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SESSION ID: CRYP-R03

Poly-Logarithmic Side Channel Rank Estimation via Exponential Sampling

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- Reveals the secret key of an encryption algorithm
- by using the side information that leaks from its implementation.
- For example:
 - Power consumption
 - Electro-magnetic radiation
 - Sound
 - Cache









Secret Key

128 bits

\$%\$#@!@#\$%^&*&^%\$%^&%^%#@\$%^&\$#@\$%^&#@!#\$!~!#%&\$*&!^





It is difficult to reveal all 128 bits in one try...



Secret Key

128 bits

\$%\$#@!@#\$%^&*&^%\$%^&%^%#@\$%^&\$#@\$%^&#@!#\$!~!#%&\$*&!^





The attacker reveals a small part of bits each time

Denoted by subkeys



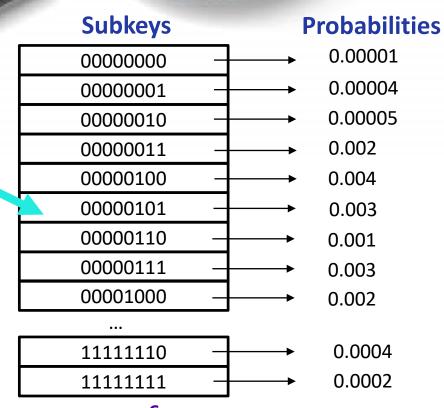
Secret Key

8 bits 8



Secret Key

The first Subkey





Secret Key

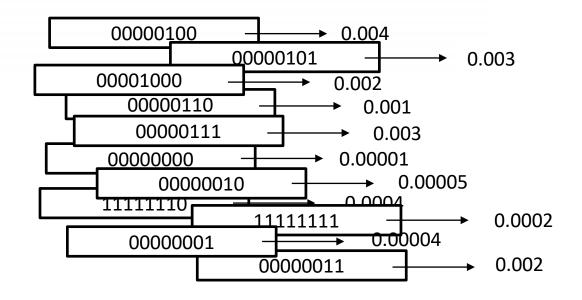
The first Subkey



Subkeys

Probabilities

We sort the subkeys according to their probabilities in decreasing order...





Secret Key

The first Subkey

 (P_1,K_1)

00010100	0.0010
10110111	0.005
11011011	0.005
01000011	0.0045
01110000	0.0043
11011010	0.003
10101110	0.003
01001111	0.002
10100110	0.0015

00000000	0.000001
11111111	0.000001



in decreasing order of probabilites



Secret Key

Sorted subkeys

in decreasing

probabilites

order of

8 bits 8 bits 8 bits \$%\$#@!@# @\$%^#& \$&@%

The Second Subkey



 (P_1,K_1)

000	
101	
110	
010	
011	
110	
101	
010	

/ [K	١
ĮΓ	21	N_2	ı

00010100	0.00
10110111	0.00
11011011	0.00
01000011	0.00
01110000	0.00
11011010	0.00
10101110	0.00
01001111	0.00
10100110	0.00

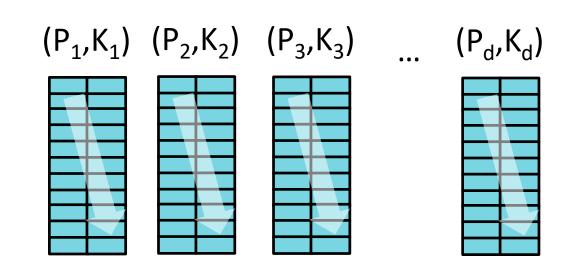
•••	
00000000	0.000001
11111111	0.000001

00010100	0.0010
10110111	0.005
11011011	0.005
01000011	0.0045
01110000	0.0043
11011010	0.003
10101110	0.003
01001111	0.002
10100110	0.0015

00000000	0.000001
11111111	0.000001



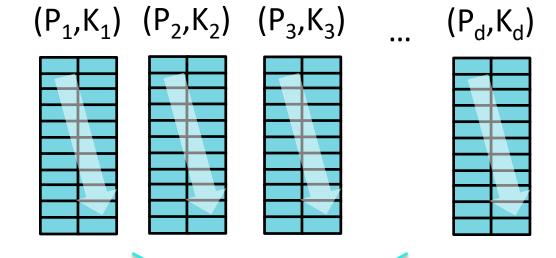
- d independent subkey
 spaces (K_i,P_i) each of size N
- **sorted** in decreasing order of proabilities.



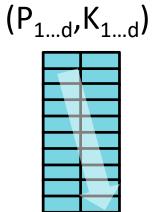


- The attacker goes over the full keys
- in **sorted order** from the most likely to the least,
- till he reaches the correct key.

The probability of a full key is defined as the product of its subkey's probabilities.



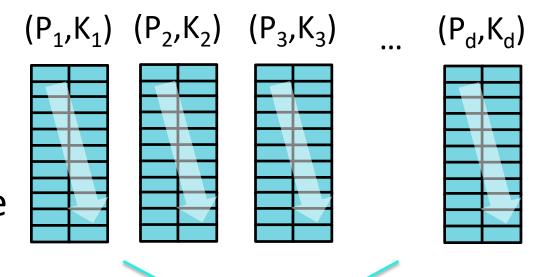


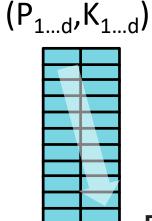


An important question is:

How many full keys the attacker needs to try before he reaches the correct key.

This allows **estimating** the **strength** of the chosen secret key after an attack has been performed.





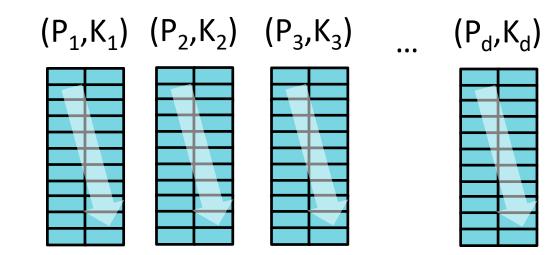


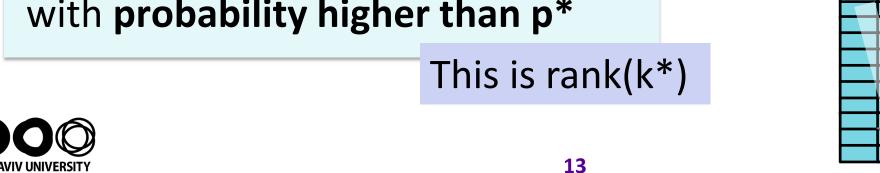
So assume we know

- The correct key k* and its probability p*
- The d subkey spaces (Ki,Pi)

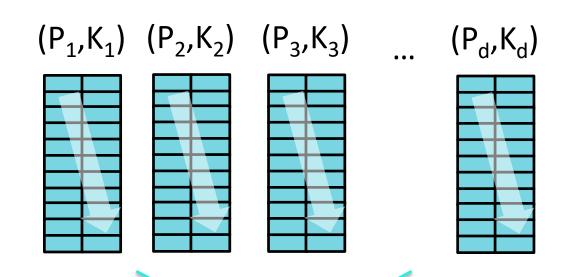
The goal:

to estimate the **number of full keys** with **probability higher than p***



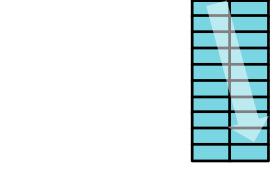


- The optimal solution
- enumerates and counts the full keys in optimal-order
- till reaches to k*



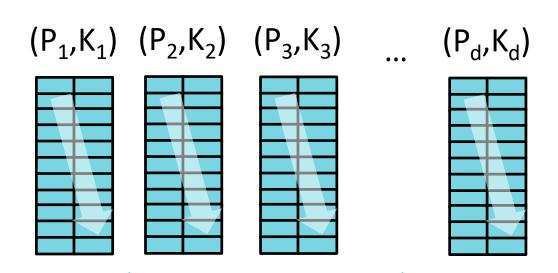


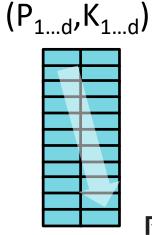
 $(P_{1...d}, K_{1...d})$





- However, key space size is 2¹²⁸
- Enumerating the whole key space in optimal-order is impossible
- Hence, estimating a rank
 without enumeration is of great
 interest.





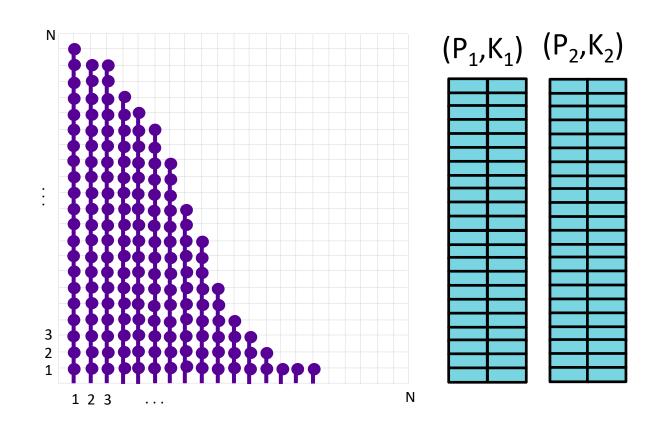


Our ESrank Algorithm: For d=2

Given

- The correct key k* whose probability is p*
- 2 subkeys (P₁,K₁), (P₂,K₂)

rank (k*) is the number of the pairs (i,j) such that $P_1[i] \cdot P_2[j] \ge p^*$



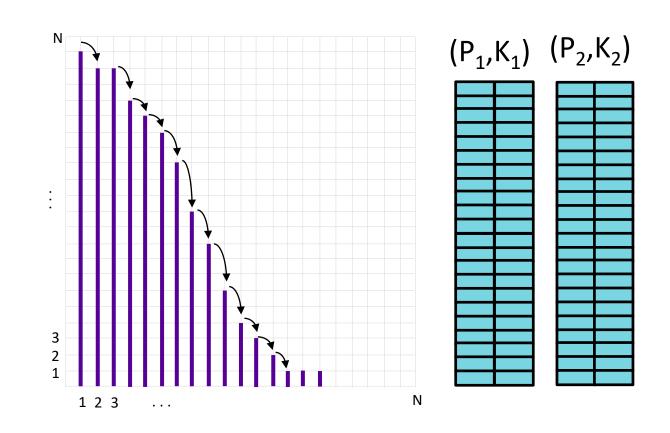


Our ESrank Algorithm: For d=2

We sum the length of bars:

Start with i=1, j=N, decrease j till $P_1[i] \cdot P_2[j] \ge p^*$ then increment i and repeat till i=N or j=1

O(N) running time.

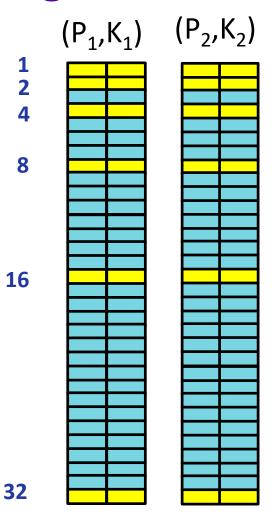




To make this algorithm faster, we use **exponential sampling**.

• Intuitively, sample indices at powers of $\gamma > 1$.

For example, If γ =2 the sampled indices are: 1,2,4,8,16,32,...



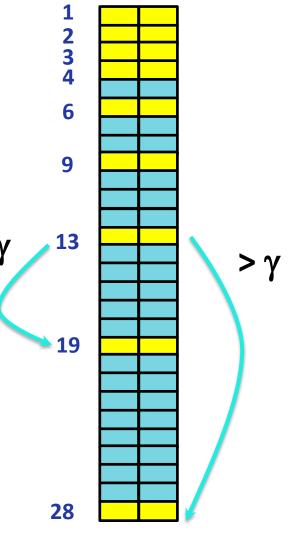


Since the power of γ are not necessarily integers

maintain an invariant
 on the ratio between sampled indices:

 $\frac{\text{i'th sampled index}}{(\text{i-1})'\text{th sampled index}} \leq \gamma$

 $\frac{\text{(i+1)'th sampled index}}{\text{(i-1)'th sampled index}} > \gamma$

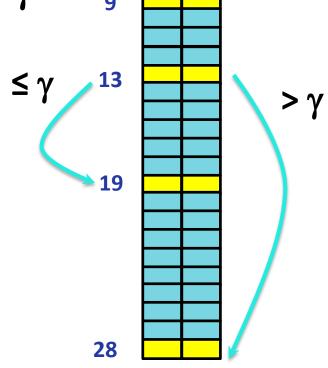




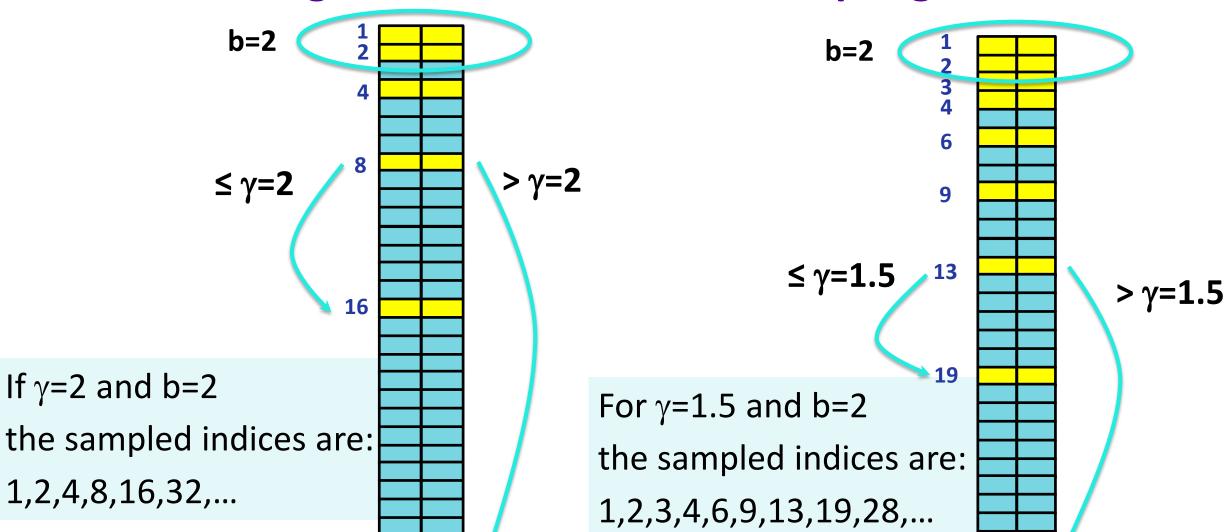
The first indices might not maintain the invariant

• since the ratio between consecutive indices is $> \gamma$

- Let b be the smallest index that maintains the invariant.
- Take the first b indices without sampling
- Sample the rest with ratio γ

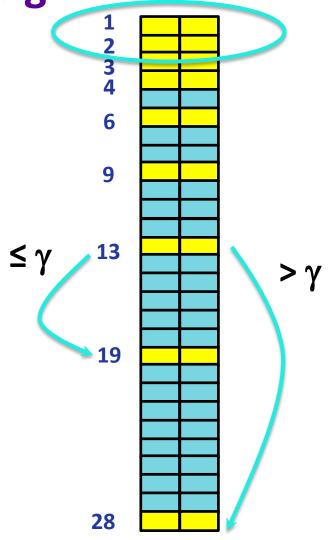








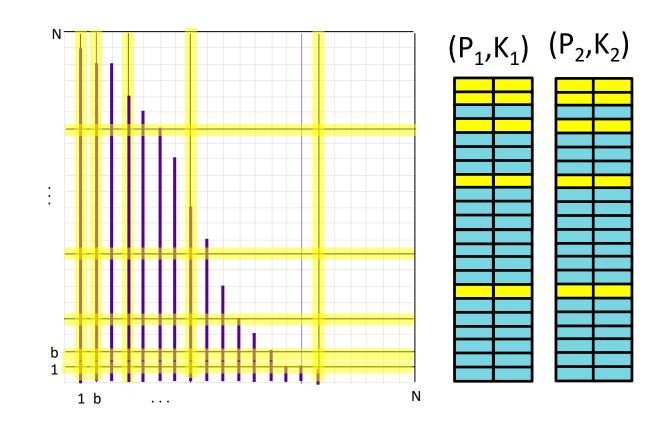
The sampled distribution is of size $O(\log_{\gamma} N)$





Now, given two sampled distibutions and the correct key k*

The goal:
To calculate rank(k*)

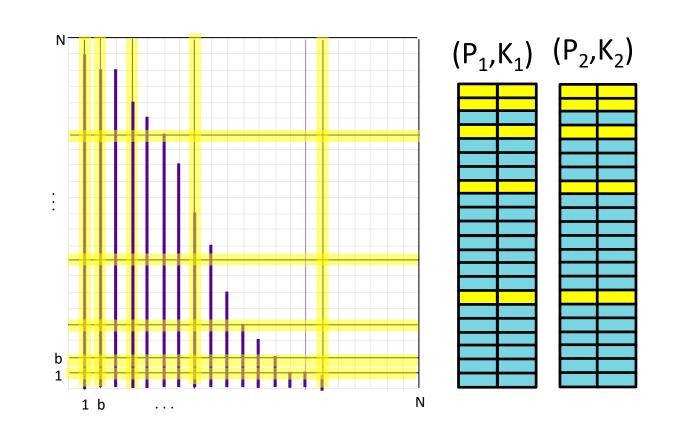




We only have an **access** to the **sampled indices**

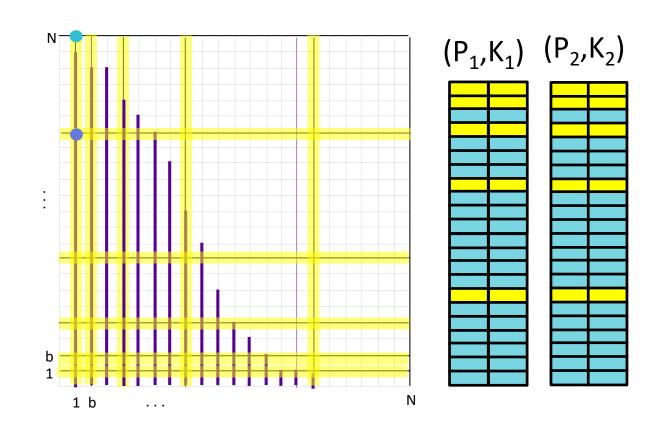
Therefore, we calculate:

- upper bound for rank(k*)
- lower bound for rank(k*)



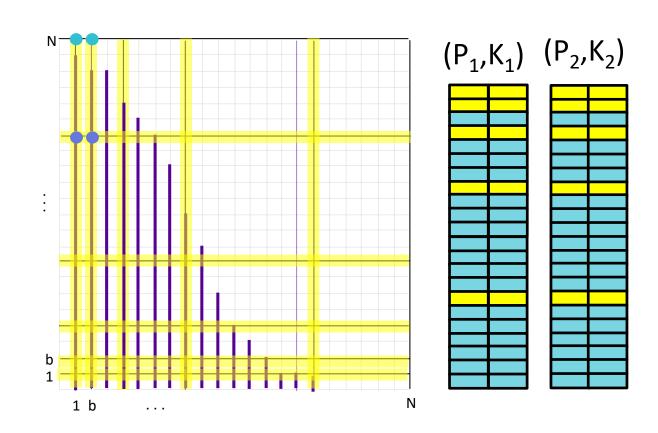


- upper bound for rank(p*)
- lower bound for rank(p*)



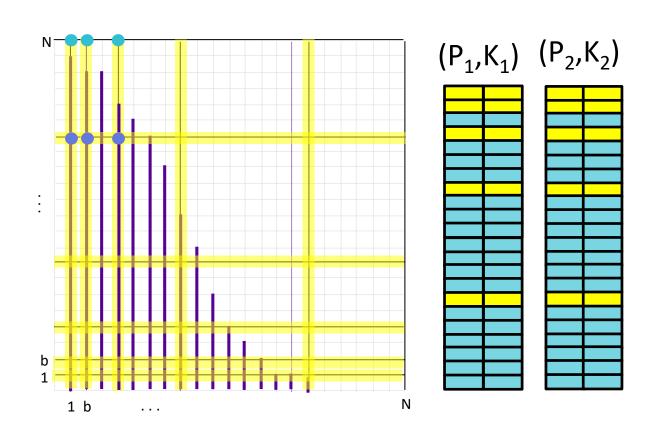


- upper bound for rank(p*)
- lower bound for rank(p*)



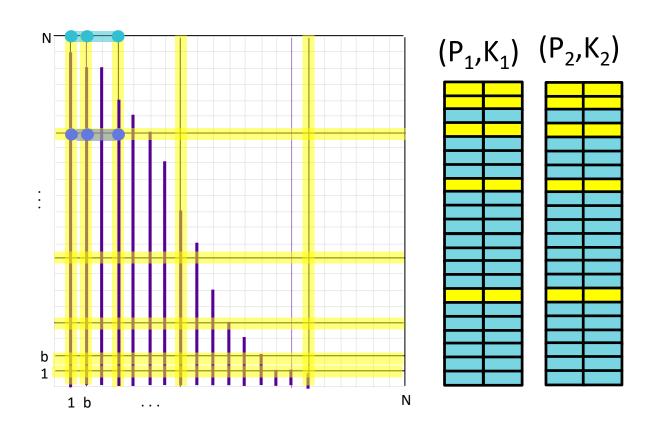


- upper bound for rank(p*)
- lower bound for rank(p*)



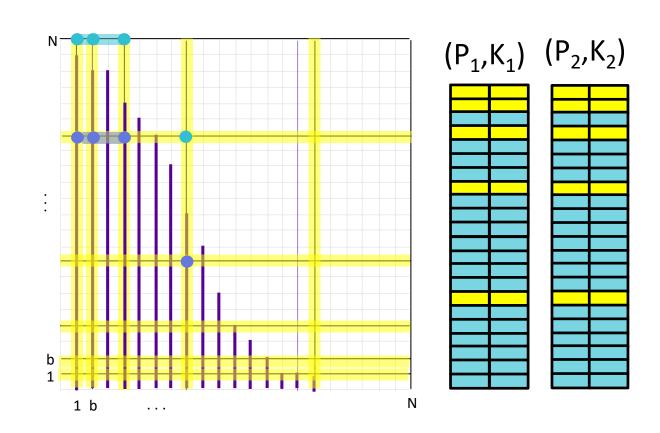


- upper bound for rank(p*)
- lower bound for rank(p*)



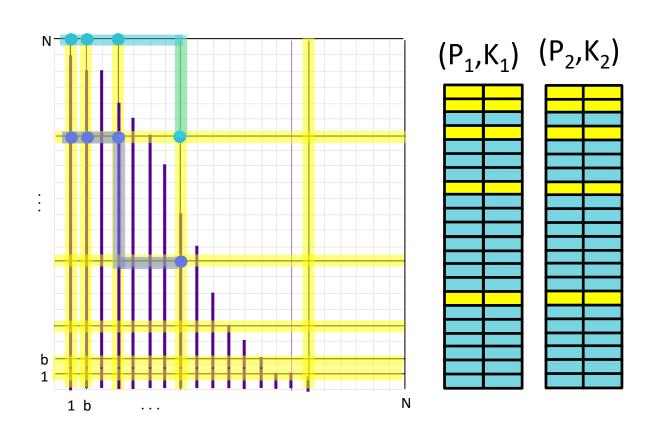


- upper bound for rank(p*)
- lower bound for rank(p*)



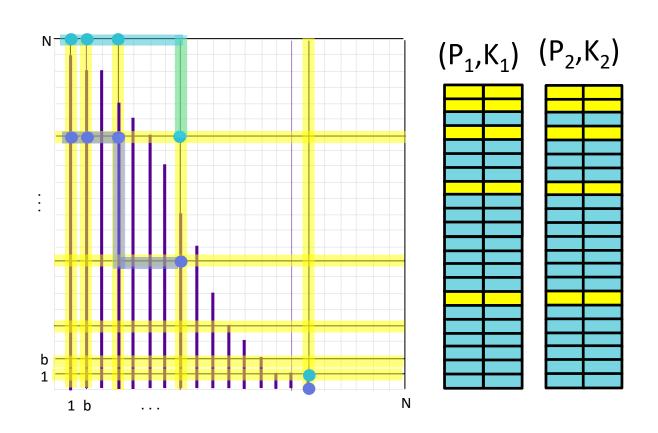


- upper bound for rank(p*)
- lower bound for rank(p*)



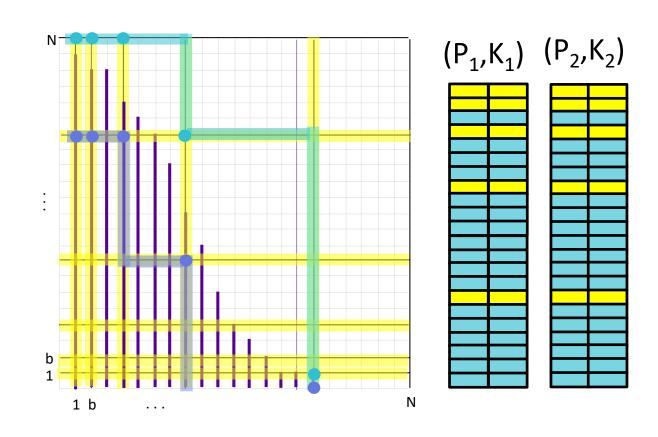


- upper bound for rank(p*)
- lower bound for rank(p*)



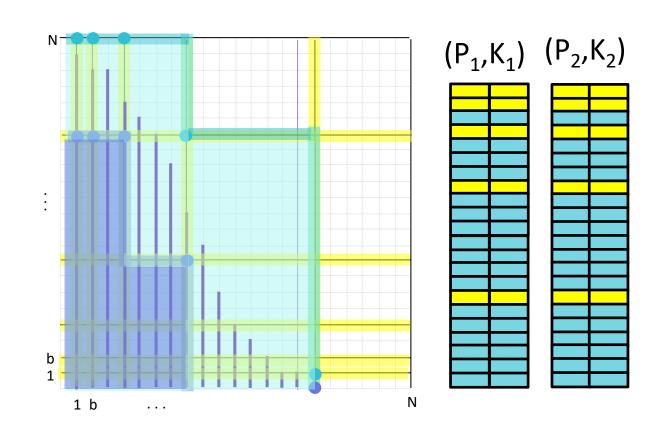


- upper bound for rank(p*)
- lower bound for rank(p*)





- upper bound for rank(p*)
- lower bound for rank(p*)

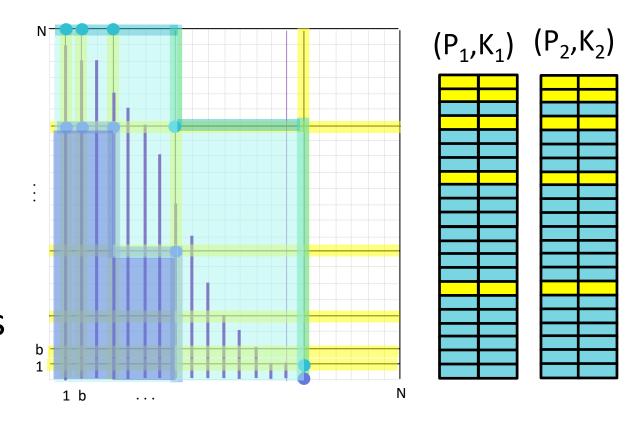




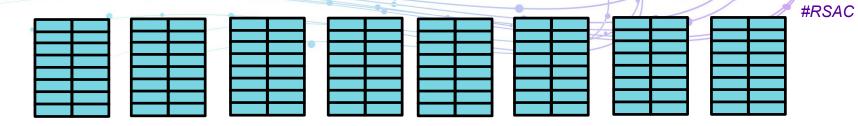
The running time is linear in the size of the sampled distribution,

Therefore $O(\log_{\gamma} N)$

The **ratio** between the **upper** and the **lower** bounds for a given correct key **is bounded by** $< \gamma^2$







d subkey distributions





Sample each distribution s.t.

the **sampled indices** maintain the **invariant with** γ **and b**

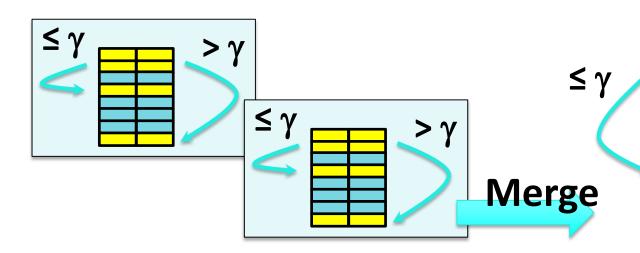
Therefore, each of size $\log_{\gamma} N$



#RSAC

Merge each two sampled distributions





Two sampled distributions

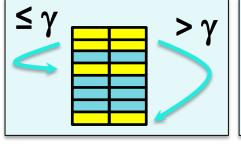
- Each maintains the sampling invariant with γ and b
- $\log_{\gamma} N$



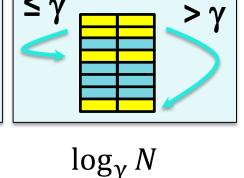


One sampled distribution

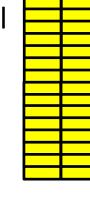
- maintains the sampling invariant with γ and b
- $\log_{\gamma} N^2 = 2 \log_{\gamma} N$



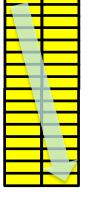
 $\log_{\nu} N$



Calculate the probabilities of all the (x,y) pairs

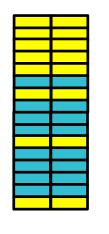


Sort the pairs in decreasing order of probabilities



 $(\log_{\gamma} N)^2$

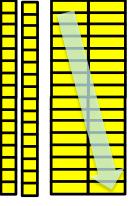
 $(\log_{\gamma} N)^2$



 $\log_{\nu} N^2 = 2 \log_{\nu} N$

Sample with γ and b





 $(\log_{\gamma} N)^2$

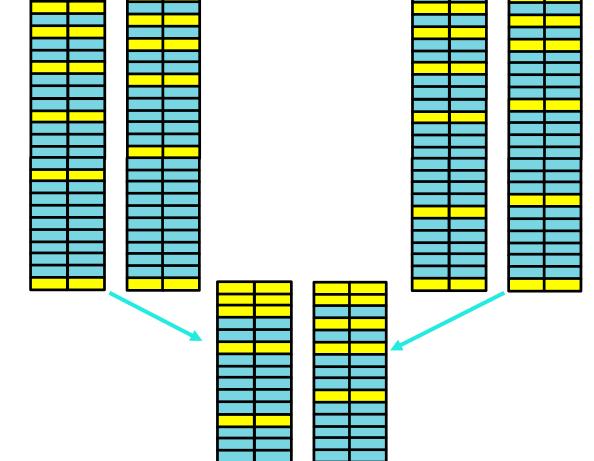
Calculate the upper and lower bounds of the pairs in accumulative way, in one linear pass over the pairs



Merge each

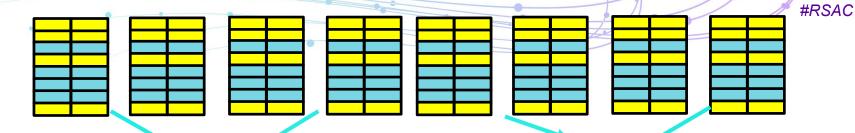
two sampled distribution with γ and b

into one sampled merged distribution with γ and b



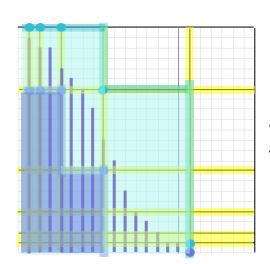


#RSAC



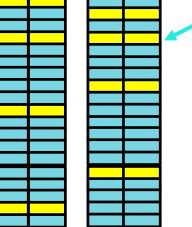
The **ratio between** the final upper and lower bounds of a given key is bounded by

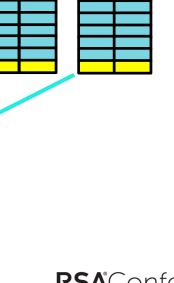
 $< \gamma^{2d-2}$



Apply ESRank for two-dimensions









Results

- Our probability distributions are gathered from a specific SCA against AES with 128-bits keys.
- It contains d = 16 probability lists each of size $N = 2^8$
- We merge them into d = 8 lists each of size $N = 2^{16}$
- The distributions are sorted in non-increasing order of probability.



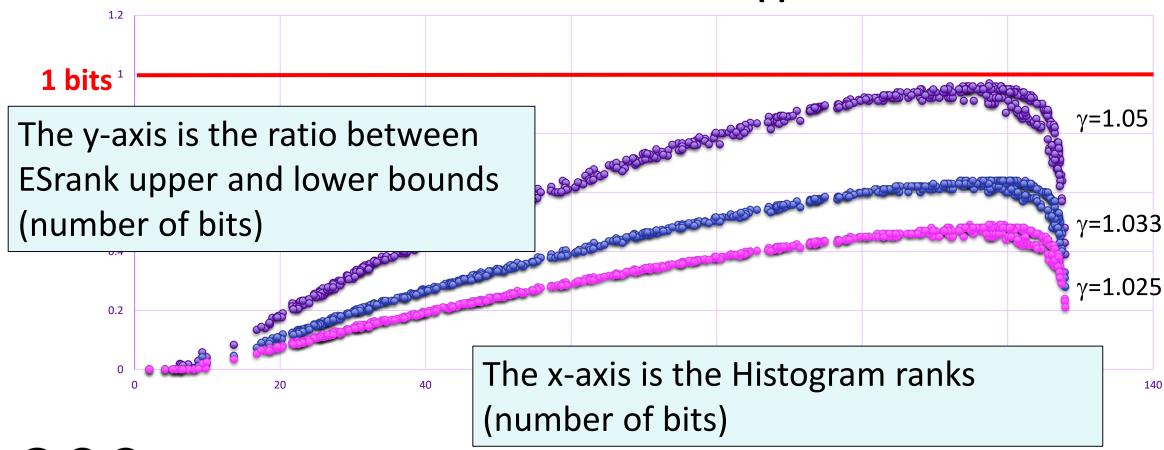
Results

- We measured the upper bound, lower bound, time and space for each trace using ESrank and the Histogram rank estimation of Glowacz et al. [GGPSS15].
- We run with different values of γ and histogram size B.



Results - Accuracy

Excellent accuracy of less than 1 bit margin between ESrank lower and upper bounds





Results – Time and Space

ESrank performance is on-par with the Histogram algorithm:

	Time	Space	Accuracy < 1 bit
	(Seconds)	(MB)	(%)
$\gamma = 1.025$	0.59	6.48	100
$\gamma = 1.033$	0.3	3.68	100
$\gamma = 1.05$	0.16	1.60	99.83
$\gamma = 1.065$	0.05	0.96	56.95
B = 50K	0.62	3.20	100
B = 35K	0.29	2.24	100
B = 20K	0.12	1.28	100
B = 5K	0.01	0.32	99.83

ESrank algorithm gives:

- Excellent accuracy of less than 1 bit
- in less than 1 second
- on a standard laptop using 6.5 MB RAM.



Conclusion

- In this paper we propose a new, simple and effective new rank estimation method called ESrank.
- Our main idea is to use exponential sampling to drastically reduce the algorithm's complexity.
- We prove ESrank has a poly-logarithmic time- and spacecomplexity.
- ESrank is simple to build from scratch, and requires no algorithmic tools beyond a sorting function.

