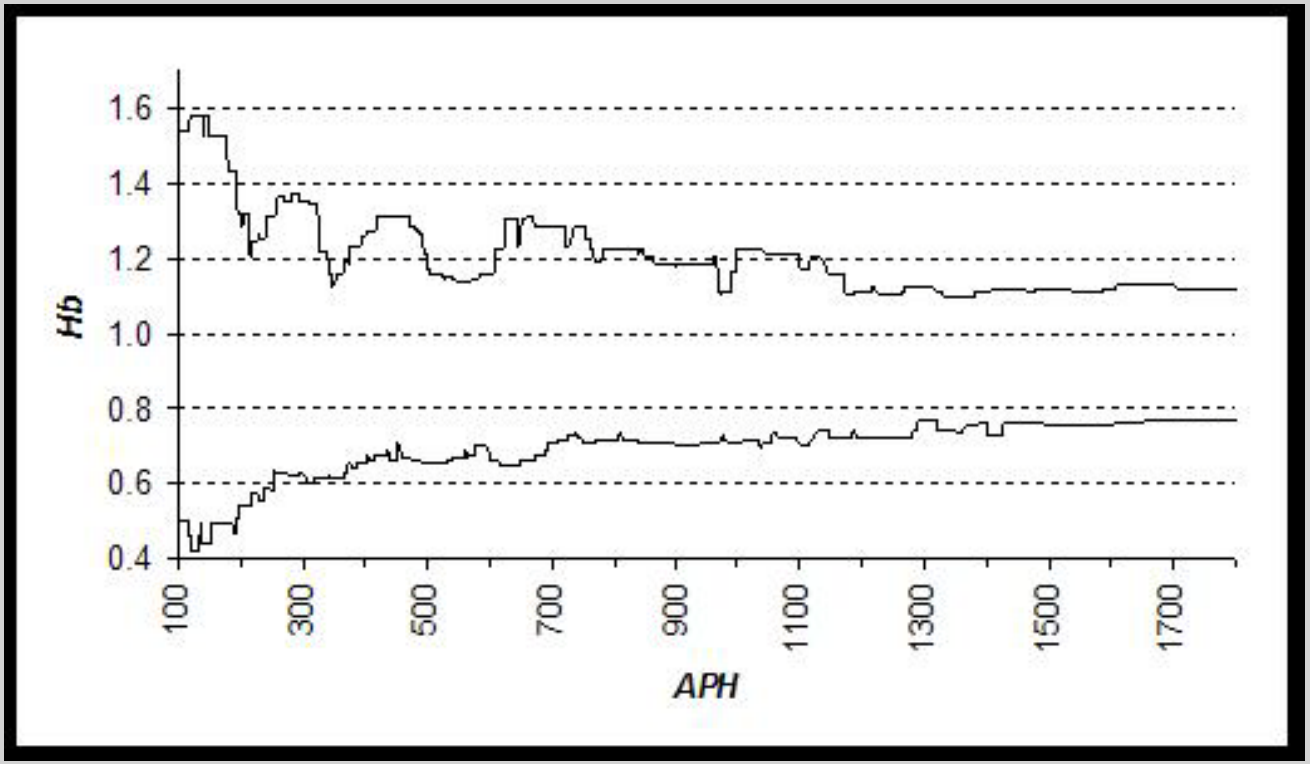

Figure 4. A plot of the bounds of the central 0.95 quantile of H_b vs *APH* for both the SAH and non-SAH combined.

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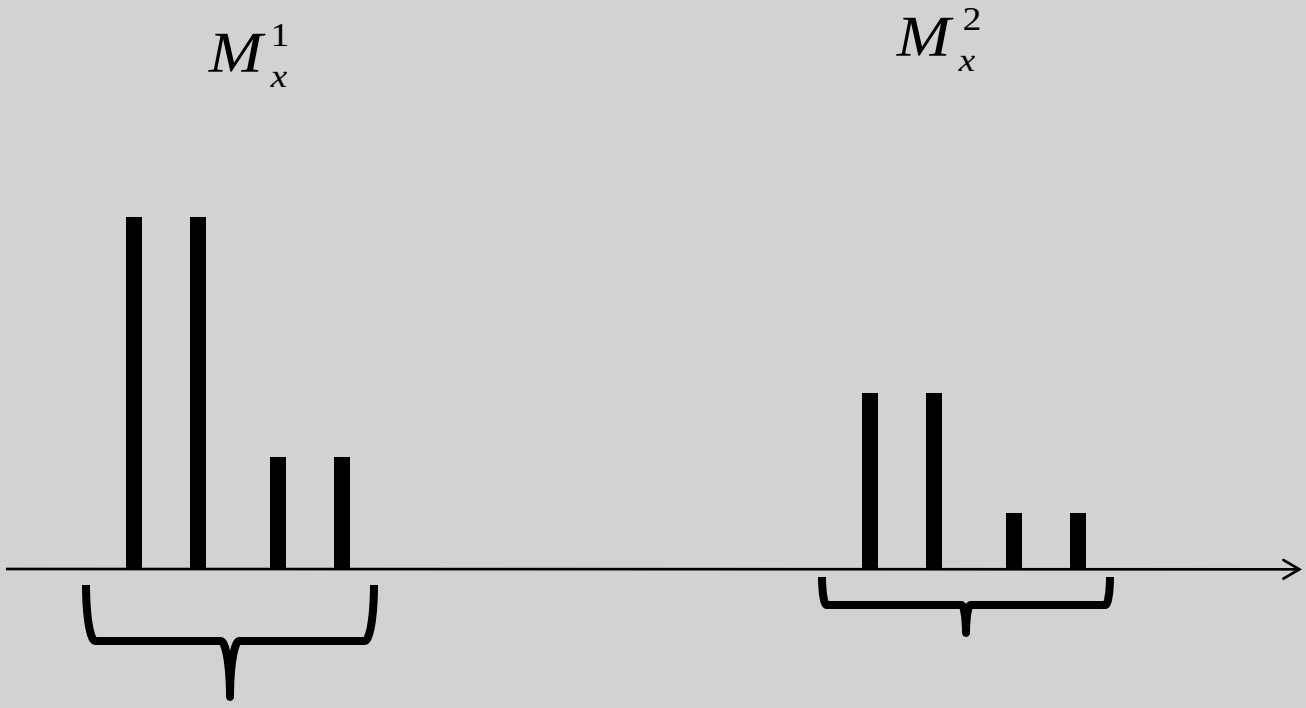
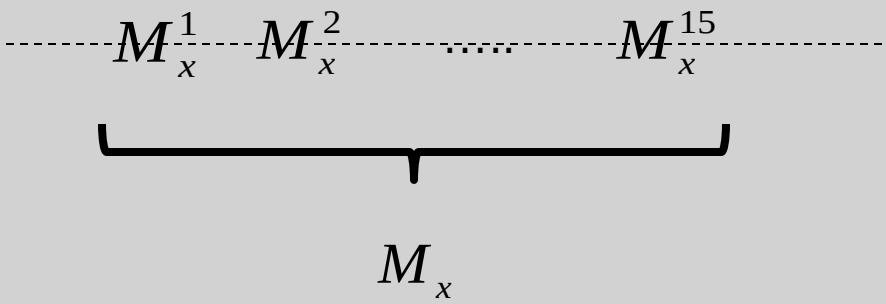
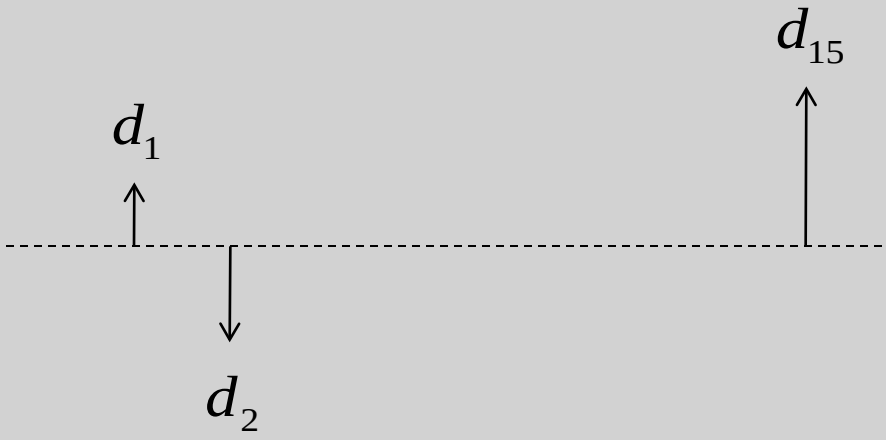
Mixture proportion – how much do mixtures vary across loci



Mixture proportion – how much do mixtures vary across loci



Mixture proportion – how much do mixtures vary across loci



28 cycles mixture proportion Identifiler

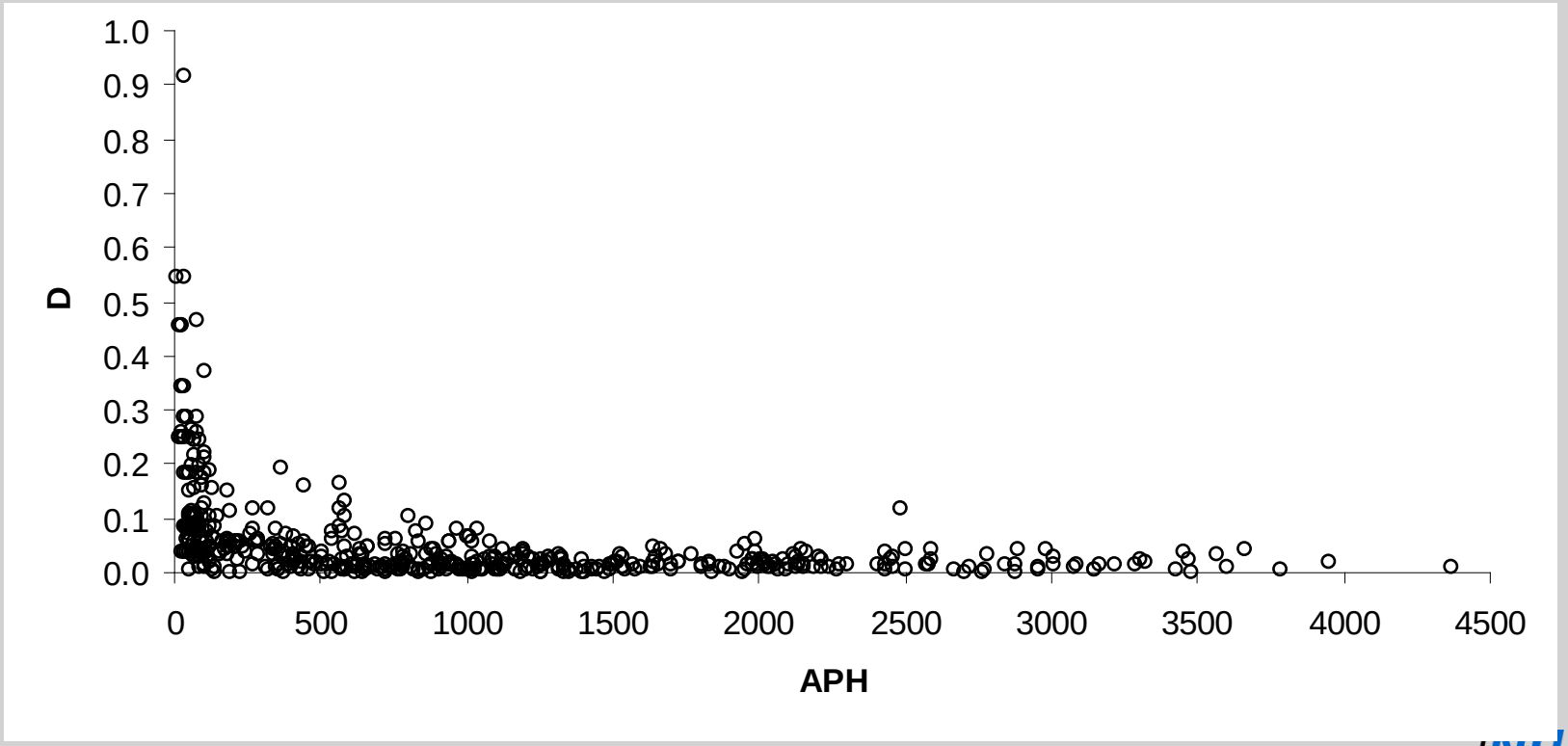
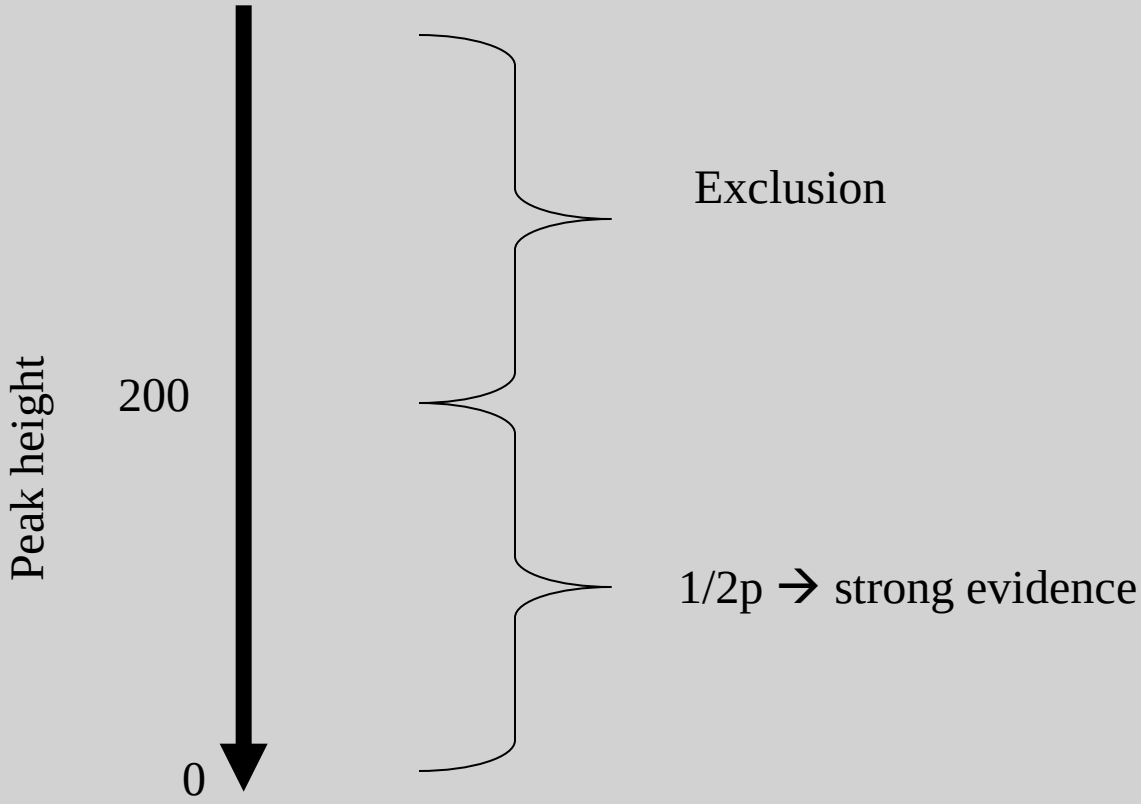


Figure 3. A plot of D vs APH

Single replicate
Suspect ab Stain a



We should have noticed something was up earlier.
We all thought 2p was "conservative"
but it's not
I need to show you the problem
this requires some heavy trawling
Then we are in a position to discuss solutions.

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Third law

- Pr(A and B) = Pr(A).Pr(B|A)
- = Pr(B).Pr(A|B)
- Pr(B|A) is the probability of event B given that event A is true
- this is called a conditional probability

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Please close your notes

Conditional probability

After Dr Evett

- **How tall is Sarah?**
- **Sarah is 3 years old?**
- **Sarah is a basketball representative?**

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Beards and Mustaches

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Terminology: Conditional probability

- Consider two events
- E: the number on the dice is Even
- L: the number on the dice is Less than 3.5
- Pr(E|L) means
- probability of an even number given that it is less than 3.5

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Exercise

- please calculate Pr(E)
- Pr(L)
- Pr(L|E)
- Pr(E|L)
- Pr(E&L)

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Exercise

- Pr(E) = 3/6
- Pr(L) = 3/6
- Pr(E|L) = 1/3
- Pr(L|E) = 1/3
- Pr(E & L) = Pr(E).Pr(L|E)
  = 3/6 . 1/3
  = 1/6
- or Pr(L & E) = Pr(L).Pr(E|L)
  = 3/6 . 1/3
  = 1/6

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Bayes theorem

- **A child abuse case**
- **Psycologist:**
- **A: This child rocks**
- **B: 60% of abused children rock.**

Borrowed from Robertson and Vignaux

Bayes theorem

- **A child abuse case**
- **Psycologist: This child rocks**
- **60% of abused children rock.**
- **C_1: 1% of non-abused children rock**
- **C_2: 60% of non-abused children rock**

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Borrowed from Robertson and Vignaux

lessons

- **You cannot interpret evidence with one hypothesis**
- **You need two hypotheses and two probabilities**
- **It is the ratio of the probabilities of the evidence given these hypotheses that matters**

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Models to interpret LCN profiles

- **This nomenclature is pretty bad but without these shortcuts the equations become VERY ugly**

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Description	Term
Drop in of an allele at a locus	C
	$\overline{C} = 1 - C$
Drop out of a specific allele of a het	D
	$\overline{D} = 1 - D$
Drop out of a hom	D_2
	$\overline{D}_2 = 1 - D_2$

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Procedure to estimate the LR

- **Nomenclature:**
- **Replicates**
- **Say, R_1 = a R_2 = ab**
- **Pr($E|H_p$) is the probability of the evidence *if* the profile is the suspect's**
- **Pr($E|H_d$) is the probability of the evidence *if* the profile is from someone else**

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$$LR = \frac{p(R_1, R_2, \ldots \mid Hp)}{p(R_1, R_2, \ldots. \mid Hd)}$$

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$$LR = \frac{p(R_1, R_2, \ldots \mid Hp)}{p(R_1, R_2, \ldots. \mid Hd)}$$

Specify all possible contributors M_j

$$= \frac{p(R_1, R_2, \ldots \mid Hp)}{\sum_j p(R_1, R_2, \ldots. \mid M_j, Hd)\, p(M_j \mid Hd)}$$

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$$LR = \frac{p(R_1, R_2, \ldots \mid Hp)}{p(R_1, R_2, \ldots. \mid Hd)}$$

$$= \frac{p(R_1, R_2, \ldots \mid Hp)}{\sum_j p(R_1, R_2, \ldots. \mid M_j, Hd)\, p(M_j \mid Hd)}$$

Assume replicate 1 and replicate 2 etc are independent?

Once M_j is specified we don't need *Hd*.

$$= \frac{\prod_i p(R_i \mid H_p)}{\sum_j \prod_i p(R_i \mid M_j)\, p(M_j)}$$

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$$2P_{ab|ab}$$

Probability of the ab genotype given POI is ab

Consider one replicate profile is ab
suspect is ab

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Explanation of the evidence under H_d

- **There may be a lot of possible 'true offender" profiles. We call these *M*j.**
- **There is no need for restriction if you have a computer but there is a need if you do it by hand.**
- **I think in this case we could have *M*j=*ab, aa, bb***

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add

*M*j	*P*(*M*j)		R_1=*ab*
ab	$2P_{ab\|ab}$	x	$\overline{D}\overline{D}\overline{C}$
aa	$P_{aa\|ab}$	x	$\overline{D}_2 C P_b$
bb	$P_{bb\|ab}$	x	$\overline{D}_2 C P_a$
$2P_{ab\|ab}\overline{D}^2\overline{C} + P_{aa\|ab}\overline{D}_2 C P_b + P_{bb\|ab}\overline{D}_2 C P_a$			

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Explanation of the evidence under H_p

- **If Hp is true then the donor is *ab***
- **If R_1 is really from the suspect how is the evidence explained?**
- **R_1= *ab* - explanation - no drop out of allele *a*, no drop out of allele *b*, no drop in**

$$p(R_1 \mid Hp) = \overline{D}\,\overline{D}\,\overline{C}$$

This has caused soooo much trouble

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$$LR = \frac{\overline{D}^2 \overline{C}}{2P_{ab|ab}\overline{D}^2\overline{C} + P_{aa|ab}\overline{D_2}CP_b + P_{bb|ab}\overline{D_2}CP_a}$$

If we assume C is low

$$LR \approx \frac{\overline{D}^2 \overline{C}}{2P_{ab|ab}\overline{D}^2\overline{C}}$$

$$= \frac{1}{2P_{ab|ab}}$$

Now the non-concordance
one replicate
profile is a low level
aF
suspect is ab

Definitions

F is any allele

Q is any allele other than those denominated

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Explanation of the evidence under H_d

- R_1 = aF
- I think in this case we could have *M*j=*aQ, ab, aa*

R_1=AF

add

*M*j	*P*(*M*j)		R_1=*aF*
aa	$P_{aa\|ab}$	x	$\overline{D}_2\overline{C}$
ab	$2P_{ab\|ab}$	x	$\overline{D}D\overline{C}$
aQ	$2P_{aQ\|ab}$	x	$\overline{D}D\overline{C}$
$P_{aa\|ab}\overline{D}_2\overline{C} + 2P_{ab\|ab}\overline{D}D\overline{C} + 2P_{aQ\|ab}\overline{D}D\overline{C}$			

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Explanation of the evidence under H_p

- **If R_1 is really from the suspect how is the evidence explained?**
- **R_1= *aF* - explanation - no drop out of allele *a*, drop out of allele *b*, no drop in**

$$p(R_1 \mid Hp) = \overline{D}D\overline{C}$$

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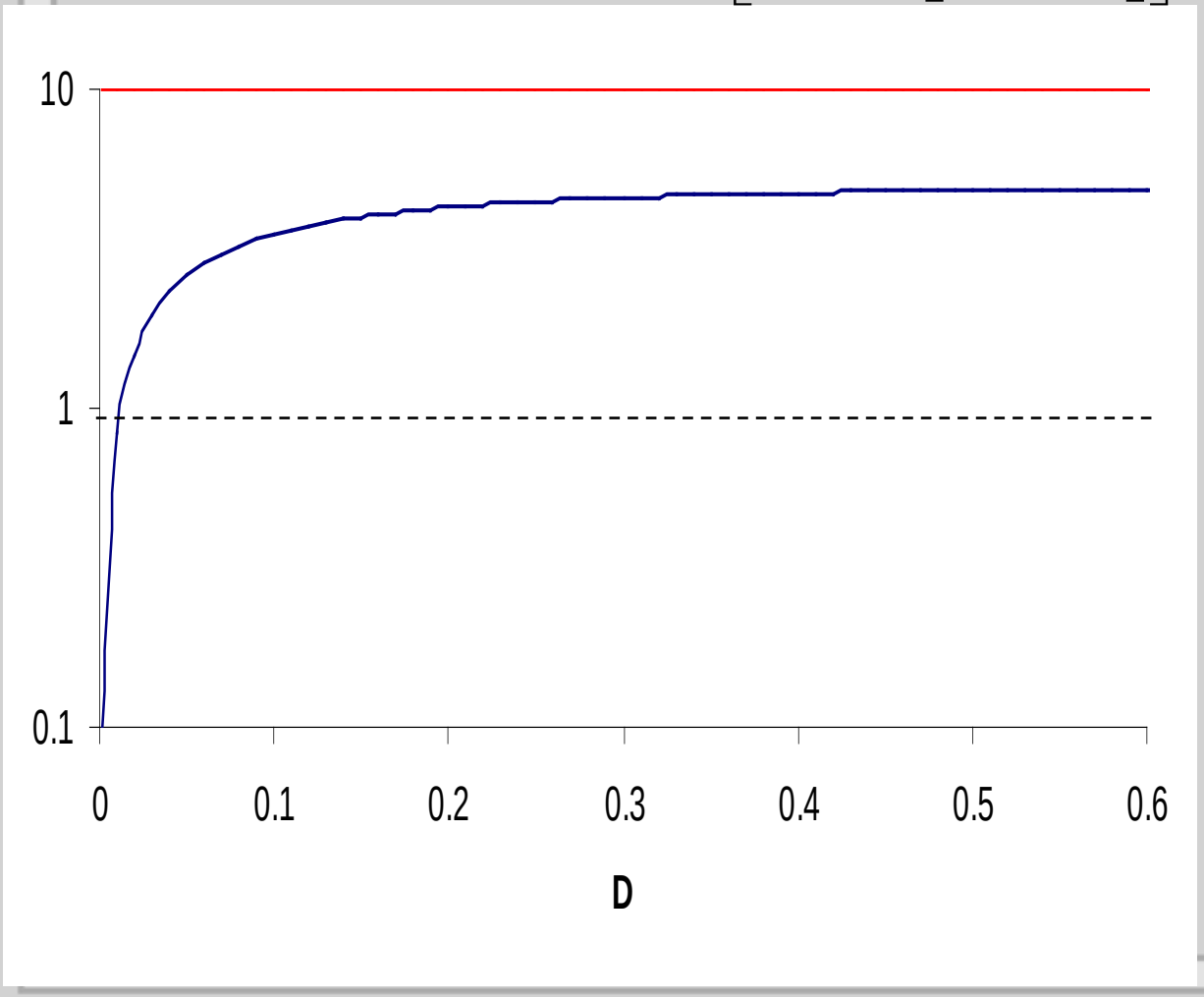
$$\frac{\overline{D}D\overline{C}}{P_{aa|ab}\overline{D}_2\overline{C}+2P_{ab|ab}\overline{D}D\overline{C}+2P_{aQ|ab}\overline{D}D\overline{C}}$$

I know you all love these equations

Write as

$$\frac{1}{2P_{a|ab}\left[1+P_{a|aab}\left[\frac{\overline{D}_2}{2\overline{D}D}-1\right]\right]}$$

Typical behaviour of $\dfrac{1}{2P_{a|ab}\left[1+P_{a|aab}\left[\dfrac{\overline{D}_2}{2\overline{D}D}-1\right]\right]}$



2p rule

$$\frac{1}{2P_{a|ab}\left[1+P_{a|aab}\left[\dfrac{\overline{D}_2}{2\overline{D}D}-1\right]\right]}$$

Ignoring the locus

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If POI = aa and stain a → no real problems

If POI = ab and stain = a (a non-concordance)

2p rule never conservative

2p rule not too bad if *D* not small

Ignoring the locus not ALWAYS conservative but OK if D not VERY small

Where do we stand in 2010?

Binary model

Under stress if non-concordant

D model

Continuous model

Can deal with non-concordances

Increasing complexity/elegance

Increasing use of available evidence

Increasing difficulty of implementation/explanation

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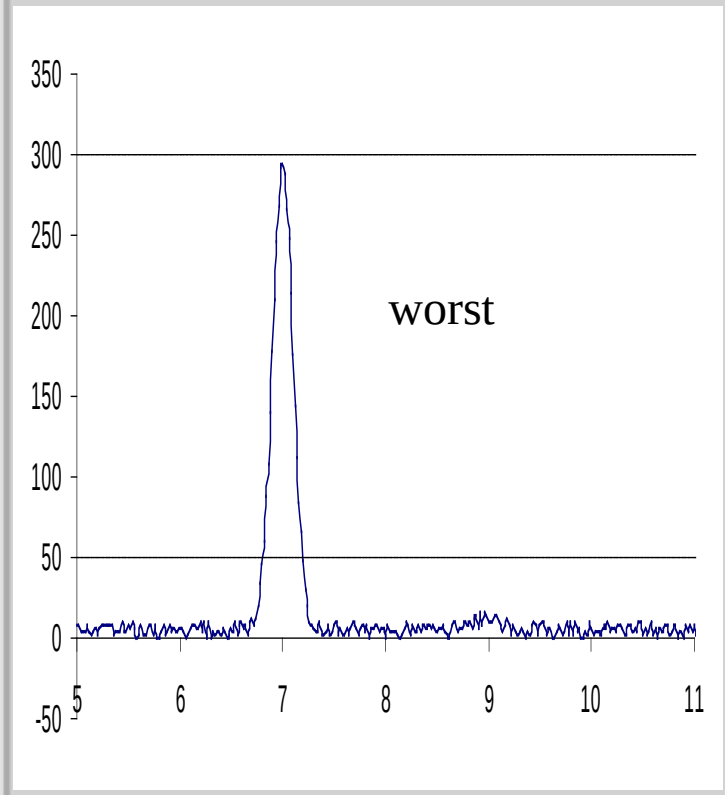
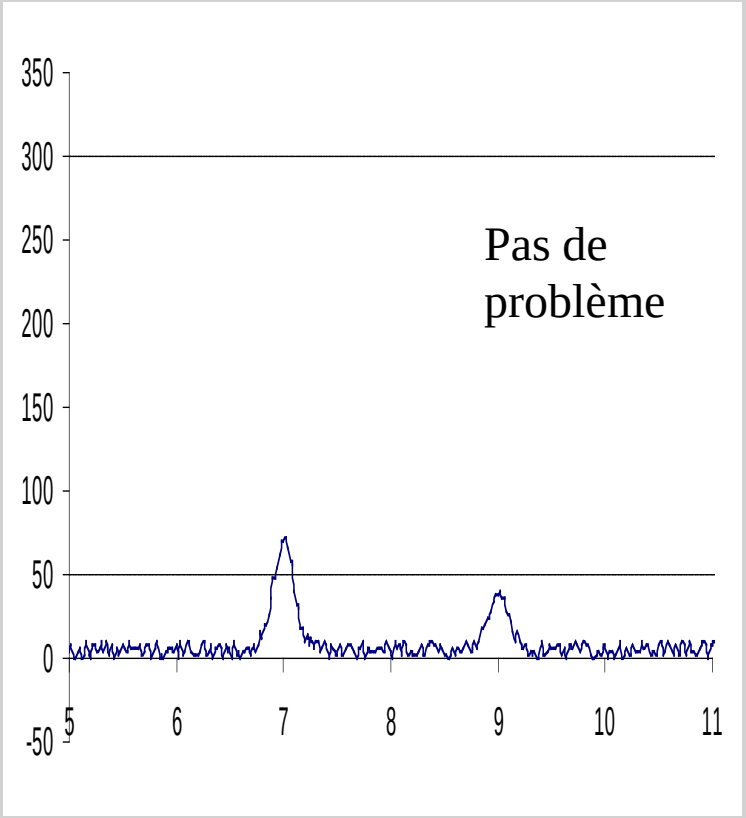
Can we nurse the binary model along a bit further?
All non-concordances are problematic but some more so than others. POI = 7,9





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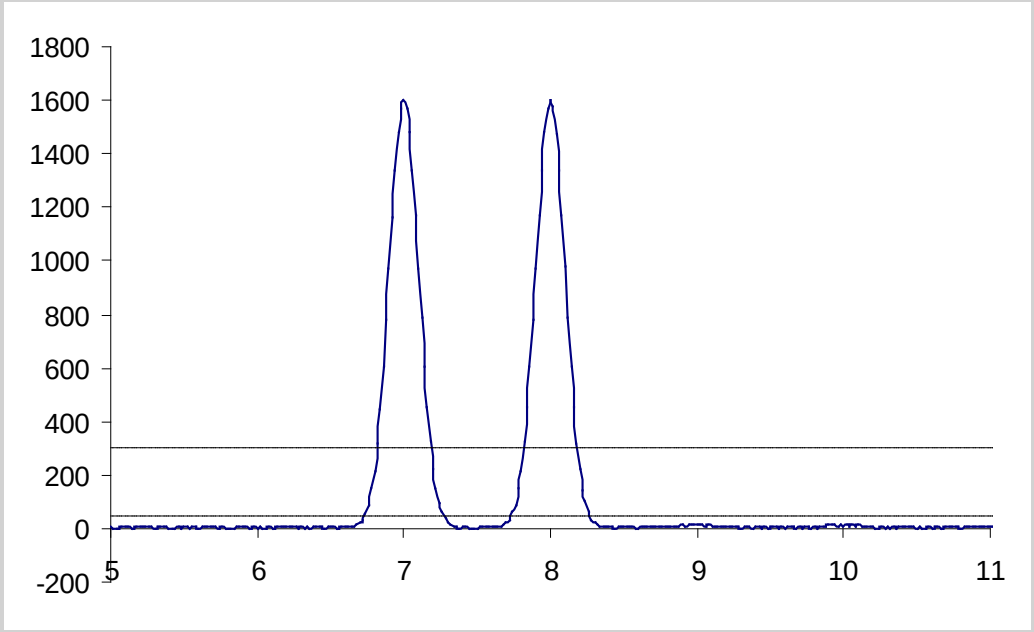
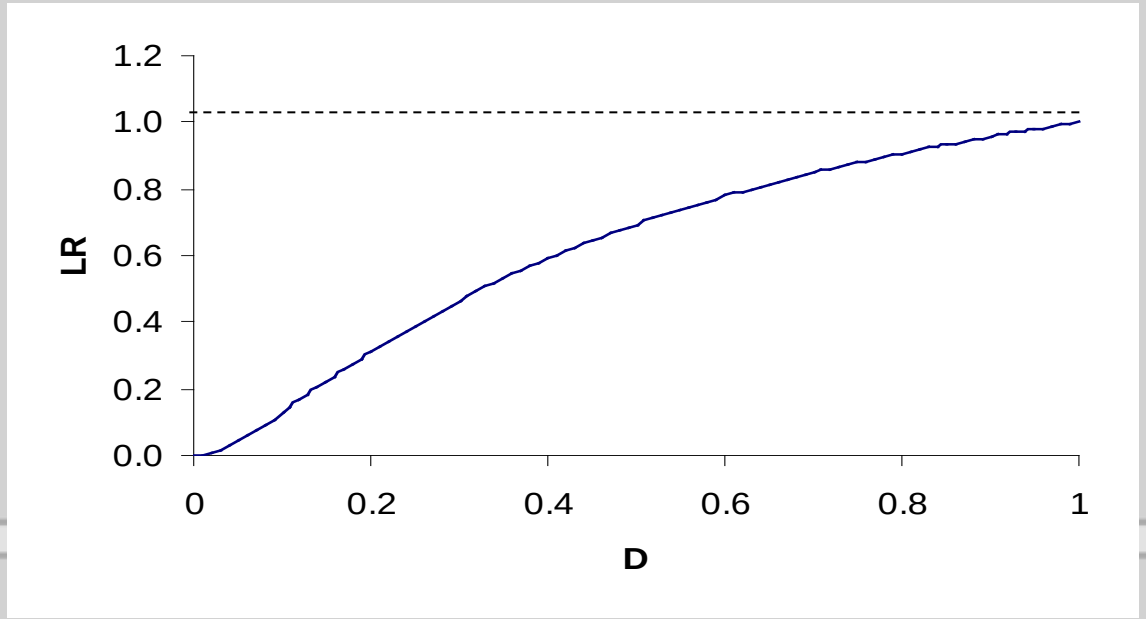


V = 7,8

POI = 9,10



Dropping locus never safe but not too bad if D very high

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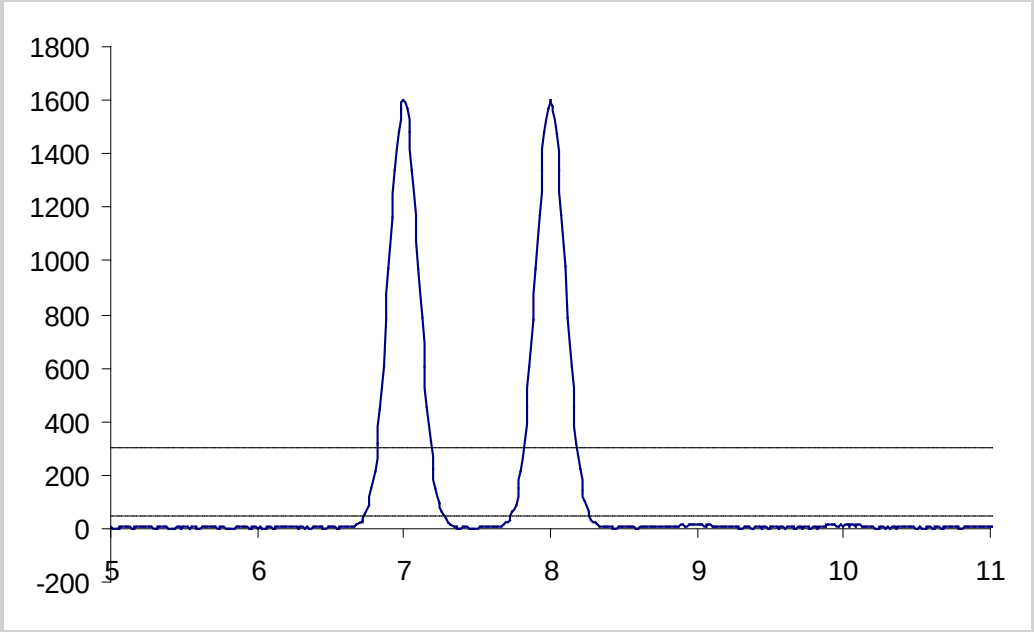
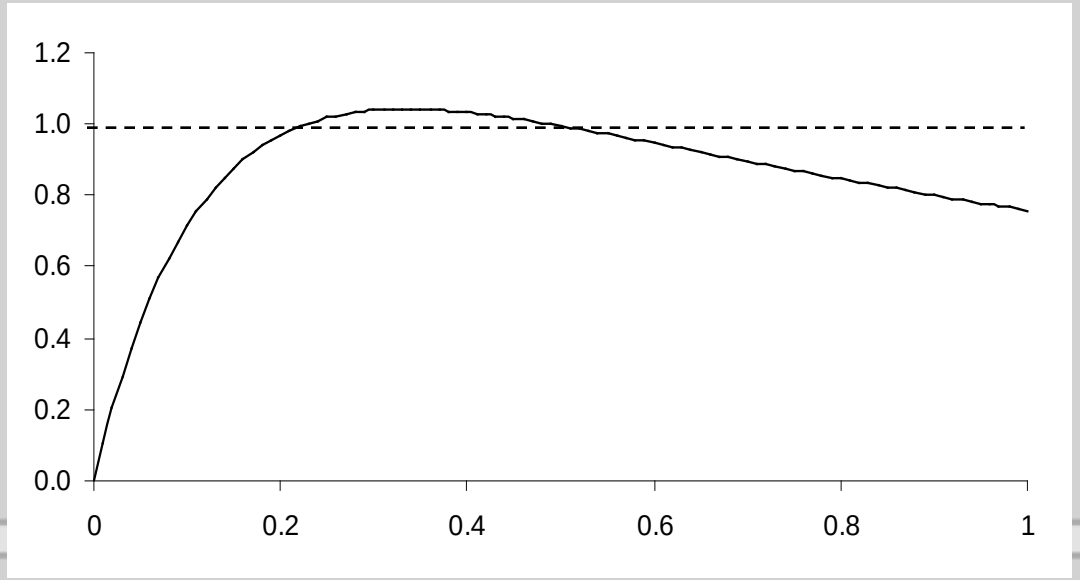


V = 7,8

POI = 8,9



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R v. Garside and Bates (2003-06)

- **Lots of victim DNA, 17 STR alleles at 10 loci.**
- **Minute trace of offender (?) DNA, 8 alleles not masked by victim alleles or artefacts.**
- **Defendant profile has 11 alleles not masked. Includes all 8 minor component alleles.**
- **What to do about 3 "missing" alleles:**
  - **trace peak in each position, not to reportable standards**
  - **1 in stutter position adjacent to homozygote peak**
  - **2 at HMW positions, more susceptible to dropout ?**

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- … Richard Bates, was convicted of murder ….
- His co-accused, James Garside, was also convicted of murder and received the same sentence.
- The victim was Marilyn Garside, the estranged wife of James Garside.
- It was the prosecution's case that Garside had hired Bates to murder her.

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- Marilyn Garside was stabbed and killed … when she answered the front door of her elderly mother's house in Rose Lane, Romford.
- The prosecution alleged that Garside was the only person who knew that Marilyn would be visiting her mother, Mrs. Barbara Rawle, that day and
- that she would answer the door rather than her mother, who walked with difficulty.

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- When calculating the probability match for each sample Dr. Evett, the expert statistician called on behalf of the prosecution, attributed a value of 1 to each of the voids, treating it as neutral.
- On that basis he calculated the probability match in the case of samples 2 and 4 to be 1 in 610,000.

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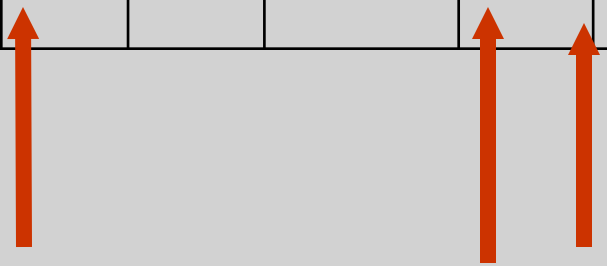
Item	Am	D3	vWA	D16	D2	D8	D21	D18	D19	THO1	FGA
M Garside	XX	16,16	15,17	11,12	20,20	12,13	30,32.2	14,14	12,14	9.3,9.3	23,25
R Bates	XY	13,16	16,16	11,12	19,22	8,13	30,31.2	12,15	12,15	7,7	21,21
SJP/22 Area 4 Chrome handle	XY	**13**,16	15,16,17	11,12	20,**22**	**8**,12,13	30,31.2,32.2	14	12,14,**15**	**7**,9.3	**21**,23,25



- In my opinion (DJB) the prosecution had a potentially arguable case but they did not make it:
- “missing” alleles were treated as neutral without any analysis or reliance on established guidelines to justify this.
- Judge accepted DNA evidence: “missing” alleles had been adequately discussed for jurors to make their own assessment.
- I disagree, and regret the lost opportunity to apply pressure for an achievable, better standard of reporting.

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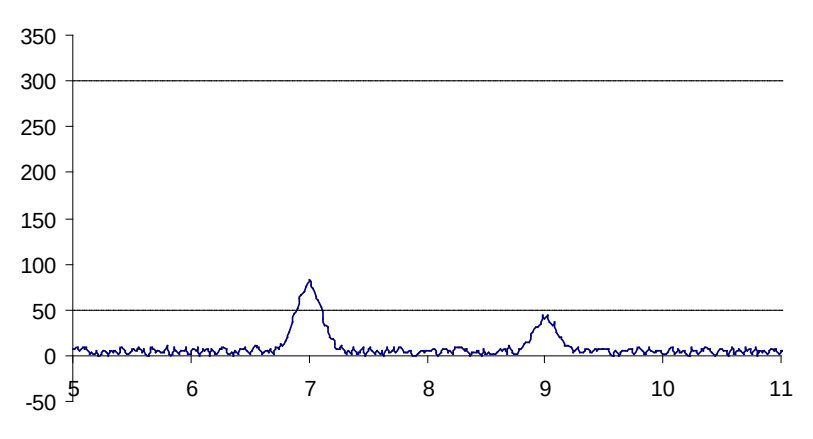
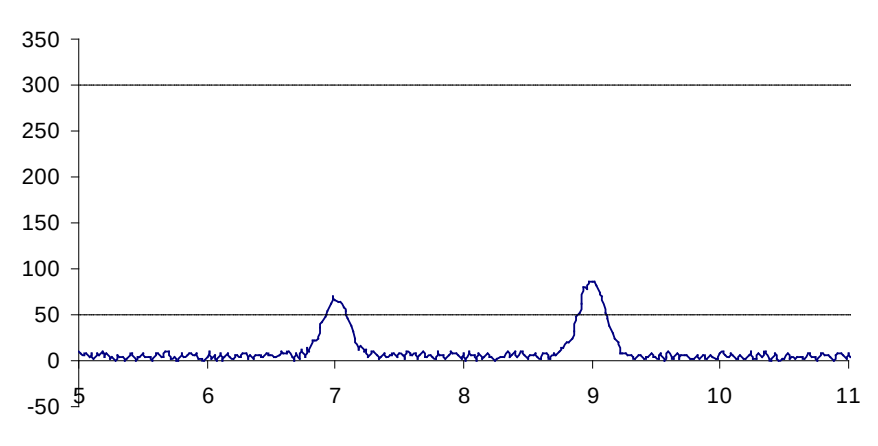
POI = 7,9

Replicate 1



Replicate 2



Practices I have heard of:

1. Report most informative or most conservative
2. Consensus 2/2 or 2/3 or…
3. Composite
4. “Mathematically” treat both
    1. D model
    2. TRUEALLELE

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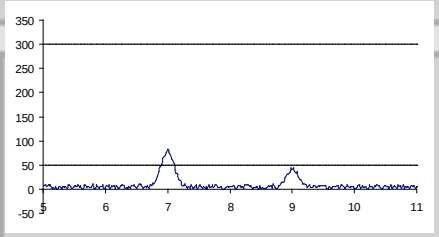

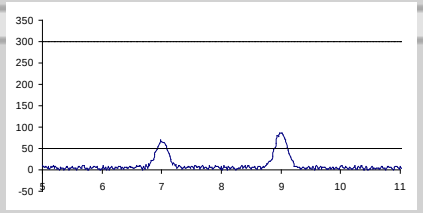

Report most informative

Accusation of bias

Which is most informative

POI = 7,7 7,9 7,11?

Replicate shopping

Report most conservative

Should be safe to accusation of prosecution bias

Most conservative does depend on POI

Wastes information

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Consensus

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Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Forensic population genetics—original research

Low template STR typing: Effect of replicate number and consensus method on genotyping reliability and DNA database search results

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amplifications (n)	reproducibility (x)	0-10%	10-25%	25-50%	>50%
3	2	57%	88%	98%	99%
4	2	64%	95%	100%	100%
6	3	63%	96%	100%	100%

Composite

- **Add any confirmed allele from any replicate**
- **Seems OK IFF**
  - **Confirmed alleles are always alleles**
  - **→C must be 0**
  - **And maybe a few other things**
  - **Risk not currently empirically assessed fully (it is in part)**
  - **But we could theoretically assess it**

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Mathematically combining - best

R_1	*ab*
R_2	*a*
POI	*ab*

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Add

Mj	P(Mj)	R1 = *ab*		$R_2 = a$		
ab	$2P_{ab\|ab}$	$\bar{D}\bar{D}\bar{C}$	X	$\bar{D}D\bar{C}$	=	$2\,\mathrm{P}_{ab\|ab}\,\bar{D}^3D\bar{C}^2$
aa	$P_{aa\|ab}$	$\bar{D}_2CP_b$	X	$\bar{D}_2\bar{C}$	=	$\mathrm{P}_{aa\|ab}\,\bar{D}_2^2\bar{C}CP_b$

$$den = 2\,\mathrm{P}_{ab|ab}\,\bar{D}^3D\bar{C}^2 + \mathrm{P}_{aa|ab}\,\bar{D}_2^2\bar{C}CP_b$$

POI = ab

$$num = \bar{D}^3D\bar{C}^2$$

POI = aa

$$num = \bar{D}_2^2\bar{C}CP_b$$

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POI = ab

POI = aa

$$num = \bar{D}^3 D \bar{C}^2$$

$$num = \bar{D}_2^2 \bar{C} C P_b$$

R_1=ab

R_2=a

$$den = 2\,\mathrm{P}_{ab|ab}\,\bar{D}^3 D \bar{C}^2 + \mathrm{P}_{aa|ab}\,\bar{D}_2^2 \bar{C} C P_b$$

POI = ab

$$LR = \frac{1}{2P_{a|ab}\left[\mathrm{P}_{b|aab} + \mathrm{P}_{a|aab}\,\dfrac{\bar{D}_2^2 C P_b}{2\bar{D}^3 D\bar{C}}\right]}$$

POI = aa

$$LR = \frac{1}{2\,\mathrm{P}_{a|ab}\left[\mathrm{P}_{b|aab}\,\dfrac{\bar{D}D\bar{C}}{2(1+D)^2 C P_b} + \mathrm{P}_{a|aab}\right]}$$

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POI = ab

$$LR = \frac{1}{2P_{a|ab}\left[\mathrm{P}_{b|aab} + \mathrm{P}_{a|aab}\,\frac{\bar{D}_2^2 C P_b}{2\bar{D}^3 D\bar{C}}\right]}$$

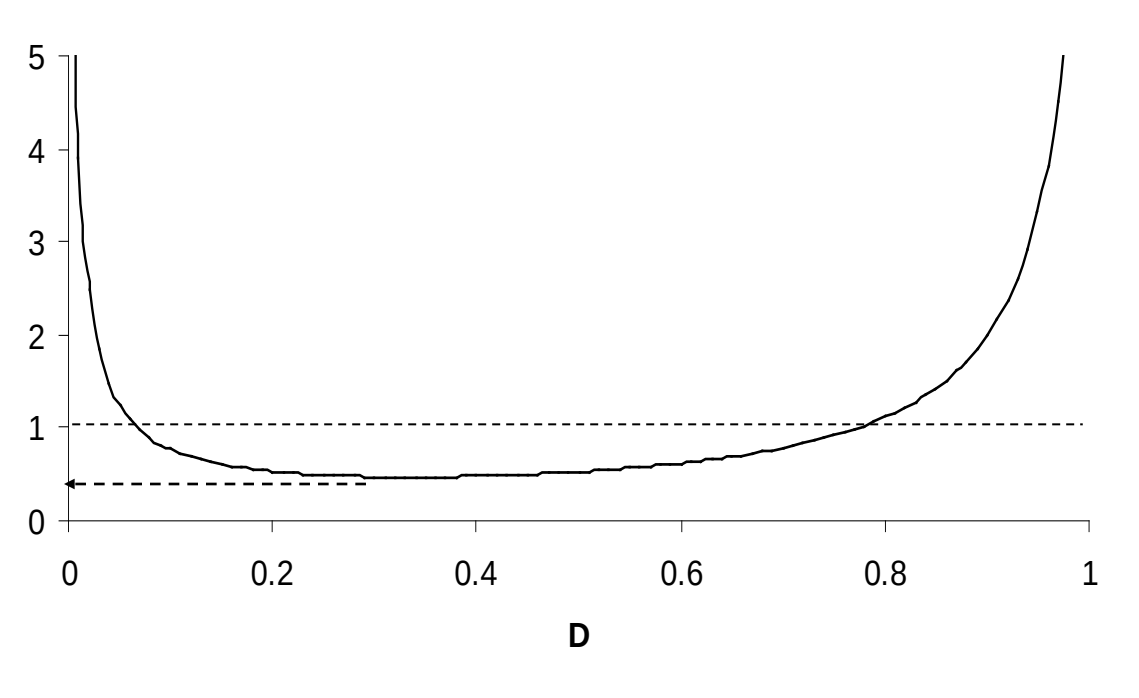
Set C = 0

$$LR = \frac{1}{2P_{ab|ab}}$$

POI = aa

$$LR = \frac{1}{2\,\mathrm{P}_{a|ab}\left[\mathrm{P}_{b|aab}\,\frac{\bar{D}D\bar{C}}{2(1+D)^2 CP_b} + \mathrm{P}_{a|aab}\right]}$$

$$\frac{1}{\left[\mathrm{P}_{b|aab}\,\frac{\bar{D}D\bar{C}}{2(1+D)^2 CP_b} + \mathrm{P}_{a|aab}\right]}$$



$P_a = P_b = 0.10$

C = 0.03

$\theta = 0.03$

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A principle of probability

- **Ignoring information is conservative, on average, if Hp is true BUT not conservative if Hd is true.**

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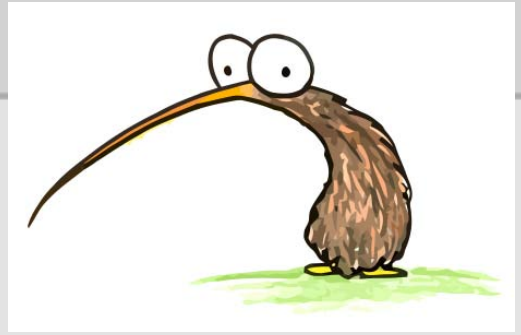
STATSWG



Unconstrained combinatorial approach

- **Alternative method is to consider all genotype combinations**
  - **Do not rule any out**
  - **Gives a lower LR**
  - **More efficient as fewer calculations required**

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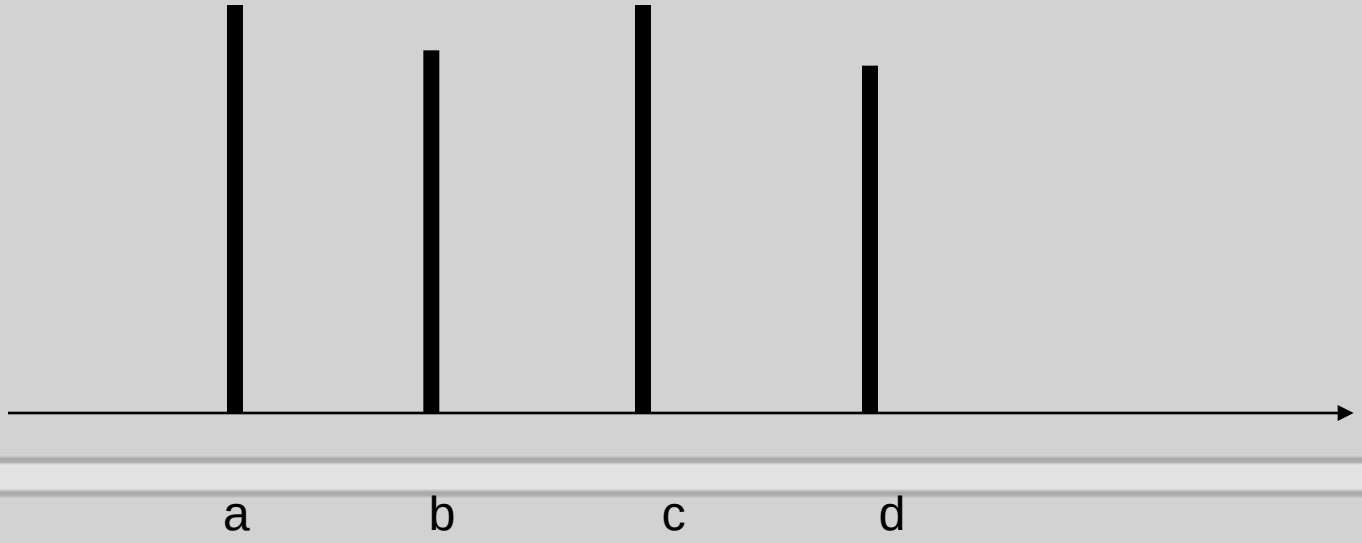
Example 1

- **2 person mixture, 4 alleles seen**
- **Hp = S1 + S2**
- **Hd = 2 unknown individuals**
- **S1 = ab, S2 = cd**



Shortcuts

- **Factorials**
- **The factorial of a positive integer N, denoted by N!, is the product of all positive integers less than or equal to N. For example,**
- **5 ! = 1 x 2 x 3 x 4 x 5 = 120**
- **The following is a table of factorials for numbers 1 through 8.**

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N	N!
1	1
2	2
3	6
4	24
5	120
6	720
7	5,040
8	40,320

Please note how quickly they “blow out”

Permutations

If the multiplicities of the elements of M are m1, m2, ..., ml and their sum is n, then the number of multiset

permutations of M is given by

$$\frac{n!}{m_1!m_2!....m_l!}$$

LRs binary method Incorporating dropout

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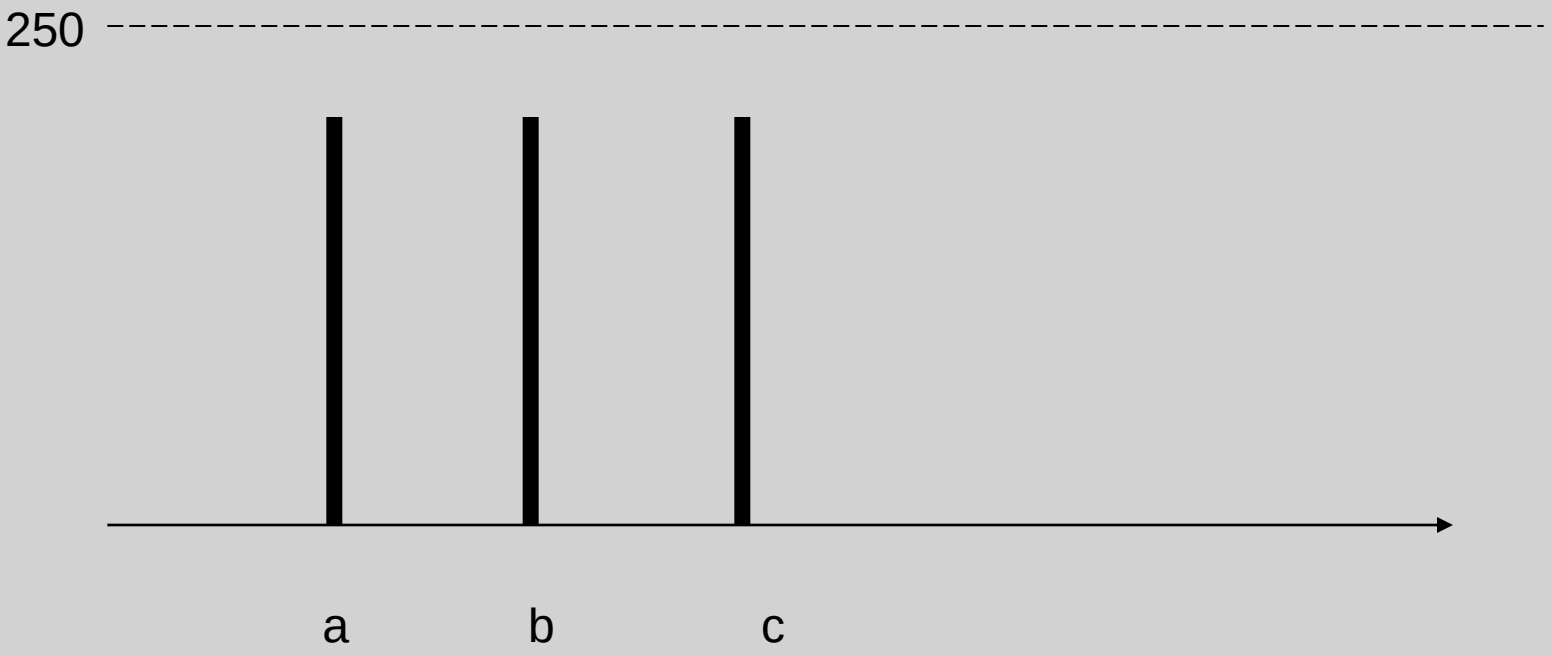
3 allele, 1 drop example



S=ab

Hp: S + U

Hd: U + U

$Hp:\{cF\}$

$Hd:\{abcF\}$

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3 allele, 1 drop example – don't concentrate please

$$LR = \frac{\Pr(CF \mid AB)}{\Pr(ABCF \mid AB)}$$

$$= \frac{2\Pr(AC \mid AB) + 2\Pr(BC \mid AB) + \Pr(CC \mid AB) + 2\Pr(CQ \mid AB)}{\begin{array}{c} 12\Pr(AABC \mid AB) + 12\Pr(ABBC \mid AB) \\ +12\Pr(ABCC \mid AB) + 24\Pr(ABCQ \mid AB) \end{array}}$$

$$= \frac{2\Pr(AC \mid AB) + 2\Pr(BC \mid AB) + \Pr(CC \mid AB) + 2\Pr(CQ \mid AB)}{12\left[\begin{array}{l} \Pr(AABC \mid AB) + \Pr(ABBC \mid AB) \\ +\Pr(ABCC \mid AB) + 2\Pr(ABCQ \mid AB) \end{array}\right]}$$

$$= \frac{\Pr(C \mid AB)\left[2\Pr(A \mid ABC) + 2\Pr(B \mid ABC) + \Pr(C \mid ABC) + 2\Pr(Q \mid ABC)\right]}{12\Pr(C \mid AB)\left[\begin{array}{l} \Pr(AAB \mid ABC) + \Pr(ABB \mid ABC) \\ +\Pr(ABC \mid ABC) + 2\Pr(ABQ \mid ABC) \end{array}\right]}$$

$$= \frac{\left[2\Pr(A \mid ABC) + 2\Pr(B \mid ABC) + \Pr(C \mid ABC) + 2\Pr(Q \mid ABC)\right]}{12\left[\begin{array}{l} \Pr(AAB \mid ABC) + \Pr(ABB \mid ABC) \\ +\Pr(ABC \mid ABC) + 2\Pr(ABQ \mid ABC) \end{array}\right]}$$

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3 allele, 1 drop example

$$LR = \frac{2\Pr(A \mid ABC) + 2\Pr(B \mid ABC) + \Pr(C \mid ABC) + 2\Pr(Q \mid ABC)}{12\begin{bmatrix}\Pr(AAB \mid ABC) + \Pr(ABB \mid ABC) \\ +\Pr(ABC \mid ABC) + 2\Pr(ABQ \mid ABC)\end{bmatrix}}$$

$$= \frac{2\Pr(A \mid ABC) + 2\Pr(B \mid ABC) + \Pr(C \mid ABC) + 2\Pr(Q \mid ABC)}{12\Pr(AB \mid ABC)\begin{bmatrix}\Pr(A \mid AABBC) + \Pr(B \mid AABBC) \\ +\Pr(C \mid AABBC) + 2\Pr(Q \mid AABBC)\end{bmatrix}}$$

but $\Pr(Q \mid ABC) = 1 - \Pr(A \mid ABC) - \Pr(B \mid ABC) - \Pr(C \mid ABC)$

$$2\Pr(A \mid ABC) + 2\Pr(B \mid ABC) + \Pr(C \mid ABC) +$$

$$= \frac{2 - 2\Pr(A \mid ABC) - 2\Pr(B \mid ABC) - 2\Pr(C \mid ABC)}{12\Pr(AB \mid ABC)\begin{bmatrix}\Pr(A \mid AABBC) + \Pr(B \mid AABBC) \\ +\Pr(C \mid AABBC) + 2\Pr(Q \mid AABBC)\end{bmatrix}}$$

$$= \frac{2 - \Pr(C \mid ABC)}{12\Pr(AB \mid ABC)\begin{bmatrix}\Pr(A \mid AABBC) + \Pr(B \mid AABBC) \\ +\Pr(C \mid AABBC) + 2\Pr(Q \mid AABBC)\end{bmatrix}}$$

but $\Pr(Q \mid AABBC) = 1 - \Pr(A \mid AABBC) - \Pr(B \mid AABBC) - \Pr(C \mid AABBC)$

$$= \frac{2\Pr(C \mid ABC)}{12\Pr(AB \mid ABC)\begin{bmatrix}\Pr(A \mid AABBC) + \Pr(B \mid AABBC) \\ +\Pr(C \mid AABBC) + 2 \\ -2\Pr(A \mid AABBC) - 2\Pr(B \mid AABBC) \\ -2\Pr(C \mid AABBC)\end{bmatrix}}$$

$$= \frac{2 - \Pr(C \mid ABC)}{12\Pr(AB \mid ABC)\left[2 - \Pr(A \mid AABBC) - \Pr(B \mid AABBC) - \Pr(C \mid AABBC)\right]}$$

Was that fun for you?

Want an easier way?

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A 'cheat's' way

- **We can demonstrate that we can treat unresolvable mixtures with dropout as for unresolvable mixtures without**
  - **Put in the Fs**
  - **Include the multiplication factor**
  - **Drop the Fs value**
- **This gives us a conservative approximation of the 'true' answer (it wastes a bit of evidence)**
- **For example:**
- **Pr(abcF) < 24Pr(abc)**

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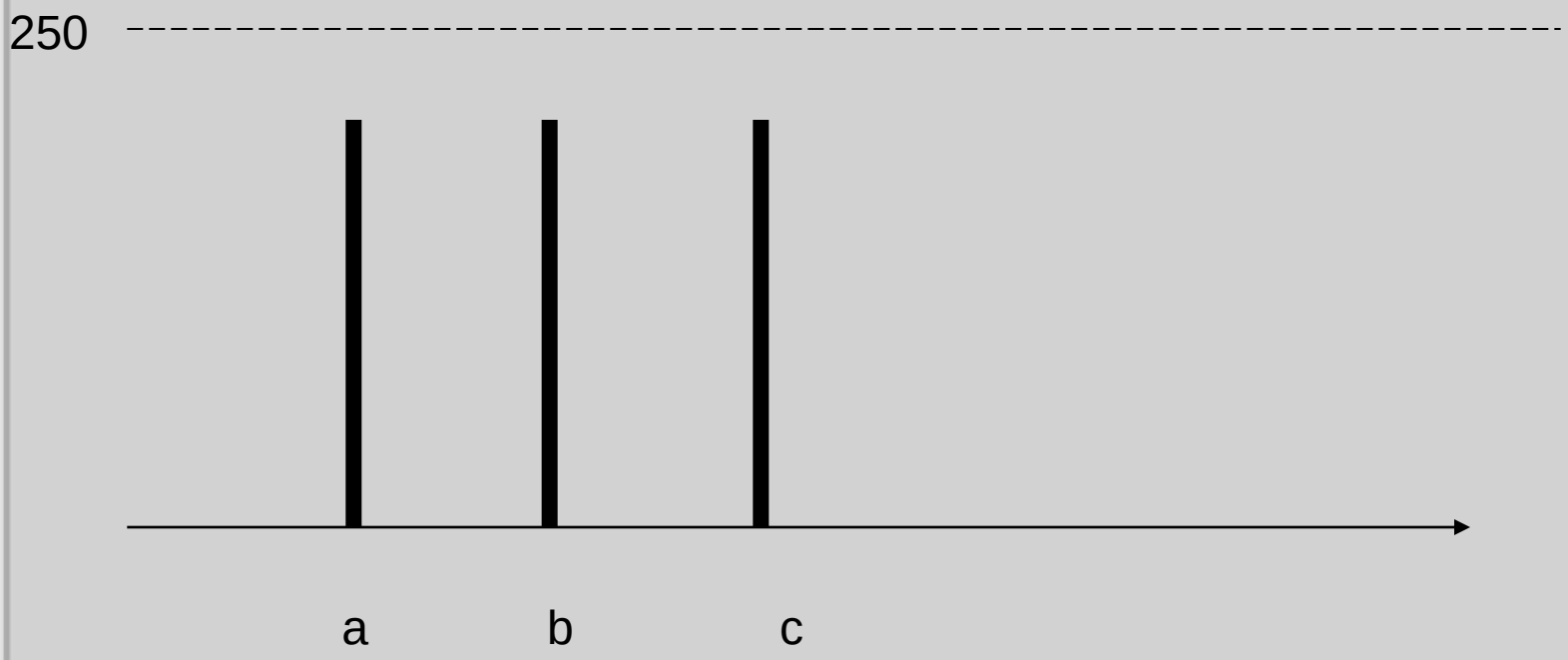
3 allele, 1 drop example



S=ab

Hp: S + U

Hd: U + U

$Hp:\{cF\}$

$Hd:\{abcF\}$

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3 allele, 1 drop example

$$LR = \frac{2\Pr(C\cancel{F})}{24\Pr(ABC\cancel{F})}$$

$$= \frac{\Pr(C)}{12\Pr(ABC)}$$

$$= \frac{\Pr(C)}{12\Pr(C)\Pr(AB)}$$

$$= \frac{1}{12\Pr(AB)}$$

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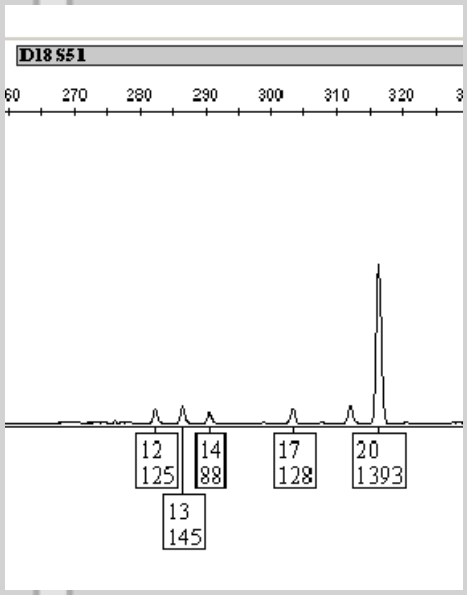


The rest of the profile looks like a three person Mmm

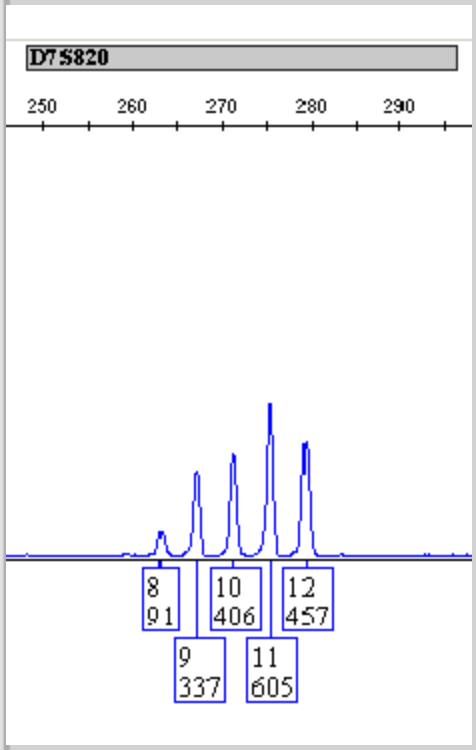
M = 20,20
mm={12,13,14,17}

If POI = 20,20 I would report LR = $1/P_{20,20}$

If POI = 12,13 I would do a full calculation
Hp = POI + 2U
Hd = 3U

Unconstrained profile = {12,13,14,15,17,20,20}

Lets try together



{8,9,10,11,12,F}

K = 8,9 POI = 11,12

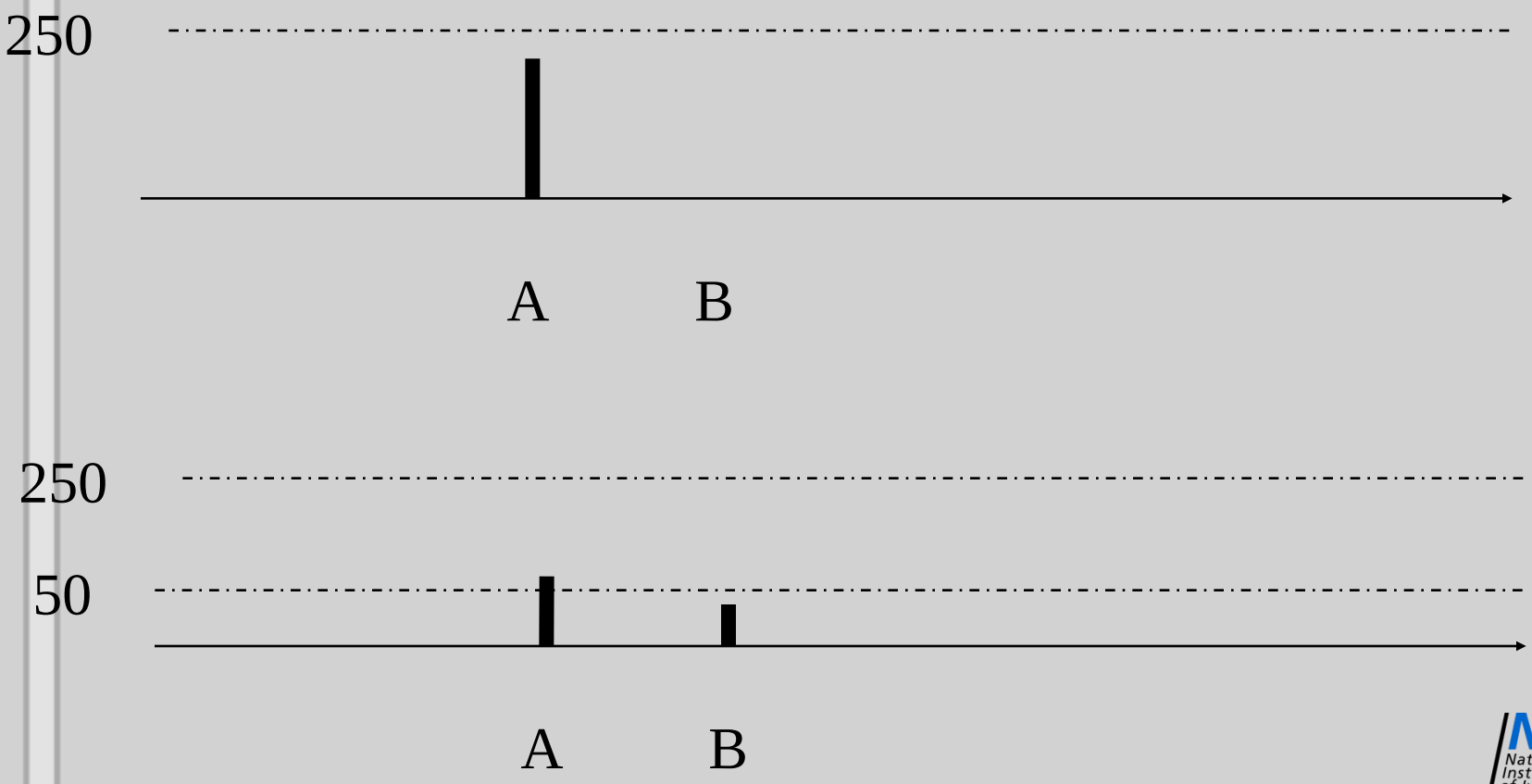
$$LR = \frac{2\Pr(10, F)}{24\Pr(10,11,12, F)}$$

$$= \frac{2\Pr(10, \cancel{F})}{24\Pr(10,11,12, \cancel{F})}$$

$$= \frac{\Pr(10)}{12\Pr(10,11,12)}$$

$$= \frac{1}{12\Pr(11,12)}$$

Please compare, POI AB



Recognising the limits - Principle

- **Non-concordance – careful term**
- **Fit to Hp**
- **The binary method, which we are doing, is SAFE if the fit to Hp is adequate**
- **I can't define "adequate" yet, maybe we are stuck with experience until we improve data**
- **In NZ I was making CHECK SAFE**
- **This is a big deal for Peter Gill and is motivating change**

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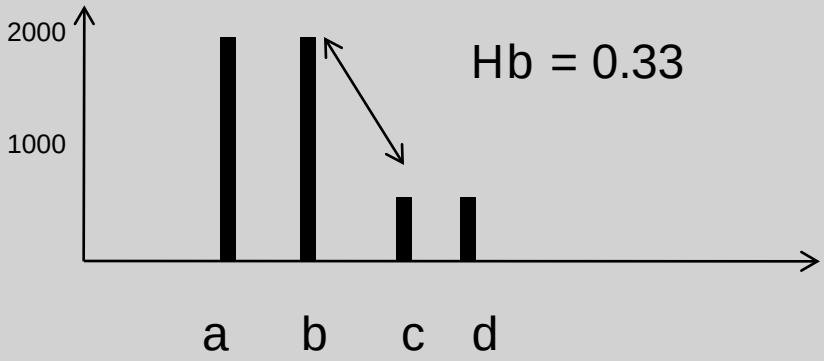
Quite a few typos coming

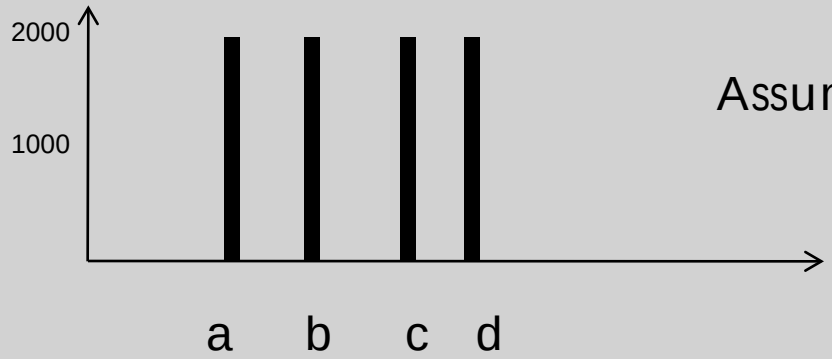
Black boxes breed bad habits



I'm using the product rule for simplicity but I don't use it in practice

$$PI = \left(p_a + p_b + p_c + p_d \right)^2$$

Assume V = ab POI = cd → *PI* conservative but wasteful
Assume V = ab POI = bc → would you exclude, I would.



Assume POI = cd

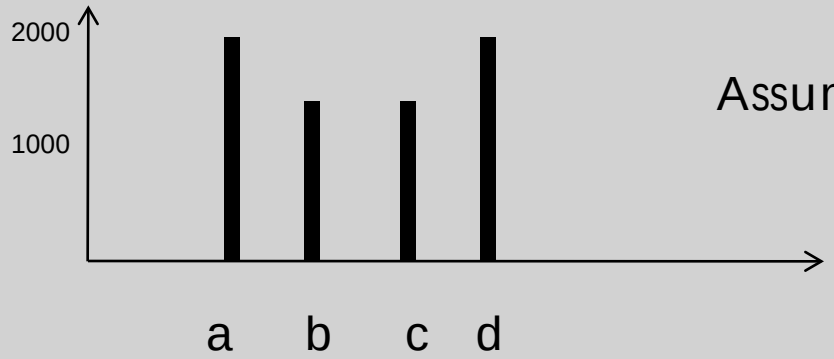
$$PI = \left(p_a + p_b + p_c + p_d \right)^2$$

$$= p_a^2 + p_b^2 + p_c^2 + p_d^2$$

$$+2p_a p_b + 2p_a p_c + 2p_a p_d + 2p_b p_c + 2p_b p_d + 2p_c p_d$$

$$RMP = 2p_a p_b + 2p_a p_c + 2p_a p_d + 2p_b p_c + 2p_b p_d + 2p_c p_d$$

$$LR = \frac{1}{12 p_c p_d} \approx \frac{1}{RMP}$$



Assume POI = cd

$$PI = \left(p_a + p_b + p_c + p_d \right)^2$$

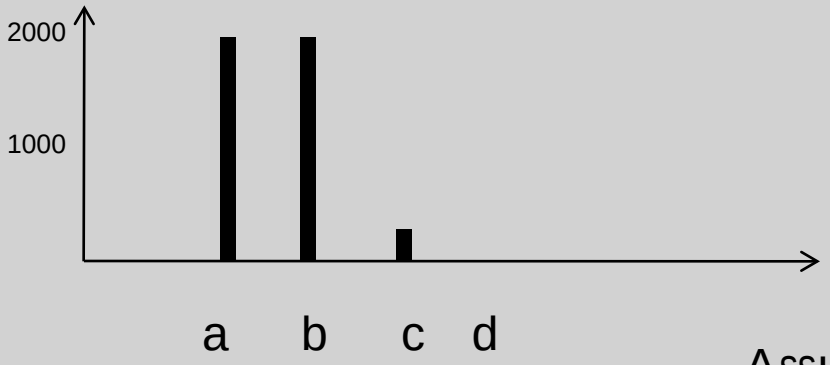
$$= p_a^2 + p_b^2 + p_c^2 + p_d^2$$

$$+2p_a p_b + 2p_a p_c + 2p_a p_d + 2p_b p_c + 2p_b p_d + 2p_c p_d$$

Everyone is at risk, only continuous approaches get this one right e.g. TRUEALLELE

$$RMP = 2p_a p_b + 2p_a p_c + 2p_a p_d + 2p_b p_c + 2p_b p_d + 2p_c p_d$$

$$LR = \frac{1}{12 p_c p_d} \approx \frac{1}{RMP}$$



Everyone is at risk, only Pr(D) or continuous approaches get this one right

Assume V = ab POI = cd
→ *PI* meaningless and dangerous

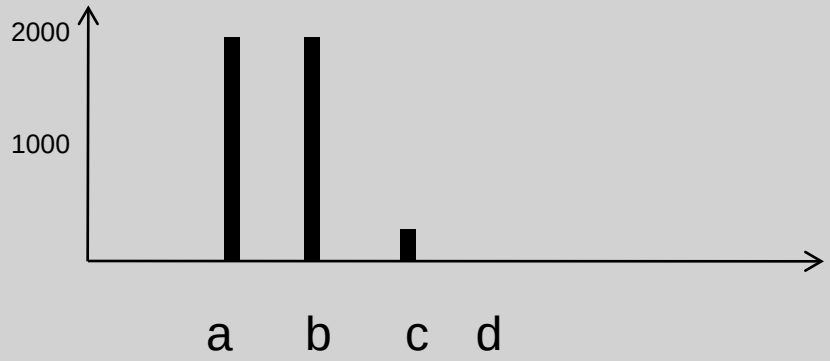
$$PI = \left(p_a + p_b + p_c \right)^2$$

$$RMP = 2p_c - p_c^2$$

$$or \quad = 2p_c$$

$$LR = \frac{1}{2p_c}$$

$$or = \frac{1}{2p_c - p_c^2}$$



$$PI = \left(p_a + p_b + p_c \right)^2$$

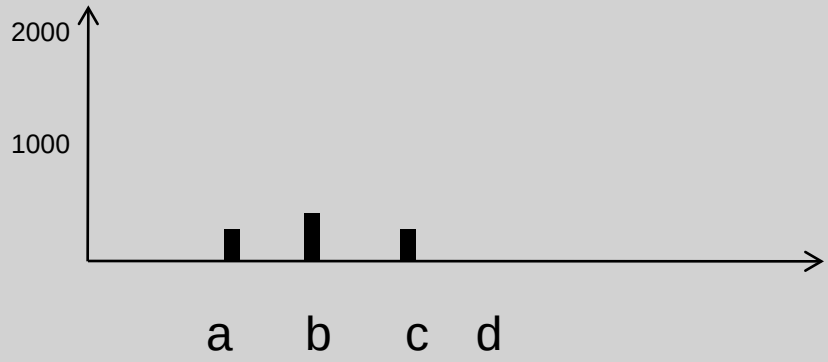
Assume V = ab POI = ac → *PI* meaningless but plausibly safe

$$RMP = 2p_c - p_c^2$$

$$or \quad = 2p_c$$

$$LR = \frac{1}{2p_c}$$

$$or = \frac{1}{2p_c - p_c^2}$$



$$PI = ?$$

$$RMP = 2p_a p_b + 2p_a p_c + 2p_b p_c + 2p_a p_Q + 2p_b p_Q + 2p_c p_Q + p_a^2 + p_b^2 + p_c^2$$

$$= 2p_a p_b + 2p_a p_c + 2p_b p_c + 2(p_a + p_b + p_c)(1 - p_a - p_b - p_c) + p_a^2 + p_b^2 + p_c^2$$

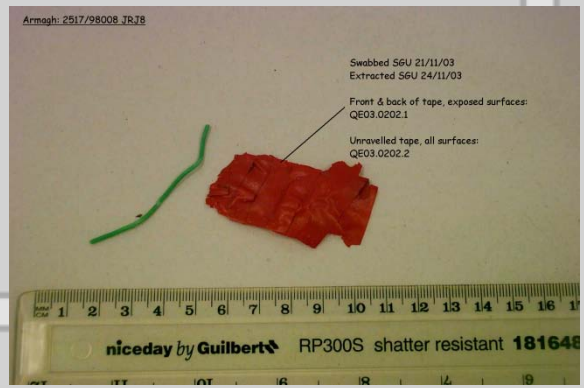
$$= 2p_a + 2p_b + 2p_c - 2p_a p_b - 2p_a p_c - 2p_b p_c - p_a^2 - p_b^2 - p_c^2$$

Assume POI = ac

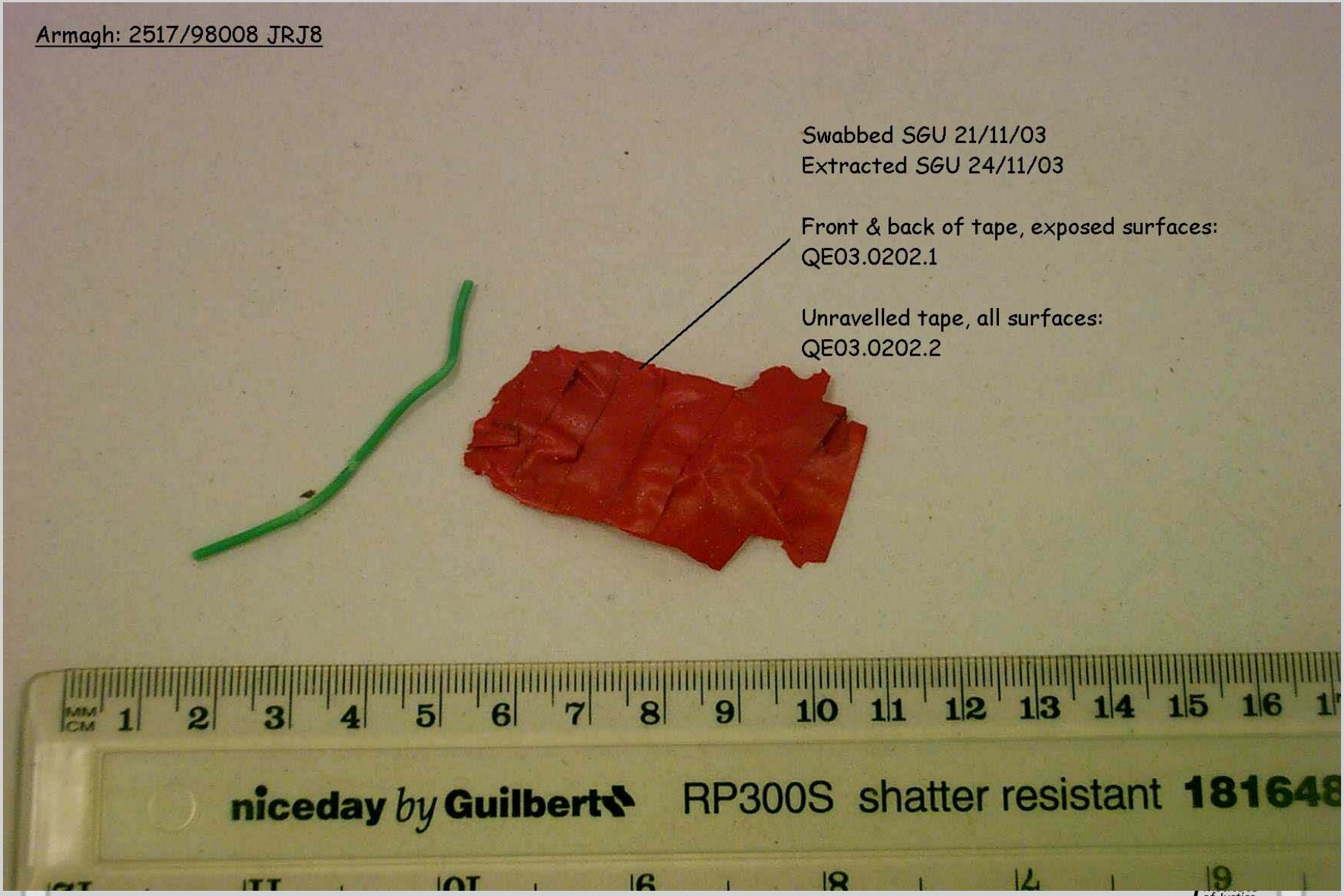
$$LR = \frac{2\Pr(bF)}{24\Pr(abcF)} = \frac{2\Pr(b\cancel{F})}{24\Pr(abc\cancel{F})} = \frac{\Pr(b)}{12\Pr(abc)} = \frac{\Pr(b)}{12\Pr(ac)\Pr(b)} = \frac{1}{12\Pr(ac)}$$

Essentials of R v Hoey

- DNA profiles matching each other were recovered from devices recovered from the main street in Lisburn (30 April 1998) and Altmore Forest (12 April 2001).
- Done blind in 1999 and 2001 from underside of tape.
- The ‘unknown’ profile obtained was matched to Mr Hoey in September 2003 – his sample could not be taken prior as he was in the south – until he crossed the border
- A further examination of a device planted at Newry Road Barracks (16 May 1998) was examined in November 2003 and also shown to match Mr Hoey.
- Omagh bombing is not linked by DNA but by similarities in the devices
- 2007 Mr Hoey Aquitted



Armagh: 2517/98008 JRJ8



Essentials or R v Hoey

- **Doubts about sample storage and handling**
- **Witness demeanour**
- **No ruling – but questioning comments regarding LCN**
  - **Only two papers**
  - **Only UK, NZ and Netherlands**
  - **US use for intelligence and triplicate**
  - **International Society of Forensic Geneticists - Azores "more work"**

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“suspect asserted he was an electrician and that his DNA (if it was his) had got onto the devices because his tape had been used in the construction by somebody else.”

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Oxford: Reliable:

1. That which may be relied on… trustworthy, safe, sure

2. Statistics. Yielding concordant results when repeated

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Is the statistic reliable?

- **Lawyers may want a yes or no answer?**
- **Were we seeking an unreal vision of certainty?**
- **“Tell me doctor, in what order were these injuries sustained?”**
- **And I want “yes” or “no” for an answer not a long lecture!**

Forty years of murder. Simpson, K. 1978. London: Grafton

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Is the statistic reliable?

- **…well we have applied the most modern and reasonable methods, blah blah**
- **But is it reliable?**
- **Within the limits of our understanding it is a fair and reasonable assignment of probability**
- **Or even some words like 99%**
- **So you are not certain that it is reliable?**
- **It is a simple question, yes or no. Is it reliable?**

R v Sean Hoey

Mr Pownall: That is what you say and the issue that I am investigating through you is whether or not the result the profile you claim is reliable or not, you understand that?

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Sydney
Me for the defence!
mitochondrial DNA
Small difference between defendant's DNA and the scene
Match/non-match?
Near match?

John Buckleton ESR

NIJ National Institute of Justice

Q. Was there a difference at the C-stretch?

John Buckleton ESR

A. Yes, I've written the entire matter out in my report and Ms Pineda was aware of this as well--

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Q. Can you answer the question?

A. Yes

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Q. Is there a difference at the C-stretch?

A. Yes, there is. Can we make that the last time you yell at me?

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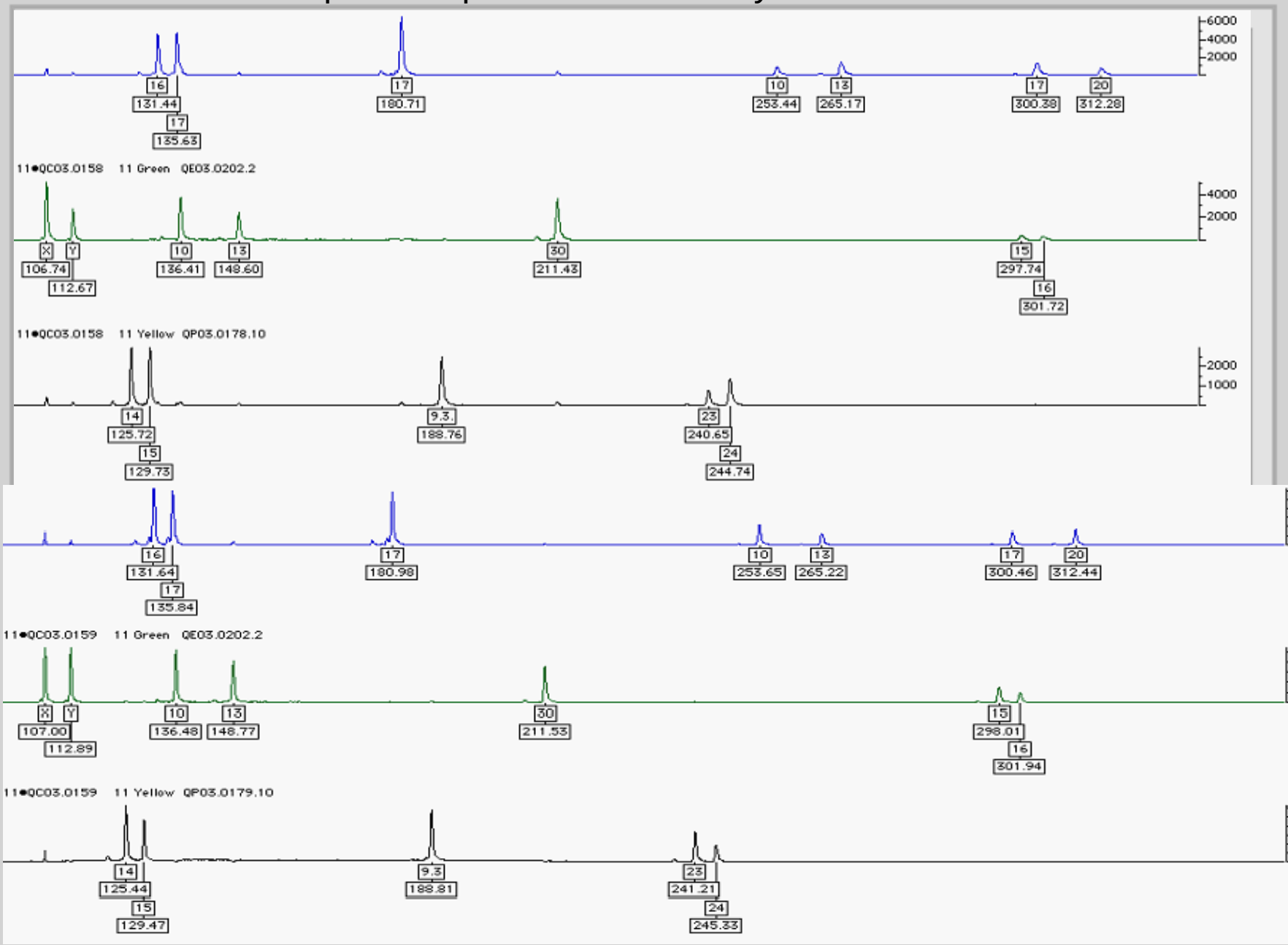
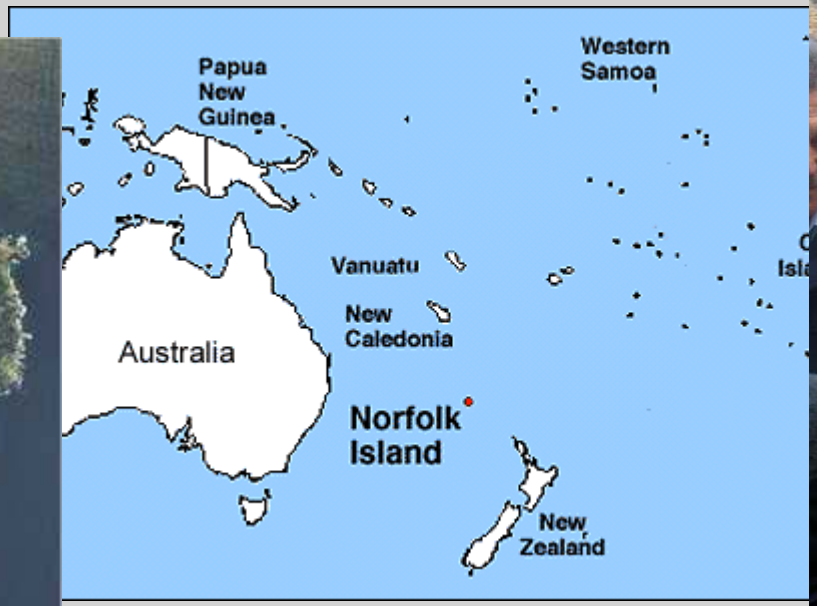
Q. Well if you'd answered the question then I wouldn't need to repeat it.

A. OK

A pair of replicates in R v Hoey





Glenn McNeill was found guilty of murdering Janelle Patton on Norfolk Island

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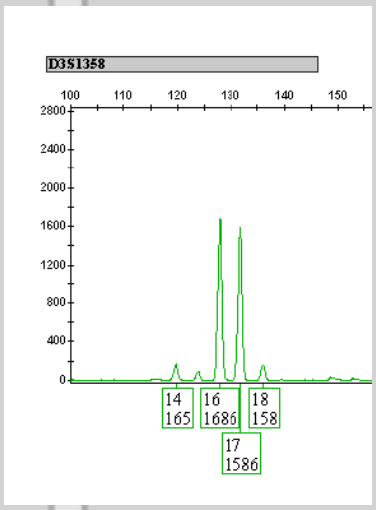
copyright 1994

Contact Information

John Buckleton

New Zealand



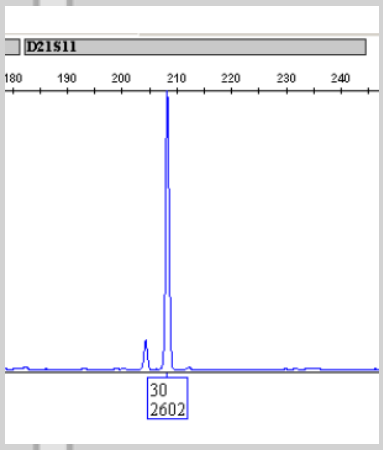
The rest of the profile looks like a two person Mm

If POI = 16,17 I would report LR = $1/2P_{16,17}$

If POI = 14,18 I would report LR = $1/2P_{14,18}$

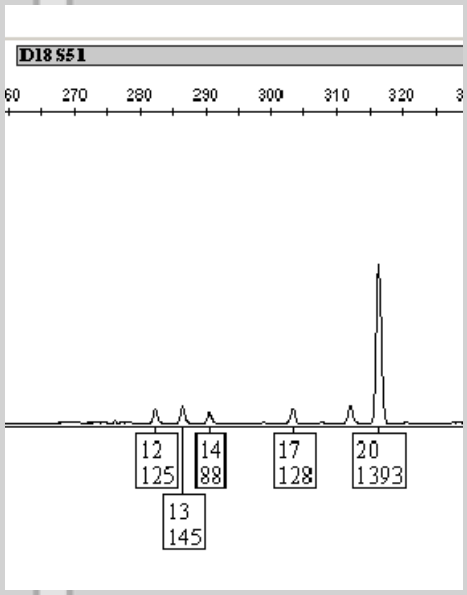
If POI = 16,17 I would report LR = $1/2P_{16,17}$

Not confident the minor would appear



If POI = 30,30 I would report LR = $1/P_{30,30}$

If POI = x,y I would report LR = 1 but I'd be worried



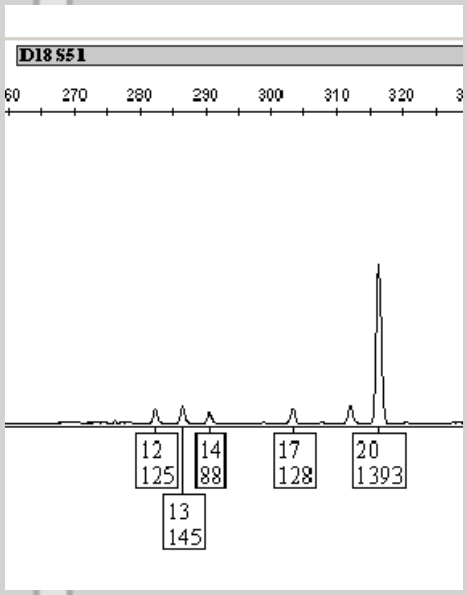
The rest of the profile looks like a three person Mmm

M = 20,20
mm={12,13,14,17}

If POI = 20,20 I would report LR = $1/P_{20,20}$

If POI = 12,13 I would do a full calculation
Hp = POI + 2U
Hd = 3U

Unconstrained profile = {12,13,14,15,17,20,20}



Hp = POI + 2U
Hd = 3U

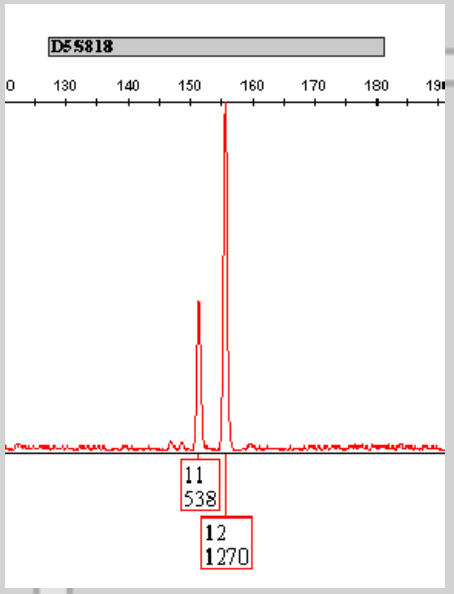
Unconstrained profile = {12,13,14,15,17,20,20}

We use different population genetic models. I'm going to product rule for simplicity but I think I could convert to your approach with some thought.

$$LR = \frac{\Pr(14,17,20,20)}{\Pr(12,13,14,17,20,20)}$$

$$= \frac{\frac{4!}{1!1!2!}P_{14,17,20,20}}{\frac{6!}{1!1!1!1!2!}P_{12,13,14,17,20,20}}$$

$$= \frac{1}{30\,f_{12}\,f_{13}}$$



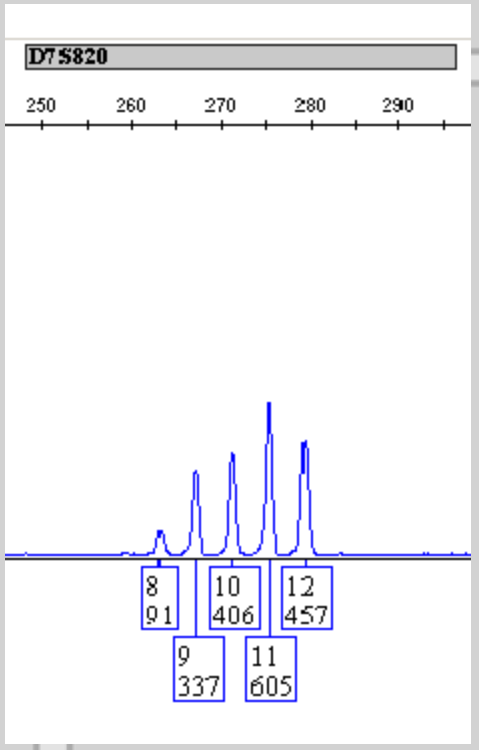
The rest of the profile looks like a three person Mmm. I can't be confident the minors would appear.

Unconstrained profile = {11,12,12,F,F,F}
If POI 11,12

$$LR = \frac{\Pr(12, F, F, F)}{\Pr(11,12,12, F, F, F)}$$

$$= \frac{\frac{4!}{1!3!} P_{12}}{\frac{6!}{1!2!3!} P_{11,12,12}}$$

$$= \frac{1}{15 f_{11} f_{12}}$$



The rest of the profile looks like a three person MMm. What is this locus?

Unconstrained profile = {8,9,10,11,12,F}
If POI 11,12

$$LR = \frac{\Pr(8,9,10,F)}{\Pr(8,9,10,11,12,F)}$$

$$= \frac{\frac{4!}{1!1!1!1!}P_{8,9,10}}{\frac{6!}{1!1!1!1!1!1!}P_{8,9,10,11,12}}$$

$$= \frac{1}{30\,f_{11}\,f_{12}}$$

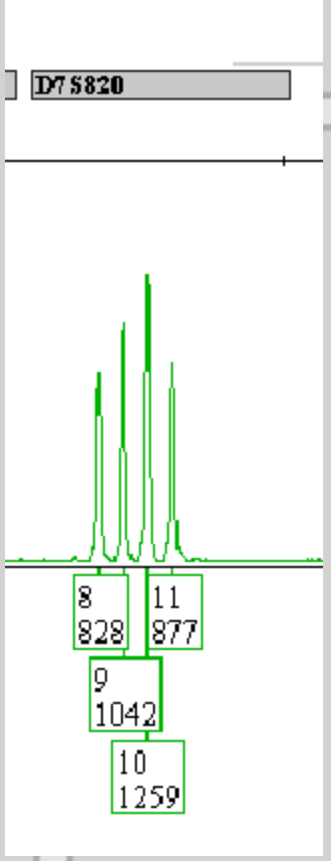
The rest of the profile looks like a three person MMm. What is this locus?

Unconstrained profile = {8,9,10,11,12,F}
If POI 11,12

$$LR = \frac{\Pr(8,9,10,F)}{\Pr(8,9,10,11,12,F)}$$

$$= \frac{\frac{4!}{1!1!1!1!} P_{8,9,10}}{\frac{6!}{1!1!1!1!1!1!} P_{8,9,10,11,12}}$$

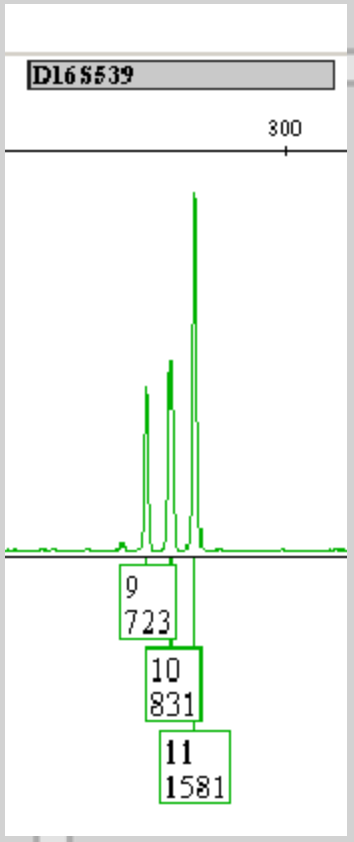
$$= \frac{1}{30 f_{11} f_{12}}$$



The rest of the profile looks like a two person MM.

Unconstrained profile = {8,9,10,11}
If POI 10,11

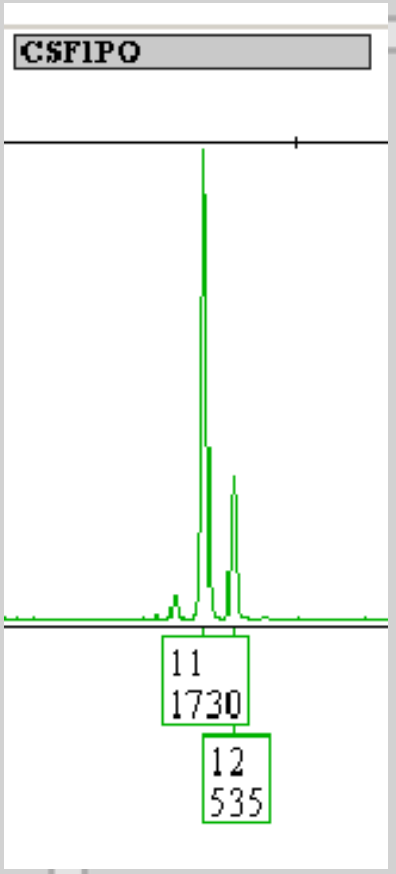
$$LR = \frac{\Pr(8,9)}{\Pr(8,9,10,11)} = \frac{\frac{2!}{1!1!}P_{8,9}}{\frac{4!}{1!1!1!1!}P_{8,9,10,11}} = \frac{1}{12\,f_{10}\,f_{11}}$$



The rest of the profile looks like a two person MM.

Unconstrained profile = {9,10,11,11}
If POI 10,11

$$LR = \frac{\Pr(9,11)}{\Pr(9,10,11,11)} = \frac{\frac{2!}{1!1!}P_{9,11}}{\frac{4!}{1!1!2!}P_{9,10,11,11}} = \frac{1}{6\,f_{10}\,f_{11}}$$



The rest of the profile looks like a two person MM.

Unconstrained profile = {11,11,11,12} or ~~{11,11,12,12)~~

If POI 11,11

$$LR = \frac{\Pr(11,12)}{\Pr(11,11,11,12)} = \frac{\frac{2!}{1!1!}P_{11,12}}{\frac{4!}{3!1!}P_{11,11,11,12}} = \frac{1}{2f_{11}^2}$$