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LFTDI

LABORATORY FOR FORENSIC TECHNOLOGY DEVELOPMENT & INTEGRATION

The probability of the number of contributors given forensic DNA data

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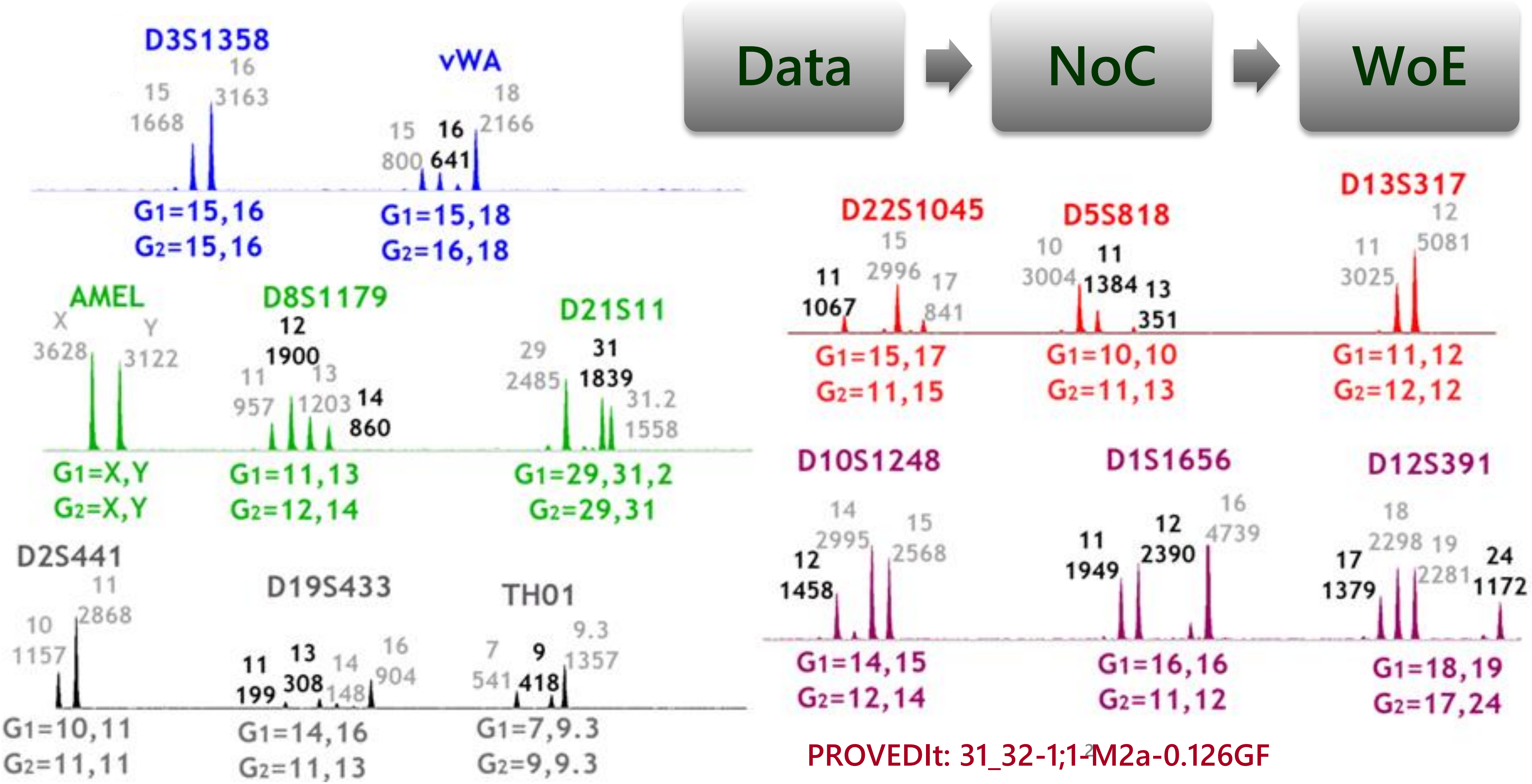
SOFTGENETICS®

DNA Mixtures and Number of Contributors (NoC)



PROVEDIt: 31_32-1;1-M2a-0.126GF

NOCIt Gives $P(N=n|H_D,I,E)$ for all N

Why $P(N=n|H_d,I,E)$?

The LR is the weighted average of the n-specific LRs, for all n

Contents lists available at ScienceDirect
Forensic Science International: Genetics
journal homepage: www.elsevier.com/locate/fsigen

Research paper

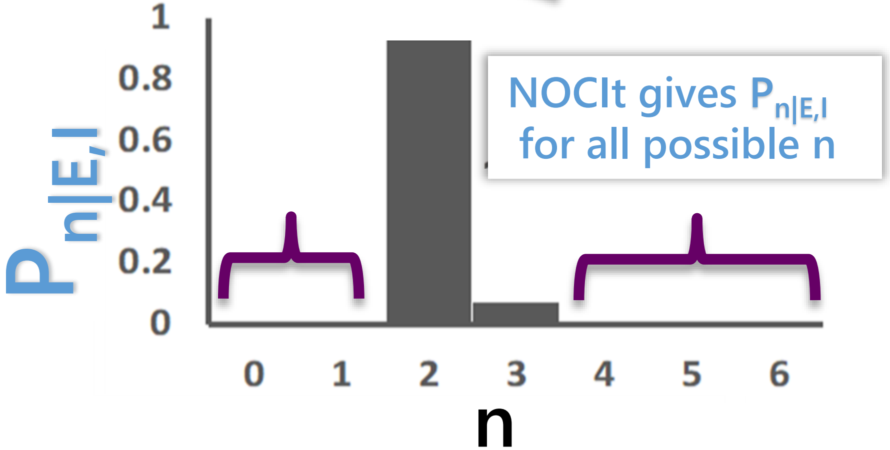
Contributors are a nuisance (parameter) for DNA mixture evidence evaluation

K. Slooten[a,*], A. Caliebe[b]

$$LR = \sum_n \left(\frac{P(E|H_p, N=n, I)}{P(E|H_d, N=n, I)} P(N=n|H_d, I, E) \right)$$

$LR^{E|n,I}$ $P_{n|E,I}$ NOCIt

$$LR = LR^{E|n=1,I}P_{n=1|E,I} + LR^{E|n=2,I}P_{n=2|E,I} + LR^{E|n=3,I}P_{n=3|E,I} + LR^{E|n=4,I}P_{n=4|E,I} + LR^{E|n=5,I}P_{n=5|E,I} + \ldots$$



NOCIt, therefore, meets 2 aims:

- Narrows *n* ranges by informing what n are associated with negligible $P_{n|E,I}$
- Supports a process that does not apply default *n* or automatic $P_{n|E,I}$

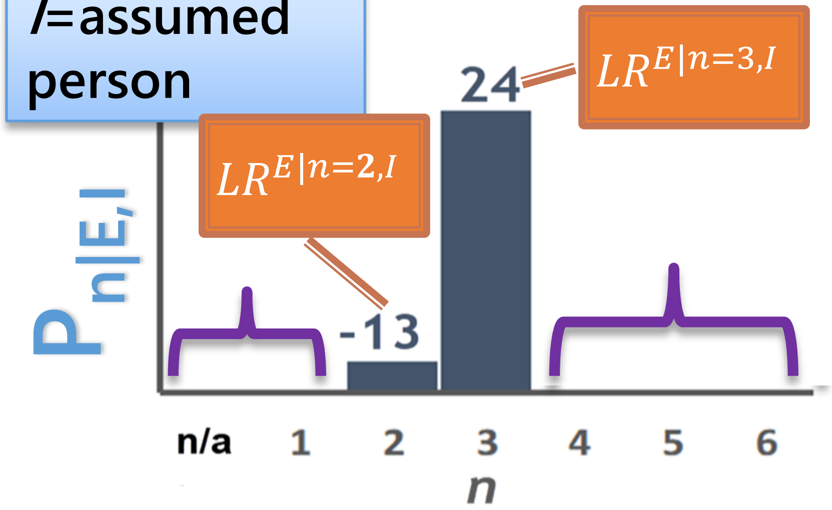
NOCIt Determines $P(N=n|H_D,I,E)$

Why $P(N=n|H_d,I,E)$ aka $P_{n|E,I}$?

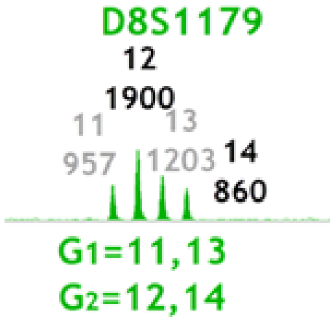
Contexts between $LR^{E|n,I}$ and $P_{n|E,I}$ are consistent

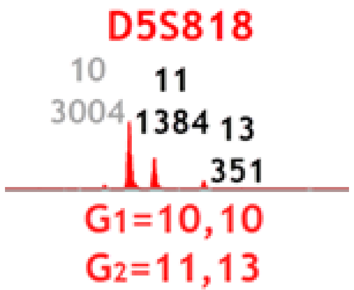
$$\mathbf{LR} = LR^{E|n=1,I}P_{n=1|E,I} + LR^{E|n=2,I}P_{n=2|E,I} + LR^{E|n=3,I}P_{n=3|E,I} + LR^{E|n=4,I}P_{n=4|E,I} + LR^{E|n=5,I}P_{n=5|E,I} + \ldots$$

I=assumed person



$$\mathbf{LR} = LR^{E|n=2,I}P_{n=2|E,I} + LR^{E|n=3,I}P_{n=3|E,I}$$
$$= 10^{-13}0.1 + 10^{24}0.9$$
$$= 10^{24}$$





NOCIt, therefore, meets a 3rd aim:

- Determines $P_{n|E,I}$ using the *same context* as assigned to $LR^{E|n,I}$

NOCIT DETERMINES $P(N=n|H_D,I,E)$

What is $P(N=n|H_d,I,E)$?

It is the posterior probability of n contributors given the data and a context

Probability of the data given n randomers

Probability that n people contributed (before seeing data – PRIOR)

$$P(N=n|H_d,I,E) = \frac{P(E|H_d,I,N=n)\cdot P(N=n|H_d,I)}{\sum_n P(E|H_d,I,N=n)\cdot P(N=n|H_d,I)}$$

Probability of n contributors after considering the data - POSTERIOR

For ease, drop I and H_d going forward

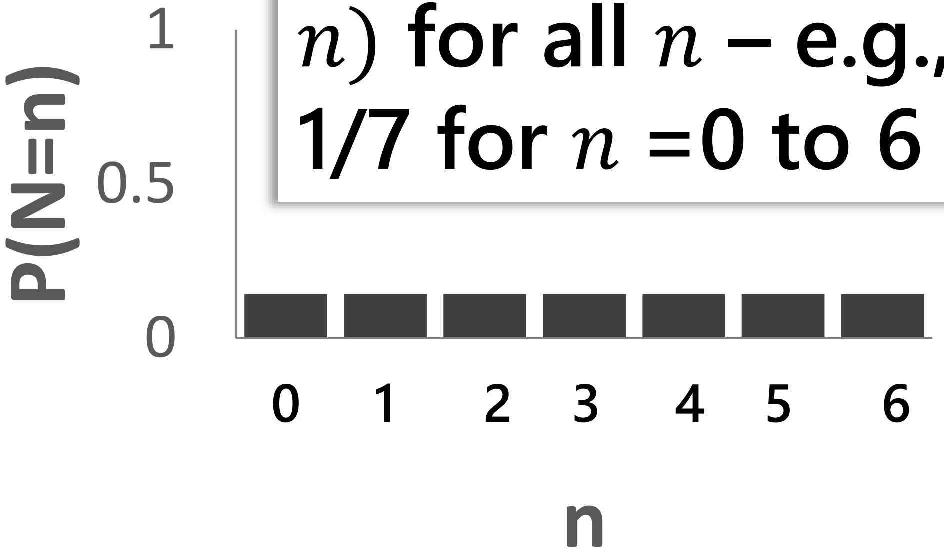
$$P(N=n|E) = \frac{P(E|N=n)\cdot P(N=n)}{\sum_n P(E|N=n)\cdot P(N=n)}$$

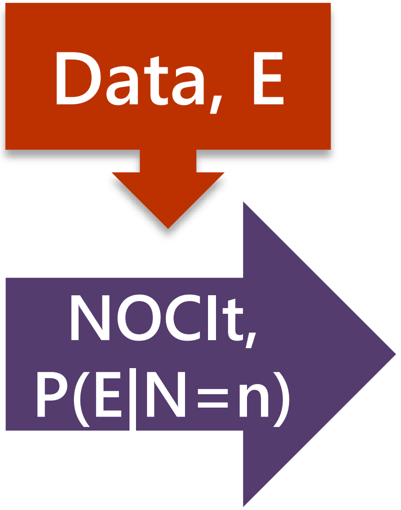
NOCIT DETERMINES $P(N=n|H_D,I,E)$

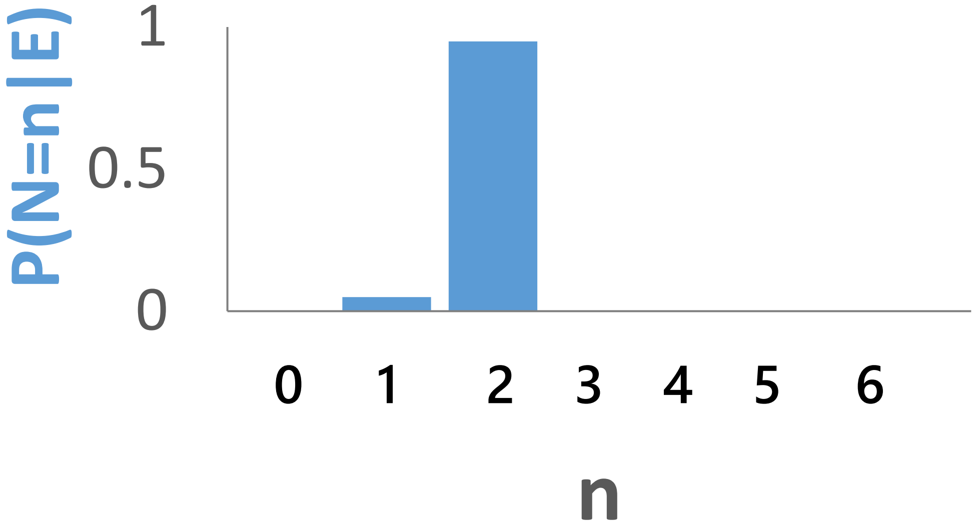
What is $P(N=n|E)$ graphically?

$$P(N=n|E) = \frac{P(E|N=n)\cdot P(N=n)}{\sum_n P(E|N=n)\cdot P(N=n)}$$

Before seeing data, set $P(N=n)$ for all n – e.g., 1/7 for n =0 to 6







What is P(*N=n|E*) *numerically*?

$$P(N=n|E) = \frac{P(E|N=n)\cdot P(N=n)}{\sum_n P(E|N=n)\cdot P(N=n)}$$

Illustrative example:

n	$P(N=n)$	$P(E\|N=n)$	$P(E\|N=n)\cdot P(N=n)$	$P(N=n\|E)$
0	1/7=0.143	0.00001	0.00000143	=0.0000014/0.0159 =0.00009
1	0.143	0.01	0.00143	0.09
2	0.143	0.1	0.0143	0.9
3	0.143	0.001	0.000143	0.009
4	0.143	0.000001	0.000000143	0.000009
5	0.143	0.0000001	1.43E-08	0.0000009
6	0.143	0.00000001	1.43E-09	0.000000009
			Sum=0.0159	**Sum=1**

Large-Scale Validation with Public Data

- Confirming NOCIt meets **predetermined** expectations
  - Unimodal distributions
    - The distribution should be peaked in one location
  - Precision
    - The apex of the distribution is the same for > 95% of the samples across 3 runs
  - Accuracy
    - $P(N=TrueNOC|H_d,I,E)$ >1% for at least 90% samples
      - TrueNOC was confirmed by running all dilutions as single-source and confirming signal
      - Used ReSOLVIt to set up a lab pipeline with LOD=1
  - Comparison
    - NOCIt outperformed current procedures
  - Robustness:
    - Resilient to sloping – i.e., degradation/inhibition effects
    - Works under different contexts

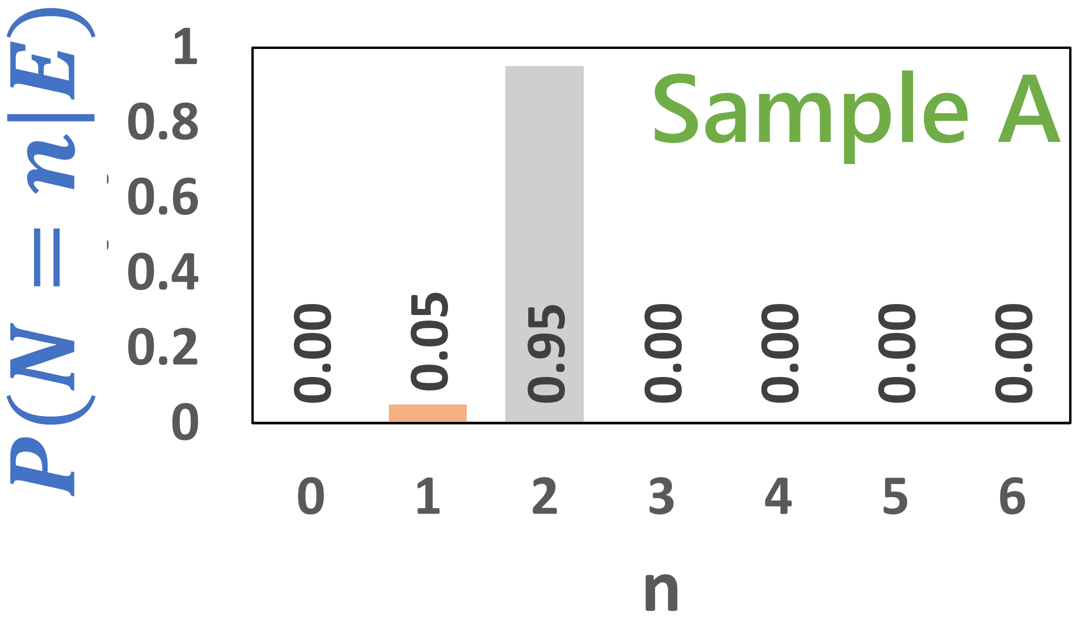
Public Mixture Data with LOD=1 are Available

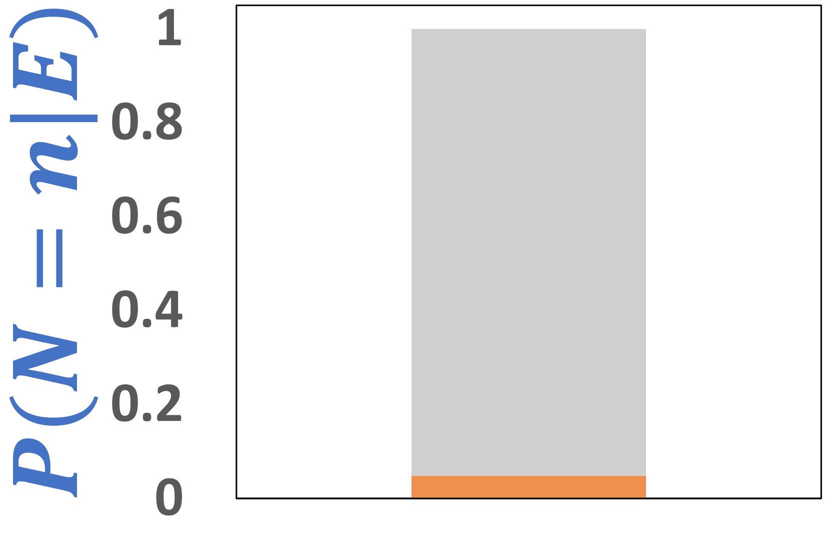
- 815 PROVEDIt samples (www.lftdi.com)
  - GlobalFiler samples (29 cycles; 25 sec 3500 Genetic Analyzer)

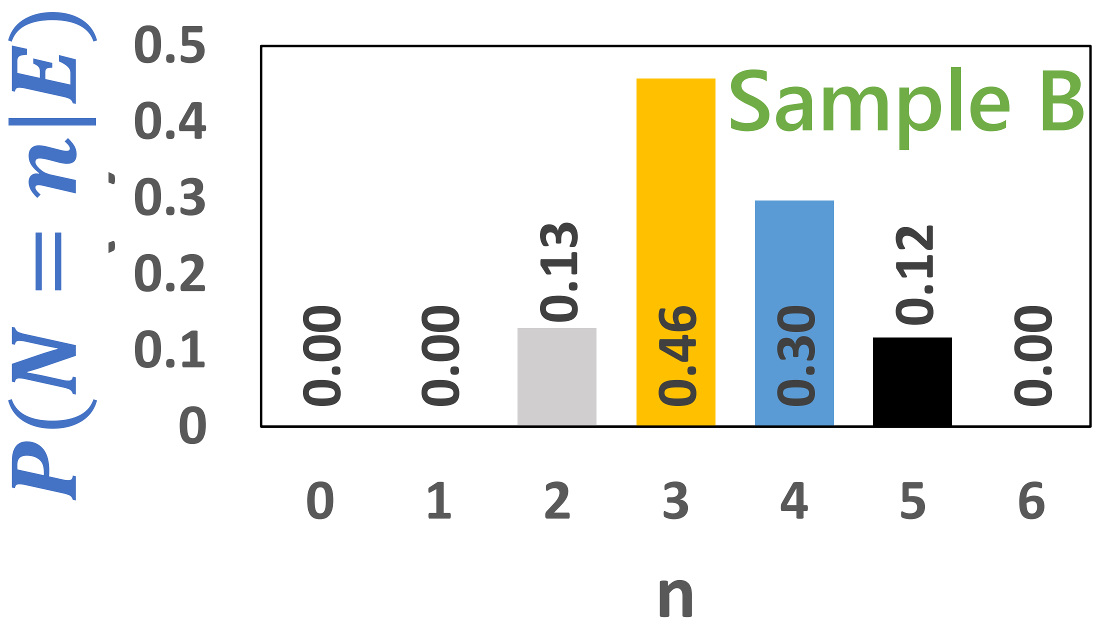
815 GlobalFiler® samples used to validate NOCIt

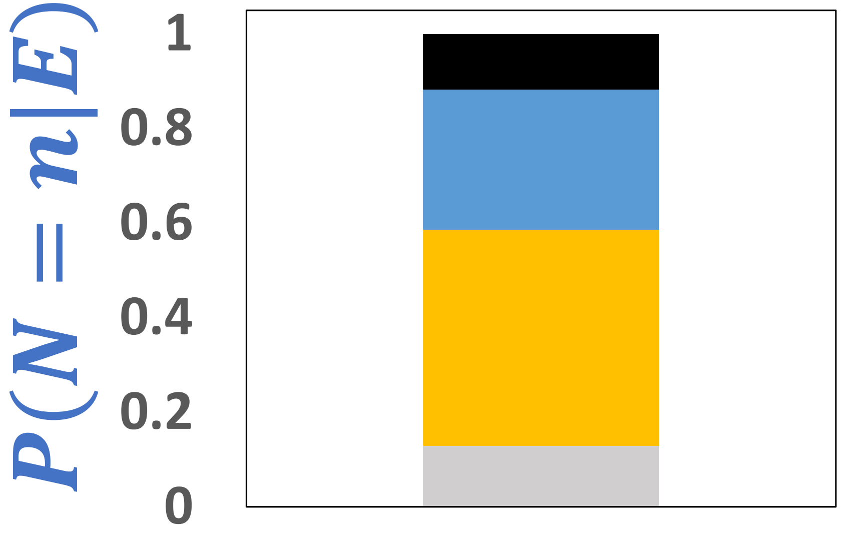
NOC	1	2	3	4	5
No. Samples	100	193	170	186	166
Tot. Template Mass (ng)	0.5 – 0.0078	0.75 – 0.03	0.75 – 0.045	0.75 – 0.06	0.75 – 0.075
Contributor Ratio	N/A	1:1 – 1:9	1:1:1 – 1:9:9	1:1:1:1 – 1:9:9:1	1:1:1:1:1 – 1:9:9:9:1

Visual Exploration is Aided by Stacked Plots

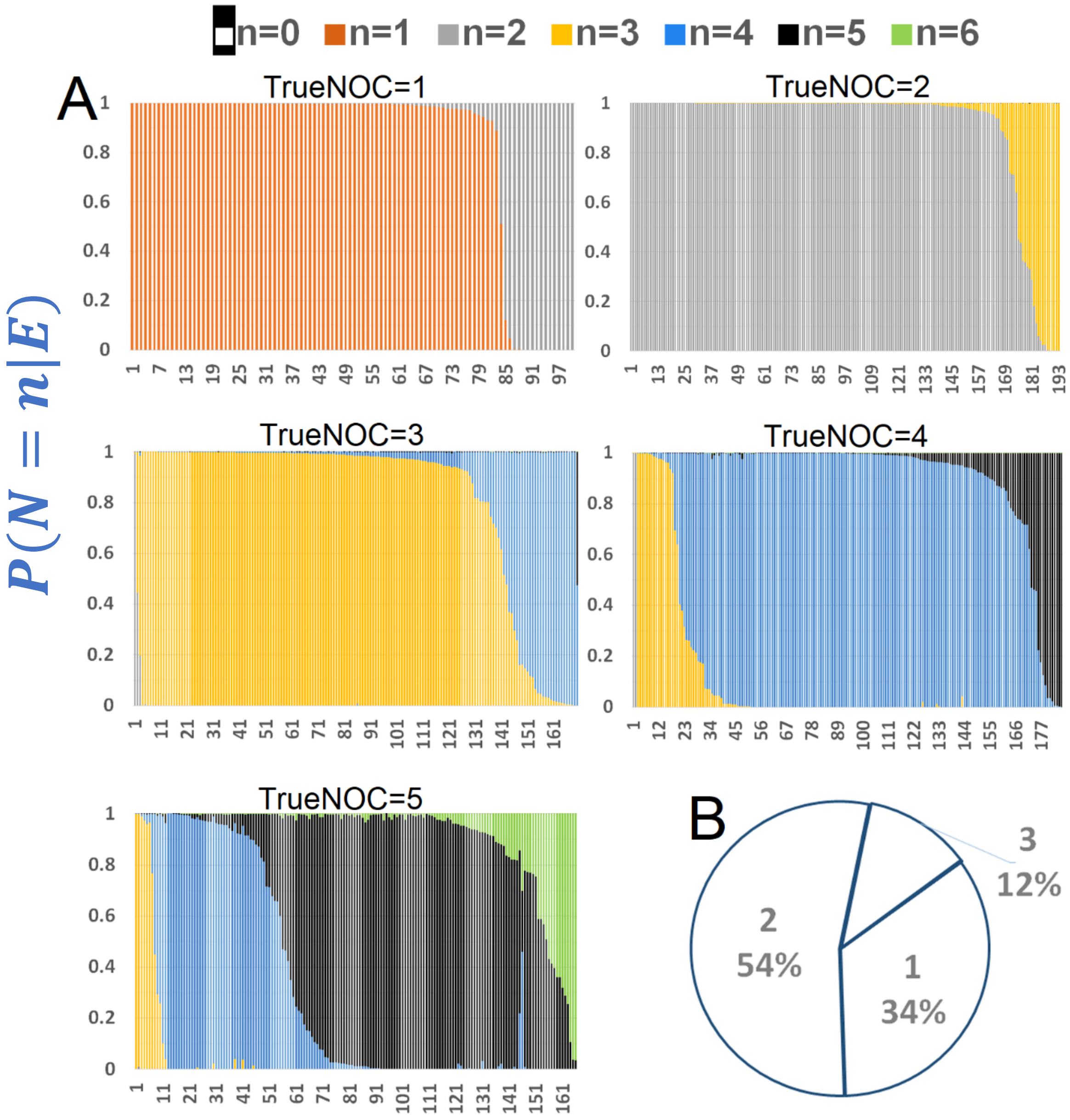








NOCIT GIVES UNIMODAL DISTRIBUTIONS



(A) Stacked Plots of APP(n) using *Condition* 1 and the APP for n= (white bar)0; ( )1; ( )2; ( )3; ( )4; and ( ) 5; and ( ) 6. X-axis is sample number.

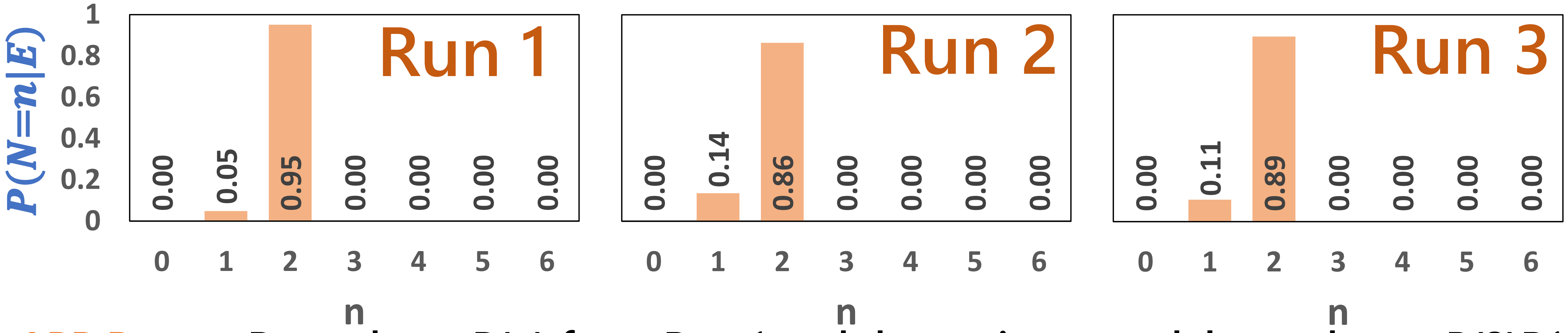
(B) Pie Chart depicting percentage of samples resulting in one, two or three APP $(n) \geq 0.001$.

Criterion: The distribution should be peaked in one location (at one n)

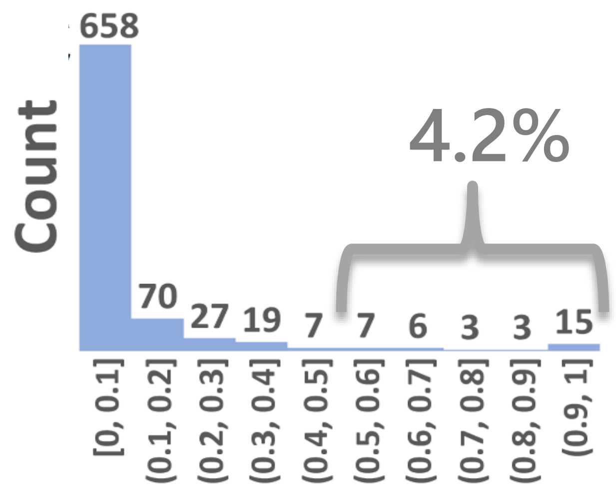
Results: Distribution was always unimodal in that there was no instance where the probability was high for small values of n, low for medium n values and then high for large n.

No sample gave more than 3 $P(N = n|E) \geq 0.001$

NOCIt is Precise Across Runs



APP Range. Record maxP(n) from Run 1 and determine max delta at that n. P(2)R1= 0.95, R2=0.86, R3=0.89. Range=(0.95-0.86)=0.09. Tells us if maxP(n) is changing.



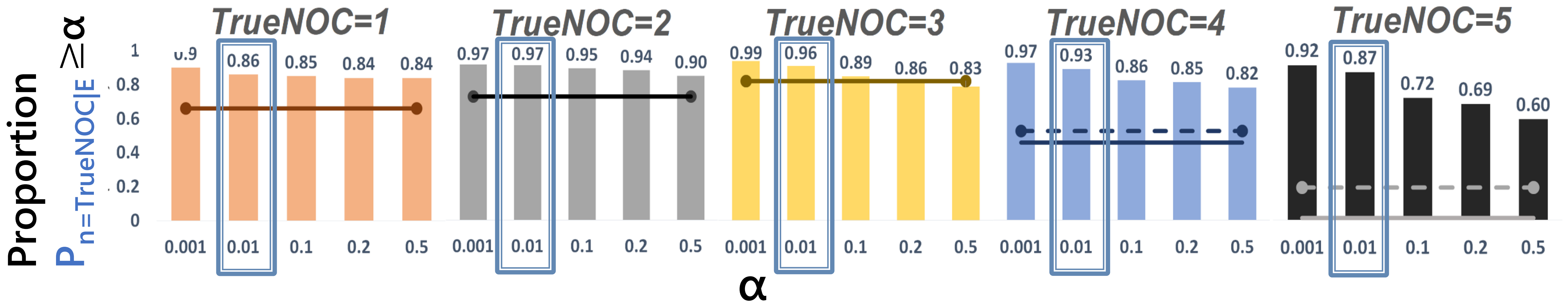
Range= max($\Delta P_{R1,R2}$; $\Delta P_{R1,R3}$; $\Delta P_{R2,R3}$)

Criterion: The distribution's apex located at the same n for > 95% of the samples across 3 runs

Results: 95.8% of the samples had repeatable distributions across 3 runs

NOCIt Is Accurate, outperforming Current Procedures

Proportion of samples giving $P(N = TrueNOC|E) \geq \alpha$, and proportion of samples for which (—) MAC and (- -) MLE (H. Haned, et al., J Forensic Sci 56(1) (2011)) estimates equaled TrueNOC



Criterion: $P(N = TrueNOC|E) \geq$ 1% for at least 90% samples

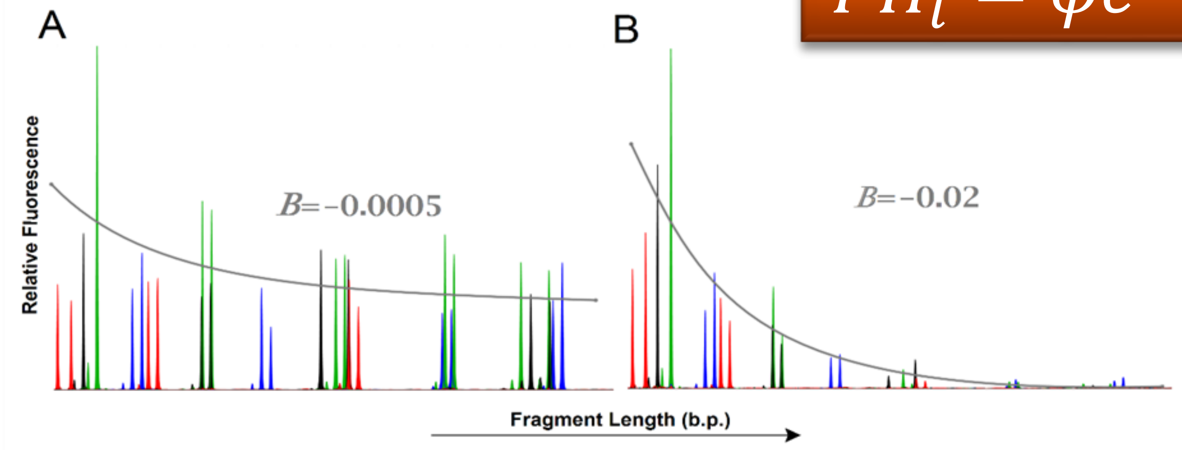
Results: 92.5% of the samples gave $P(N = TrueNOC|H_d, I, E) \geq 1\%$

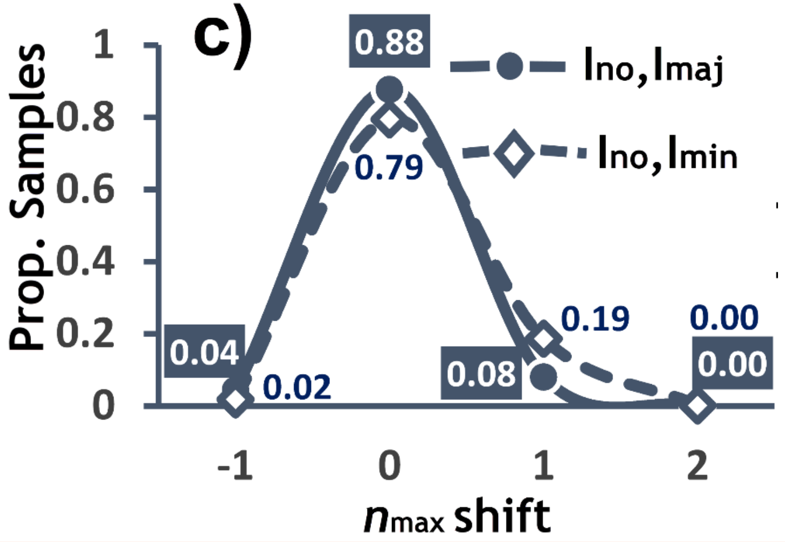
Criterion: NOCIt must outperform current procedures

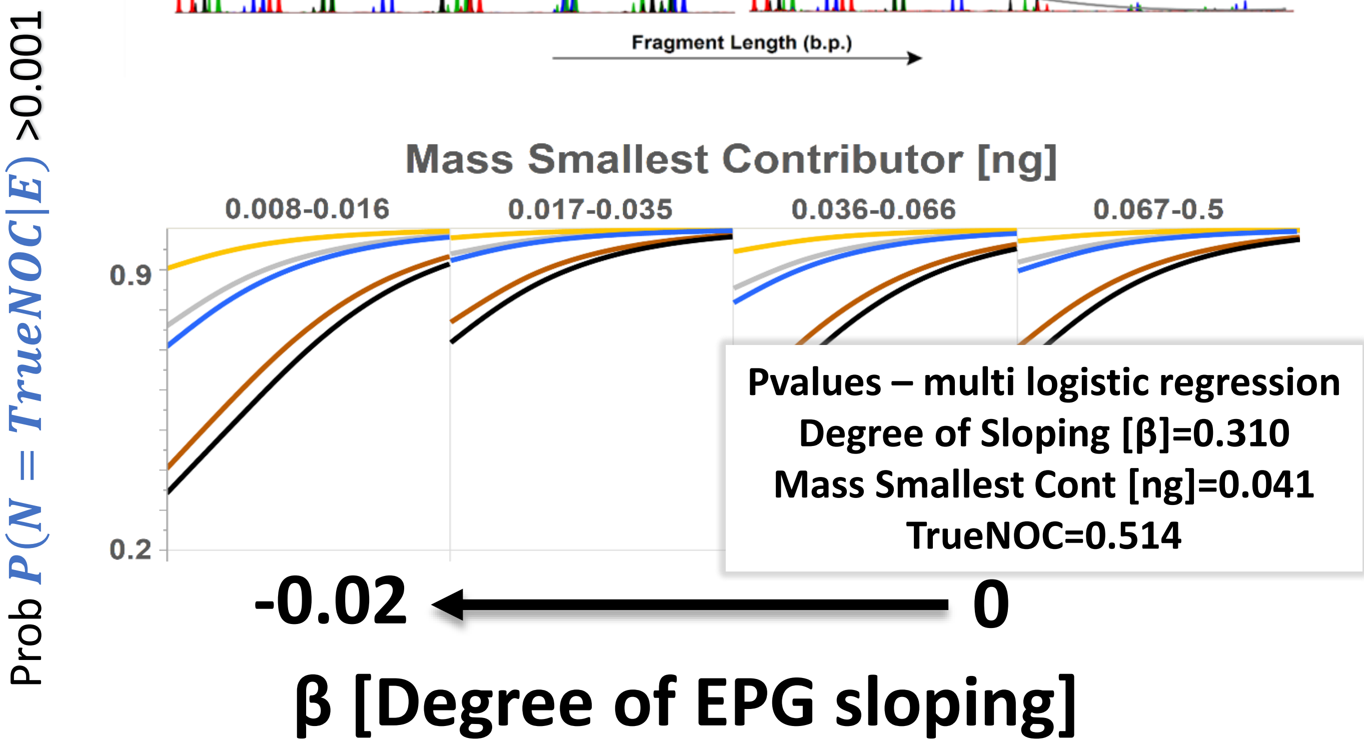
Results: NOCIt performance equals or exceeds current procedures at all α

NOCIt is Robust across Contexts and DNA Qualities

$$PH_l = \varphi e^{\beta \overline{w_l}}$$







Pvalues – multi logistic regression
Degree of Sloping [β]=0.310
Mass Smallest Cont [ng]=0.041
TrueNOC=0.514

***Criterion*: Resilient to sloping – i.e., degradation/inhibition effects**

***Results*: Pvalue of 0.310 suggests sloping [β] does not significantly affect probability of including TrueNOC when α=0.001 (or 0.5)**

***Criterion:* Works under different contexts**

***Results*: Most apexes shifted when a known contributor was assumed and it was the minor**

SUMMARY

NOCIt reports $P(N = n|E)$ – i.e., the posterior distribution for all n up to 6

Supports pipelines that do not apply default or subjective n, or automatic $P(N = n|E)$

Helps target n with non-negligible $P(N = n|E)$

Engineered to use all data (even noise)

Full descriptions in:

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Research paper

A large-scale validation of NOCIt's *a posteriori* probability of the number of contributors and its integration into forensic interpretation pipelines

Catherine M. Grgicak[a,b,*], Slim Karkar[b], Xia Yearwood-Garcia[c], Lauren E. Alfonse[c], Ken R. Duffy[d], Desmond S. Lun[b,e,f]

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ELSEVIER

Research paper

The a posteriori probability of the number of contributors when conditioned on an assumed contributor

FUNDING, COLLABORATORS & STUDENTS

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