md5bloom: Forensic Filesystem Hashing Revisited

By

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`md5bloom`: Forensic Filesystem Hashing Revisited

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One-slide Hashing Refresher

- Hashing:
  - Mapping of a large/infinite domain (e.g., all strings) to a small/finite one (e.g., 128-bit strings)
- Properties:
  - Different hashes → different objects
  - Identical hashes (strongly) suggest identical objects
    - Chance collisions (false positives) are possible
    - Good hash functions minimize such probability
    - For **cryptographic** ones it should be virtually zero

Forensic Use of Hashes

- Basic use
  - Assume that identical hashes imply identical objects
  - Compare *before* and *after* hashes
- Scenarios
  - Verify integrity of evidence
  - Automatically identify known content during an investigation
- Hashing pros:
  - Fast, generic, reliable
- Hashing cons:
  - Fragile!

Open Issues

- Evidence validation works just fine, thank you!
- How about content identification?
  - Example scenario:
    - Simple HDD correlation: 500GB vs. 500GB (vs. 500GB …)
    - Related Q: what summaries should we keep of old cases?
  - Approach #1: use NSRL
    - ~ 50,000,000 ***file*** hashes—a **drop** in the bucket!
    - Static reference DB vs. dynamic application installations
  - Approach #2: generate custom hashes
    - File hashes ➔ non-sequential I/O ➔ not scalable!
      ➔ will not identify versions of known files

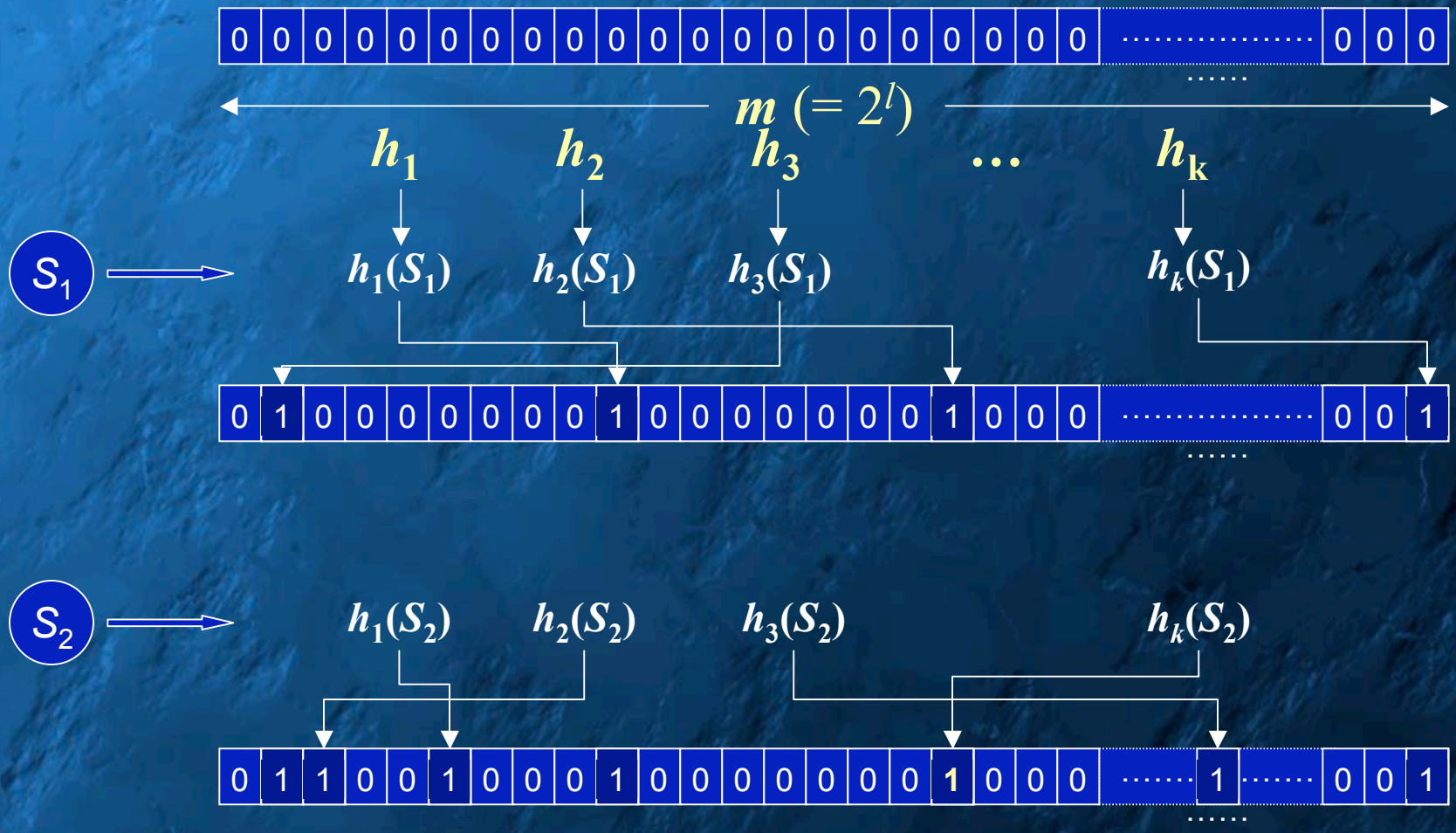
Better Content Identification

- Basic ideas:
  - Finer-grain hashing (e.g. block-level)
    - Linear I/O access—optimal performance
    - Showstopper: RAM
      - Block-level MD5s for 512GB == 16GB
      - ➔ need ~32GB RAM hash table for efficient access
      - RAM & HDD capacities grow at approx the same rate
    - ➔ Need better in-memory representation
  - Structure-based hashing of composite objects
    - Hash logical sub-components (e.g. functions in a library)
    - ➔ Need a unified 'hash bag' representation & comparison rules

Bloom Filters as Hash Bags

- Bloom filter:
  - A simple, space-efficient probabilistic set representation.
    - Operations: insert, lookup, (delete)
      - No false negatives
      - False positives possible (the price of efficiency)
  - Allows quantified trade off between space efficiency and error rate (false positives)
- Numerous variations and uses:
  - Counting, hierarchical, compressed, …
  - Dictionaries, network ID, distributed caching …
  - All uses based on membership queries
  - ➔ no direct comparisons of filters

Bloom Filter Basics



Using MD5s in a *Bloom* Filter

- For all practical purposes, MD5 (SHA-xxx, etc.) is a perfect hash function
  - We can use *any* subset of bits ('subhash) as an independent hash value
  - Predicted FP rates have actually been observed
  - E.g.: $l = 16$ ($m = 2^{16}$)

False Positive (Error) Rates

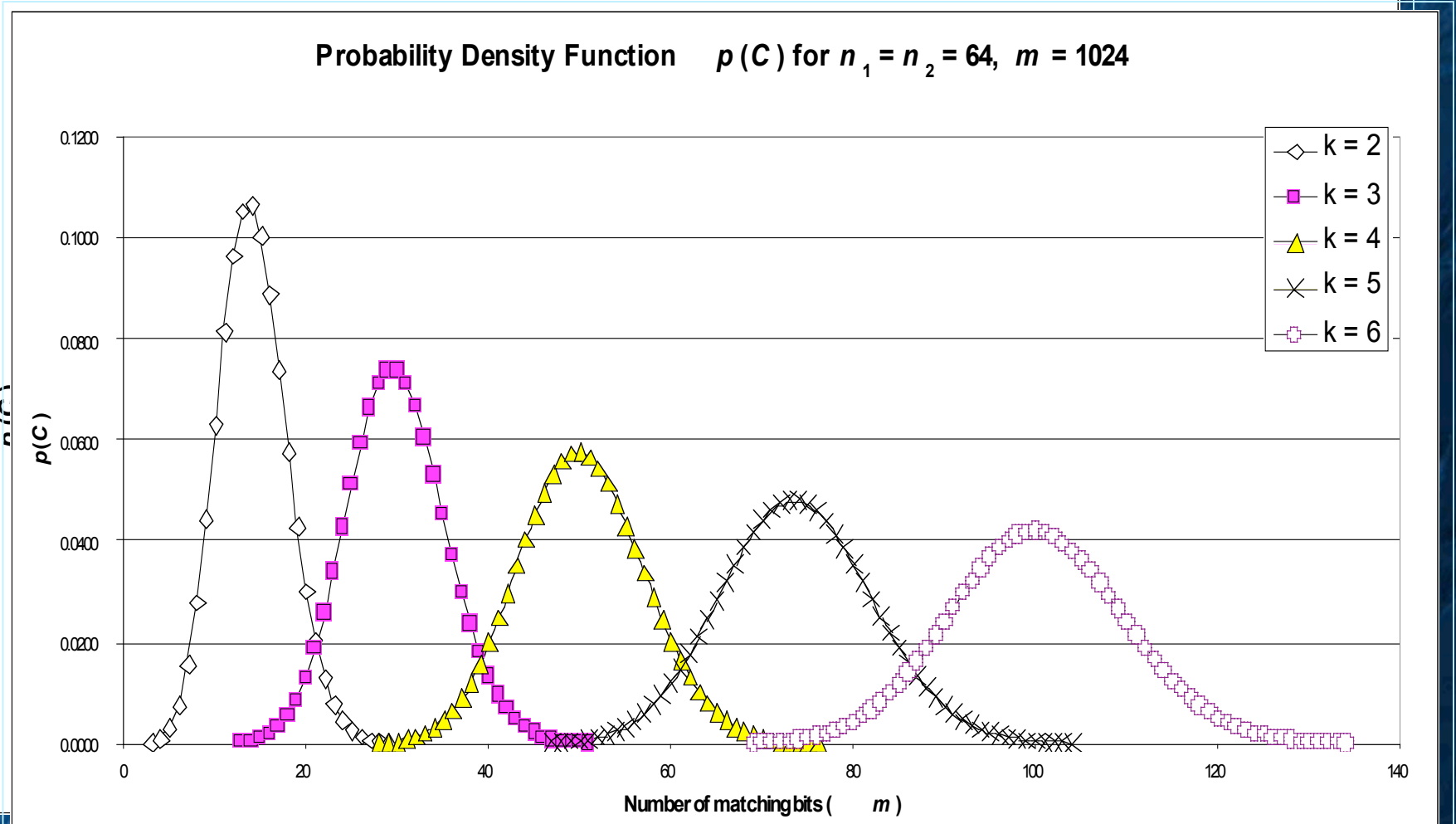
m = 1024		*k*					
		2	4	6	8	12	16
m / *n*	16	0.0138	0.0024	0.0009	0.0006	0.0005	0.0007
	14	0.0177	0.0038	0.0018	0.0013	0.0013	0.0022
	12	0.0236	0.0065	0.0037	0.0032	0.0041	0.0075
	10	0.0329	0.0118	0.0085	0.0085	0.0136	0.0272
	8	0.0490	0.0240	0.0216	0.0255	0.0484	0.0979
	4	0.1549	0.1598	0.2201	0.3128	0.5423	0.7444

- ***n*** = number of elements inserted
- *m*/*n* = bits per element

Bloom Filter Comparison

- Q: How to compare two filters?
- A: Count the number of matching bits
  - ***m***, ***k***, and hash functions fixed, ***n*** may vary
- Q: How to interpret the results?
- A: Estimate the probability that the observed number of matching bits happened by chance (*p*-value)
  - I.e., lower is better
  - E.g., $p = 0.01$ ⇔ there is 1% chance for two random filters with the given parameters to have the observed number of matching bits
  - Matching bits ⇔ inverse of Hamming distance
- Formulas—see paper

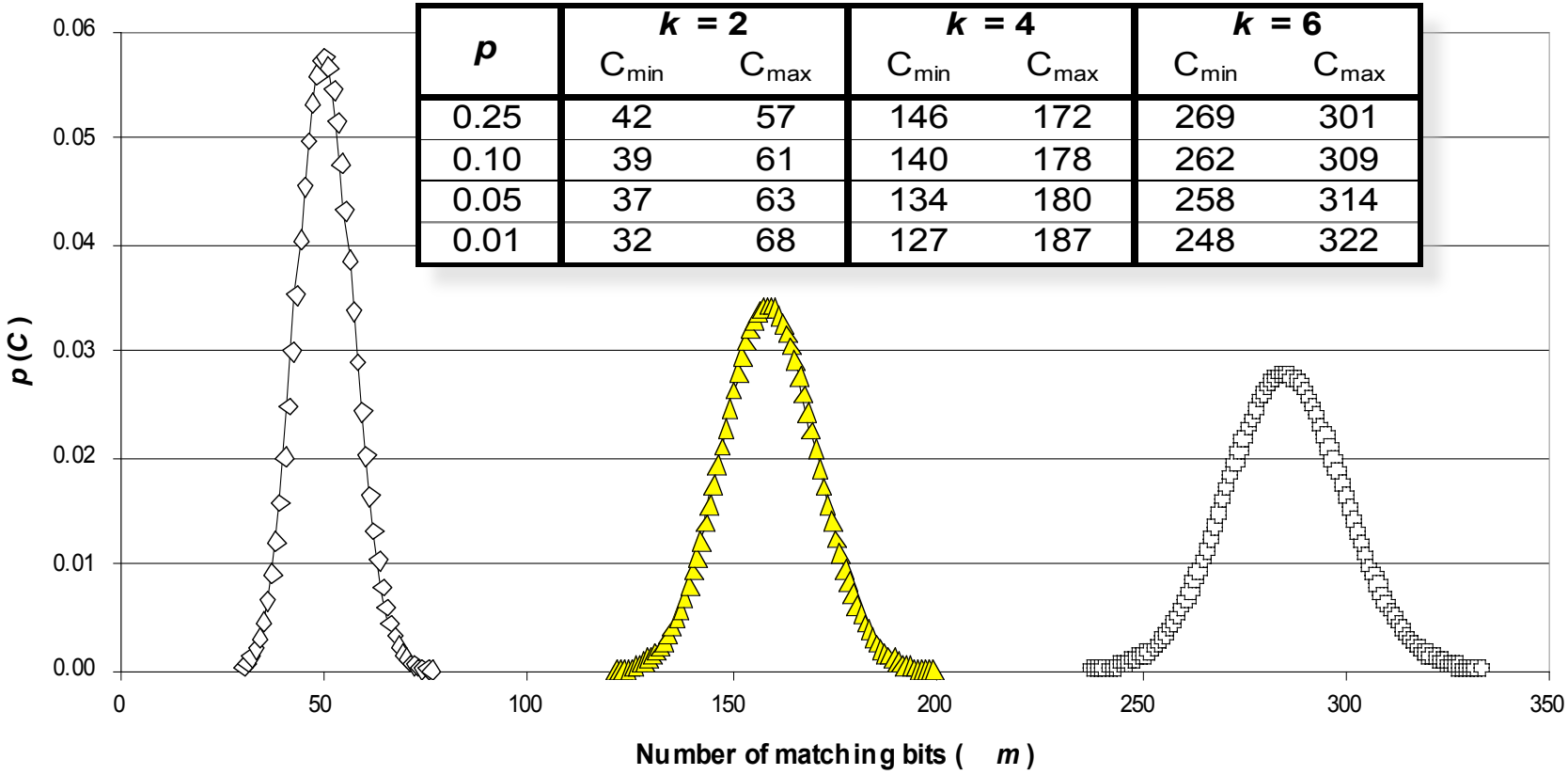
Interpretation: Example *PDFs*



Filter Comparison Interpretation

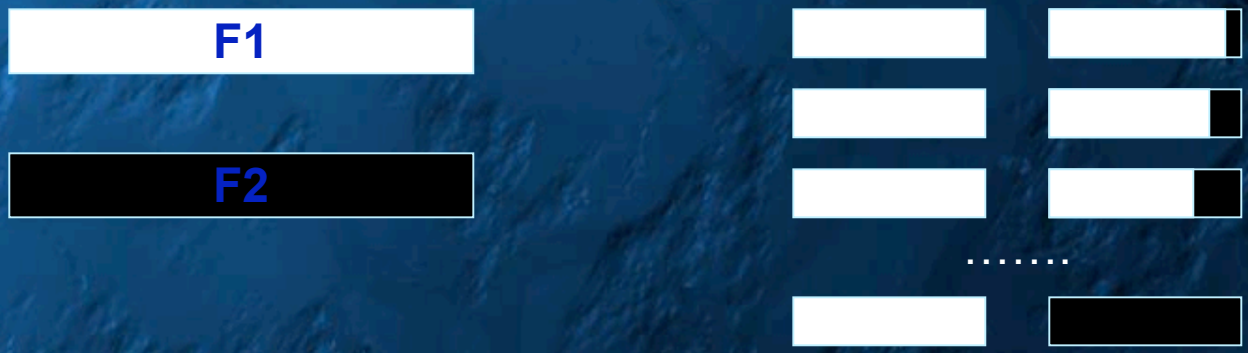
Probability Density Function $p(C)$ **for** $n_1 = n_2 = 128$, $m = 1024$

p	$k = 2$		$k = 4$		$k = 6$	
	C_{min}	C_{max}	C_{min}	C_{max}	C_{min}	C_{max}
0.25	42	57	146	172	269	301
0.10	39	61	140	178	262	309
0.05	37	63	134	180	258	314
0.01	32	68	127	187	248	322

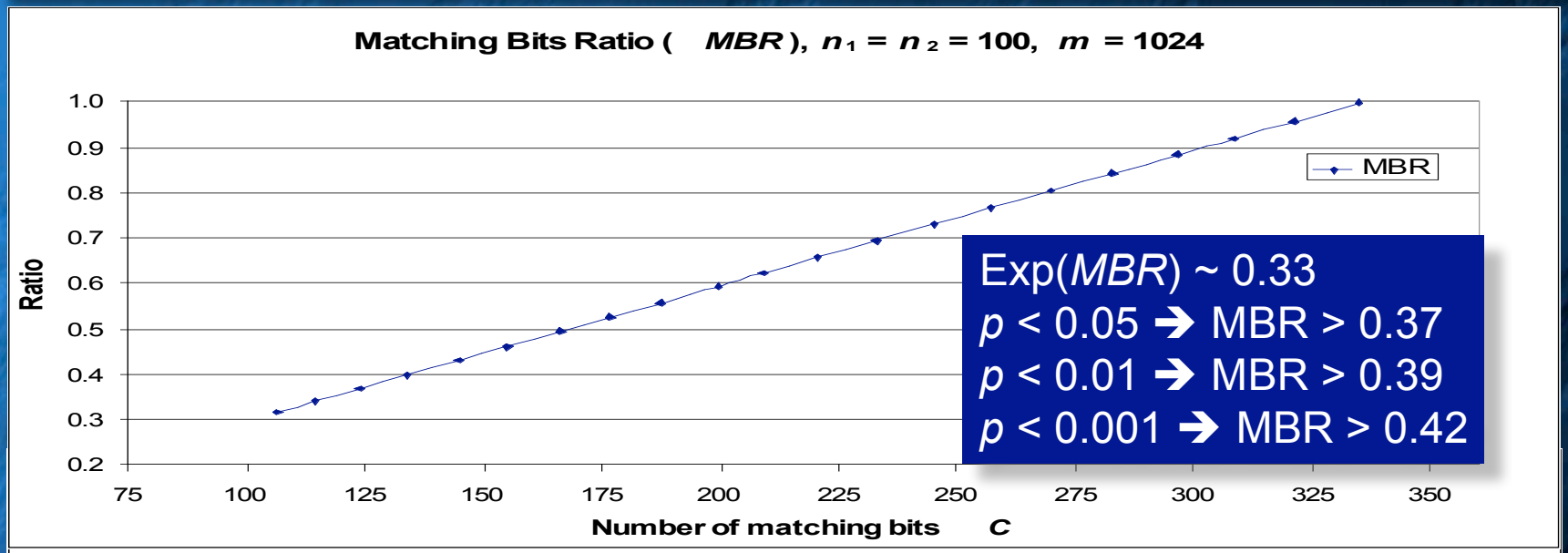


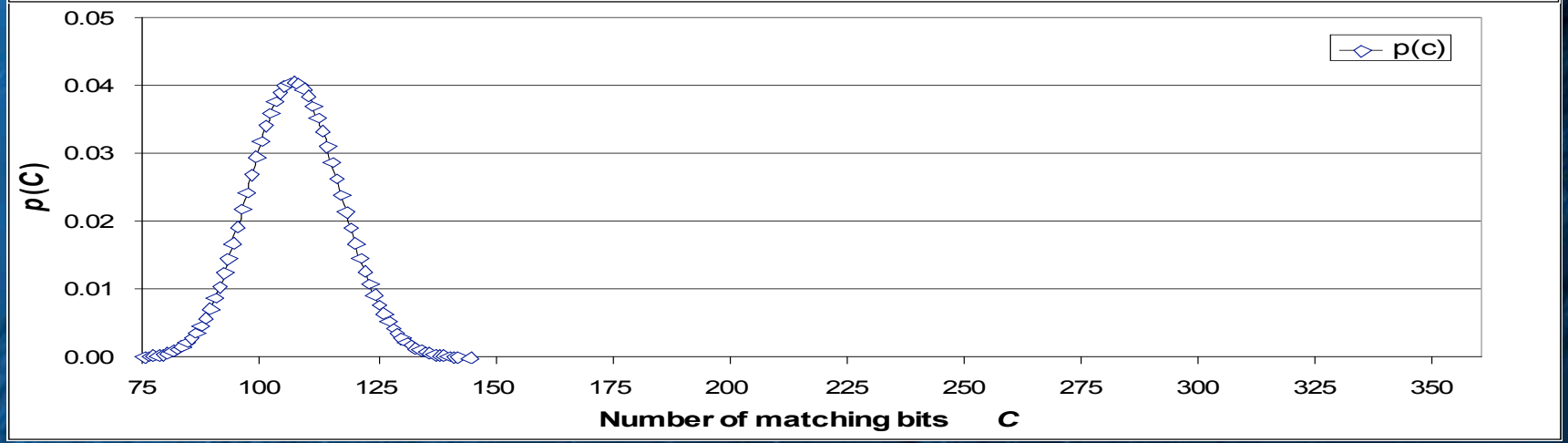
Filter Comparison Interpretation (2)

- Q: Can we relate the fraction of matching bits to the *p*-value?
- A: Demonstration experiment
  - Generate two random filters of MD5 hashes—100 each
  - Compare one filter w/ controlled mix of the two:
    - F_1 vs. 100x/0, F_1 vs. 95/5, F_1 vs. 90/10, …, F_1 vs. 0/100 (F_2)



MBR vs. PDF

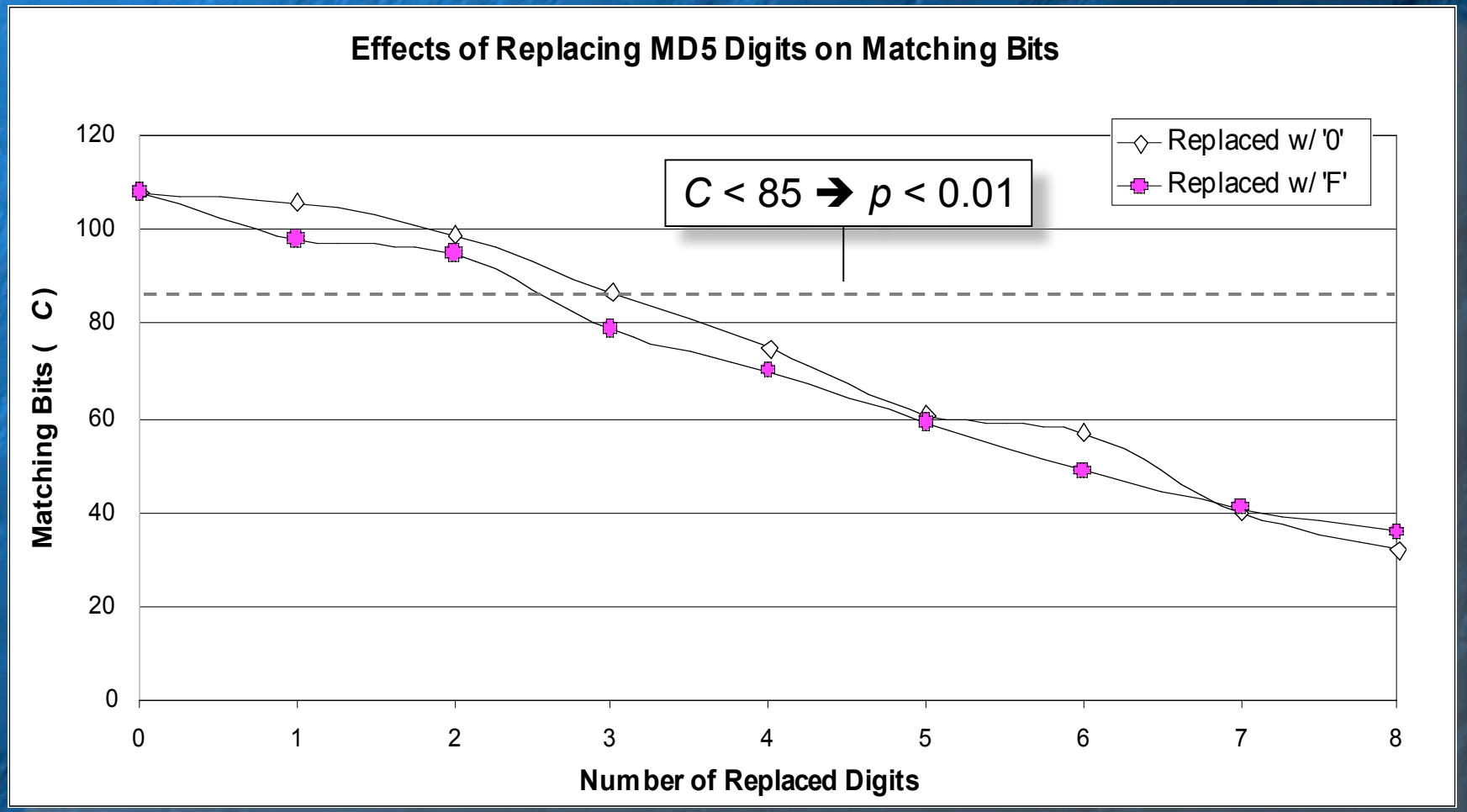

Matching Bits Ratio (MBR), $n_1 = n_2 = 100$, $m = 1024$
Ratio
1.0
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
MBR
75
100
125
150
175
200
225
250
275
300
325
350
Number of matching bits C
Exp(MBR) ~ 0.33
p < 0.05 ➔ MBR > 0.37
p < 0.01 ➔ MBR > 0.39
p < 0.001 ➔ MBR > 0.42


p(C)
0.05
0.04
0.03
0.02
0.01
0.00
p(c)
75
100
125
150
175
200
225
250
275
300
325
350
Number of matching bits C

Hash Set Tampering

- Q1: Is it possible for two hash sets to have too few matching bits?
  - I.e., *C* is to the left of the bell curve
- Q2: If so, what does it mean?
- A: Based on hashing function properties, it is extremely (and quantifiably) unlikely to achieve this by chance or by tampering with the original objects.
  - ➔ Any tampering must have happened afterwards
  - E.g., the reference set has been made deliberately different

Tampering Example: MD5 Digit Replacement



Detecting Object Versioning

Name	Reference	Functions
liboskit_fsnamespace.a	fs1	54
liboskit_fsnamespace_r.a	fs2	54
liboskit_posix.a	posix1	103
liboskit_posix_r.a	posix2	127
libpng10.a	png1	303
libpng12.a	png2	329

Detecting Object Versioning (2)

	fs	fs	posix	posix	png
m	256	512	512	1024	1024
n_1	54	54	103	103	303
n_2	54	54	127	127	329
m / n	4.74	9.48	4.45	8.90	3.24
$S_1 \cap S_2$	19	19	53	53	239
C	101	98	218	230	657
p	< 0.015	< 0.001	< 0.001	< 0.001	< 0.01

$k = 4$

Detecting Object Versioning (3)

	fs	posix	png
m / n	4.74	4.45	3.24
$S_1 \cap S_2$	35%	46%	76%
p	< 0.015	< 0.001	< 0.01

- Observations
  - Detecting object versions works very well
  - Depending on the level of overlap, even filters with very low bits per element ratio work reliably
  - In contrast, using similar filters for individual membership queries would be pointless:

$m = 1024$		k					
		2	4	6	8	12	16
m / n	4	0.1549	0.1598	0.2201	0.3128	0.5423	0.7444

Implementation: `md5bloom`

- Goals
  - Develop an open-source solution
  - Efficient, flexible, extendable, reliable
  - Compatible with existing practices
  - Both a standalone utility and a library to be used in other tools
- Design
  - Back-end (*bloom server*): filter management
    - Create, insert, lookup, store/load
    - Hash function independent
  - Front-end (*bloom client*): hash/query management
- Usage scenarios:
  - Same address space
  - Single client/server
  - Multiple client/server

`md5bloom`: Quick Overview

- Functions:
  - Creation
    - Byte stream
    - Existing MD5 hashes
    - Client hashes (over the network)
  - Query lookup
    - Byte stream
    - Existing MD5 hashes
  - Filter comparison

`md5bloom`: Server Examples

- Creation:

  `md5bloom -genstream 10 4 8 512 -daemon 2024`

  - Create filter: $m = 2^{10}$, $k = 4$, $m/n \leq 8$
  - Hash `stdin` every 512 bytes
  - Listen for queries on port 2024

  `md5bloom -genmd5 10 4 8 [-daemon] 2024`

  - Create filter: $m = 2^{10}$, $k = 4$, $m/n \leq 8$
  - Read (hexadecimal) hashes (one per line) from `stdin`
  - No `daemon` ➔ send to `stdout`, else keep in memory

  `md5bloom -genclient 10 4 8 [-daemon] 2024`

  - Create filter: $m = 2^{10}$, $k = 4$, $m/n \leq 8$
  - No `daemon` ➔ send to `stdout`, else keep in memory

`md5bloom`: Client Examples

- Creation
  - **`md5bloom -clientstream host 2024 512`**
    - Connect to server at **`host:2024`**
    - Hash `stdin` every 512 bytes and send to server
  - **`md5bloom -genmd5 host 2024`**
    - Connect to server at **`host:2024`**
    - Read hashes from `stdin` and send to server
- Queries
  - **`md5bloom -querystream host 2024 512`**
    - Hash `stdin` every 512 bytes and query the server
  - **`md5bloom -querymd5 host 2024`**
    - Read hashes from `stdin` and query the server
    - Hash `stdin` every 512 bytes and query the server
- Comparison
  - **`md5bloom -diff <file_1> <file_2>`**

Conclusions

- Bloom filters can be a valuable tool in filesystem forensics to
  - Alleviate scalability problems
  - Provide a framework for finer-grain content identification
- Developed a probabilistic framework that treats filters as first-class objects
  - Direct comparison
  - Reliable interpretation of results
- Provided simulation-based verification of theoretical results
- Developed a practical tool—*md5blooom*—that can be used as a standalone utility, or a component of a system
- Initial testing results
  - Confirm the predicted results
  - Provide new insights into the use and performance of *Bloom* filters

Future Work

- Transition *md5bloom* from alpha to beta
  - Stable code
  - Stable client/server protocol & storage format
  - Competitive performance
- Large-scale testing
  - Various file types
  - HDD-to-HDD correlation
- Develop front-end extensions for various variations of *Bloom* filters
- Explore the use of
  - Chained multi-filter comparisons
  - Recursive filters

Thank You!

Questions?