Data Structures and Algorithms

Exam 5 Review and Bloom Filters

CS 225

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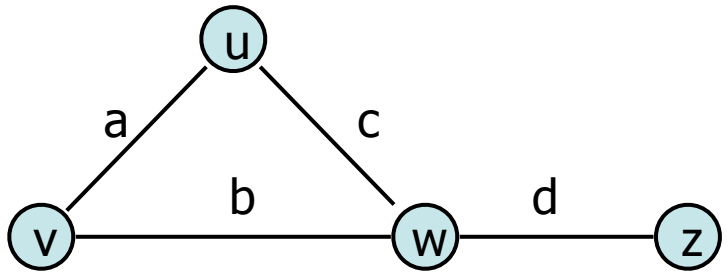
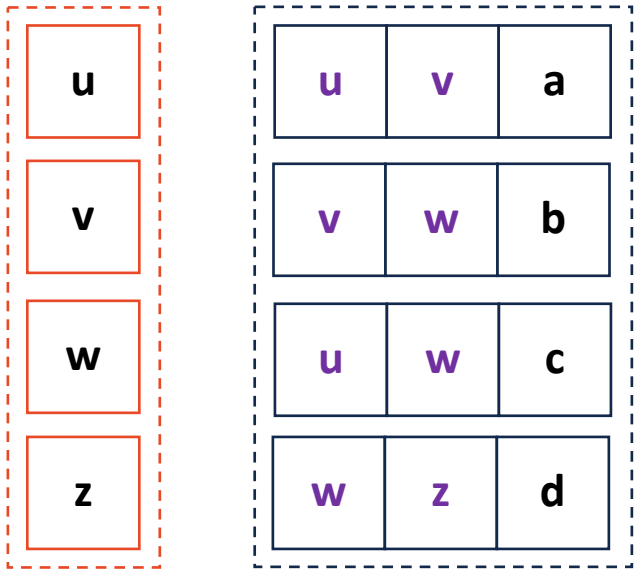
Graph Implementation: Edge List `|V|= n, |E|= m`

The equivalent of an 'unordered' data structure





Vertex Storage:

An optional list of vertices

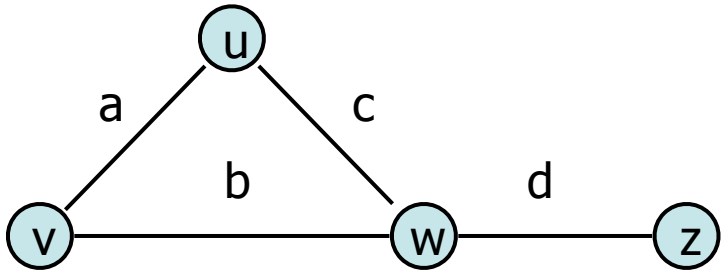
Edge Storage:

A list storing edges as (V1, V2, Weight)

Most graphs are stored as just an edge list!

Graph Implementation: Adjacency Matrix

|V|= n, |E|= m



u	0
v	1
w	2
z	3

	0	1	2	3
0	-	a	c	0
1		-	b	0
2			-	d
3				-

Vertex Storage:

A hash table of vertices

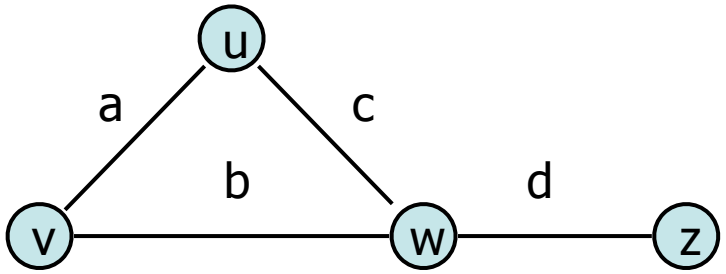
Implicitly or explicitly store index

Edge Storage:

A |V| x |V| matrix of edges

Weight is stored at position (u, v)

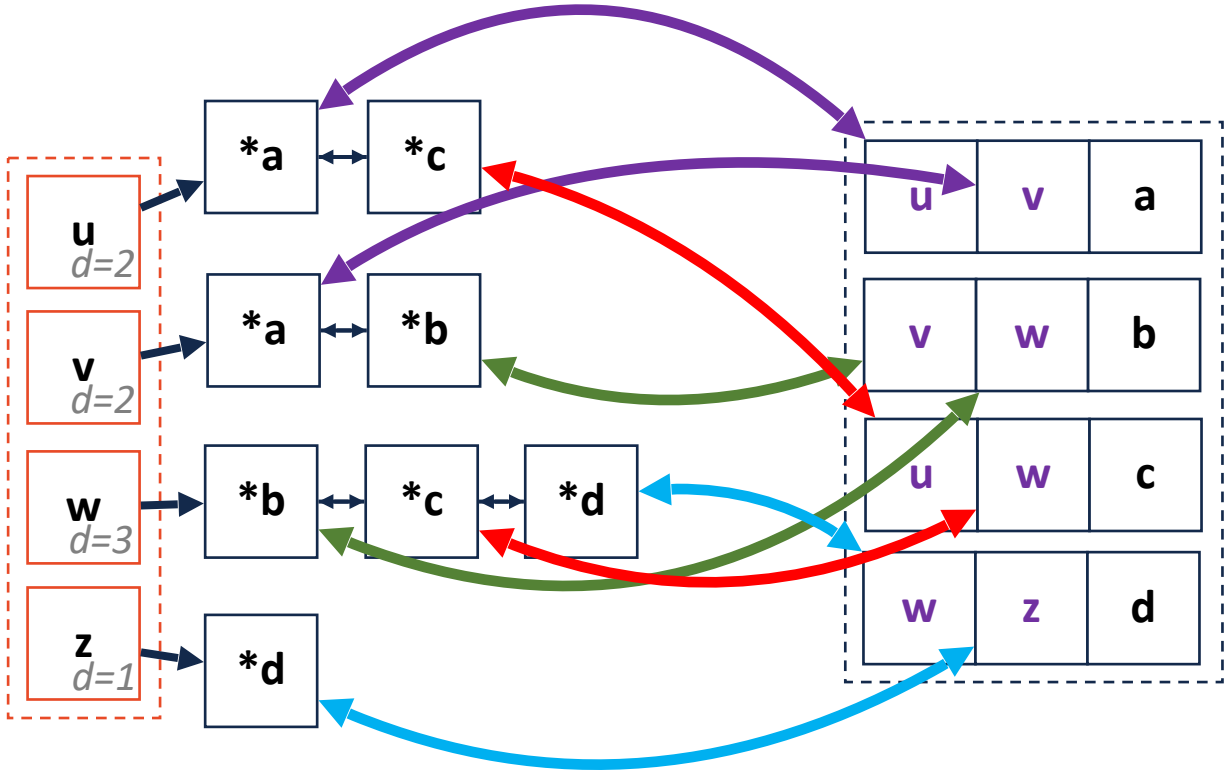
Adjacency List



Vertex Storage:

A bidirectional linked list with size variable

Each node is a pointer to edge in edge list



Edge Storage:

A list of (v1, v2, weight) edges

Also store pointers back to nodes

|V|= n, |E|= m

Expressed as O(f)	Edge List	Adjacency Matrix	Adjacency List
Space	n+m	n^2	n+m
insertVertex(v)	1*	n*	1*
removeVertex(v)	n+m	n	deg(v)
insertEdge(u, v)	1	1	1*
removeEdge(u, v)	m	1	min(deg(u), deg(v))
incidentEdges(v)	m	n	deg(v)
areAdjacent(u, v)	m	1	min(deg(u), deg(v))

Summary: DFS and BFS

$|V| = n, |E| = m$

Both are **O(n+m)** traversals! They label every edge and every node

BFS	**DFS**
Solves unweighted MST	Solves unweighted MST
Solves shortest path	
Solves cycle detection	Solves cycle detection
Memory bounded by width	Memory bounded by longest path

Kruskal's Algorithm

```
1  KruskalMST(G):
2    DisjointSets forest
3    foreach (Vertex v : G.vertices()):
4      forest.makeSet(v)
5
6    PriorityQueue Q     // min edge weight
7    Q.buildFromGraph(G.edges())
8
9    Graph T = (V, {})
10
11   while |T.edges()| < n-1:
12     Vertex (u, v) = Q.removeMin()
13     if forest.find(u) != forest.find(v):
14        T.addEdge(u, v)
15        forest.union( forest.find(u),
16                      forest.find(v) )
17
18   return T
19
```

1) Build a **priority queue** on edges

   A minheap

   or

   A sorted array

2) Build a **disjoint set** on vertices

   All vertices start as their own set

3) Loop through min edges

   If edge connects two disjoint sets

   Union sets and record edge in MST

4) Stop when:

   N-1 edges recorded

   Only a single disjoint set remains

Kruskal's Algorithm

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17
18    return T
19
```

|V|= n,|E|= m

What is the Big O?

2 — 4: O(n)

6 — 7: Heap: O(m)
Sorted List: O(m log m)

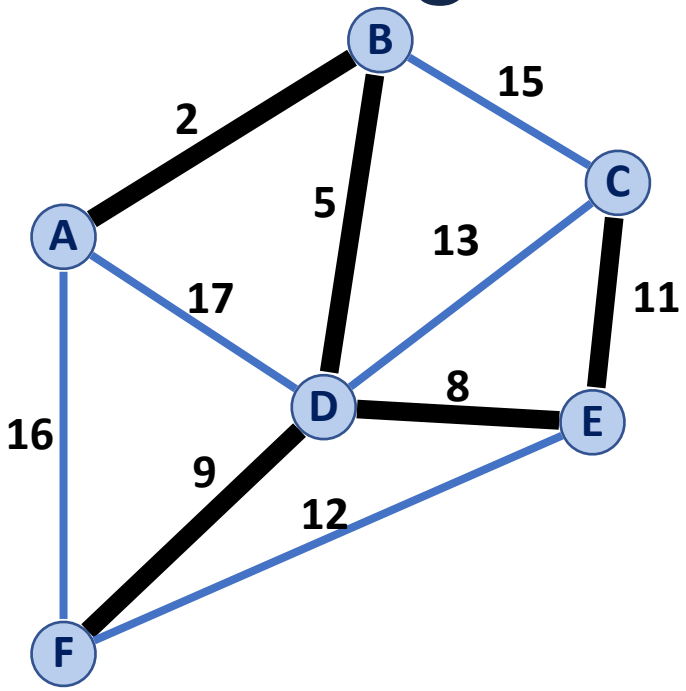
11: m x <12-17>

12—17: Heap: O(log m)
Sorted List: O(1)

O(n + m + m log m)

Simplified: O(n + m log n)

Prim's Algorithm



A	B	C	D	E	F
0, —	2, A	11, E	5, B	8, D	9, D

```
1  PrimMST(G, s):
2    Input: G, Graph;
3           s, vertex in G, starting vertex
4    Output: T, a minimum spanning tree (MST) of G
5
6    foreach (Vertex v : G.vertices()):
7      d[v] = +inf
8      p[v] = NULL
9    d[s] = 0
10
11   PriorityQueue Q   // min distance, defined by d[v]
12   Q.buildHeap(G.vertices())
13   Graph T           // "labeled set"
14
15   repeat n times:
16     Vertex m = Q.removeMin()
17     T.add(m)
18     foreach (Vertex v : neighbors of m not in T):
19       if cost(v, m) < d[v]:
20         d[v] = cost(v, m)
21         p[v] = m
22
23   return T
```

Prim's Big O

|V|= n, |E|= m

7 — 9: O(n)

12—14:

MinHeap: O(n)

Unsorted Array: O(1)

16—22: Complicated!

```
 6  PrimMST(G, s):
 7    foreach (Vertex v : G.vertices()):
 8      d[v] = +inf
 9      p[v] = NULL
10    d[s] = 0
11
12    PriorityQueue Q // min distance, defined by d[v]
13    Q.buildHeap(G.vertices())
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20        if cost(v, m) < d[v]:
21          d[v] = cost(v, m)
22          p[v] = m
23
```

Depends on choice of **PriorityQueue** (MinHeap vs Unsorted Array)

Depends on choice of **Graph** (Adjacency Matrix vs Adjacency List)

Prim's Algorithm

Sparse Graph: ($m \sim n$)

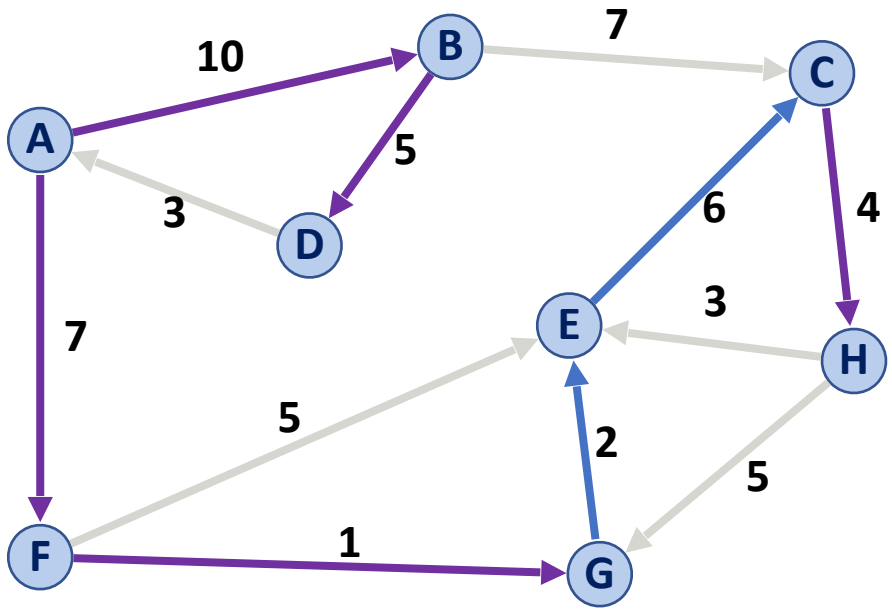
Dense Graph: ($m \sim n^2$)

```
 6  PrimMST(G, s):
 7    foreach (Vertex v : G.vertices()):
 8      d[v] = +inf
 9      p[v] = NULL
10    d[s] = 0
11
12    PriorityQueue Q // min distance, defined by d[v]
13    Q.buildHeap(G.vertices())
14    Graph T          // "labeled set"
15
16    repeat n times:
17      Vertex m = Q.removeMin()
18      T.add(m)
19      foreach (Vertex v : neighbors of m not in T):
20        if cost(v, m) < d[v]:
21          d[v] = cost(v, m)
22          p[v] = m
23
```

Lines 7 — 14 are O(n) [at most]

	Adj. Matrix	Adj. List
Heap	$O(n^2 + m \lg(n))$	$O(n \lg(n) + m \lg(n))$
Unsorted Array	$O(n^2)$	$O(n^2)$

Dijkstra's Algorithm (SSSP)




```
    DijkstraSSSP(G, s):
 6    foreach (Vertex v : G.vertices()):
 7      d[v] = +inf
 8      p[v] = NULL
 9    d[s] = 0
10
11    PriorityQueue Q // min distance, defined by d[v]
12    Q.buildHeap(G.vertices())
13    Graph T           // "labeled set"
14
15    repeat n times:
16      Vertex u = Q.removeMin()
17      T.add(u)
18      foreach (Vertex v : neighbors of u not in T):
19        if cost(u, v) + d[u] < d[v]:
20          d[v] = cost(u, v) + d[u]
21          p[v] = u
```

A	B	C	D	E	F	G	H
--	A	E	B	G	A	F	C
0	10	16	15	10	7	8	20

Floyd-Warshall Algorithm

Floyd-Warshall's Algorithm is an alternative to Dijkstra in the presence of negative-weight edges (not negative weight cycles).

```
 1  FloydWarshall(G):
 2    Let d be a adj. matrix initialized to +inf
 3    foreach (Vertex v : G):
 4      d[v][v] = 0
 5    foreach (Edge (u, v) : G):
 6      d[u][v] = cost(u, v)
 7
 8    foreach (Vertex u : G):
 9      foreach (Vertex v : G):
10        foreach (Vertex w : G):
11          if (d[u, v] > d[u, w] + d[w, v])
12            d[u, v] = d[u, w] + d[w, v]
```

A Hash Table based Dictionary

User Code (is a map):

```
1  Dictionary<KeyType, ValueType> d;
2  d[k] = v;
```

A **Hash Table** consists of three things:

1. A hash function

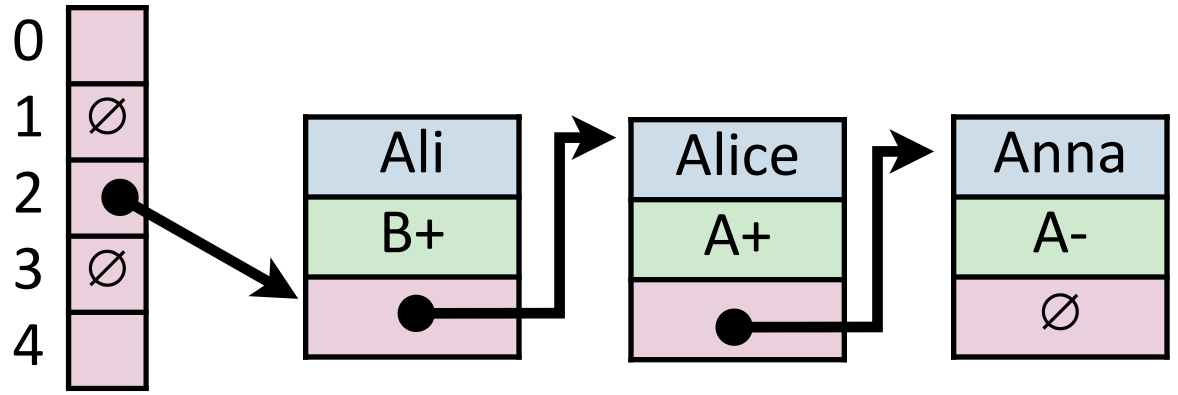
2. A data storage structure

3. A method of addressing *hash collisions*

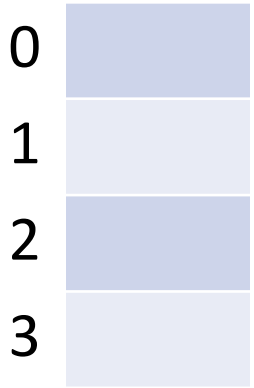
Open vs Closed Hashing

Addressing hash collisions depends on your storage structure.

- **Open Hashing:** store *k,v* pairs externally



- **Closed Hashing:** store *k,v* pairs in the hash table



Separate Chaining Under SUHA

Claim: Under SUHA, expected length of chain is $\frac{n}{m}$

Table Size: m

Num objects: n

α_j = expected # of items hashing to position j

$$\alpha_j = \sum_i H_{i,j}$$

$$H_{i,j} = \begin{cases} 1 \text{ if item i hashes to j} \\ 0 \text{ otherwise} \end{cases}$$

$$E[\alpha_j] = E[\sum_i H_{i,j}]$$

$$Pr[H_{i,j} = 1] = \frac{1}{m}$$

$$E[\alpha_j] = n * Pr(H_{i,j} = 1)$$

$$\mathbf{E[\alpha_j] = \frac{n}{m}}$$

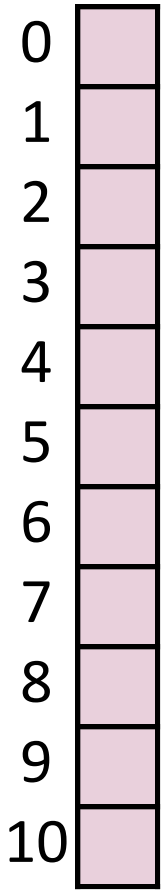
Separate Chaining Under SUHA

Under SUHA, a hash table of size *m* and *n* elements:

Find runs in: $O(1 + \alpha)$

Insert runs in: $O(1)$

Remove runs in: $O(1 + \alpha)$



Running Times *(Don't memorize these equations, no need.)*

The expected number of probes for find(key) under SUHA

Linear Probing:

- Successful: **$\frac{1}{2}(1 + 1/(1-\alpha))$**
- Unsuccessful: **$\frac{1}{2}(1 + 1/(1-\alpha))^2$**

Double Hashing:

- Successful: **$1/\alpha * \ln(1/(1-\alpha))$**
- Unsuccessful: **$1/(1-\alpha)$**

Separate Chaining:

- Successful: **$1 + \alpha/2$**
- Unsuccessful: **$1 + \alpha$**

Instead, observe:

- As α increases:

Runtime approaches infinity!

- If α is constant:

Runtime is a constant!

Resizing a hash table

When and how do you resize?

Any (review) questions?

Learning Objectives

Review when you would prefer different data structures

Build a conceptual understanding of a bloom filter

Review probabilistic data structures and one-sided error

Formalize the math behind the bloom filter

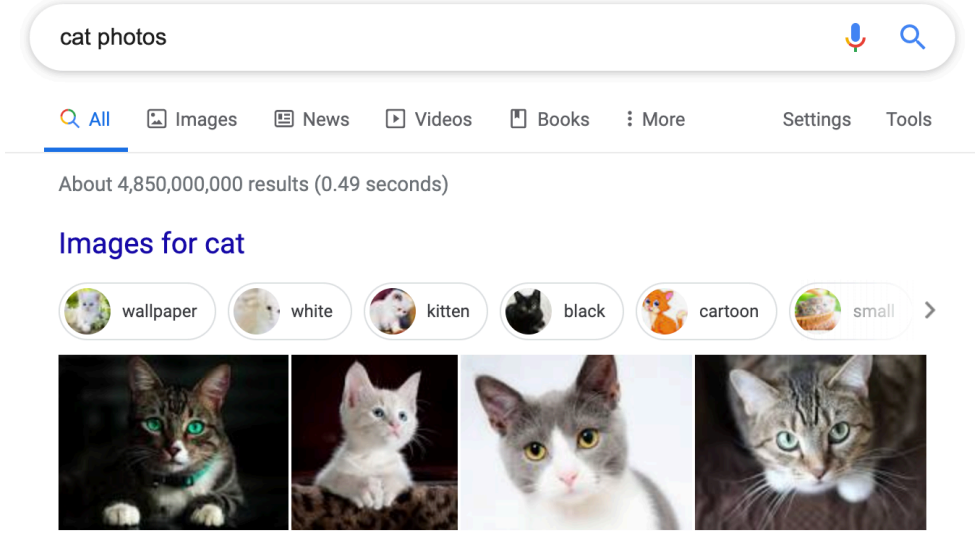
Running Times (Tradeoff Highlights)

	Hash Table	AVL	Linked List
Find	Expectation*: O(1)*** Worst Case: O(n)	O(log n)	O(n)
Insert	Expectation*: O(1)*** Worst Case: O(n)	O(log n)	O(1)
Storage Space	O(n)	O(n)	O(n)

Memory-Constrained Data Structures

What method would you use to build a search index on a collection of objects *in a memory-constrained environment*?

Constrained by Big Data (Large N)



Google Index Estimate: >60 billion webpages

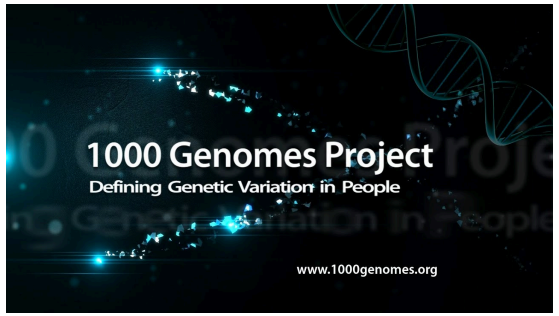
Google Universe Estimate (2013): >130 trillion webpages

Memory-Constrained Data Structures

What method would you use to build a search index on a collection of objects *in a memory-constrained environment*?

Constrained by Big Data (Large N)

ENA
European Nucleotide Archive



GTEx

SRA

Sequence Read Archive (SRA) makes biological sequence data available to the research community to enhance reproducibility and allow for new discoveries by comparing data sets. The SRA stores raw sequencing data and alignment information from high-throughput sequencing platforms, including Roche 454 GS System®, Illumina Genome Analyzer®, Applied Biosystems SOLiD System®, Helicos Heliscope®, Complete Genomics®, and Pacific Biosciences SMRT®.

Sequence Read Archive Size: >60 petabases (10^{15})

Memory-Constrained Data Structures

What method would you use to build a search index on a collection of objects *in a memory-constrained environment*?

Constrained by Big Data (Large N)

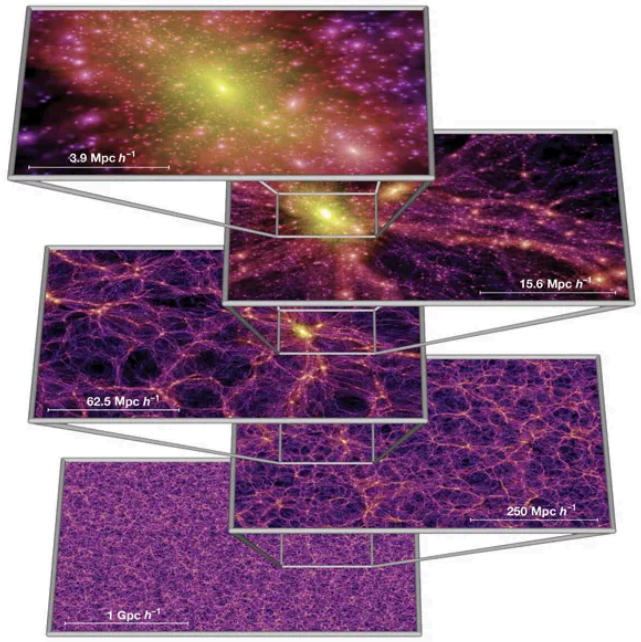


Image: https://doi.org/10.1038/nature03597

Sky Survey Projects	Data Volume
DPOSS (The Palomar Digital Sky Survey)	3 TB
2MASS (The Two Micron All-Sky Survey)	10 TB
GBT (Green Bank Telescope)	20 PB
GALEX (The Galaxy Evolution Explorer)	30 TB
SDSS (The Sloan Digital Sky Survey)	40 TB
SkyMapper Southern Sky Survey	500 TB
PanSTARRS (The Panoramic Survey Telescope and Rapid Response System)	~ 40 PB expected
LSST (The Large Synoptic Survey Telescope)	~ 200 PB expected
SKA (The Square Kilometer Array)	~ 4.6 EB expected

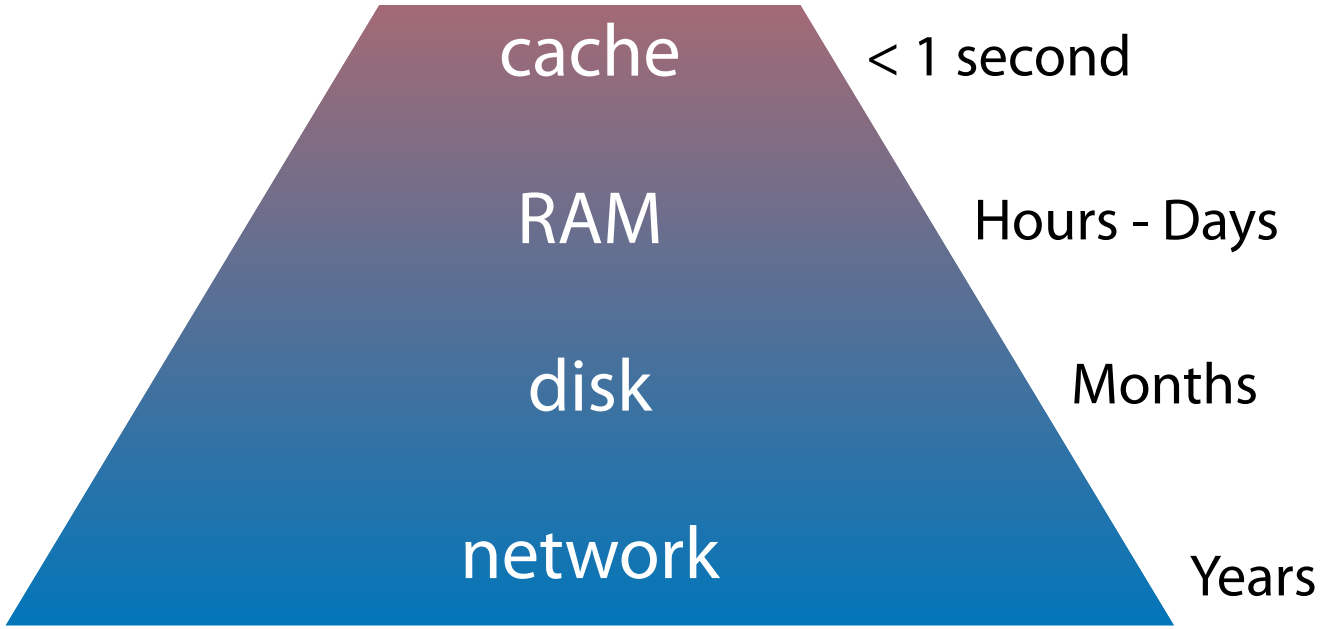
Table: http://doi.org/10.5334/dsj-2015-011

Estimated total volume of one array: 4.6 EB

Memory-Constrained Data Structures

What method would you use to build a search index on a collection of objects *in a memory-constrained environment*?

Constrained by resource limitations



(Estimates are Time x 1 billion courtesy of https://gist.github.com/hellerbarde/2843375)

Memory-Constrained Data Structures

What method would you use to build a search index on a collection of objects *in a memory-constrained environment*?

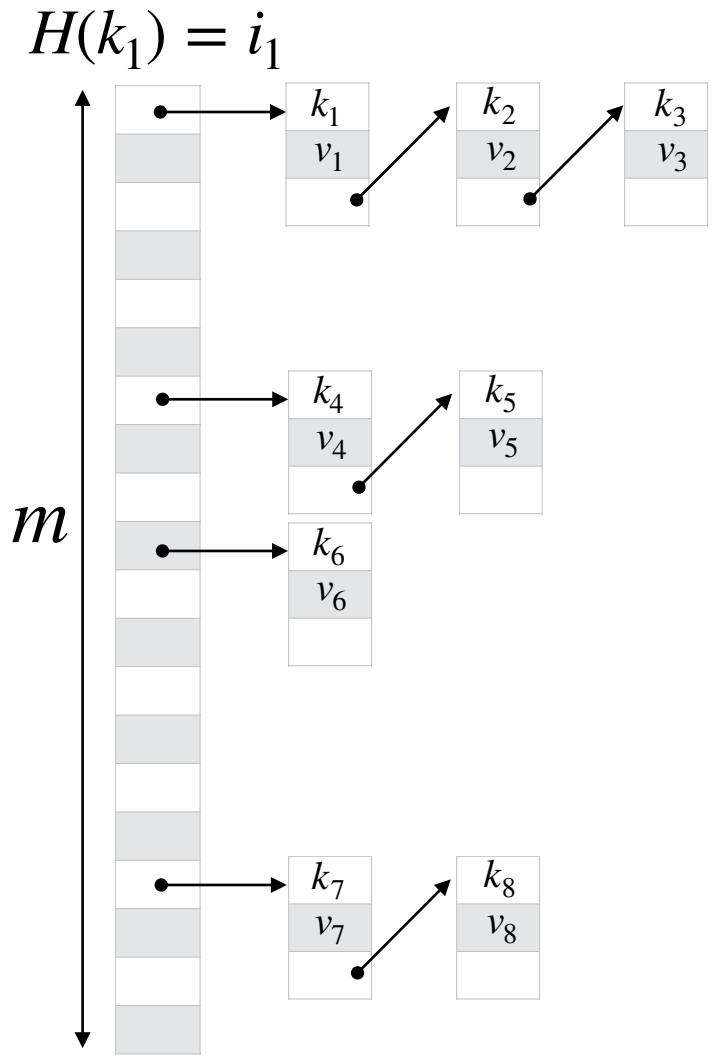
Reducing storage costs

1) Throw out information that isn't needed

2) Compress the dataset

Reducing a hash table

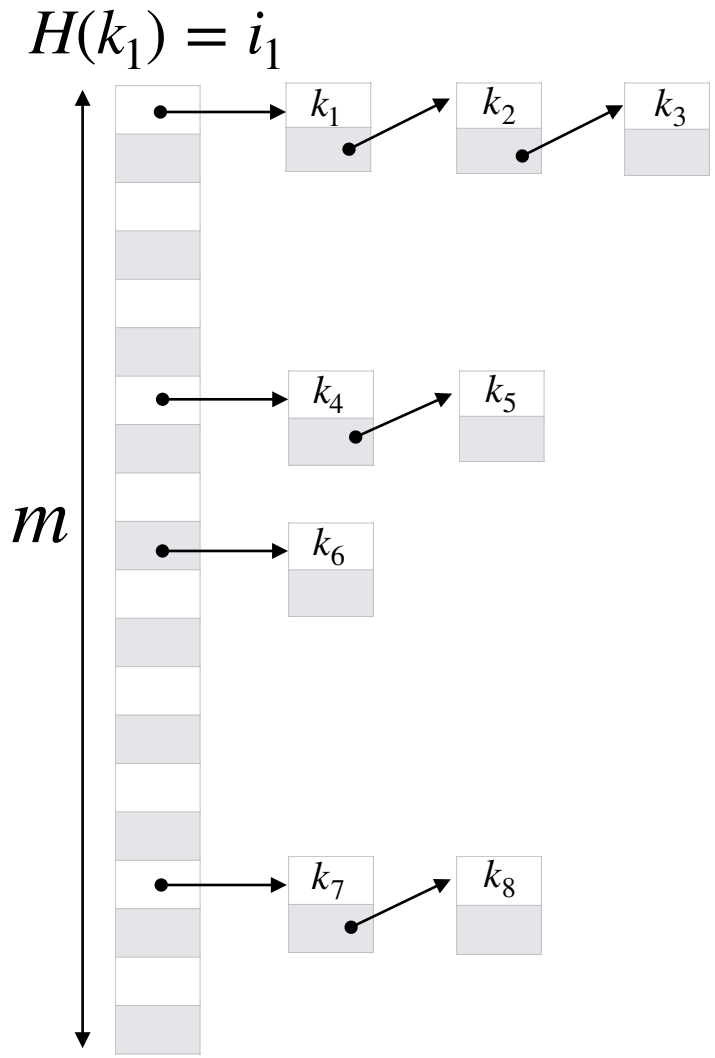
What can we remove from a hash table?



Reducing a hash table

What can we remove from a hash table?

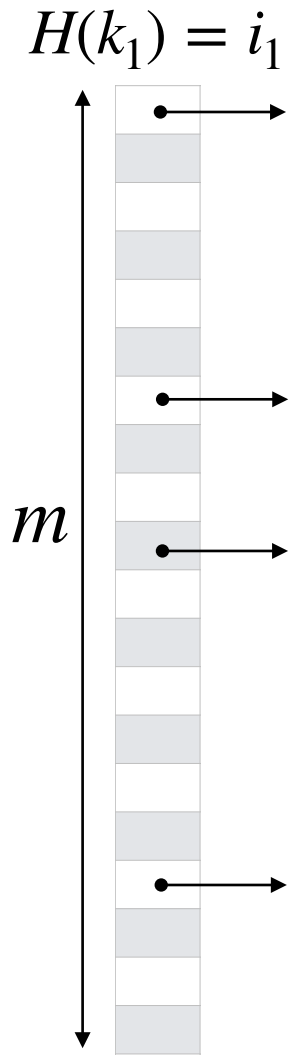
Take away values



Reducing a hash table

What can we remove from a hash table?

Take away values and keys

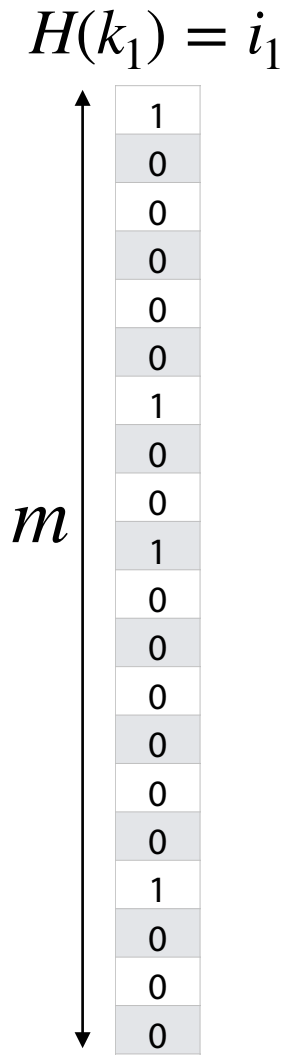


Reducing a hash table

What can we remove from a hash table?

Take away values and keys

This is a ***bloom filter***



Bloom Filter ADT

Constructor

Insert

Find

Bloom Filter: Insertion

S = { 16, 8, 4, 13, 29, 11, 22 }

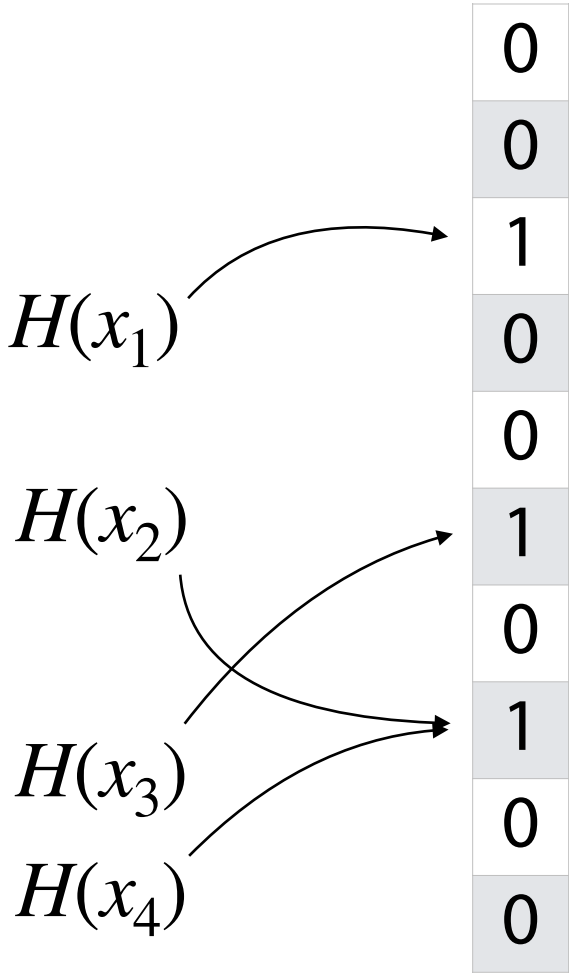
h(k) = k % 7

0	0
1	0
2	0
3	0
4	0
5	0
6	0

Bloom Filter: Insertion

An item is inserted into a bloom filter by hashing and then setting the hash-valued bit to 1

If the bit was already one, it stays 1



Bloom Filter: Deletion

S = { 16, 8, 4, 13, 29, 11, 22 }

h(k) = k % 7

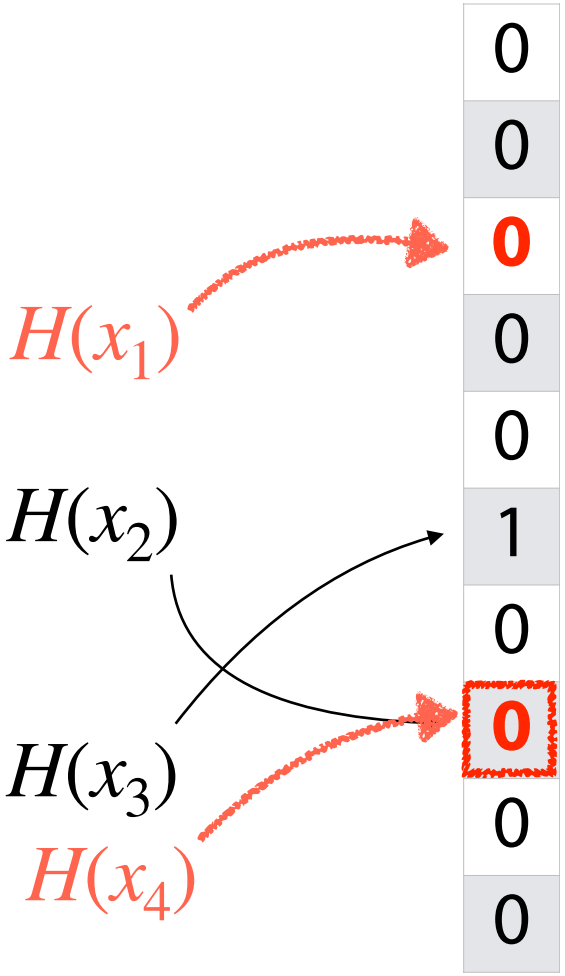
0	0
1	1
2	1
3	0
4	1
5	0
6	1

`_delete(13)`

`_delete(29)`

Bloom Filter: Deletion

Due to hash collisions and lack of information, items cannot be deleted!



Bloom Filter: Search

S = { 16, 8, 4, 13, 29, 11, 22 }

h(k) = k % 7

0	0
1	1
2	1
3	0
4	1
5	0
6	1

```
_find(16)
```

```
_find(20)
```

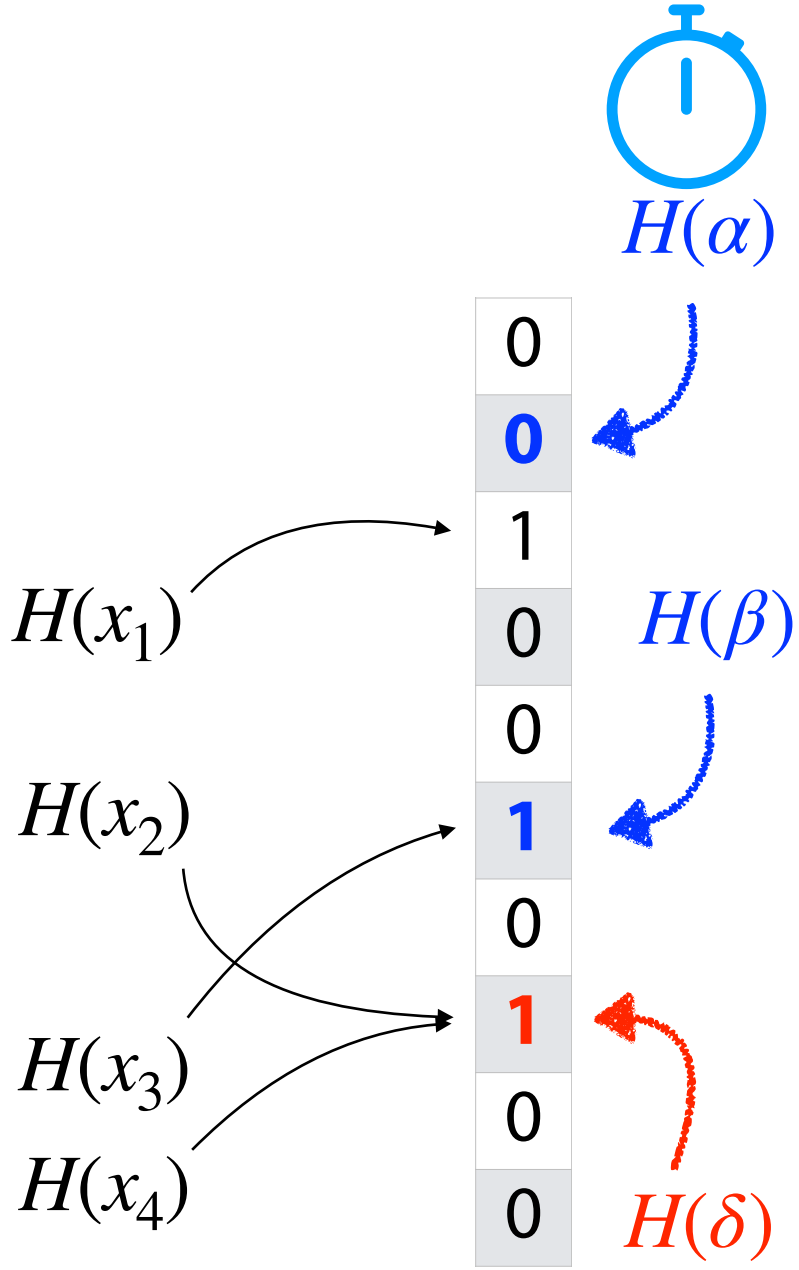
```
_find(3)
```

Bloom Filter: Search

The bloom filter is a *probabilistic* data structure!

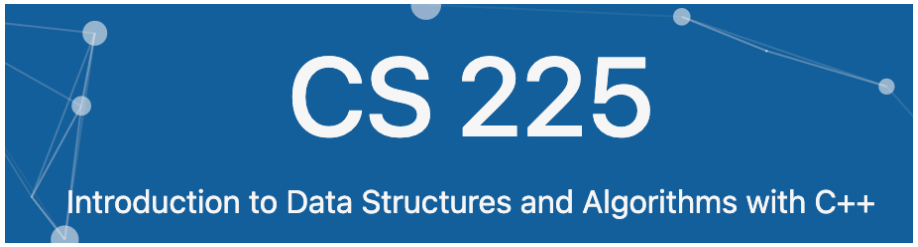
If the value in the BF is 0:

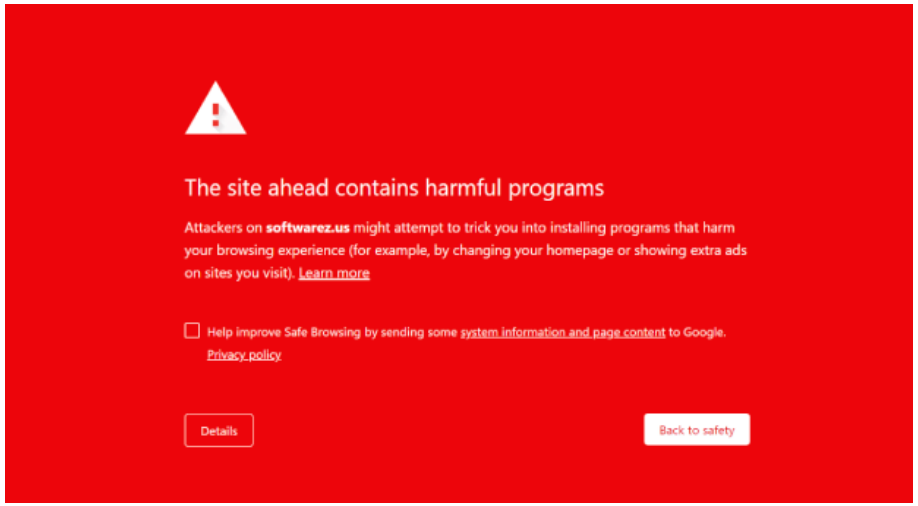
If the value in the BF is 1:

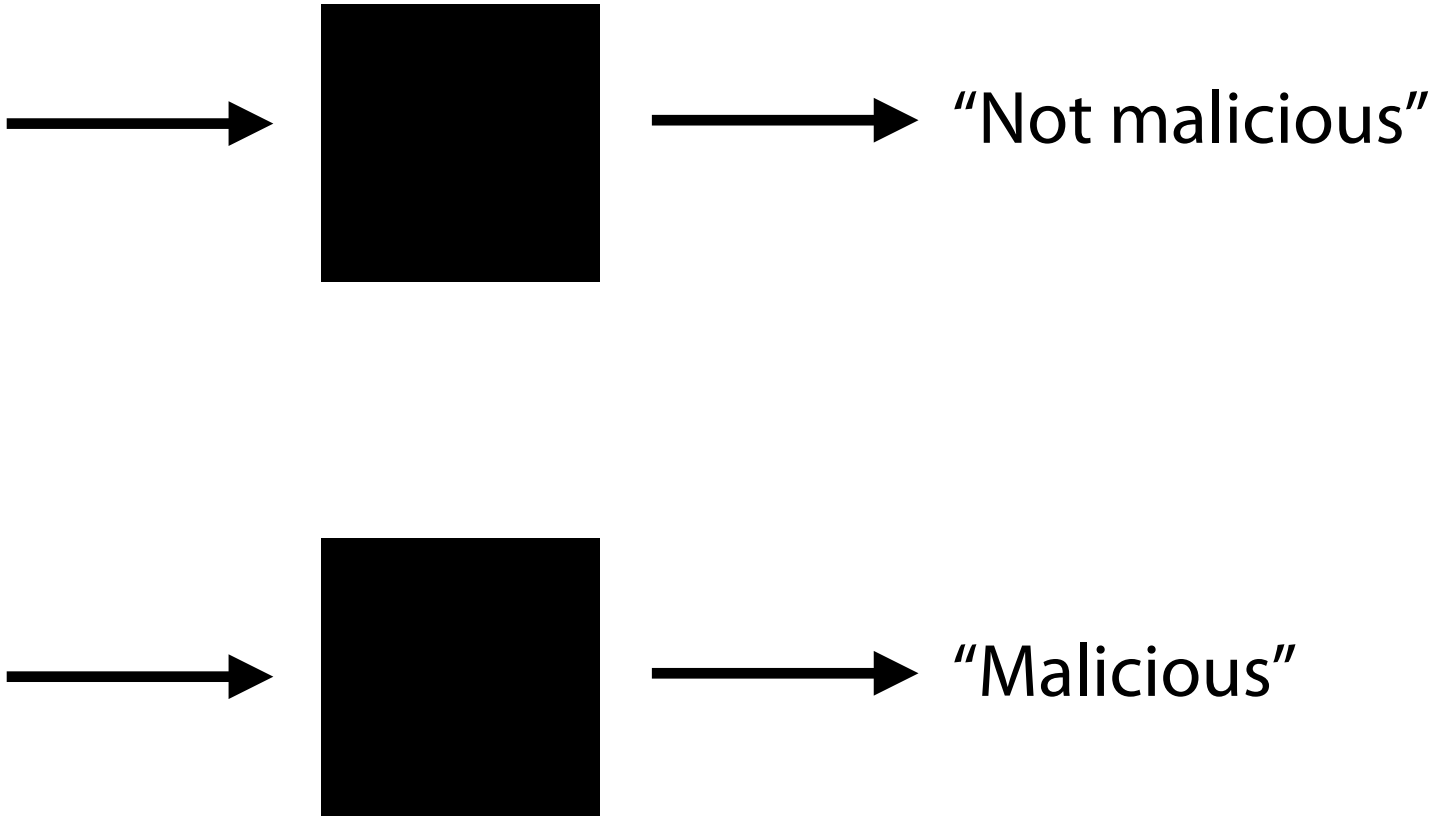


Probabilistic Accuracy: Malicious Websites

Imagine we have a detection oracle that identifies if a site is malicious







Probabilistic Accuracy: Malicious Websites

Imagine we have a detection oracle that identifies if a site is malicious

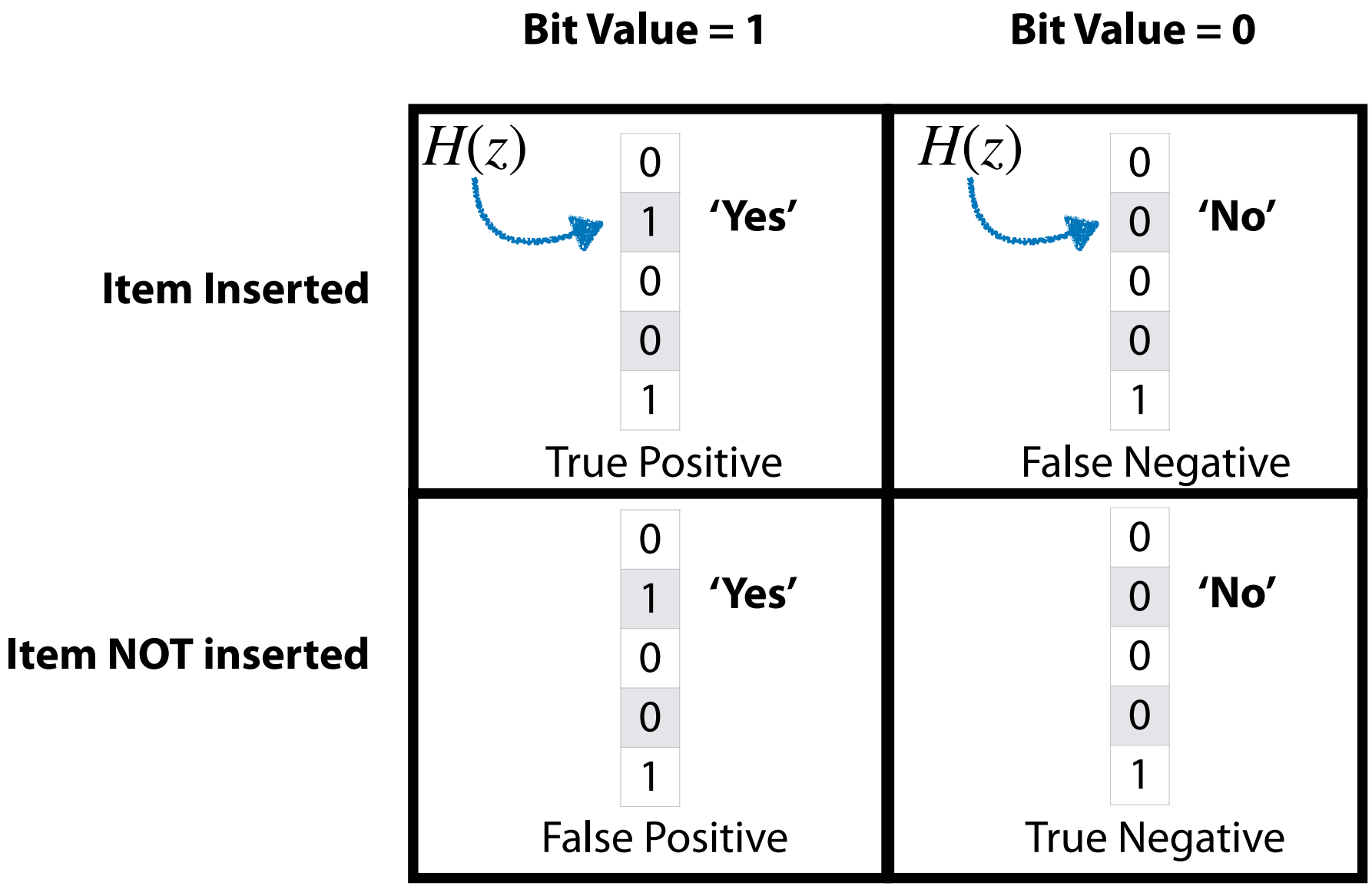
True Positive:

False Positive:

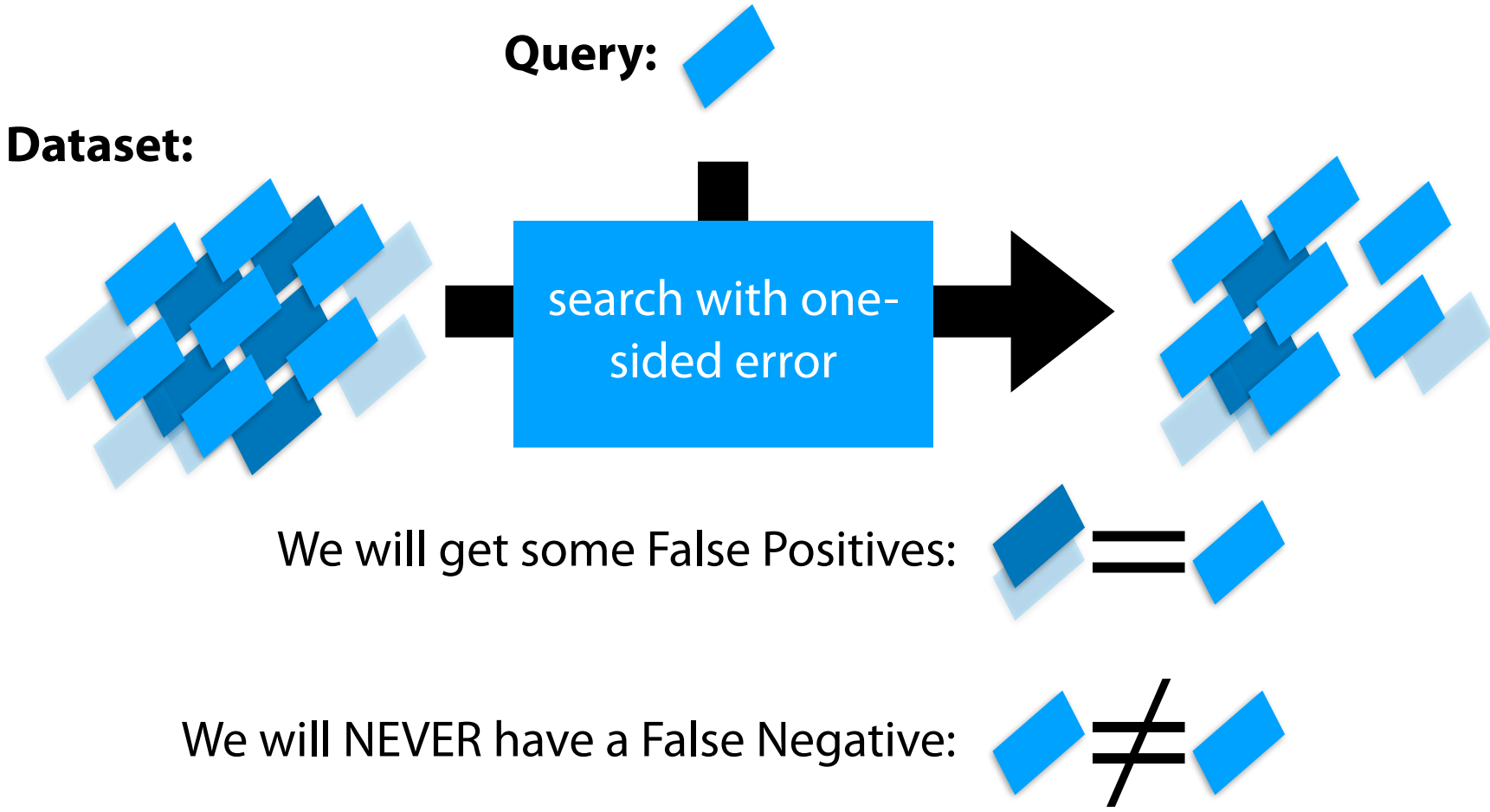
False Negative:

True Negative:

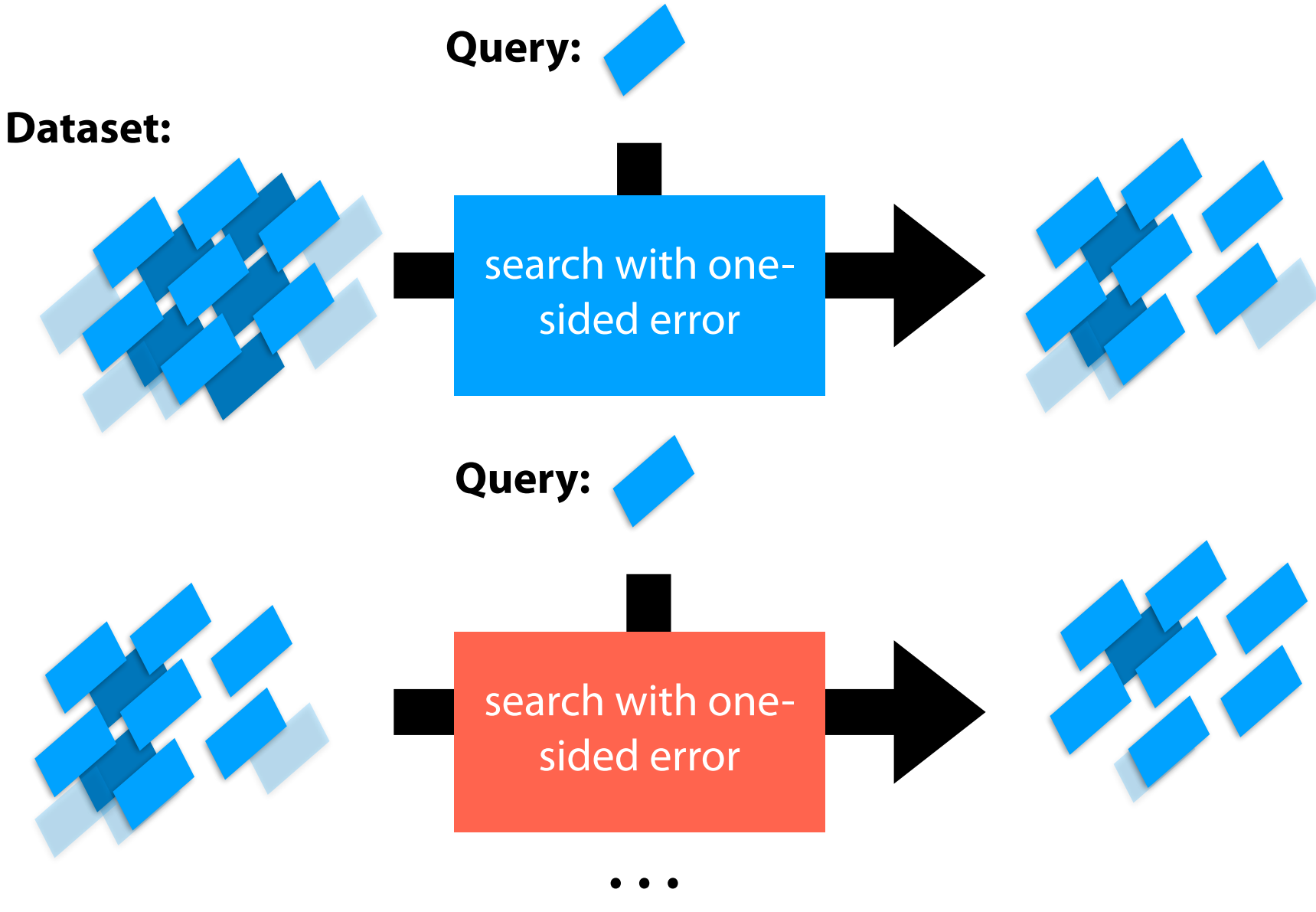
Imagine we have a **bloom filter** that **stores malicious sites…**



Probabilistic Accuracy: One-sided error



Probabilistic Accuracy: One-sided error

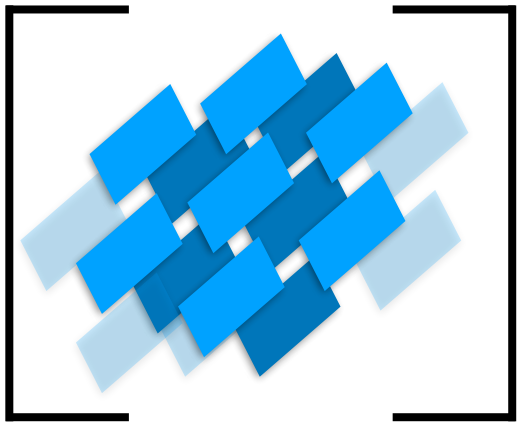


Bloom Filter: Repeated Trials

Use many hashes/filters; add each item to each filter

0
1
0
1
0
0
0
1
0
1
1
0
1
0
1
1
0
1
0
1

h_1



Bloom Filter: Repeated Trials

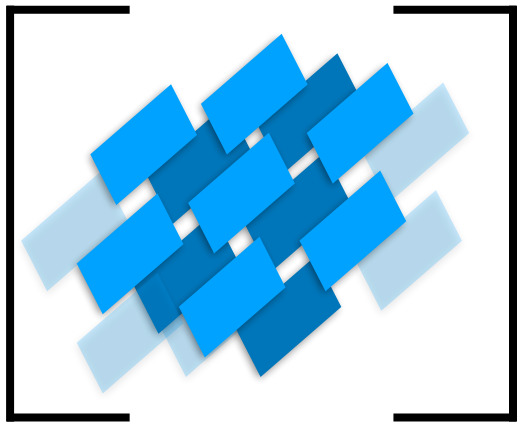
Use many hashes/filters; add each item to each filter

h_1

0
1
0
1
0
0
0
1
0
1
1
0
1
0
1
1
0
1
0
1

0
0
0
1
0
0
0
1
0
1
0
0
1
1
1
0
0
1
0
0

h_2



Bloom Filter: Repeated Trials

Use many hashes/filters; add each item to each filter

h_1

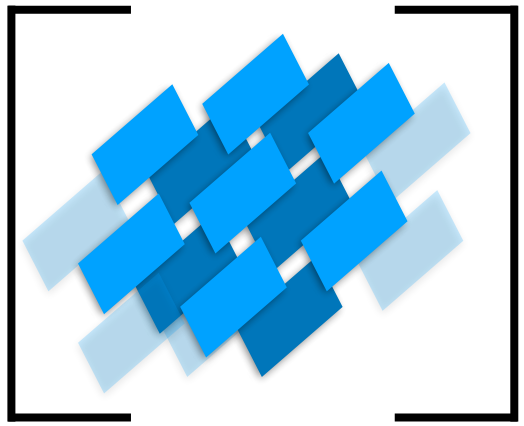
0
1
0
1
0
0
0
1
0
1
1
0
1
0
1
1
0
1
0
1

h_2

0
0
0
1
0
0
0
1
0
1
0
0
1
1
1
0
0
1
0
0

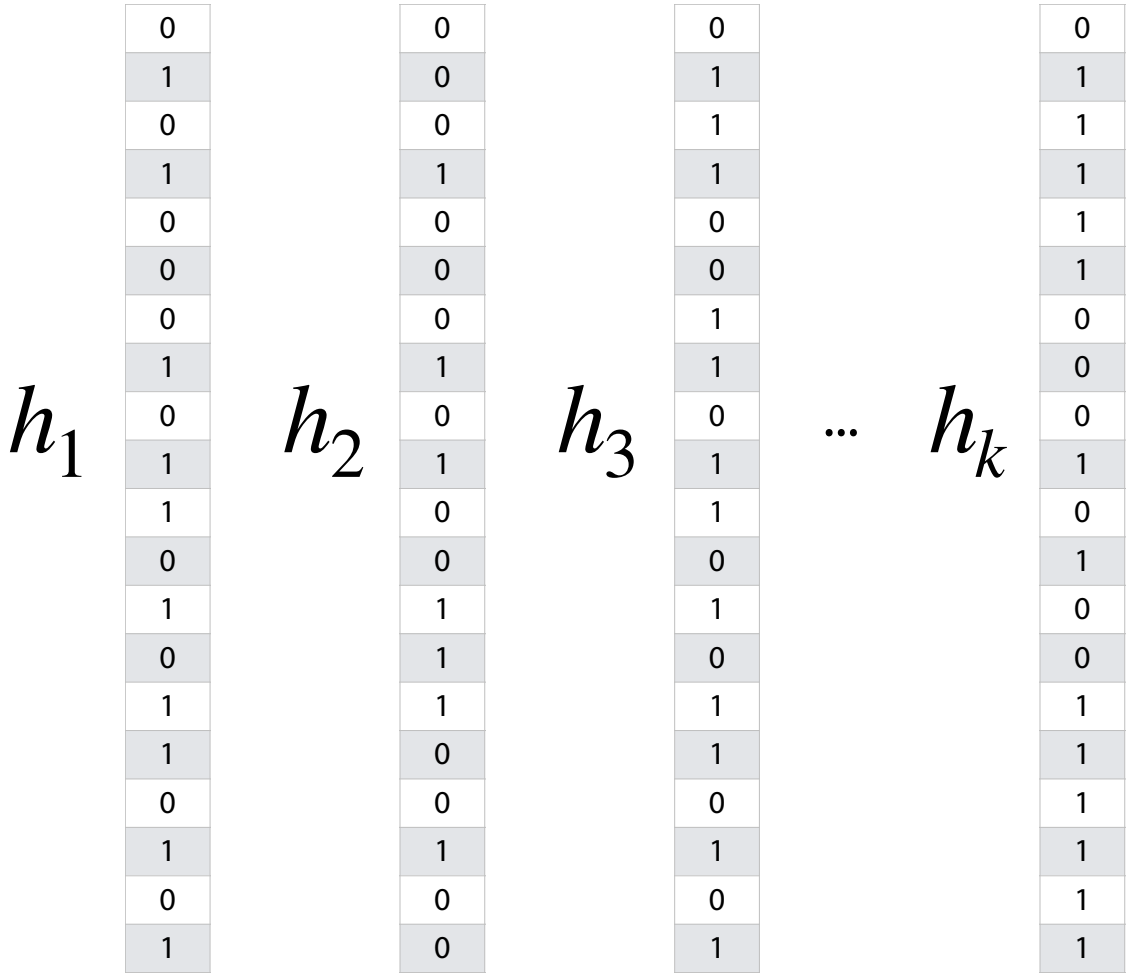
h_3

0
1
1
1
0
0
1
1
0
1
1
0
1
0
1
1
0
1
0
1

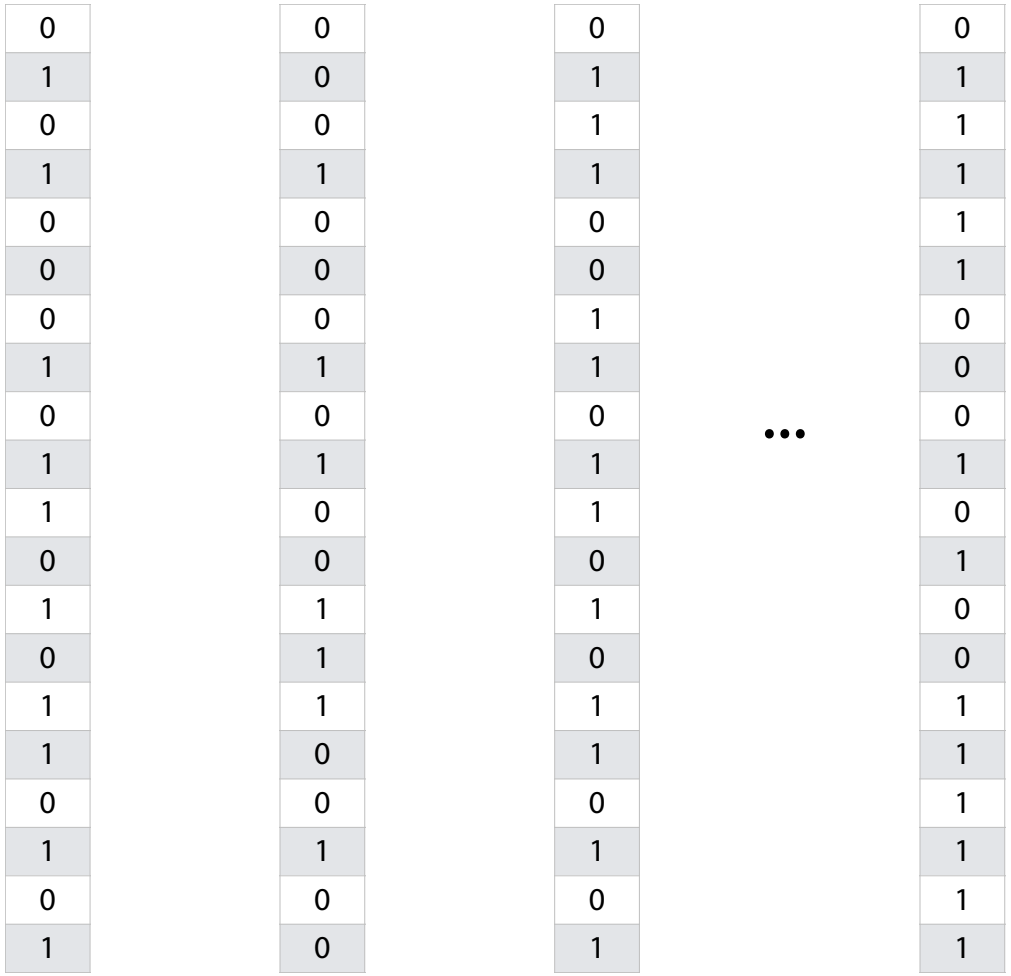


Bloom Filter: Repeated Trials

Use many hashes/filters; add each item to each filter

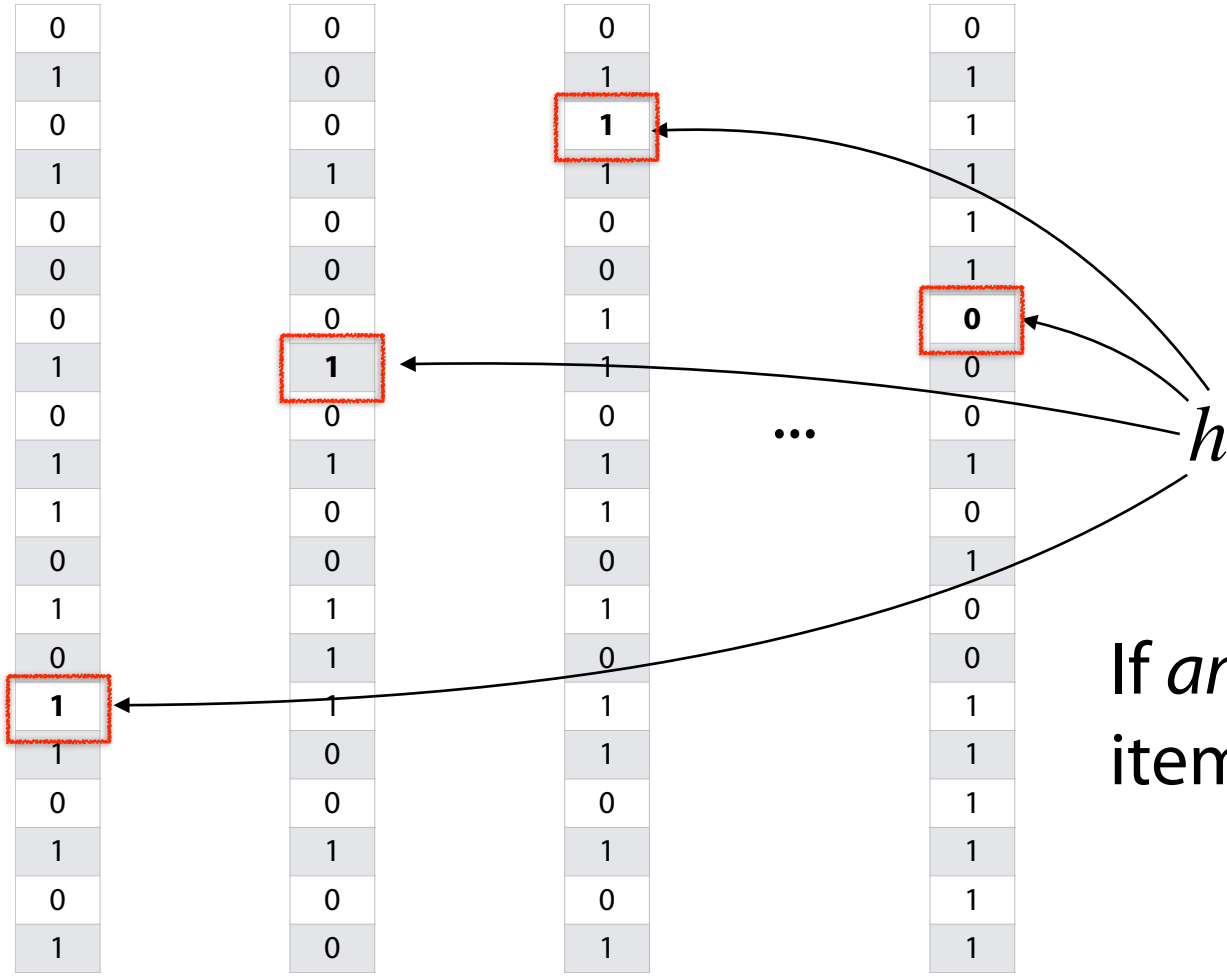


Bloom Filter: Repeated Trials



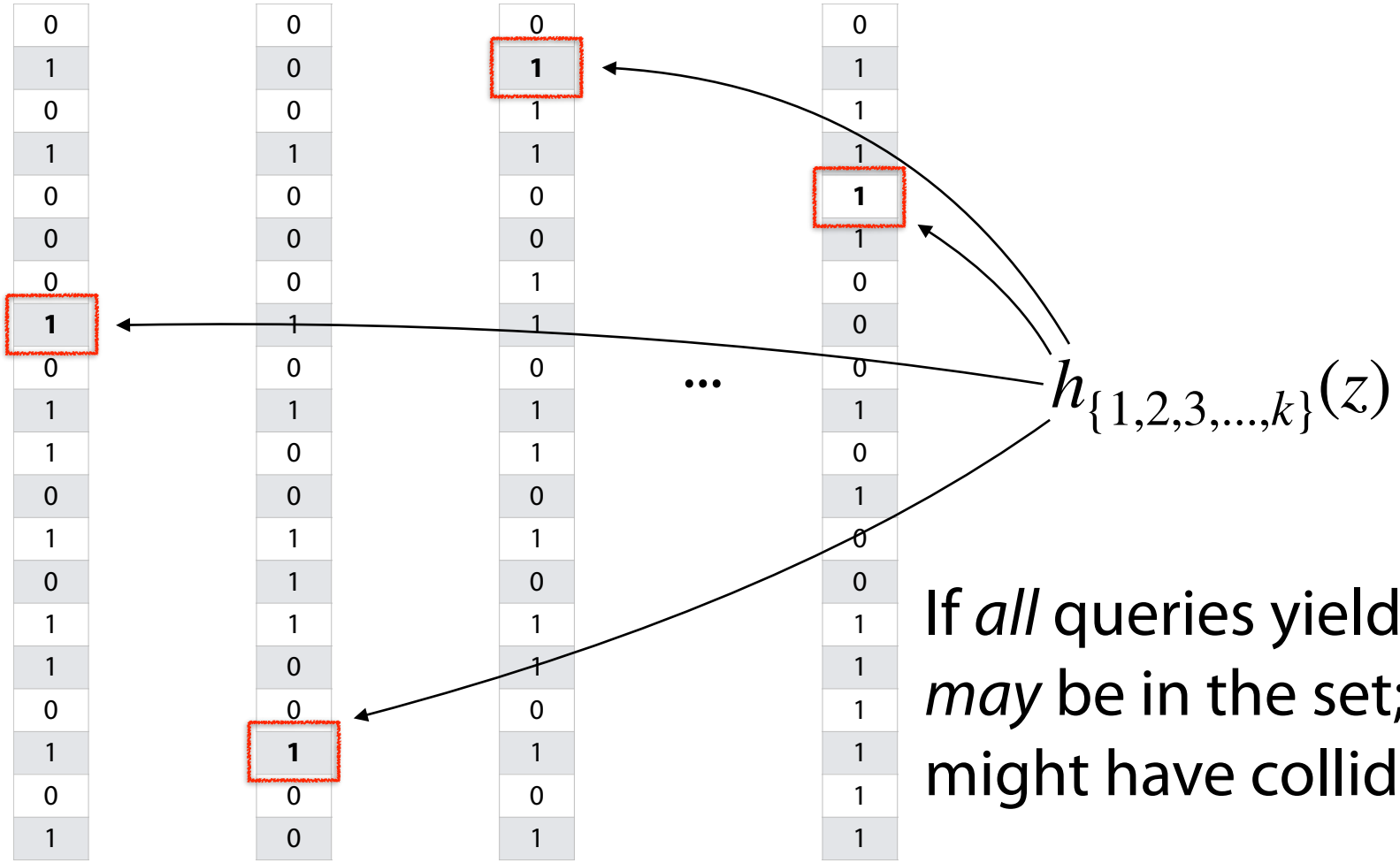
$$h_{\{1,2,3,\ldots,k\}}(y)$$

Bloom Filter: Repeated Trials



If *any* query yields 0, item is not in the set

Bloom Filter: Repeated Trials



If *all* queries yield 1, item *may* be in the set; or we might have collided *k* times

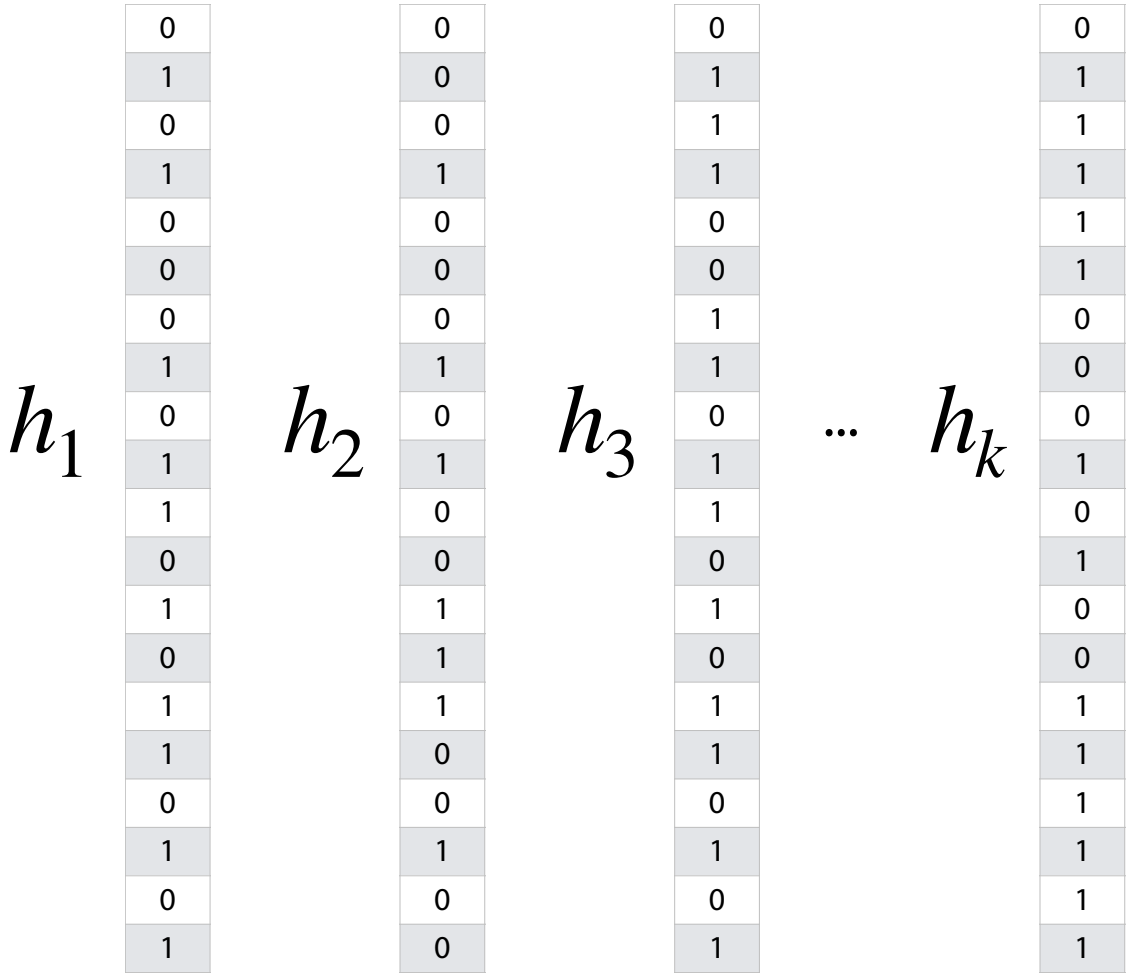
Bloom Filter: Repeated Trials

Using repeated trials, even a very bad filter can still have a very low FPR!

If we have k bloom filter, each with a FPR p, what is the likelihood that ***all*** filters return the value '1' for an item we didn't insert?

Bloom Filter: Repeated Trials

But doesn't this hurt our storage costs by storing k separate filters?



Bloom Filter: Repeated Trials

Rather than use a new filter for each hash, one filter can use k hashes

S = { 6, 8, 4 }

$h_1(x) = x \% 10$ **$h_2(x) = 2x \% 10$** **$h_3(x) = (5+3x) \% 10$**

Bloom Filter: Repeated Trials

Rather than use a new filter for each hash, one filter can use k hashes

0	0
1	0
2	1
3	1
4	1
5	0
6	1
7	1
8	1
9	1

$h_1(x) = x \% 10$ **$h_2(x) = 2x \% 10$** **$h_3(x) = (5+3x) \% 10$**

```
_find(1)
```

```
_find(16)
```

Bloom Filter

$H = \{h_1, h_2, \ldots, h_k\}$

A probabilistic data structure storing a set of values

Built from a bit vector of length m and k hash functions

Insert / Find runs in: _____

Delete is not possible (yet)!

0
0
1
0
0
1
0
1
0
0