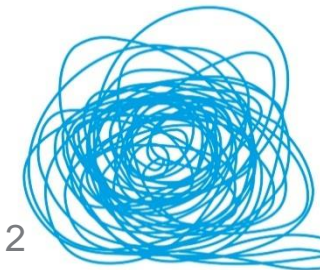




STRmix™
RESOLVE
MORE DNA
MIXTURES.

<http://STRmix.esr.cri.nz>

The number of contributors



- Q: *What's your opinion about how likely it is that there are more than four contributors to this mixed DNA sample*
- A: *I have absolutely no idea and nor does [the prosecution witness].*

IN

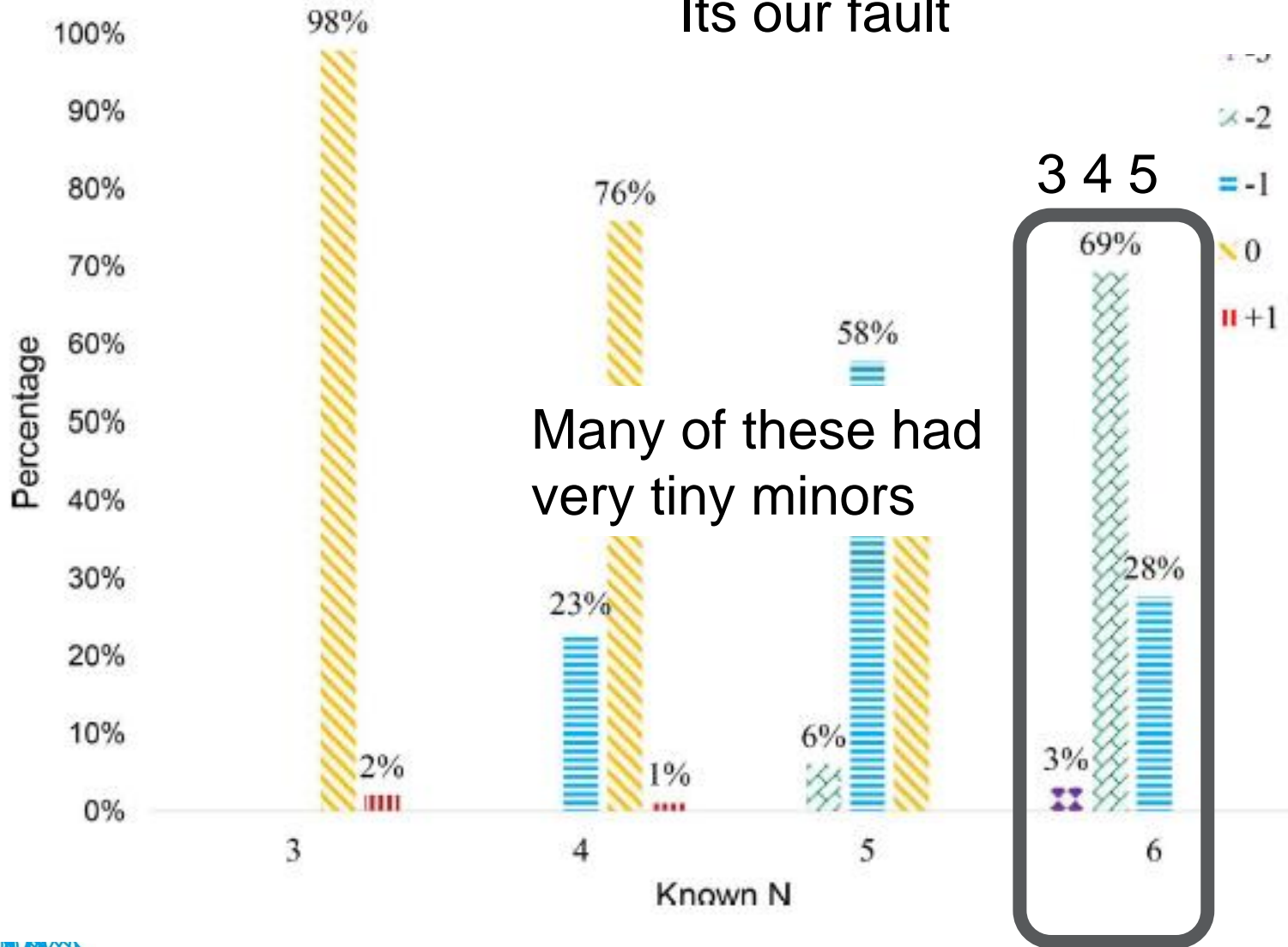


=

OUT

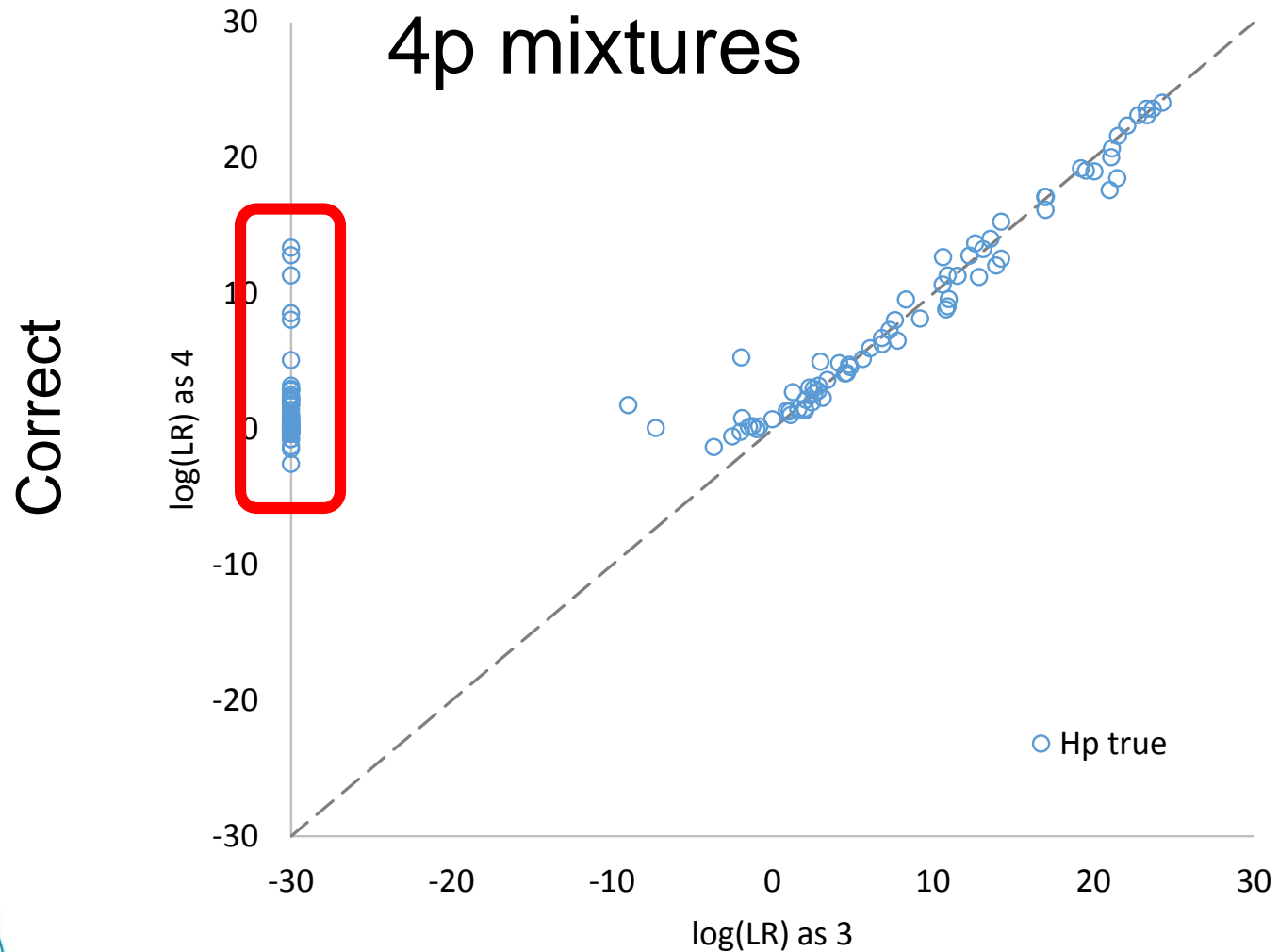


A bit of over interpretation
Its our fault



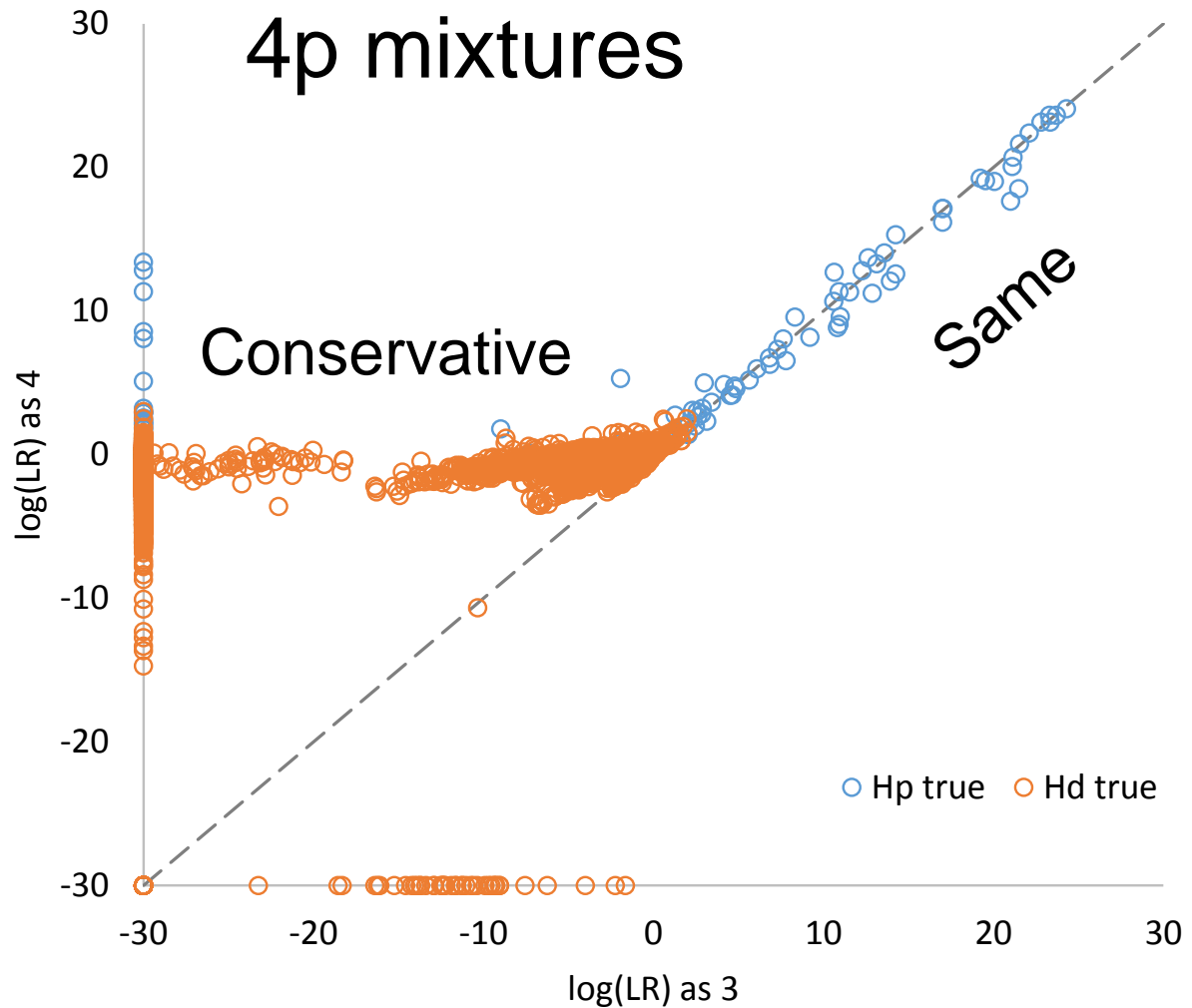
Many of these had
very tiny minors

Underestimating – H_p true



One under

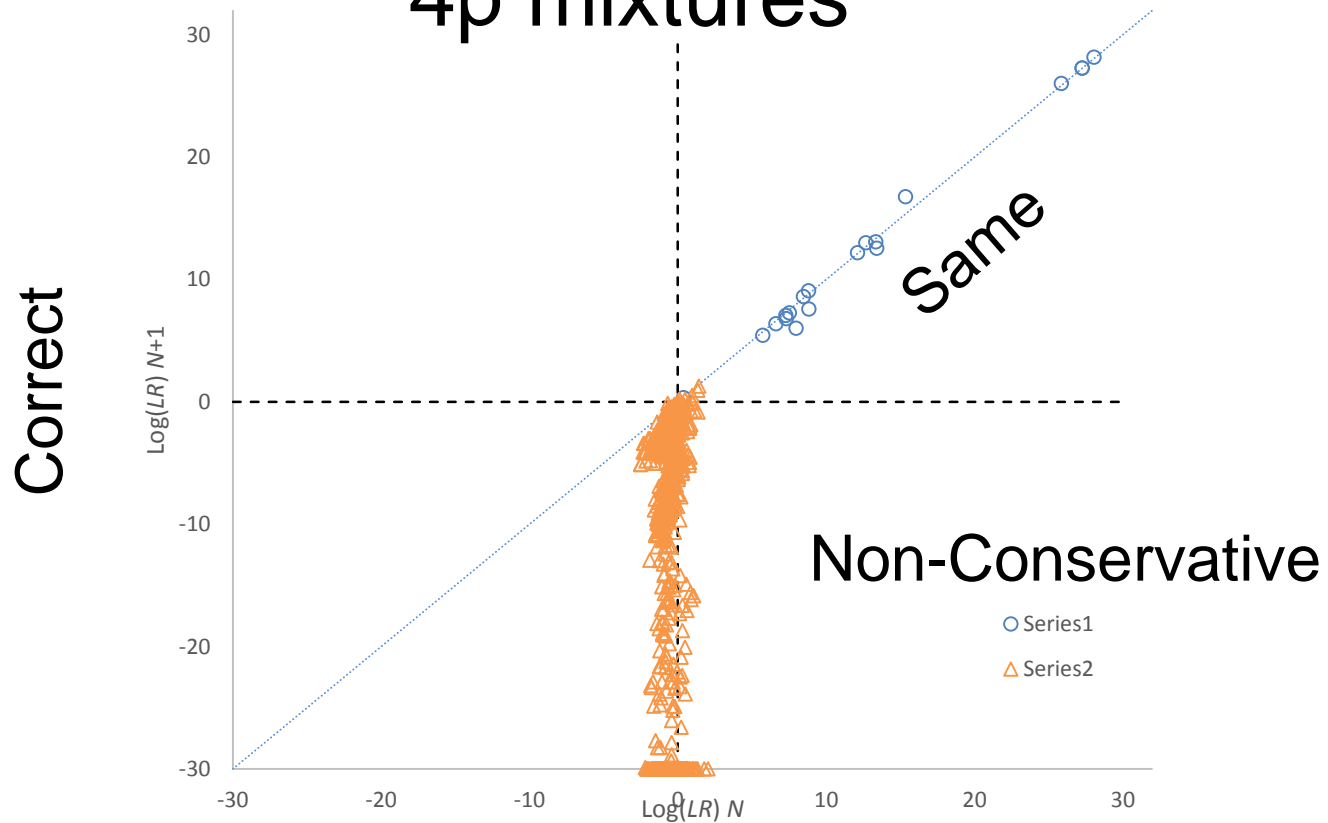
Underestimating – H_a true



Overestimating – H_p true

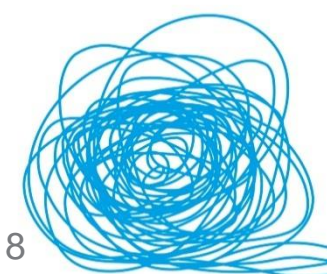
4p N vs 4p $N+1$

4p mixtures

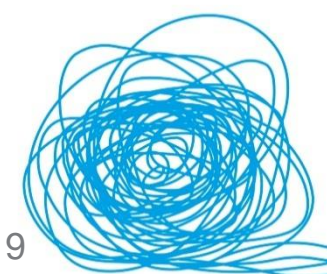


One over

	True donors	False donors
One under	Kicks out the smallest, you didn't think it was there	Some inc → excl

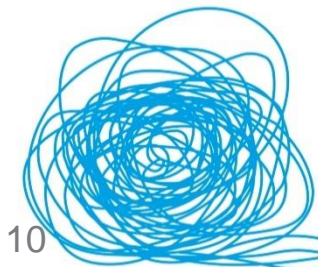


	True donors	False donors
One under	Kicks out the smallest, you didn't think it was there	Some inc → excl
One over	Big ones stay the same smallest → down 2-3 orders	Some excl → inc



	True donors	False donors
One under	Kicks out the smallest, you didn't think it was there	Some inc → excl
One over	Big ones stay the same smallest → down 2-3 orders	Some excl → inc
One over and Mx prior	Stay the same	Some excl → inc

As long as your LR is big then you are correct or conservative





Contents lists available at ScienceDirect

Forensic Science International: Genetics

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



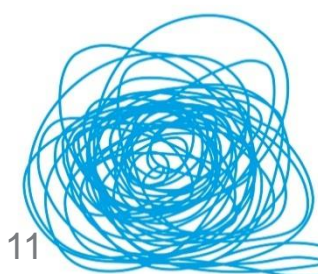
Research paper

Contributors are a nuisance (parameter) for DNA mixture evidence evaluation

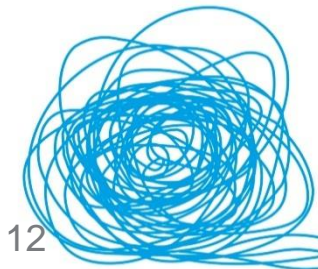
K. Slooten^{a,*}, A. Caliebe^b

^a VU University Amsterdam, Netherlands Forensic Institute (NFI), The Netherlands

^b Institut für Medizinische Informatik und Statistik, Christian-Albrechts-Universität zu Kiel, Germany



- “*Thus...the LR will be determined as a weighted average of $LR(n)$ each with the **same** number n in the numerator and in the denominator.*”



Consider the weights

$$w_n = \Pr(N = n | G_P, G_C, H_a) \frac{\Pr(N = n | H_p)}{\Pr(N = n | H_a)}$$

where

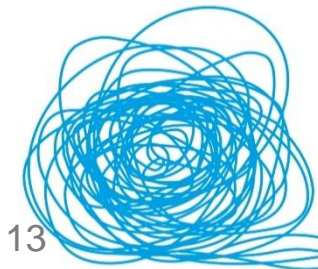
H_p : The POI is a donor

H_a : The POI is not a donor

N is the number of contributors

G_C is the profile of the crime stain and

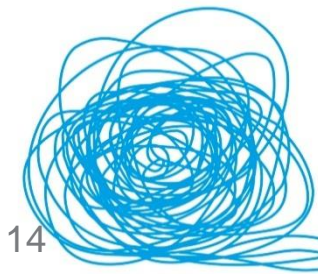
G_P is the profile of the person of interest.



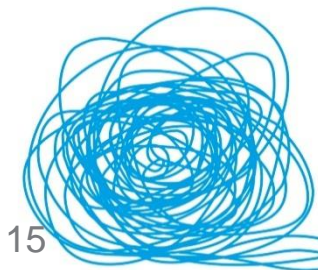
Consider the weights

$$w_n = \Pr(N = n \mid G_P, G_C, H_a)$$

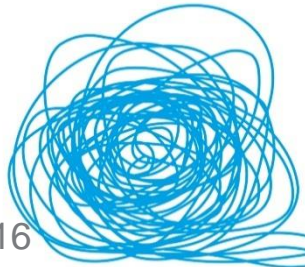
- You need to assign N
- You know the POI's genotype
- You know the crime sample
- You assume POI is not a donor



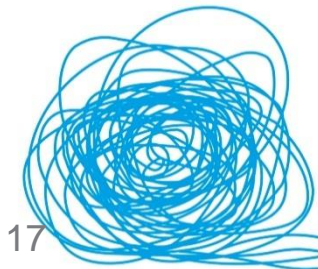
- This suggests no justification
- To look at G_p and G_c and add 1 to “fit” P
- This suggests little justification for different N in numerator and denominator



Verbal scales



Adventitious matches can
happen...
and always could





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Forensic Science International: Genetics

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



Research paper

Internal validation of STRmix™ – A multi laboratory response to PCAST

Jo-Anne Bright^{a,*}, Rebecca Richards^a, Maarten Kruijver^a, Hannah Kelly^a, Catherine McGovern^a, Alan Magee^b, Andrew McWhorter^c, Anne Ciecko^d, Brian Peck^e, Chase Baumgartner^f, Christina Buettner^g, Scott McWilliams^g, Claire McKenna^h, Colin Gallacherⁱ, Ben Mallinderⁱ, Darren Wright^j, Deven Johnson^k, Dorothy Catella^l, Eugene Lien^m, Craig O'Connor^m, George Duncanⁿ, Jason Bundy^o, Jillian Echard^p, John Lowe^q, Joshua Stewart^r, Kathleen Corrado^s, Sheila Gentile^s, Marla Kaplan^t, Michelle Hassler^u, Naomi McDonald^v, Paul Hulme^w, Rachel H. Oefelein^x, Shawn Montpetit^y, Melissa Strong^y, Sarah Noël^z, Simon Malsom^A, Steven Myers^B, Susan Welti^C, Tamyra Moretti^D, Teresa McMahon^E, Thomas Grill^F, Tim Kalafut^G, MaryMargaret Greer-Ritzheimer^H, Vickie Beamer^I, Duncan A. Taylor^{J,K}, John S. Buckleton^{a,L}



False inclusions (Adventitious)

- 2%
- A
- 2%
- tc

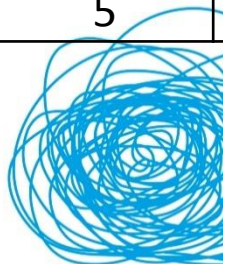


Factors

1% and up

Number
1
2
3
4
5

Overlapping elements
1%
0%
3%
3%
3%





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

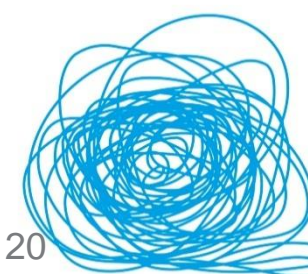


Searching mixed DNA profiles directly against profile databases

Jo-Anne Bright^{a,b,*}, Duncan Taylor^c, James Curran^b, John Buckleton^a

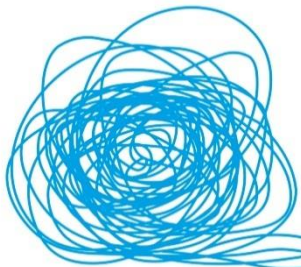


Highest adventitious match 730,000

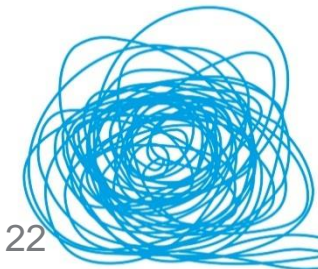


False donor testing

- This tests known false donors against the profile
- Either use a database (say staff) or
- Simulate
- Run against the profile with your system,
- Record the results and present (?)
- Problem To test $LR = x$ you need at least x

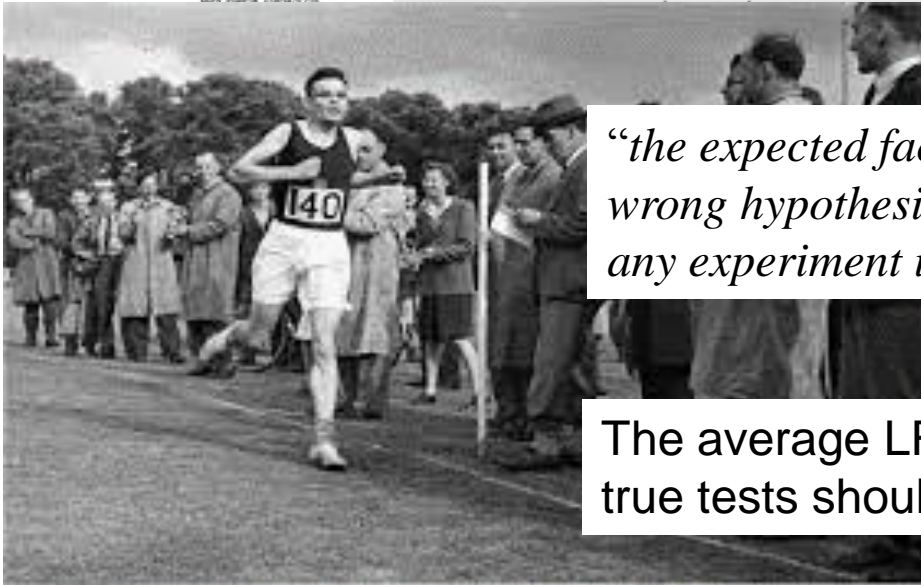


- Turing informs us that an LR of x happens less than 1 in x



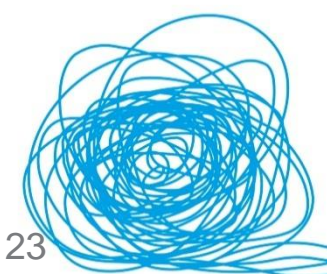
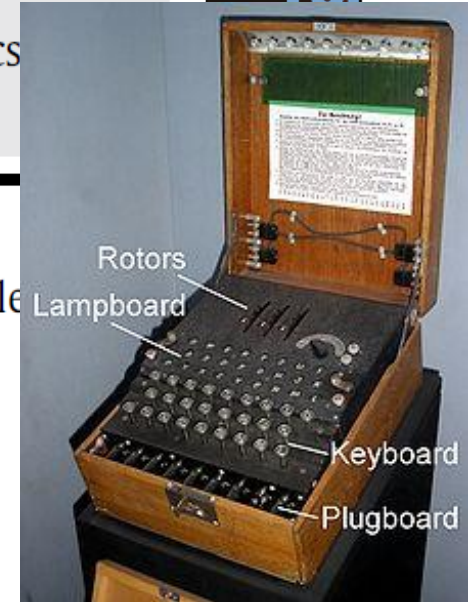


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“the expected factor for a wrong hypothesis in virtue of any experiment is 1.”

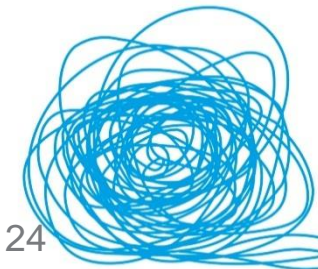
The average LR for the H_a true tests should be 1



Internal validation compilation

2,825 mixtures 28,250,000 false donors

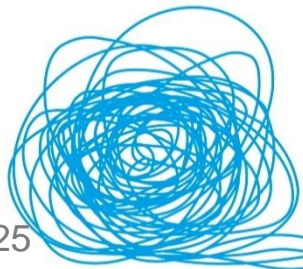
LR for H_p Support and $1/\text{LR}$ for H_d Support	Verbal Qualifier	Expected less than
[1-2)	Uninformative	1 in 2
[2-99)	Limited Support	1 in 99
[99-9999)	Moderate Support	1 in 9,999
[9999-999,999)	Strong Support	1 in 999,999
$\geq 999,999$	Very Strong Support	



Internal validation compilation

2,825 mixtures 28,250,000 false donors

LR for H _p Support and 1/LR for H _d Support	Verbal Qualifier	Expected less than	Fraction of false donor LRs in this range (N = 28,250,000)
[1-2)	Uninformative	1 in 2	1 in 312
[2-99)	Limited Support	1 in 99	1 in 318
[99-9999)	Moderate Support	1 in 9,999	1 in 18,000
[9999-999,999)	Strong Support	1 in 999,999	1 in 1,400,000
≥999,999	Very Strong Support		0





Contents lists available at ScienceDirect

Forensic Science International: Synergy

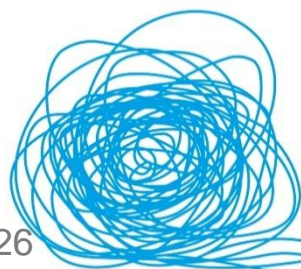
journal homepage: <https://www.journals.elsevier.com/forensic-science-international-synergy/>



Juror comprehension of forensic expert testimony: A literature review and gap analysis

Heidi Eldridge

RTI International, 3040 E. Cornwallis Rd., Research Triangle Park, NC, 27709, USA



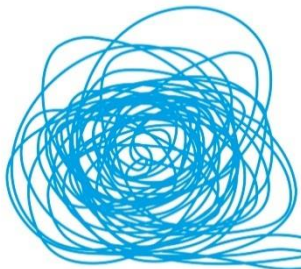
From Turing we can infer that

$$\tilde{p} \leq \frac{1}{LR_{POI}}$$

Equation 2

The chance of an LR greater than or equal to LR_{POI} is less than $1/LR_{POI}$

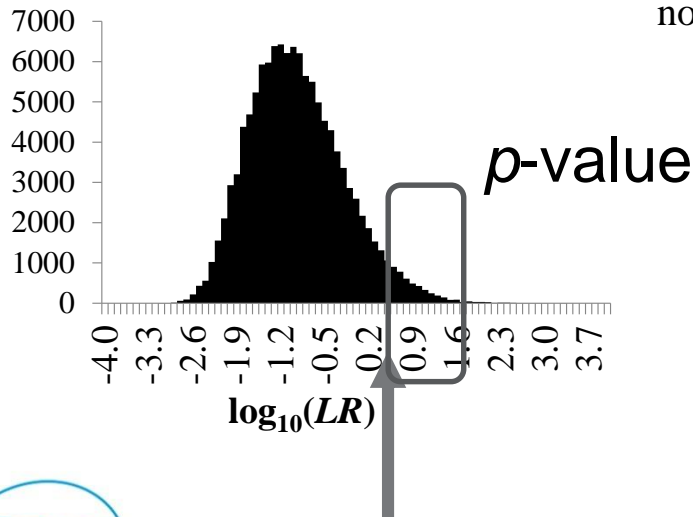
This is true for every LR not just LR_{POI}



The distribution of Ha true

- the shape depends on the profile
- there will be a maximum,
 - Not directly known to us but potentially calculable
 - this is probably slightly bigger than the largest Hp true

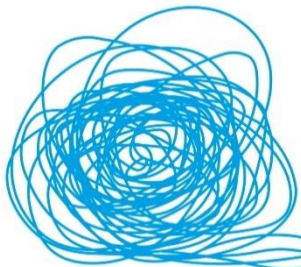
A low level four person mixture (4:3:2:1 pg) 12 loci where none of contributors are assumed.



Equation 2

$$\tilde{p} \leq \frac{1}{LR_{POI}}$$

Average LR		LR for Hp true	logLR
0.93	C ₁	4	0.60
	C ₂	7	0.85
	C ₃	5	0.70
	C ₄	6	0.78





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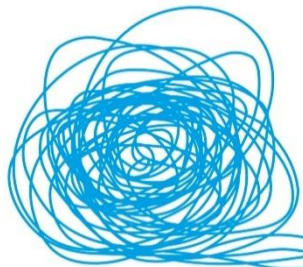


Research paper

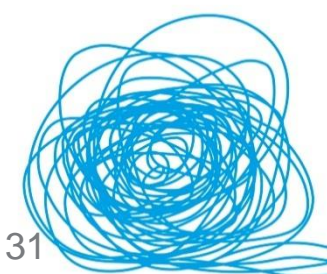
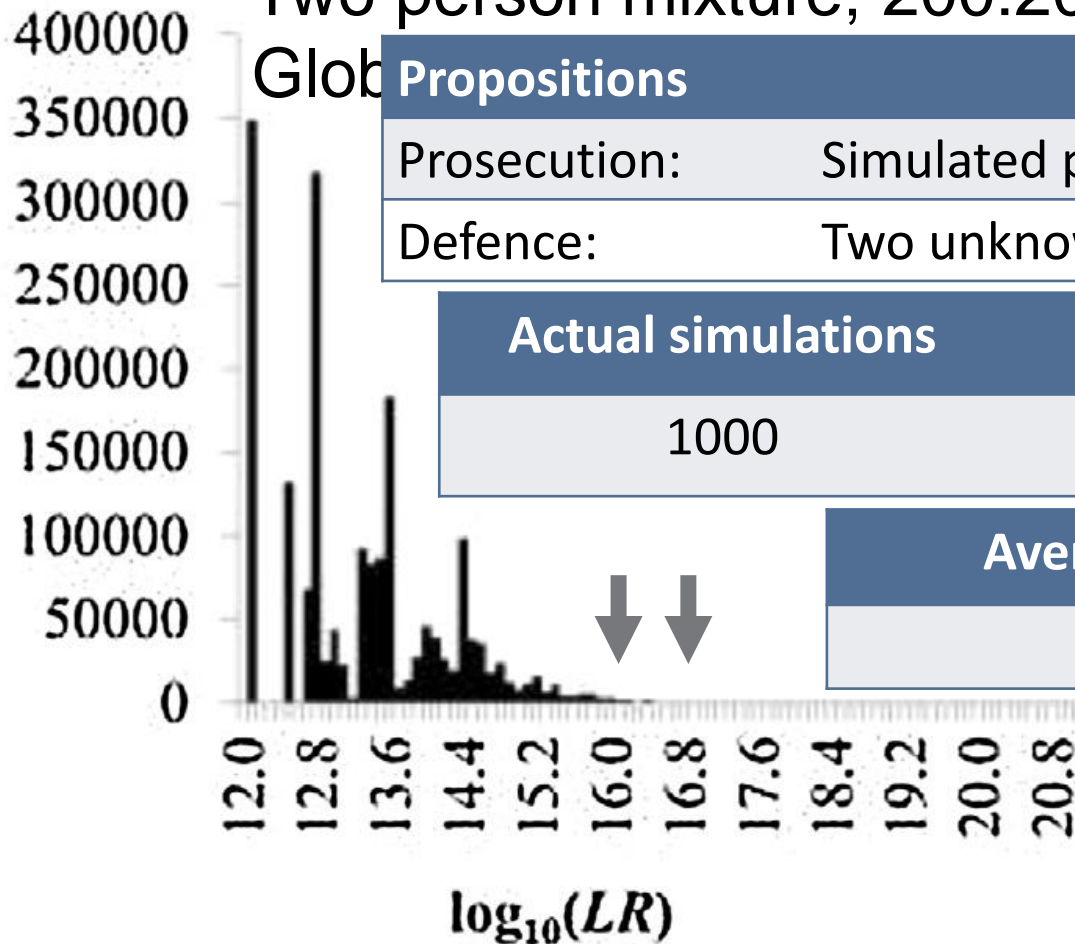
Importance sampling allows H_d true tests of highly discriminating DNA profiles

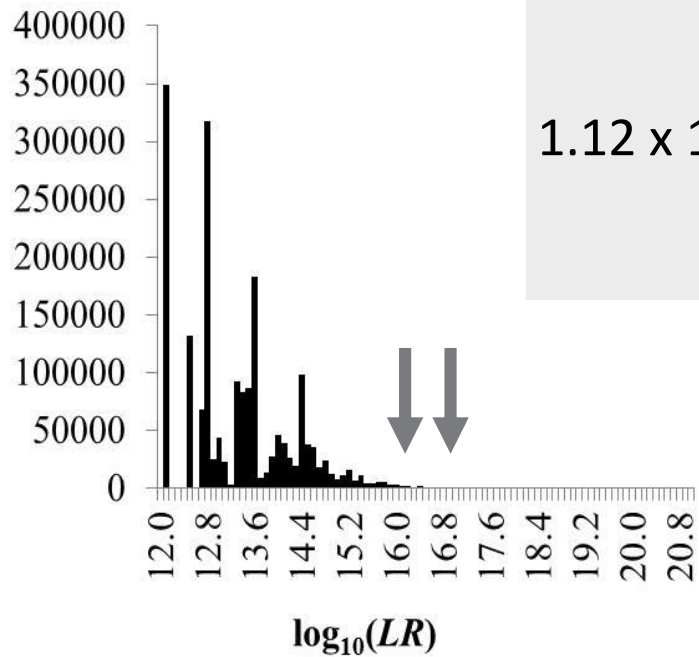


Duncan Taylor^{a,b,*}, James M. Curran^c, John Buckleton^{d,e}

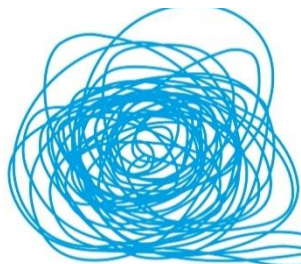


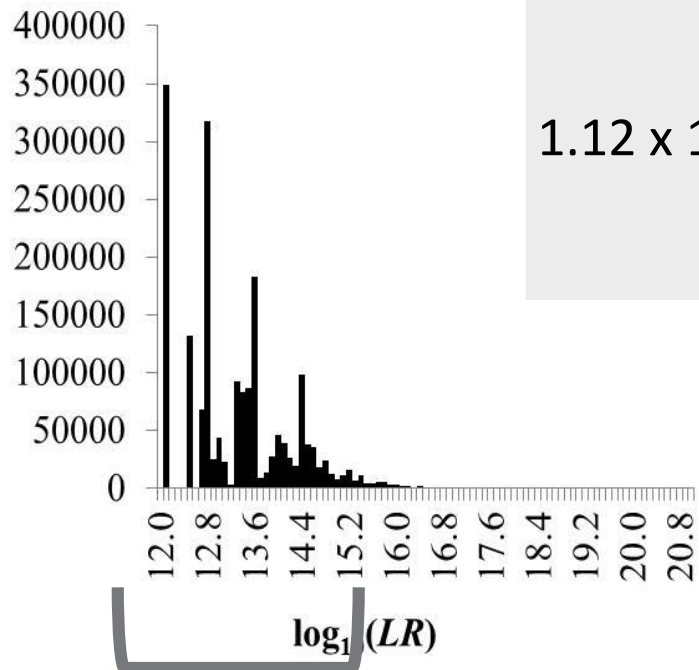
Two person mixture; 200:200 pg;





equivalent # naïve simulations	Average LR	LR for Hp true	Log(LR)
1.12×10^{21}	1.12	6.54×10^{16}	16.81
		1.22×10^{16}	16.08





equivalent # naïve simulations	Average LR	LR for H_p true	Log(LR)	p-value 1 in
1.12×10^{21}	1.12	6.54×10^{16}	16.81	4.34×10^{17}
		1.22×10^{16}	16.08	9.35×10^{16}

- Saying p is
- Always an overstatement
- Ignores these





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Forensic Science International

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



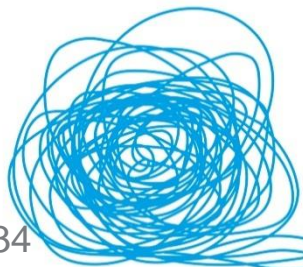
Reliable support: Measuring calibration of likelihood ratios[☆]

Daniel Ramos^{*}, Joaquin Gonzalez-Rodriguez

Research Institute on Forensic Science (ICFS), ATVS, Biometric Recognition Group, Escuela Politecnica Superior, Universidad Autonoma de Madrid, C/ Francisco Tomas y Valiente 11, E-28049 Madrid, Spain



Calibration

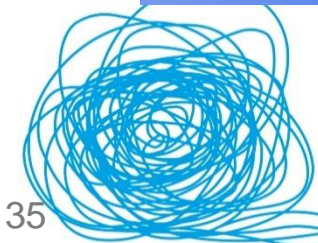




50% chance of rain

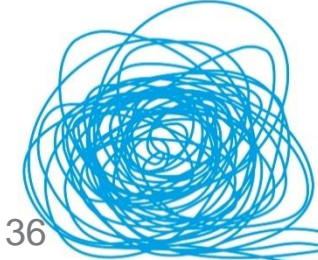
How could we check

Collect times he says 50% and see if 50% of these have rain



In the 31 lab set

- 28,250,000 false donors
- 10,297 true donors
- Prior odds $10,297/28,250,000$
- Each LR can be turned into a posterior odds and
- Then into a posterior probability
- Are we “right” the “right” number of times



Range of posterior probabilities	Observed	Number of false donors in this interval	Number of true donors in this interval
0.977 to 1.000		4	7657
0.891 to 0.977			$\frac{7,657}{4 + 7,657} = 0.9995$
0.813 to 0.891			
0.398 to 0.813			
0.158 to 0.398		200	201
0.063 to 0.158		563	162
0.025 to 0.063		1,366	165
0.010 to 0.025		3,533	131
0.004 to 0.010		9,569	133
0.002 to 0.004		24,603	115
0.001 to 0.002		64,106	112
0.0003 to 0.0006		156,994	115
0.0000 to 0.0003		28,037,070	760

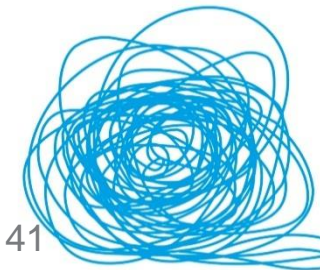
Range of posterior probabilities	Observed	Number of false donors in this interval	Number of true donors in this interval
0.977 to 1.000	0.9995	4	7657
0.891 to 0.977		5	342
0.813 to 0.891		7	111
0.398 to 0.813		60	314
0.158 to 0.398		200	201
0.063 to 0.158		563	162
0.025 to 0.063		1,366	165
0.010 to 0.025		3,533	131
0.004 to 0.010		9,569	133
0.002 to 0.004		24,603	115
0.001 to 0.002		64,106	112
0.0003 to 0.0006		156,994	115
0.0000 to 0.0003		28,037,070	760

Range of posterior probabilities	Observed	Number of false donors in this interval	Number of true donors in this interval
0.977 to 1.000	0.9995	4	7657
0.891 to 0.977	0.9856		2
0.813 to 0.891			1
0.398 to 0.813		50	514
0.158 to 0.398		200	201
0.063 to 0.158		563	162
0.025 to 0.063		1,366	165
0.010 to 0.025		3,533	131
0.004 to 0.010		9,569	133
0.002 to 0.004		24,603	115
0.001 to 0.002		64,106	112
0.0003 to 0.0006		156,994	115
0.0000 to 0.0003		28,037,070	760

We are "right" too often
Not enough false donors
up here

Range of posterior probabilities	Observed	Number of false donors in this interval	Number of true donors in this interval
0.977 to 1.000	0.9995	4	7657
0.891 to 0.977	0.9856	5	342
0.813 to 0.891	0.9407	7	111
0.398 to 0.813	0.8396	60	314
0.158 to 0.398	0.5012	200	201
0.063 to 0.158	0.2234	563	162
0.025 to 0.063	0.1078	1,366	165
0.010 to 0.025	0.0358	3,533	131
0.004 to 0.010	0.0137	9,569	133
0.002 to 0.004	0.0047	24,603	115
0.001 to 0.002	0.0017	64,106	112
0.0003 to 0.0006	0.0007	156,994	115
0.0000 to 0.0003	0.000027	28,037,070	760

Communication





The Forensic Institute

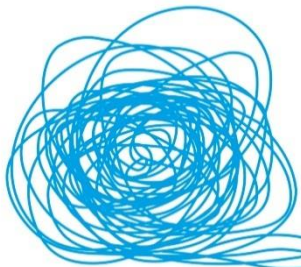


Report of Professor Allan Jamieson in the case of Donte Lee

8th May 2017

Occupation: Director of The Forensic Institute

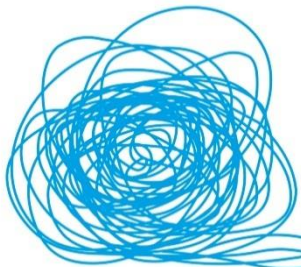
No one understand the LR



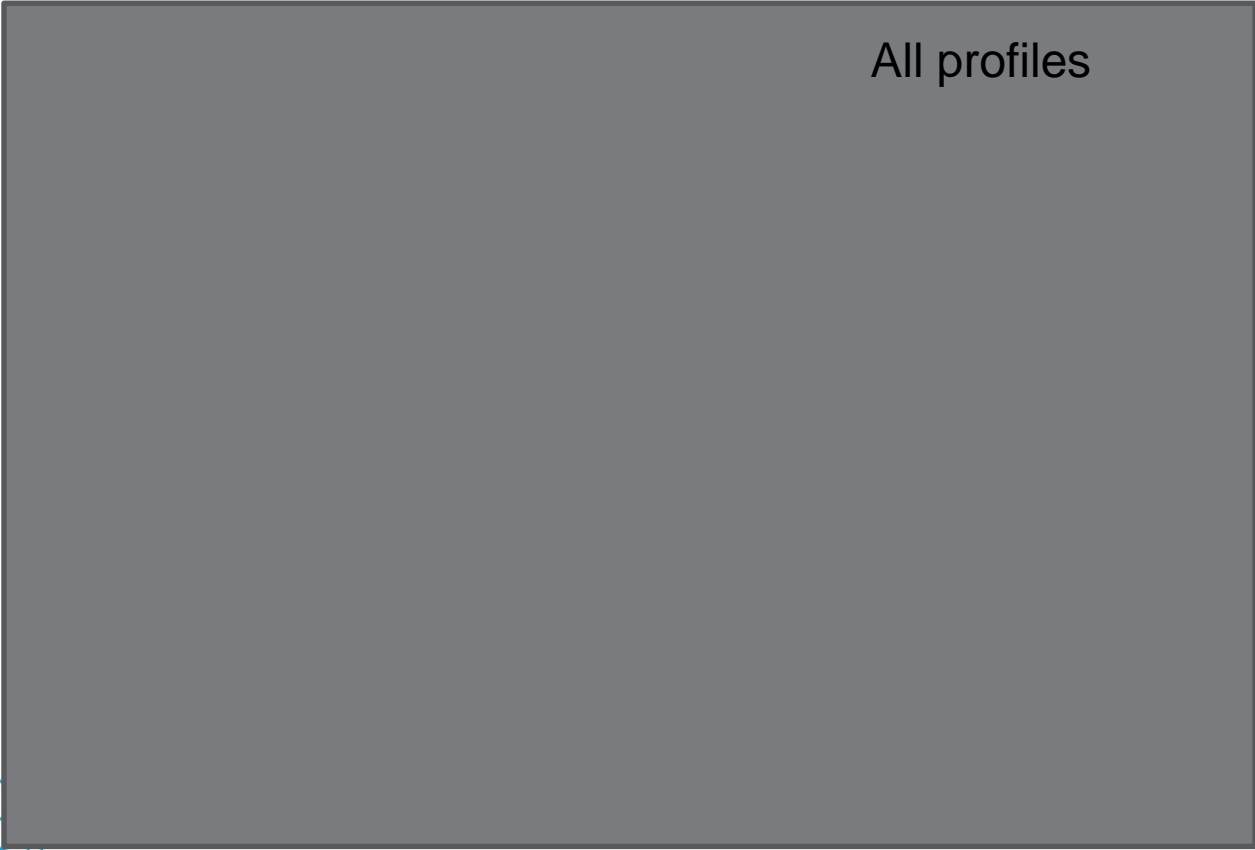
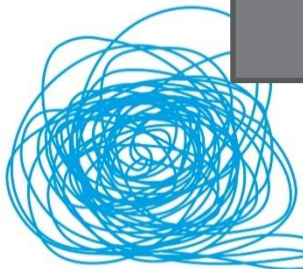
This illustrates that if the LRs of all the millions of potential genotypes from a mixture were calculated and then arranged in order of size, the suspect is unlikely to be the highest LR.

In other words, the LR provides only the weight of evidence against the specific defendant without reference to other people who would also have a LR greater than 1 (i.e. support for the prosecution hypothesis).

In effect, the LR is a sophisticated version of the disparaged 'consistent with' statement.

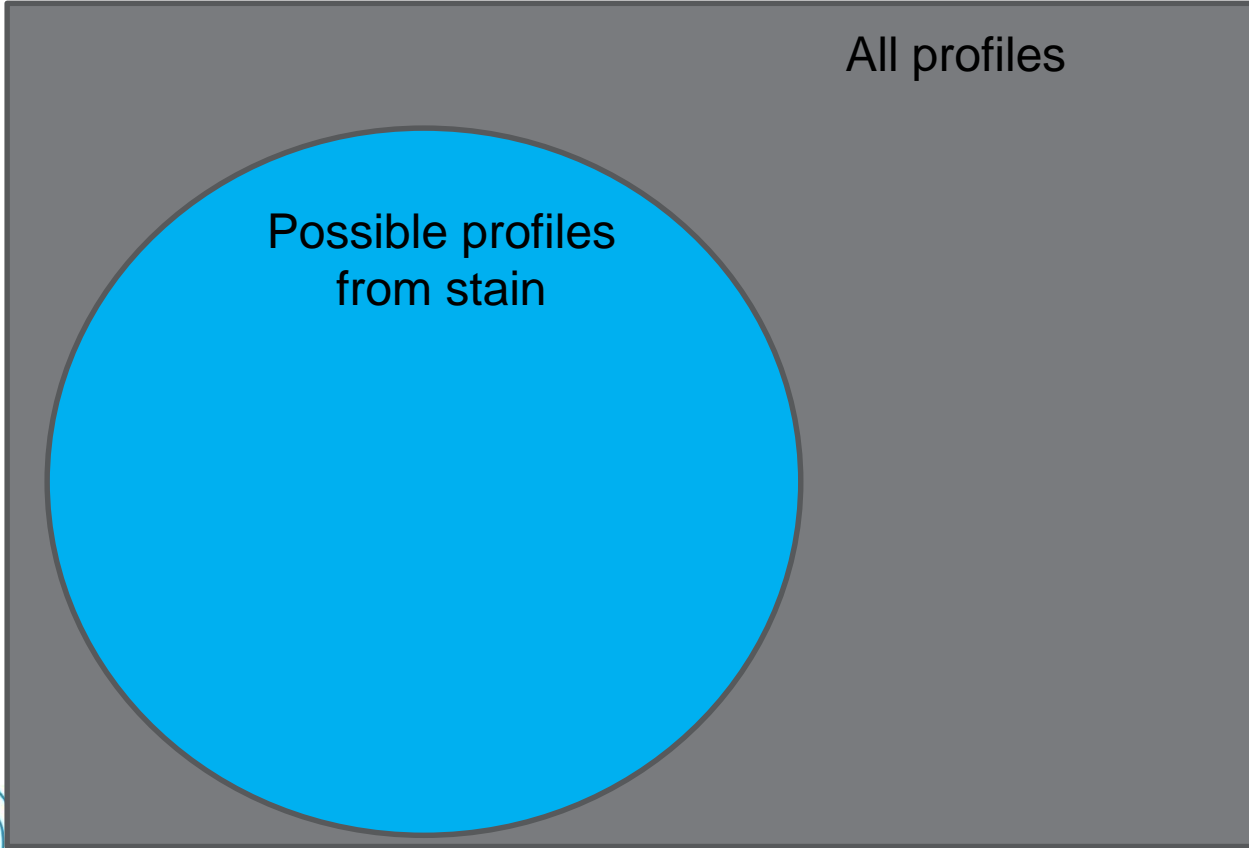
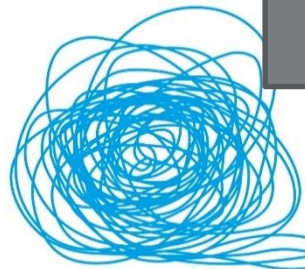


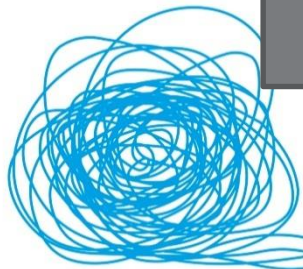
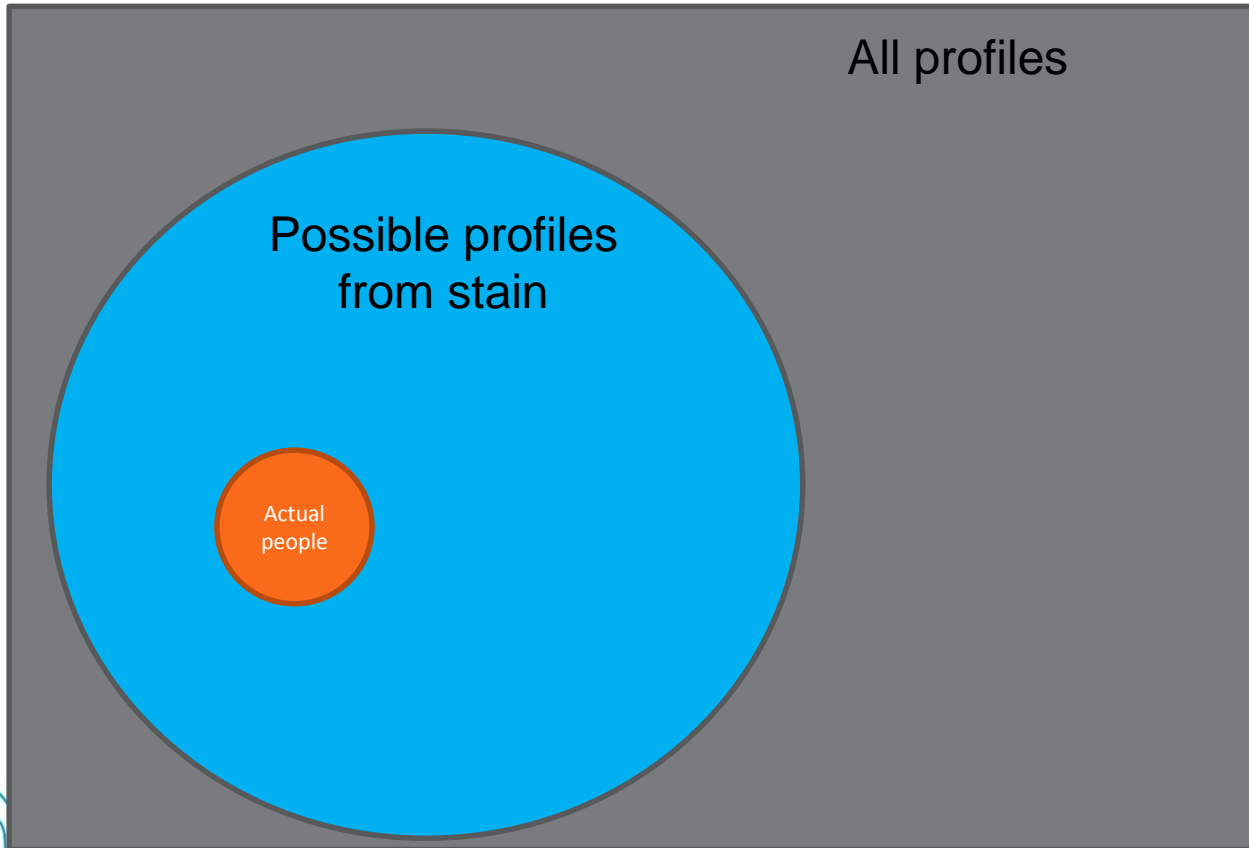
All profiles

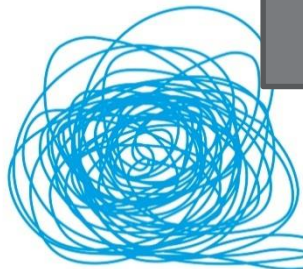
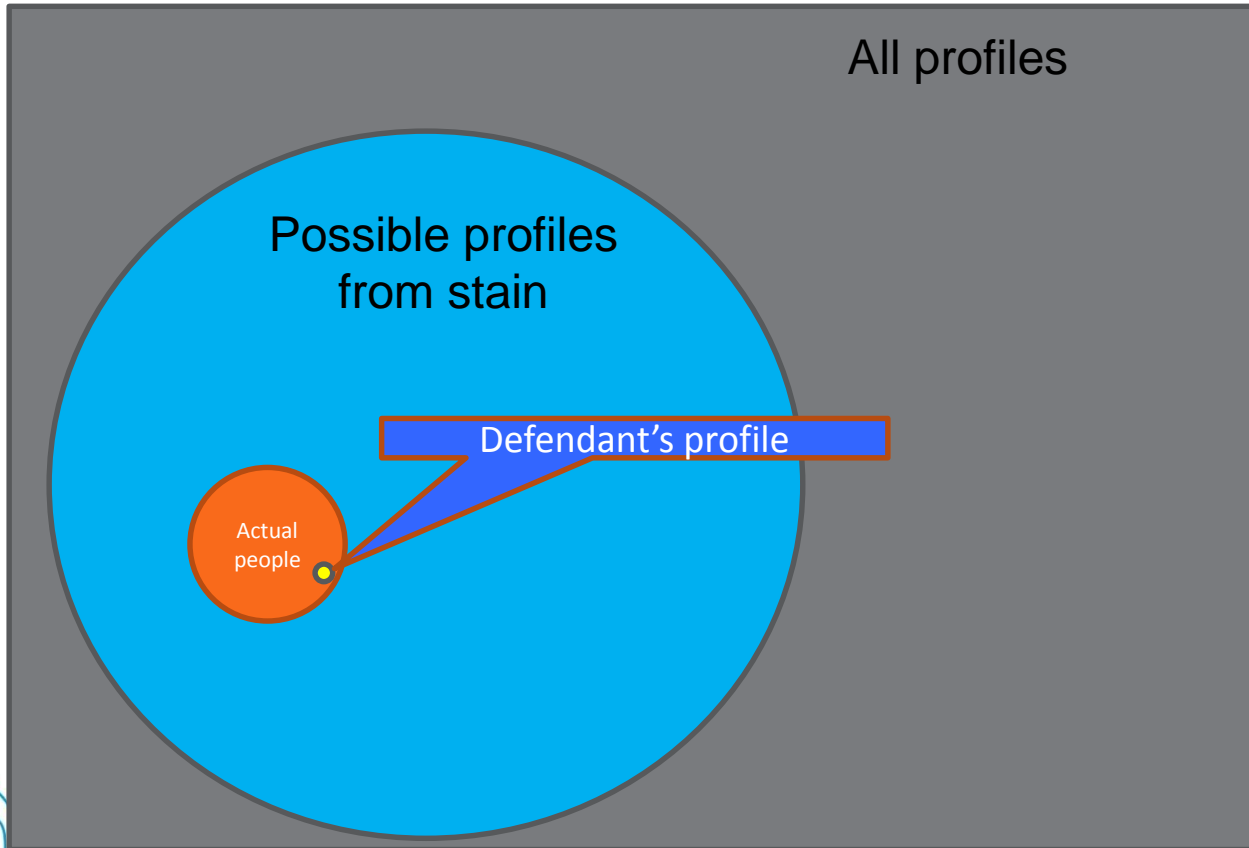


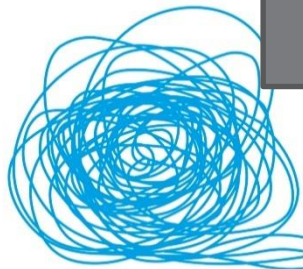
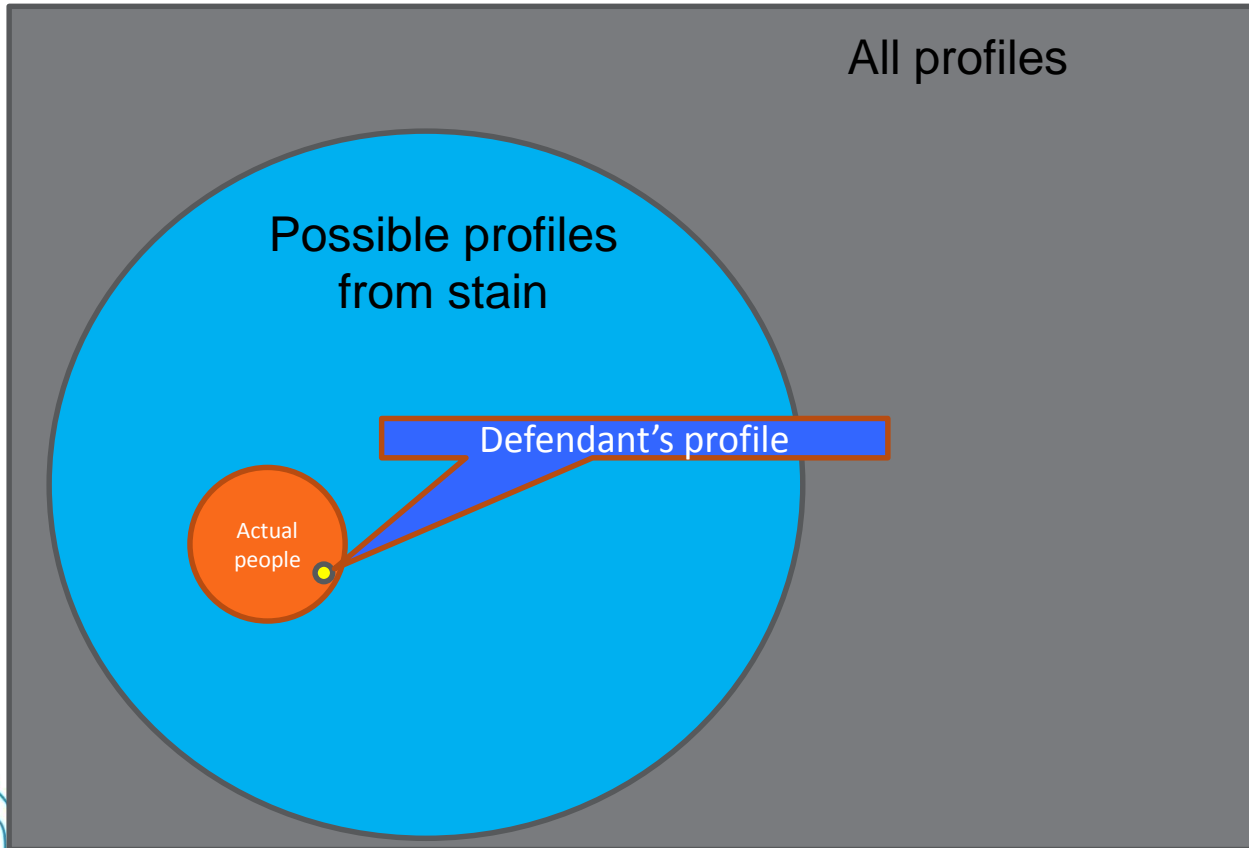
All profiles

Possible profiles
from stain

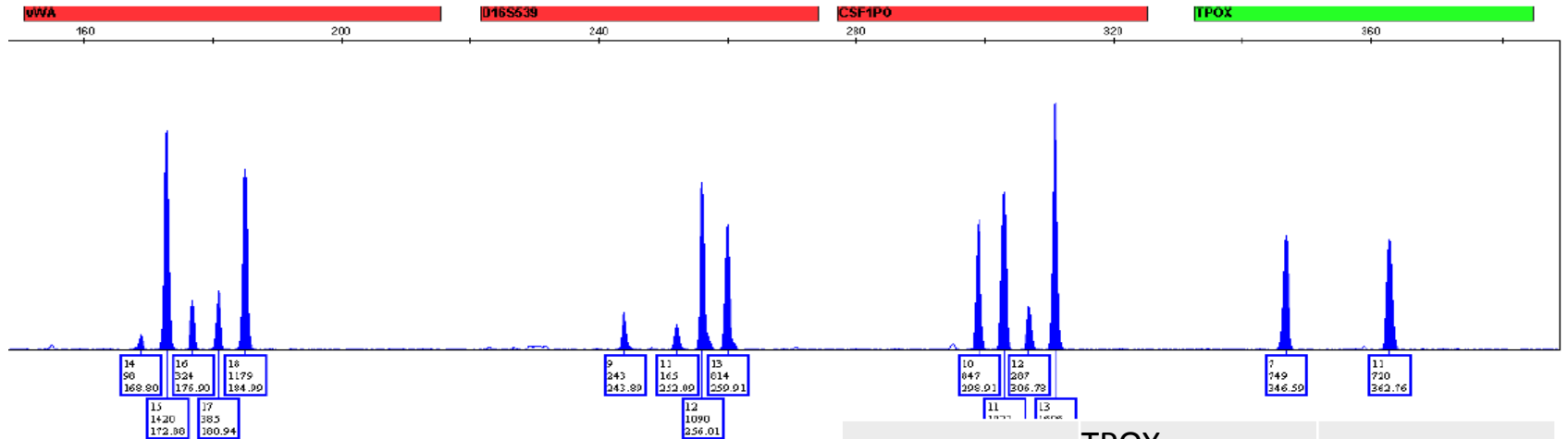




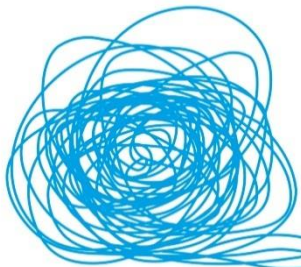




Weights and ranks



	TPOX	
C1	7,11	100.00%
C2	7,7	23.42%
	7,Q	5.85%
	7,11	37.80%
	11,11	25.73%
	11,Q	5.67%
	Q,Q	1.53%



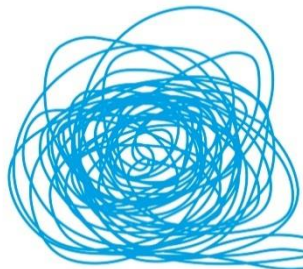
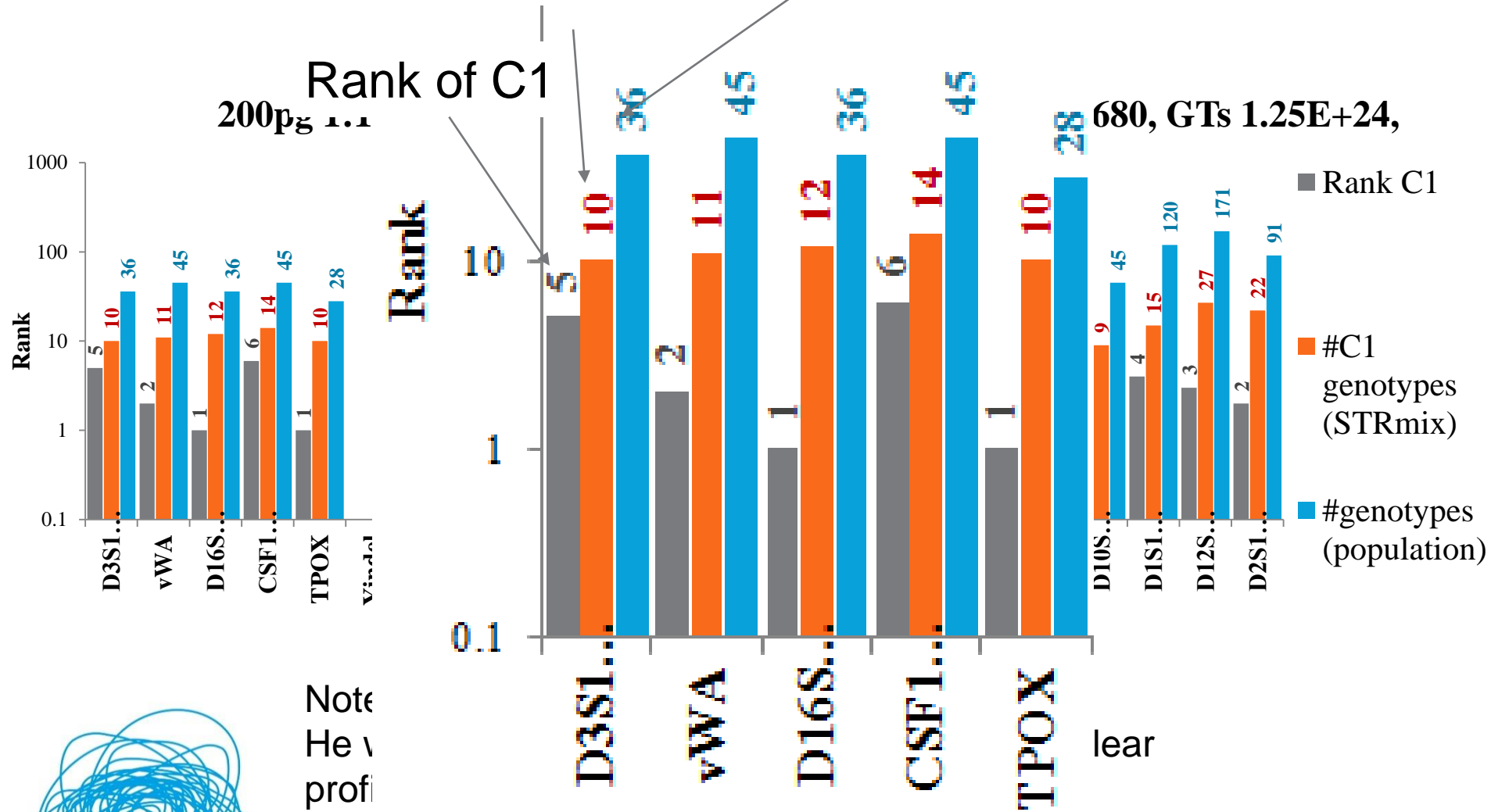
Number of genotypes
STRmix considered

Number of genotypes at
this locus

Rank of C1

200pg

680, GTs 1.25E+24,



In our example 8.55×10^{38} genotypes
 7.5×10^9 people

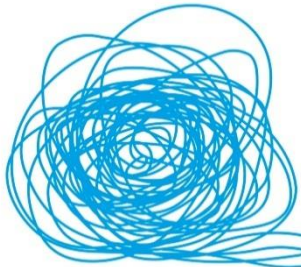
Only about 1 in 10^{29} genotypes exist

There are about 6×10^7 genotypes above our rank

Hence potentially no actual people above our rank

Most genotypes do not exist

Weir, BS

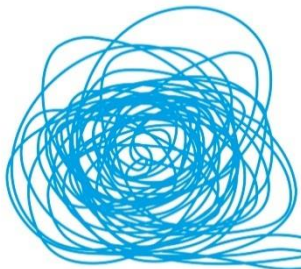


Likelihood ratio

“The probability of observing this evidence is n times more likely if it arose from Mr X + an unknown person rather than two unknowns”



- Is NOT measuring the probability of Mr Lee being a contributor – many profiles will produce a high LR
- High LRs can be obtained for false propositions
- Depends on the number of contributors
- Does not test all of the possible explanations for the evidence



A statement about the probability that Mr Smith left the stain can only be made from all the evidence, not from the DNA alone.

The DNA evidence by itself increases the odds that Mr Smith is the donor LR times Over what they would be from the other evidence

This represents extremely strong support that he is the donor





Ev

p-Values should not be used for evaluating the strength of DNA evidence



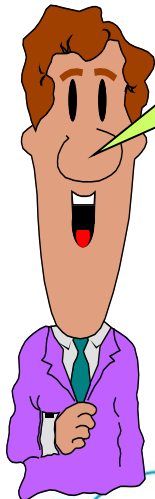
Maarten Kruijver^a, Ronald Meester^a, Klaas Slooten^{a,b,*}

^a Department of Mathematics, VU University, De Boelelaan 1081a, 1081 HV Amsterdam, The Netherlands

^b Netherlands Forensic Institute, P.O. Box 24044, 2490 AA The Hague, The Netherlands

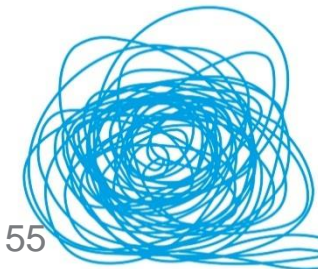
Its not quite a *p*-value. But there has been considerable criticism.

The LR is the best summary of the evidence.



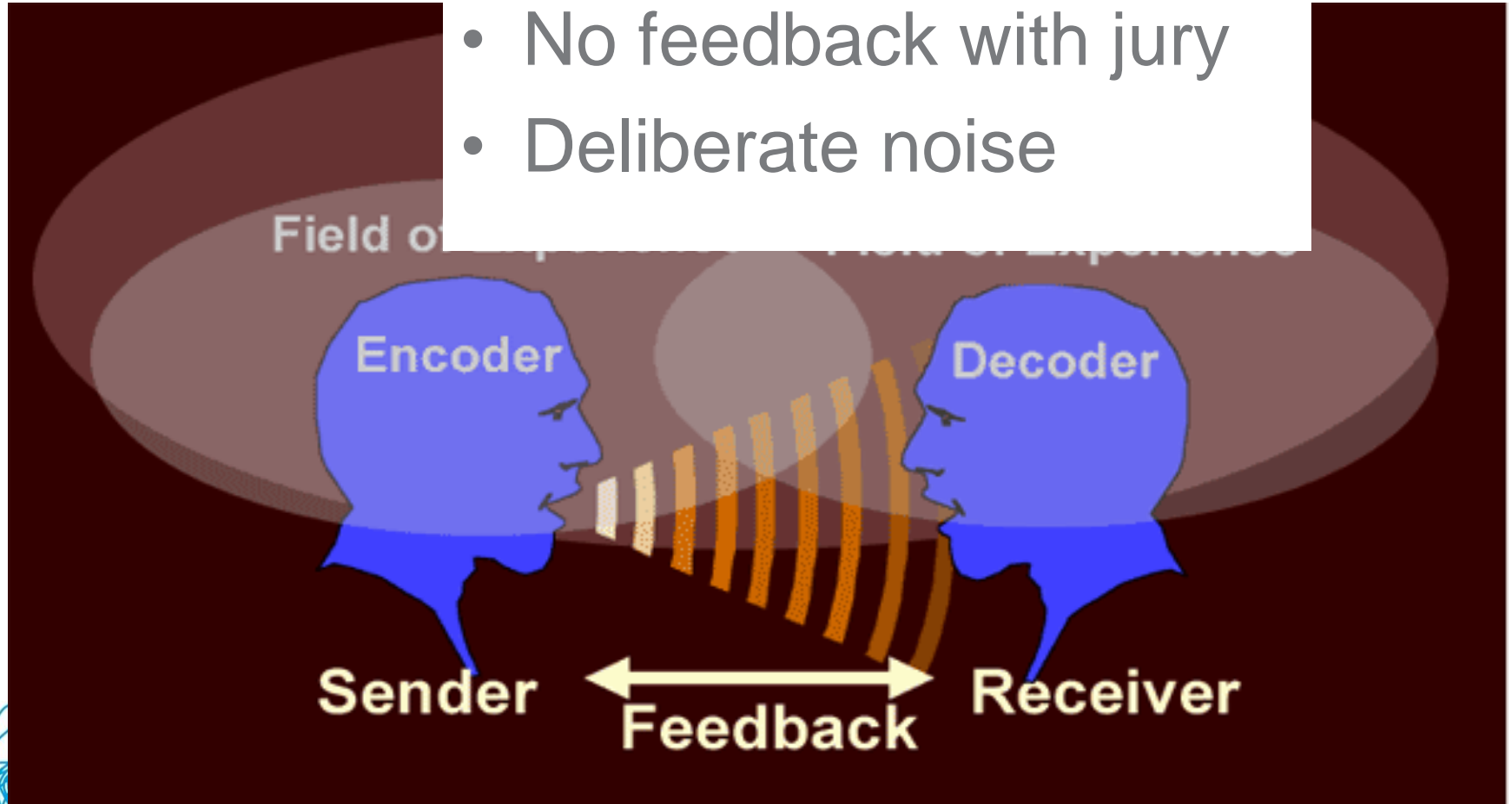
Rewording

- Concern about pseudo-frequentist expression
- Other profiles “near-by”
- Loss of posterior = LR x prior construct
- Trying to “not change”

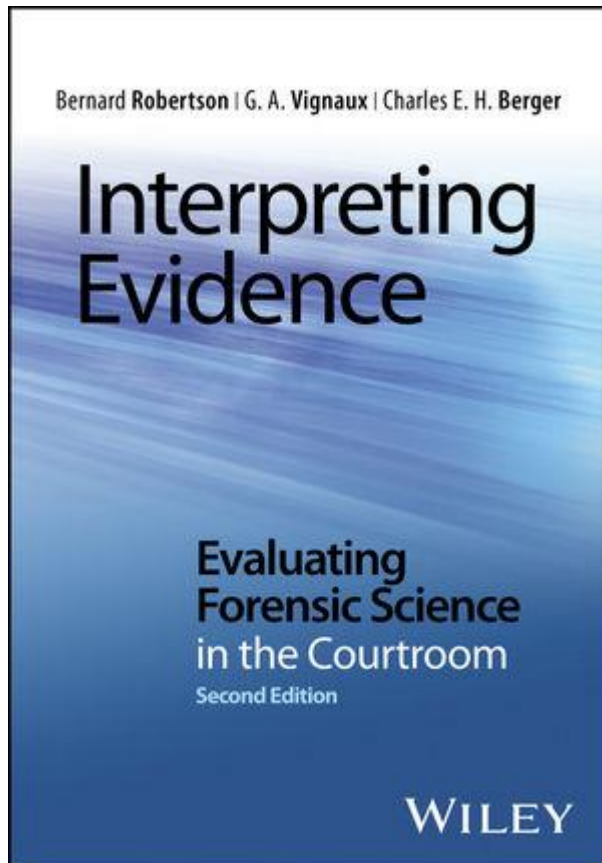


Theory of communication

- Q&A
- No feedback with jury
- Deliberate noise



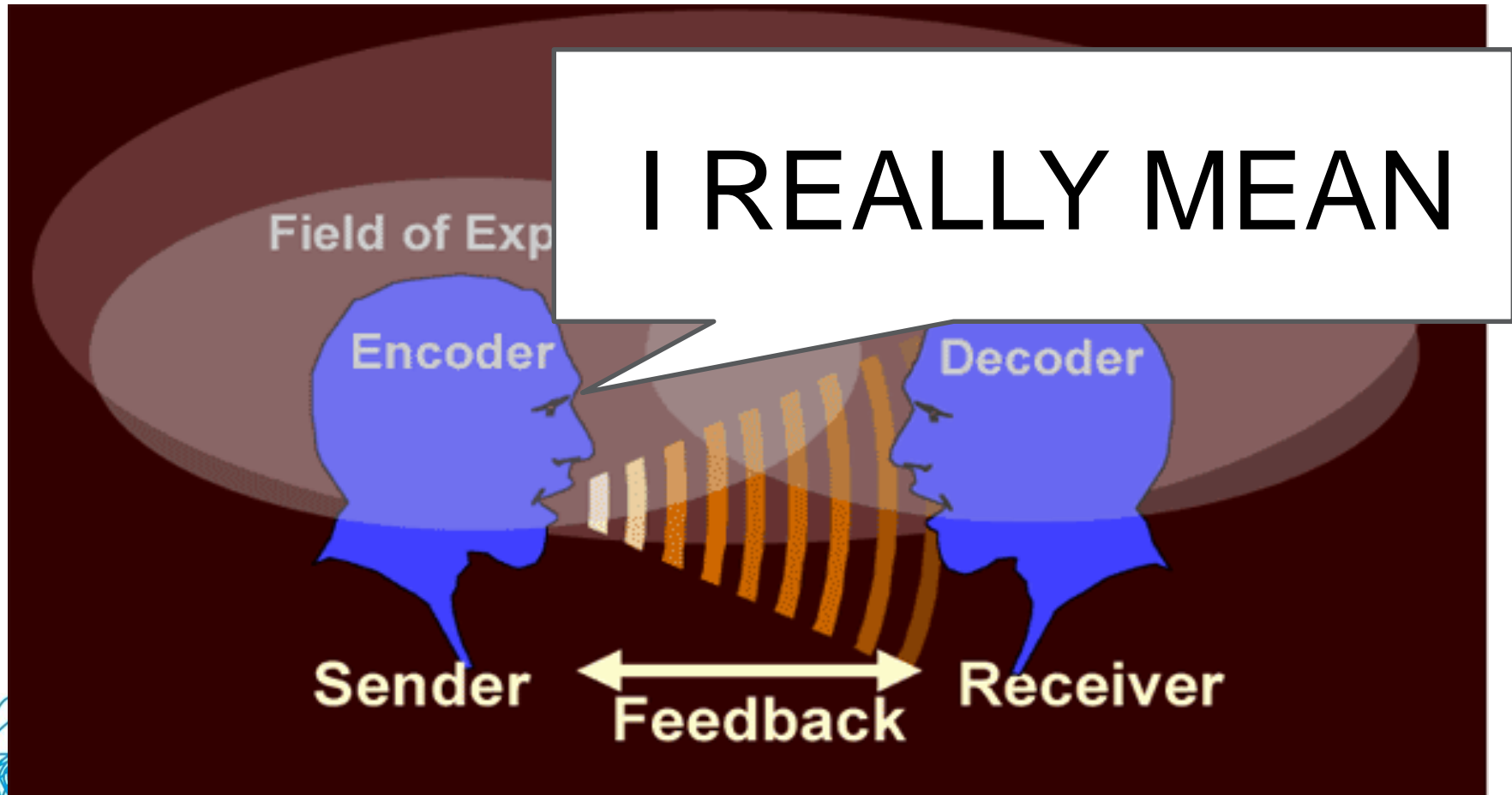
Saying it better does not guarantee understanding better



They have some great analogies
But they are long and I suspect you cannot do them in court



Saying it better does not guarantee understanding better



Conclusion

- Number of Contributors
 - LR stable over NoC
- Adventitious matches do happen
 - Actually at less than the expected rate
- Reliable support – calibration
- Communication – cannot be fixed at one end



Acknowledgement and disclaimer

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- Professor Bruce Budowle
- Lynn Garcia