

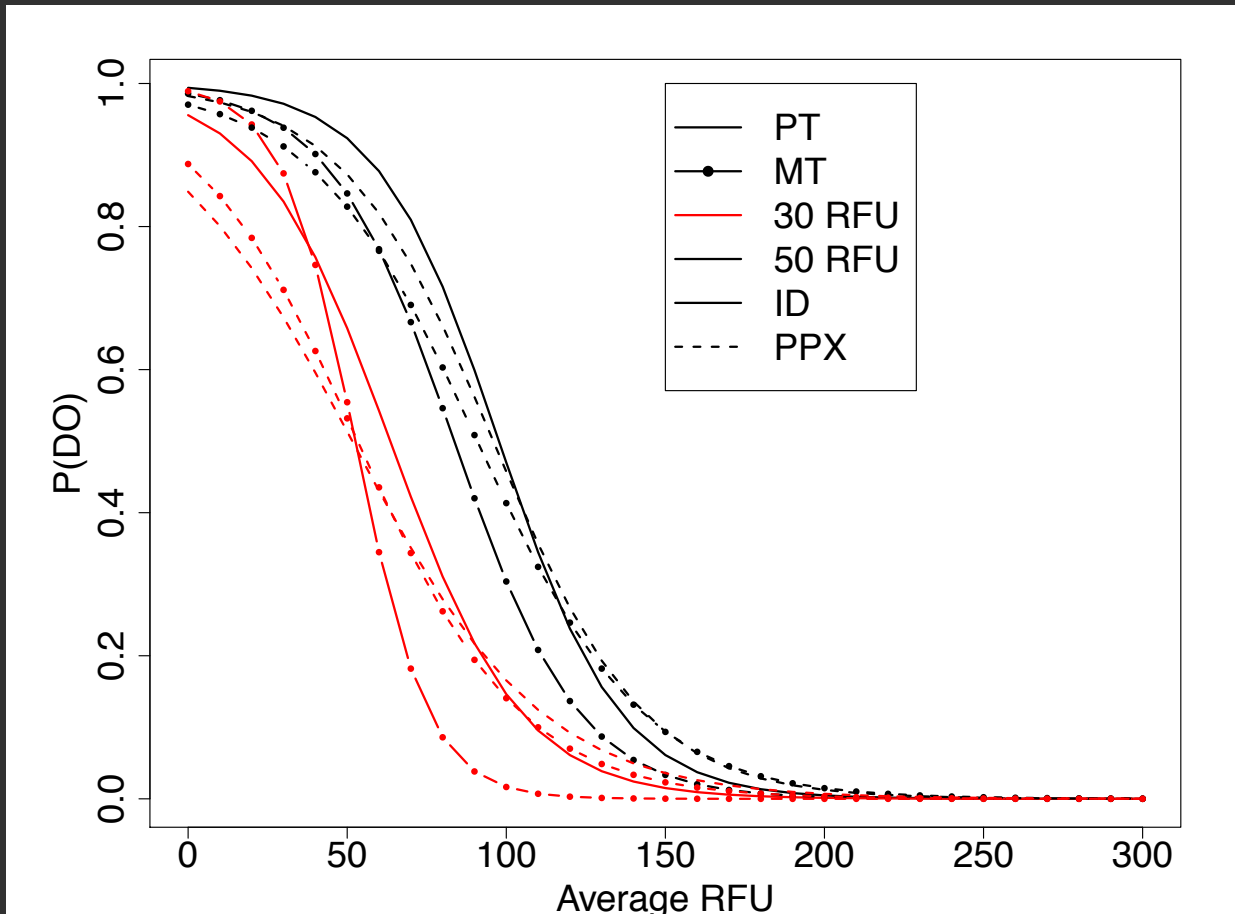
Analysis of Allelic Drop-out

II. Evaluation of drop-out probabilities

Some initial findings

- Previous work found several statistically significant differences when estimating
 - Drop-out between different samples
 - Relationship between peak heights and experimental conditions.
- Could estimating dropout probabilities from peak heights compromise accuracy of LR?

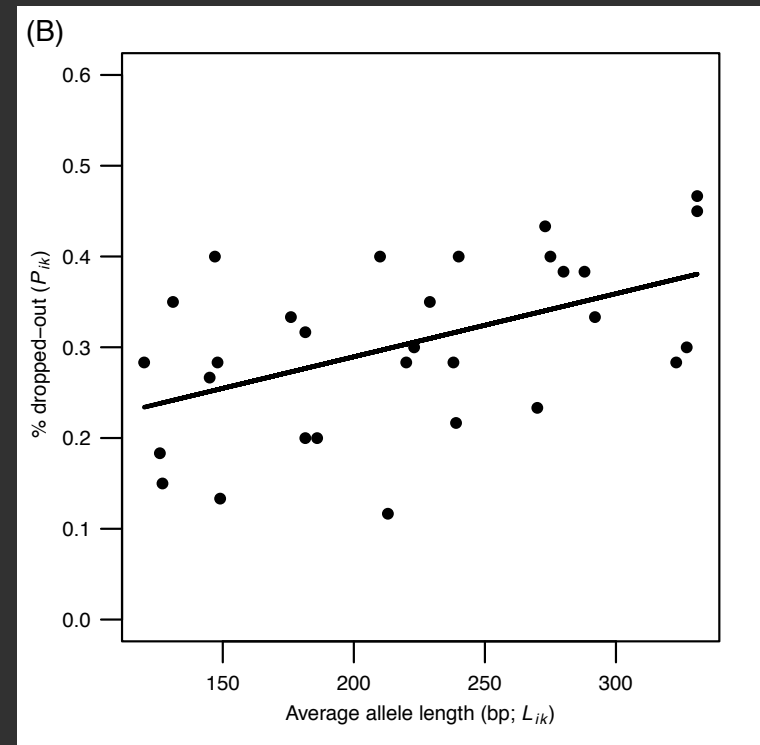
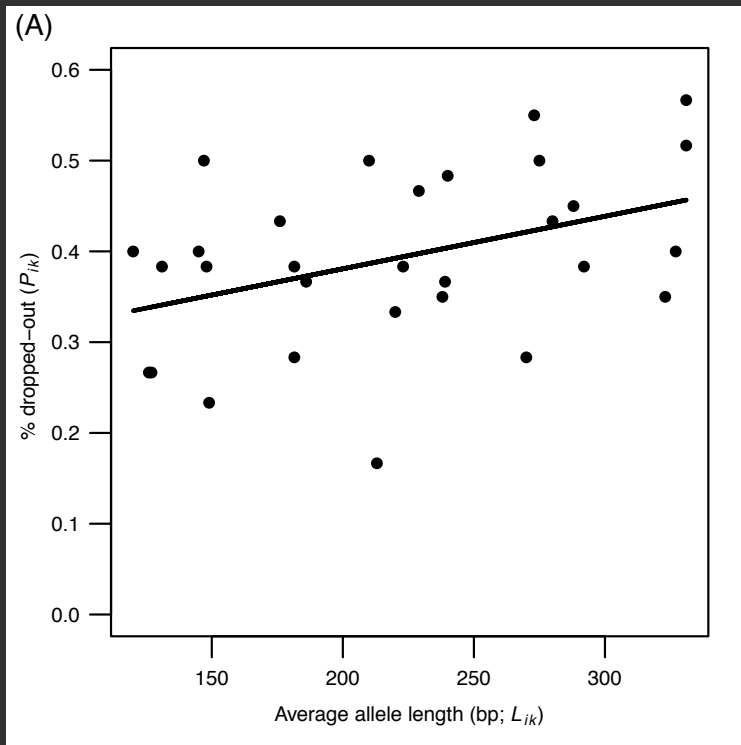
Less than perfect overlay



Dropout as a function of average RFU

Do the differences matter?

Identifiler data



Need to know...

- The practical effect of these differences remained unclear.
- Performed simulation studies to evaluate accuracy and practical applicability of estimated drop-out probabilities.

Testing the model

- Assume that each profile is an evidence profile
- Compare the evidence to a suspected contributor
- Compute two LR's
 - One uses our estimated probability of dropout
 - The other uses the true dropout
 - If estimated dropout is accurate, then

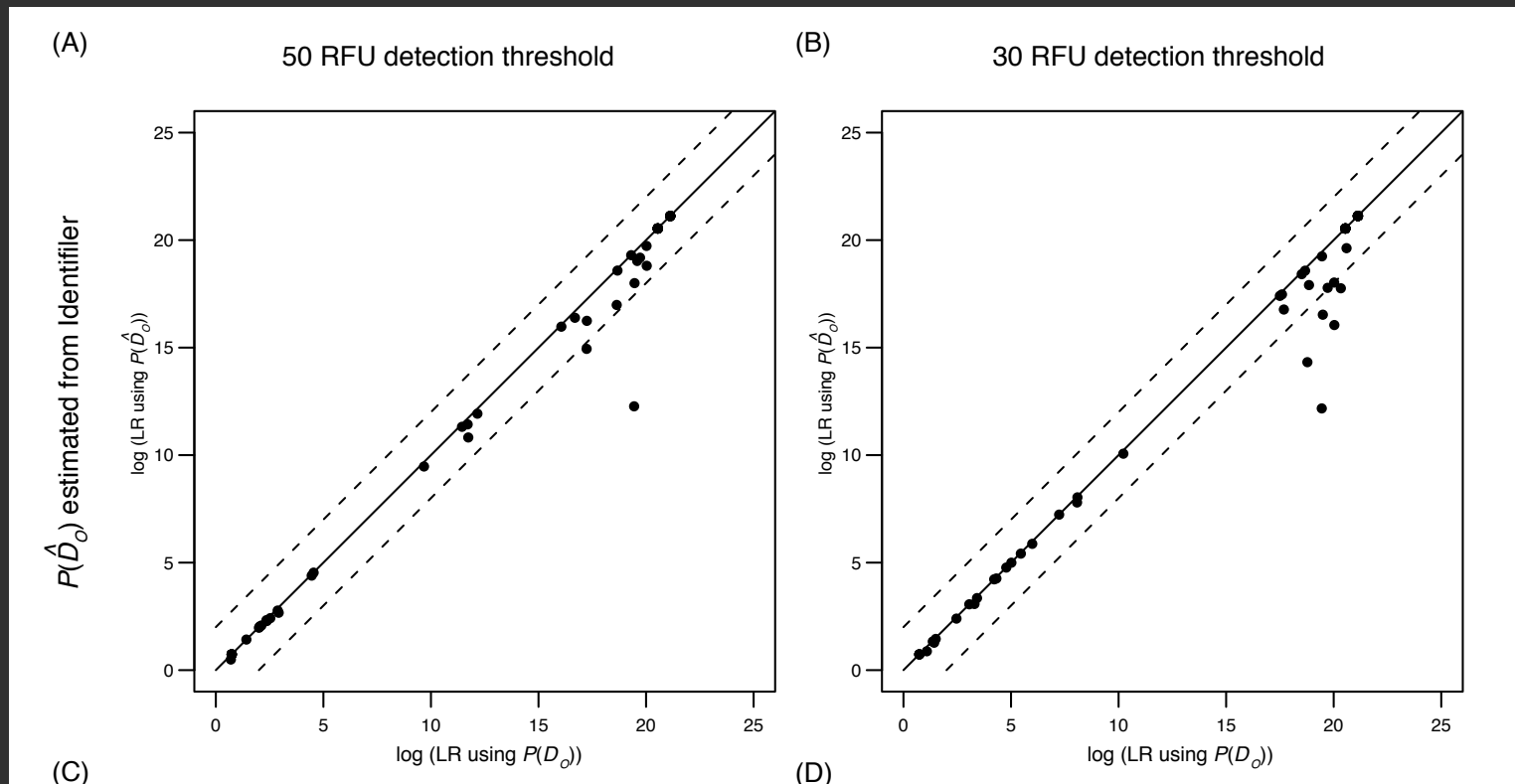
- $LR_{\text{estimated}P(D_o)} \cong LR_{\text{true}P(D_o)}$

Study One: True contributor

- Evaluated the true contributor as the suspected contributor of the LT DNA evidence.
 - For MT97150
 - Genotype of suspected contributor was MT97150
 - For PT84411
 - Genotype of suspected contributor was PT84411
 - Denominator was a random individual
 - Frequency data from Butler (2003) or Levadokou (2001)
 - LRs calculated using Balding and Buckleton (2009) R program.

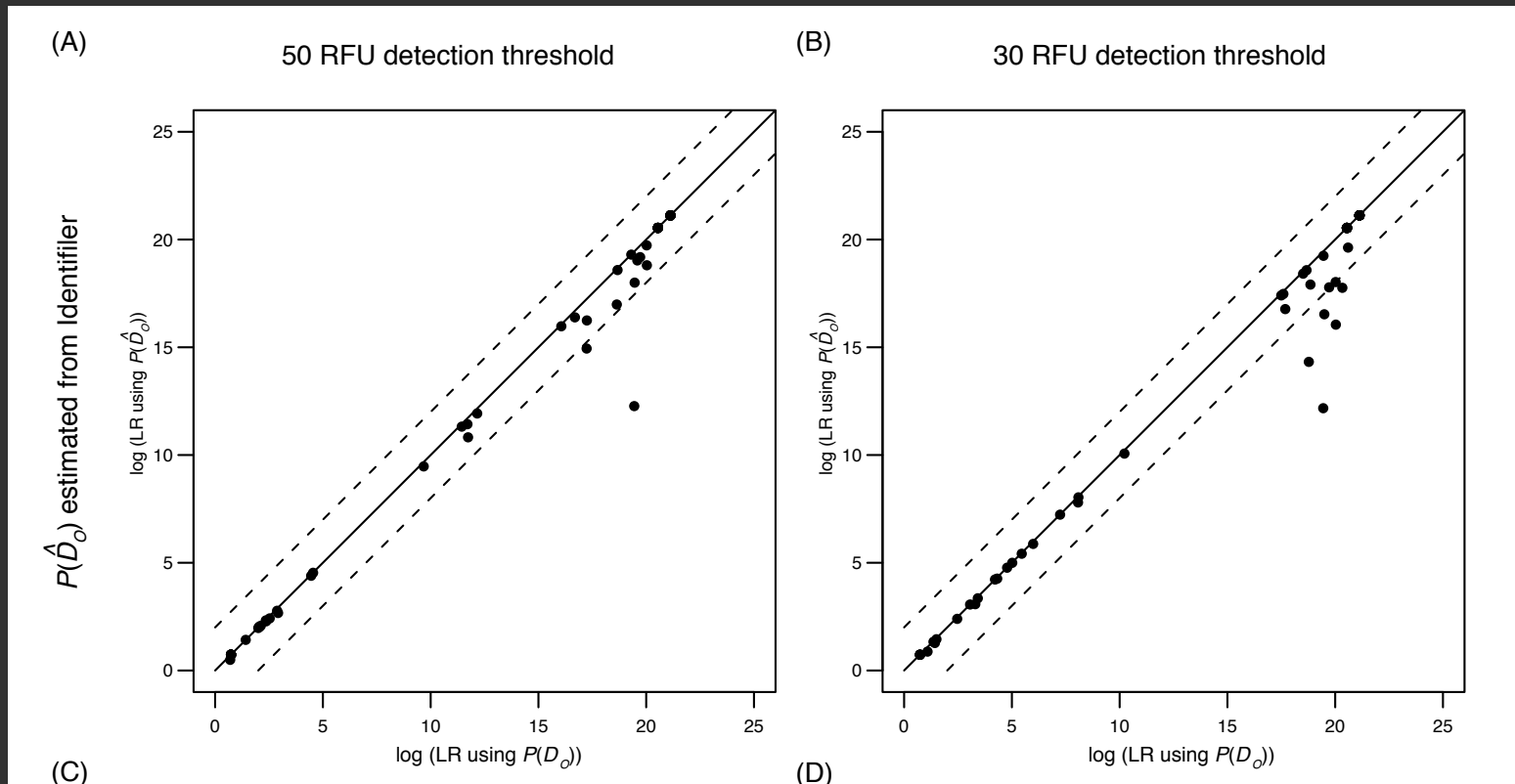
Study One: Comparing all four sets

LRs calculated using $\hat{P}(D_0)$ typically fall within two orders of magnitude of those calculated using $P(D_0)$.

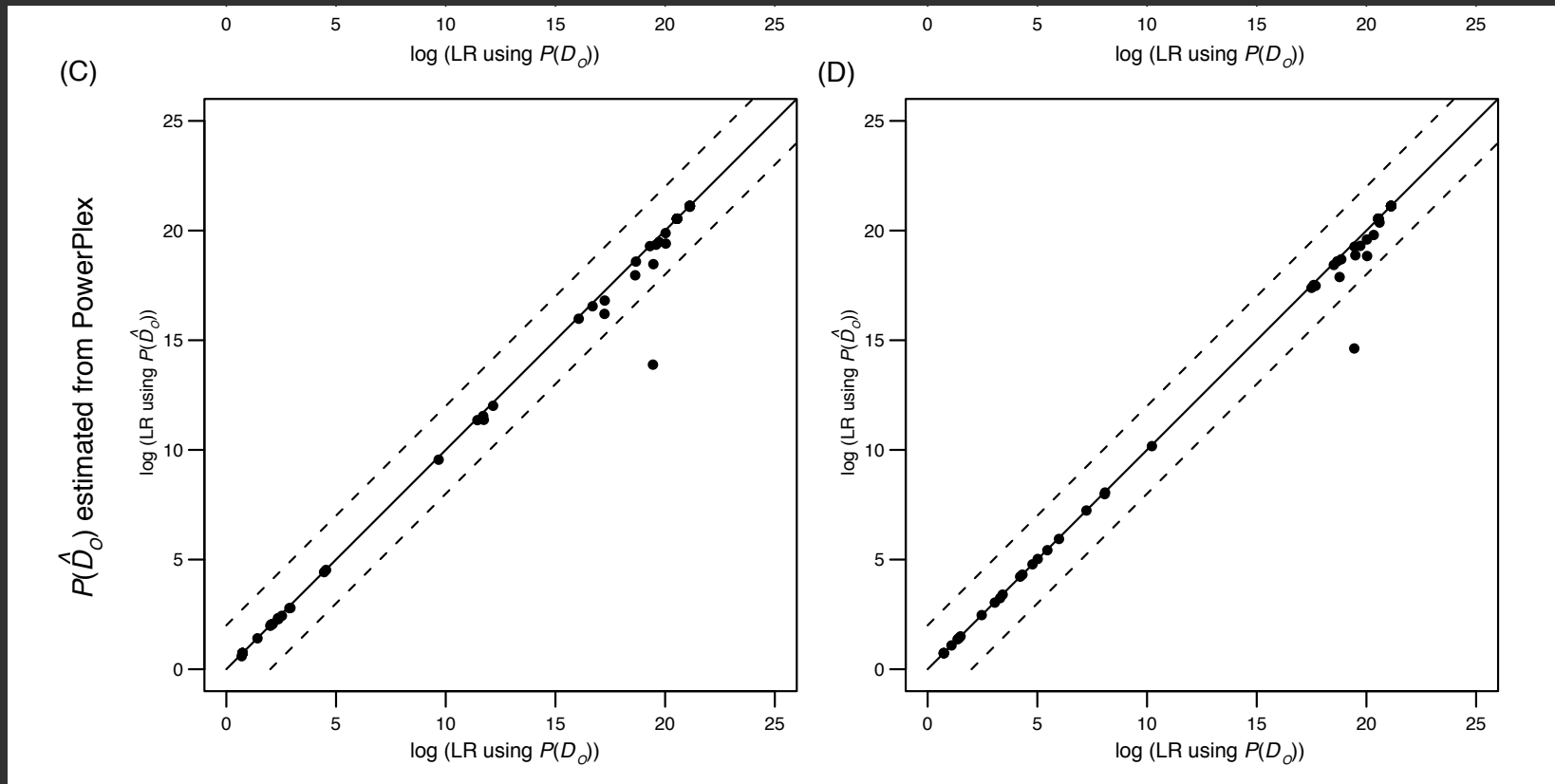


Study One: Comparing all four sets

When LRs differ by $>$ two orders of magnitude, LRs using $\hat{P}(D_o)$ lower than $P(D_o)$.



Powerplex data



Study Two: Known non-contributor

- Evaluated a true non-contributor as the suspected contributor of the LT DNA evidence
 - Suspected contributor was a random individual simulated from a US population database
 - Denominator was a random individual
 - Frequency data from *Butler (2003)* or *Levadokou (2001)*
 - LRs calculated using Balding and Buckleton (2009) R program.

When you've got the wrong guy (or gal)...

Detection threshold	Drop-out probability ^b	% LRs <1	% LRs <2	% LRs >100	% LRs >1000	99.9% of LRs are < than...	Max LR
50 RFU	True $P(D_o)$	84.199%	99.432%	0.053%	0.010%	33.8	66,029.3
	Estimated using Identifiler	84.302%	99.532%	0.031%	0.001%	27.1	2,398.4
	Estimated using PPX	84.230%	99.504%	0.030%	0.001%	27.1	2,403.1
30 RFU	True $P(D_o)$	92.861%	99.593%	0.041%	0.005%	31.3	1,481,404.0
	Estimated using Identifiler	92.845%	99.600%	0.012%	0.001%	16.7	323,282.4
	Estimated using PPX	92.848%	99.589%	0.012%	0.001%	17.6	340,162.9

When you've got the wrong guy (or gal)

...

Detection threshold	Drop-out probability ^b	% LRs <1	% LRs <2	% LRs >100	%LRs >1000	99.9% of LRs are < than...	Max LR
50 RFU	True $P(D_o)$	99.975%	99.981%	0.005%	0.001%	0.001	2,663.7
	Estimated using PPX	99.982%	99.986%	0.004%	0.0%	0.038	525.1
	Estimated using Identifiler	99.984%	99.985%	0.004%	0.0%	0.029	487.7
30 RFU	True $P(D_o)$	100%	100%	0%	0%	0	6.6×10^{-7}
	Estimated using PPX	100%	100%	0%	0%	2.84×10^{-13}	1.4×10^{-2}
	Estimated using Identifiler	100%	100%	0%	0%	4.92×10^{-13}	7.3×10^{-2}

Summary of Study Two

- For the majority of the comparisons (>80%), the LRs were < 1 ,
- regardless of detection threshold, typing system, or how was estimated
- LRs correctly reflected support for the hypothesis that the known non-contributor was not the true donor.

What it all means

- For both simulations
 - LRs from estimated drop-out probabilities similar to true drop-out probabilities
 - **estimates** of drop-out probability are accurate and useful.
- Trend holds for PowerPlex® 16 data as well
- Thus, while some logistic regression model parameters show statistically significant differences
 - Results are similar enough to have little practical effect on the final LRs calculated using estimated drop-out probabilities.
- We demonstrate that use of LR using empirically estimated allelic drop-out probabilities provides a reliable means for extracting maximum information from LT forensic DNA profiles.

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