

## Agenda for today:

- Bloom filters
- Suffix trees
- Birgit & Shirin: Information about project courses
- Sketching

## Upcoming Deadlines



### Python Programming 3

Available until May 2 | Due Apr 29 at 10am | -/5 pts



### Assignment 3

Available until May 7 | Due May 4 at 10am | -/17 pts

Next lecture: April 29

Background material for 2<sup>nd</sup> part of the course  
<https://chalmers.instructure.com/courses/9360/pages/advanced-databases-background>

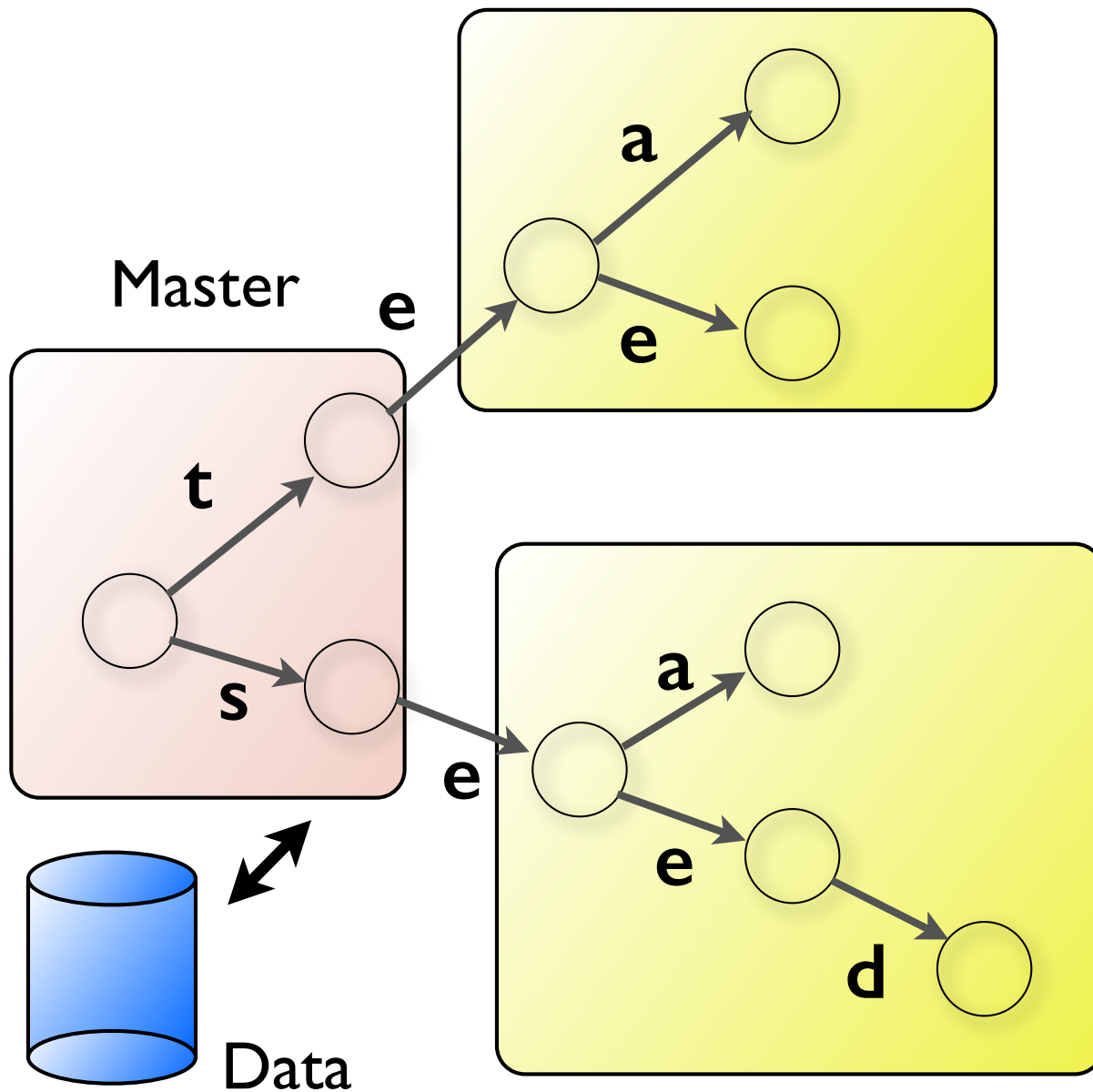
# Recap

# Application: Count Frequent Items

- Frequent items:
  - Heavy hitters
  - Top search queries
  - Most frequently requested items in a database
- Very important in Genomics/DNA sequencing

# Trie: applications & parallelization

Workers



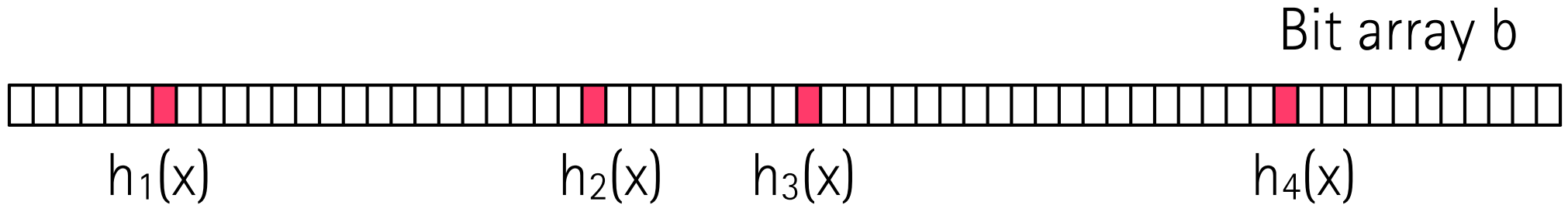
- Duplicates: Second visit to leaf
- Counting: Integer variables in leaf

Trie (Retrieval Tree)

# Frequent items: problem sizes

- Billions of items ( $\sim$  coverage  $\times$  genome size)  
*E.g. 264 Billions for an 80x Human sequencing data set*
- Billions of frequent items ( $\sim$ genome size)  
*> 3 Billion for Human*
- Billions of infrequent items  
*100s of Billions*

# Bloom filter



- Given  $k$  hash functions  $h_1, h_2, \dots, h_k$
- Insert: for item  $x$  set bits  $h_1(x), h_2(x), \dots, h_k(x)$  in a bit array  $b$
- Query: Check whether bits  $h_1(x), h_2(x), \dots, h_k(x)$  are set in  $b$
- No false negatives

# Bloom filter example

	Text	Python Dict	Trie	Bloom Filter $p = 0.01$	Bloom filter $p = 0.001$	Bloom filter $p = 0.0001$
10 000	146 kb	2.5 MB	1.17 MB	12 KB	18 kB	24 kB
100 000	1.43 MB	19.2 MB	~11.44 MB	117 KB	175 kB	243 kB
1M	14.4 MB	179.9 MB	~112 MB	1.14 MB	1.71 MB	2.29 MB

Assuming 15 unique characters per string. E.g URL

<http://hur.st/bloomfilter>

Continuing ...

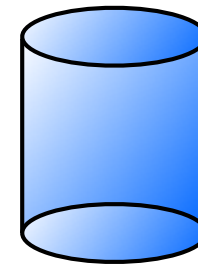
# Counting with Bloom Filters?

# Counting with Bloom Filters

```
from pybloom import BloomFilter
f = BloomFilter(capacity=len(X), error_rate=p)
from collections import defaultdict
d = defaultdict(int)
```

```
for x in X:
    if x in f:
        d[x] += 1
    else:
        f.add(x)
```

```
for x in d.keys():
    if (d[x] + 1) > tau:
        print x, d[x]
```



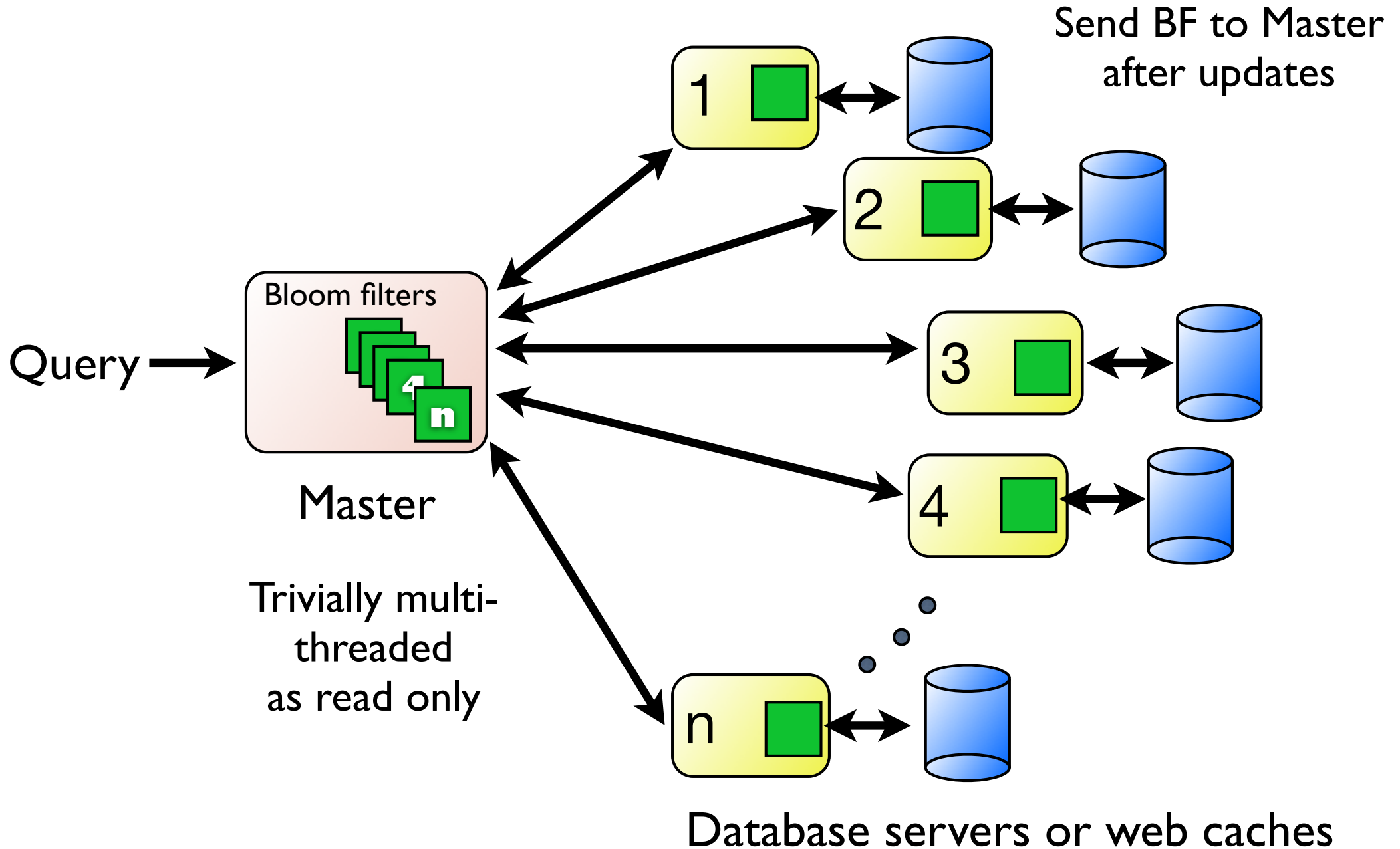
Have we seen the  
k-mer before?



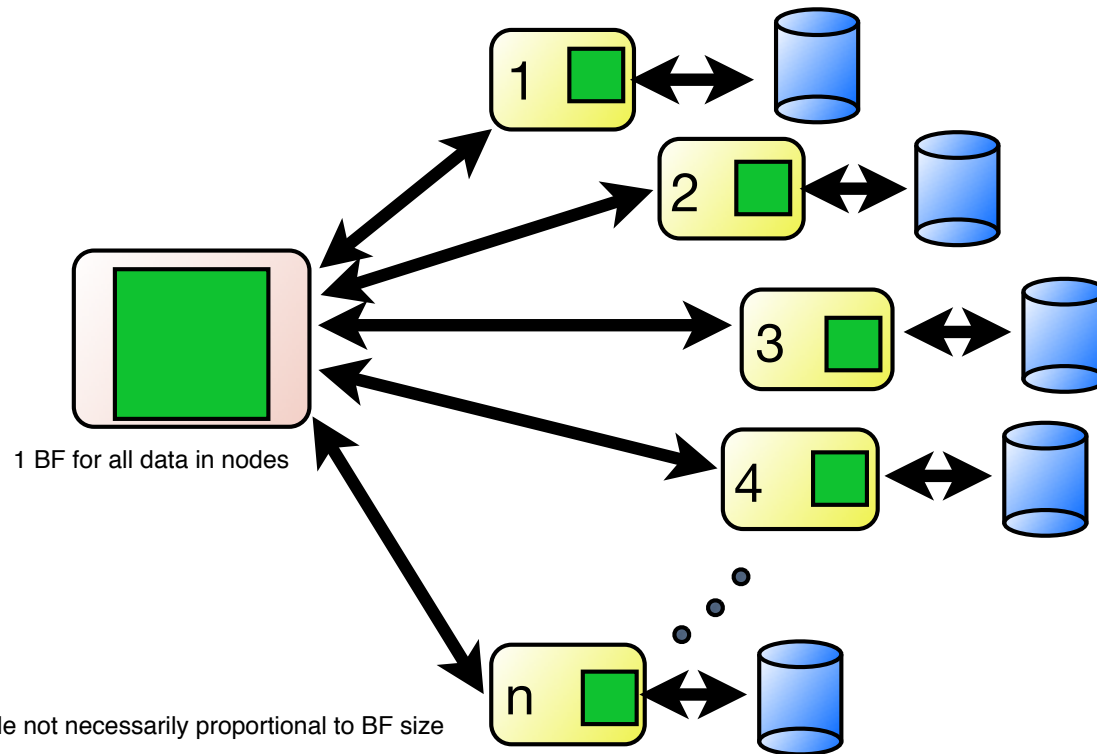
Only count k-mers  
seen at least twice

Counting Data  
Structure

# Distributed Data Store

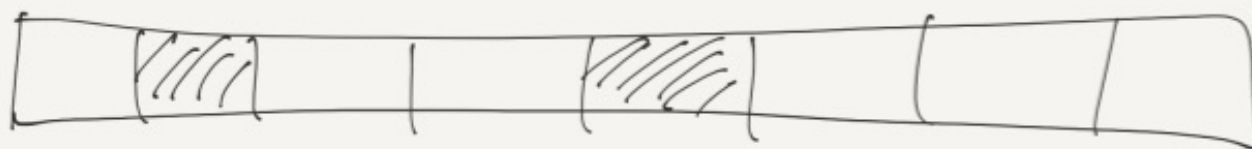


Can the creation of Bloom filters be efficiently distributed; e.g. with Map Reduce?



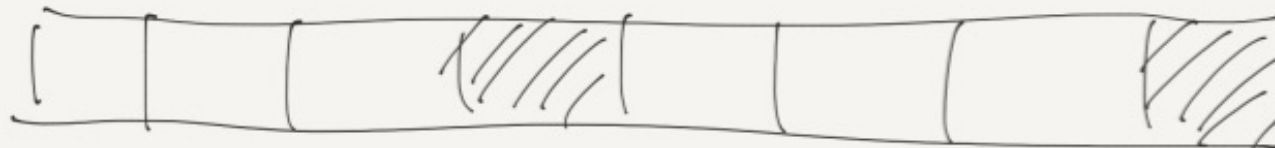
A	B	C	D	E
True	False			

Insert X



Node 1

Insert y



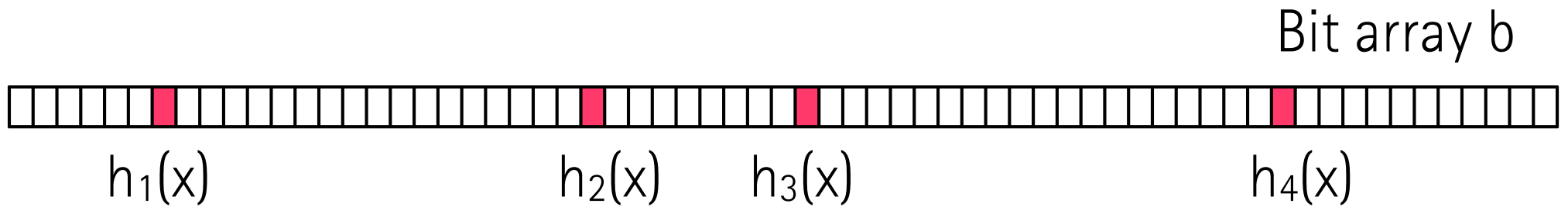
Node 2

Bitwise

OR



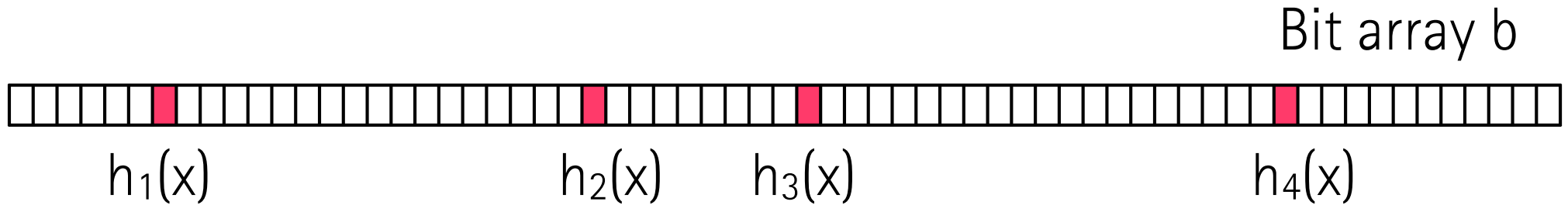
Insert x, y



For sufficiently large  $b$ , accessing each bit will likely cause a cache miss. The expected number of cache misses for insert and query operations, when the item is not in the Bloom filter is the same.

A	B	C	D	E
True	False			

# Bloom filter: Cache Behaviour



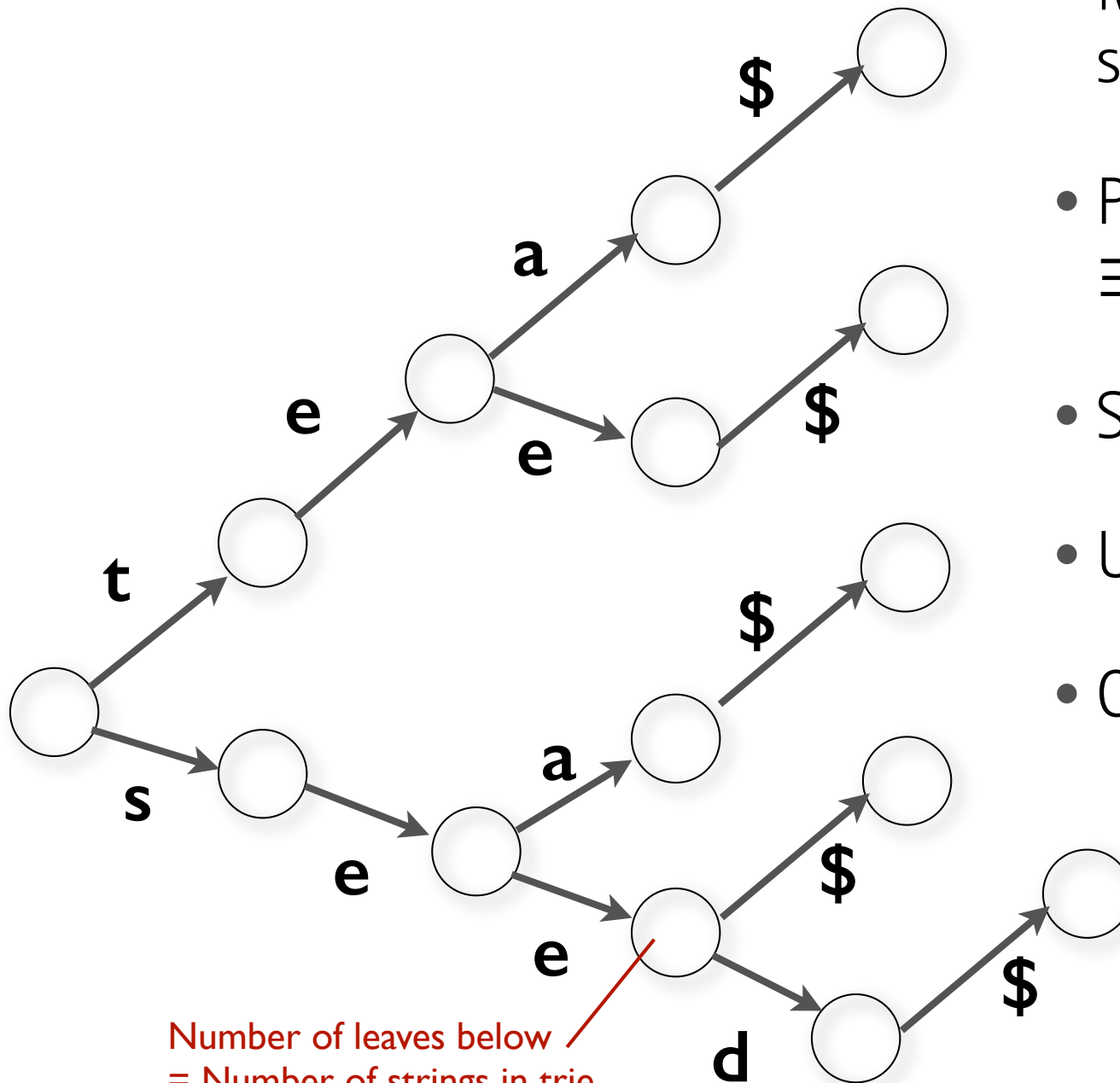
- Insert:
  - Worst-case:  $n$  cache misses (average close) per Insert
- Query:
  - item present / false positive: like insert
  - item not-present: average much lower than worst-case

# Suffix trees

# Data analysis on large texts

- Text T:
  - Natural language
  - Error or event logs (error codes/event types = alphabet)
  - Biological sequences, any other sequence of discrete observations
- Questions:
  - Is  $s$  a substring of  $T$ ?
  - How often appears  $s$  in  $T$ ?

# Recall: Tries



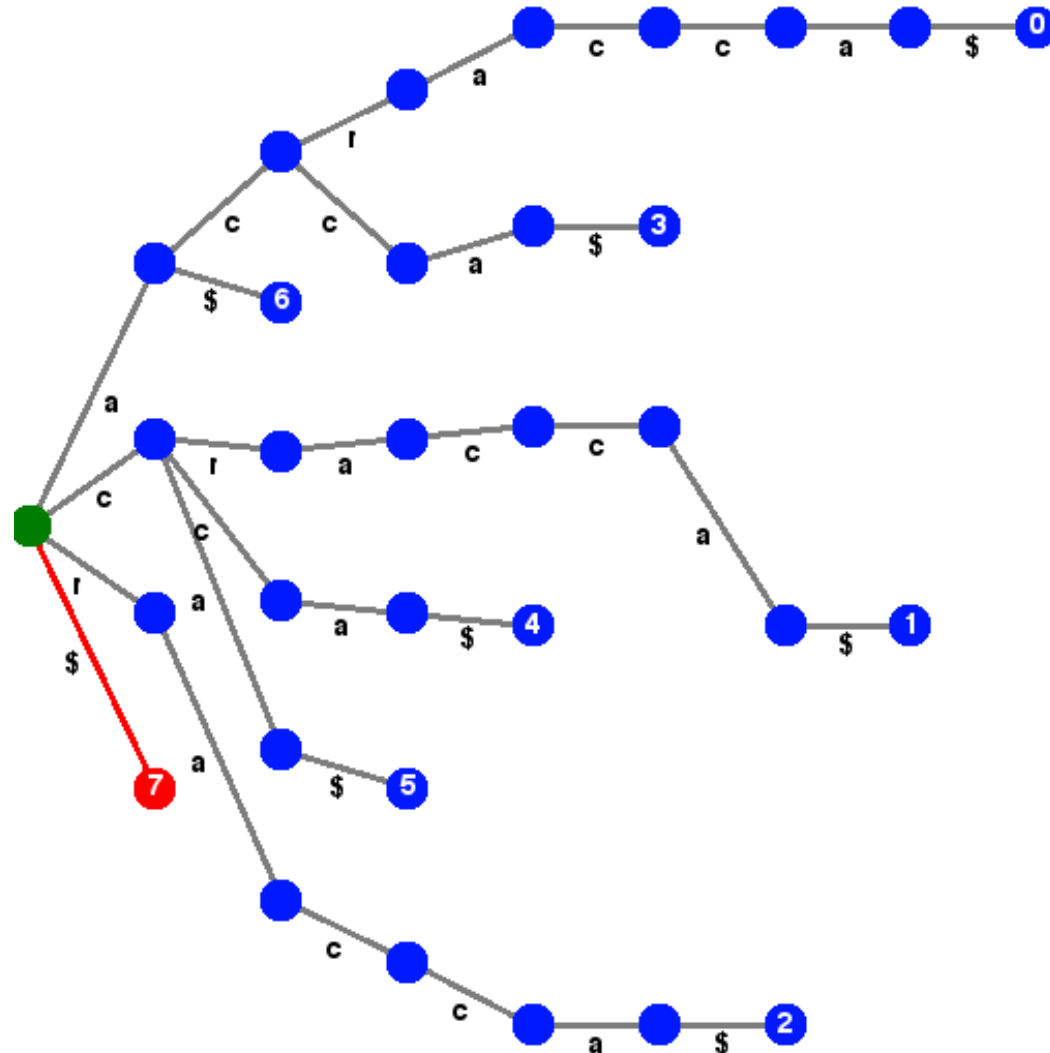
Number of leaves below  
= Number of strings in trie  
with prefix "see"

- Membership query:  
 $s \in S$
- Prefix query:  
 $\exists t \in S: s \text{ is prefix of } t$
- Sorting string
- Unique strings
- Count strings

# Example: T = acracca\$

acracca\$  
cracca\$  
racca\$  
acca\$  
cca\$  
ca\$  
a\$  
\$

Trie of all  
suffixes of T



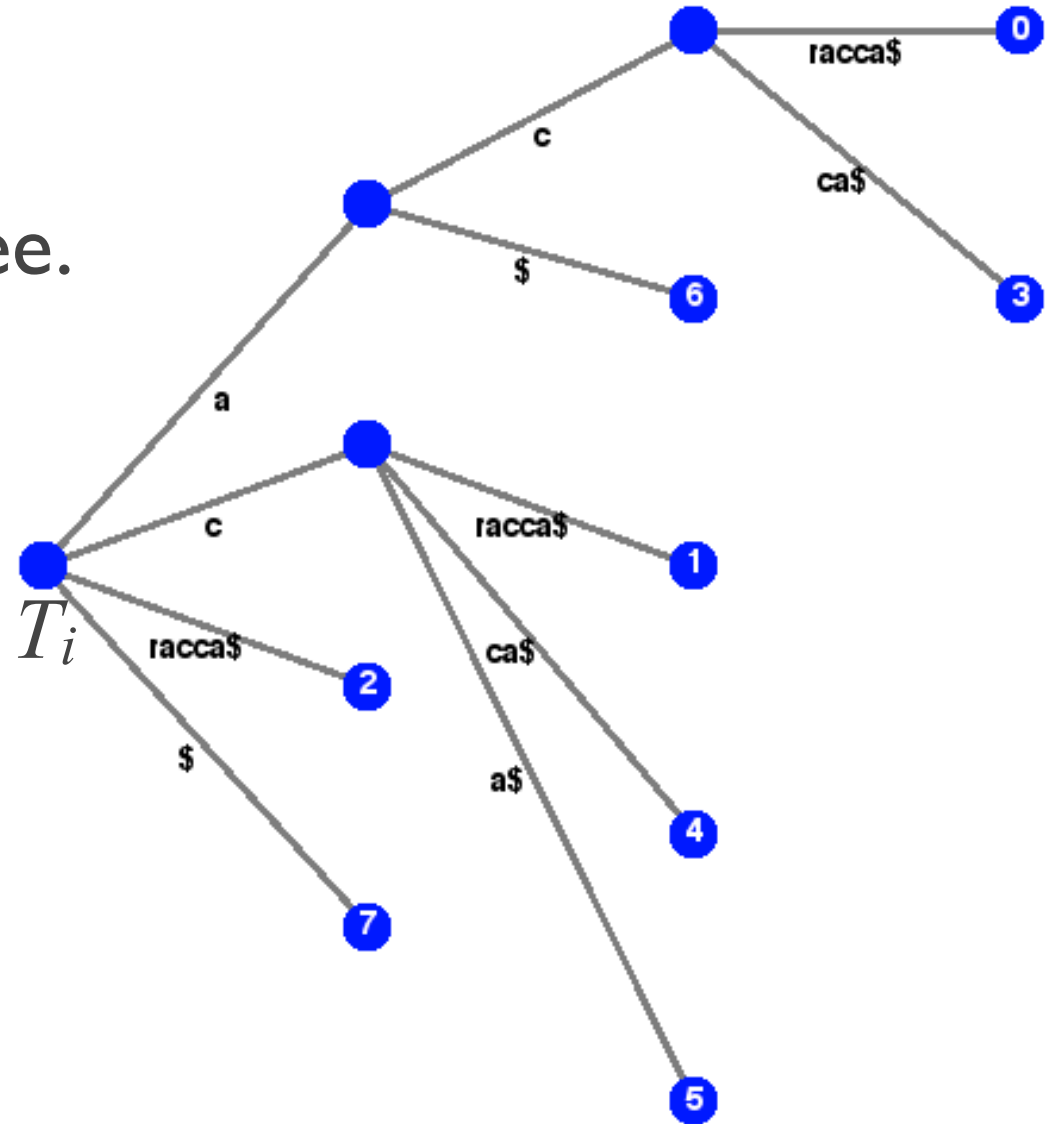
T = banana

Is "na" a substring of T

nana are suffixes  
na of banana

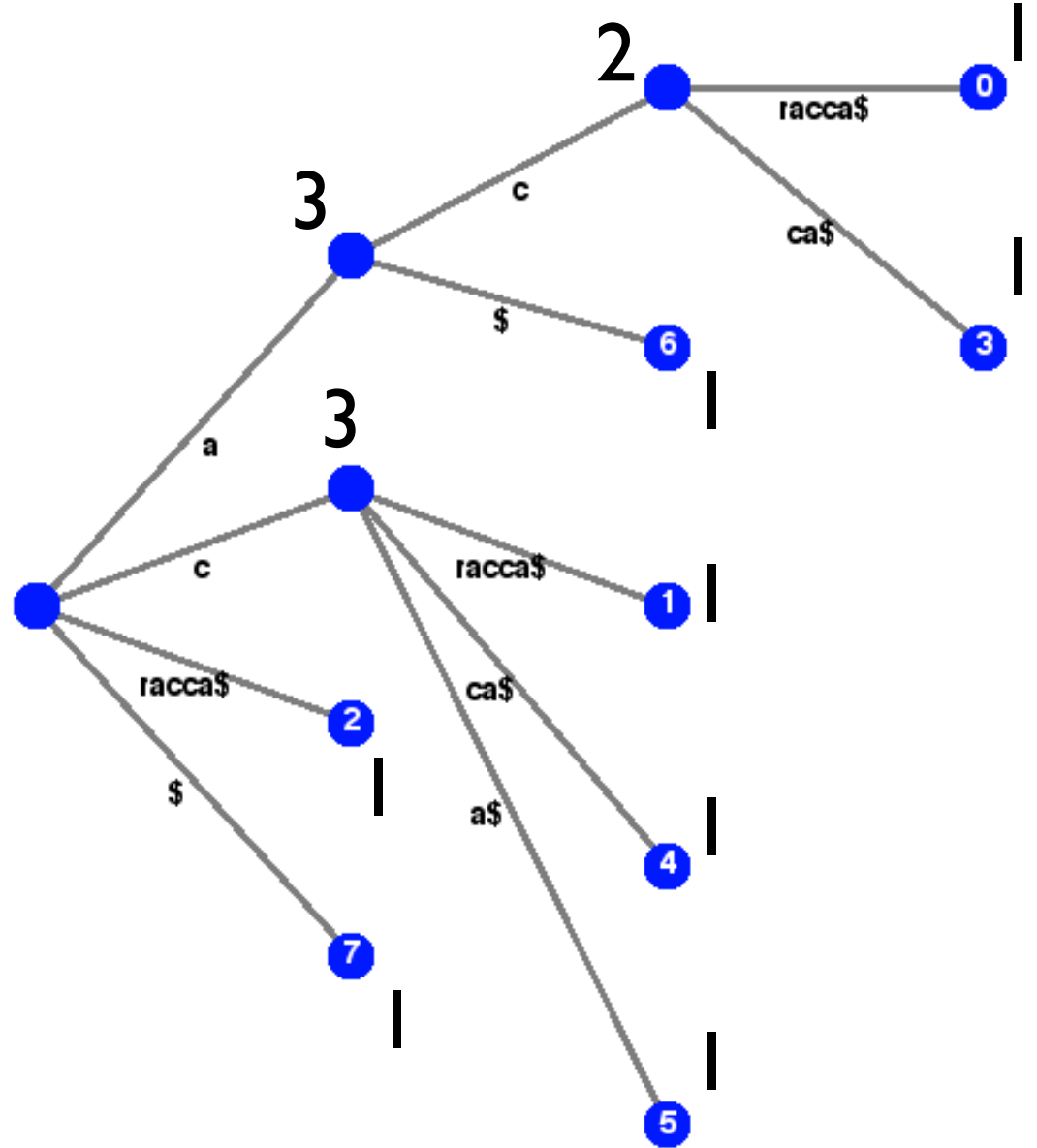
# Definition: Suffix tree

- Given  $T = t_1 t_2 \dots t_n$  its suffix tree  $\mathcal{T}_T$  is a rooted tree.  $\mathcal{T}_T$  has
  - $n$  leaves; leaf  $l_i$  corresponds to suffix  $T_i$
  - edge label  $\text{label}(u, v)$ : sub-string
- Can be constructed in  $O(|T|)$



# Application: #occurrences of $s$ in $T$ ?

- Use tree-traversal to populate leaf-counts for all internal nodes (once!)
- If for some explicit or implicit vertex  $u$ ,  $L[u] = s$  then  $s$  is a substring and its count is given by  $u$  (or its least explicit predecessor)
- Complexity:  $O(|s|)$
- Independent of  $|T|$  !



# Outlook:

- Suffix tree for Human Genome ~40GB
- Burrows-Wheeler-Transform (BWT) and FM-index support same operations with same complexity but index is compressed to ~4 GB

# Accelerating computations

Sketches

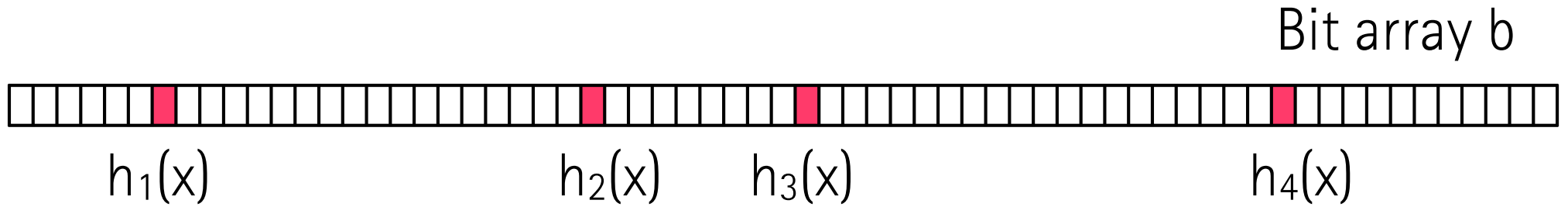
# Counting observations

- Data:  $m$  elements from  $\{1, 2, \dots, n\}$ ,  $m \gg n$
- $f_i$  frequency of  $i$
- Query types:
  - Point query: frequency  $f_i$  of  $i$
  - Range Query: for  $i, j$  estimate  $f_i + f_{i+1} + \dots + f_j$
  - Quantile query: find  $i$  s.t.  $f_1 + f_2 + \dots + f_i \sim x$
  - Heavy hitters: find  $i$  s.t.  $f_i \geq m \cdot x$

# Subsampling

- Randomly select a small subset of the data
- Compute summary statistics on this

# Bloom filter

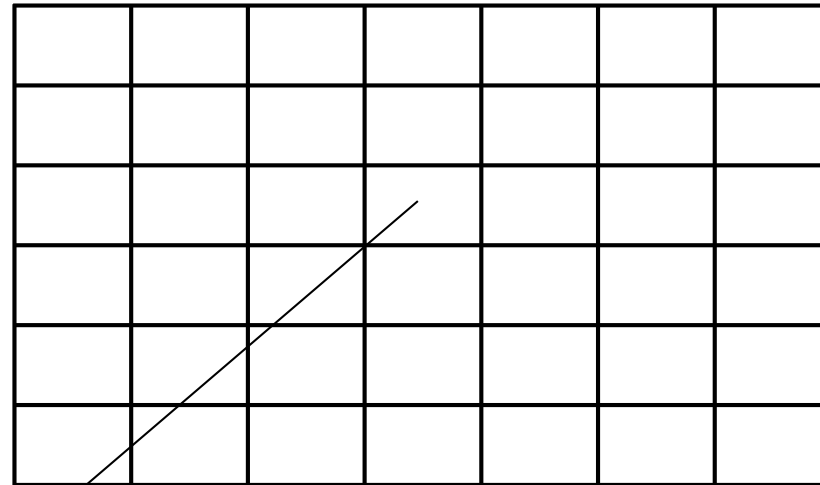


How to change a Bloom Filter so that it can count?

# Count-min sketch

*Image of hash functions*

**W**




**d**

*Hash  
functions*

$c_{i,j} = \# \text{ of elements with } h_i(x) = j$

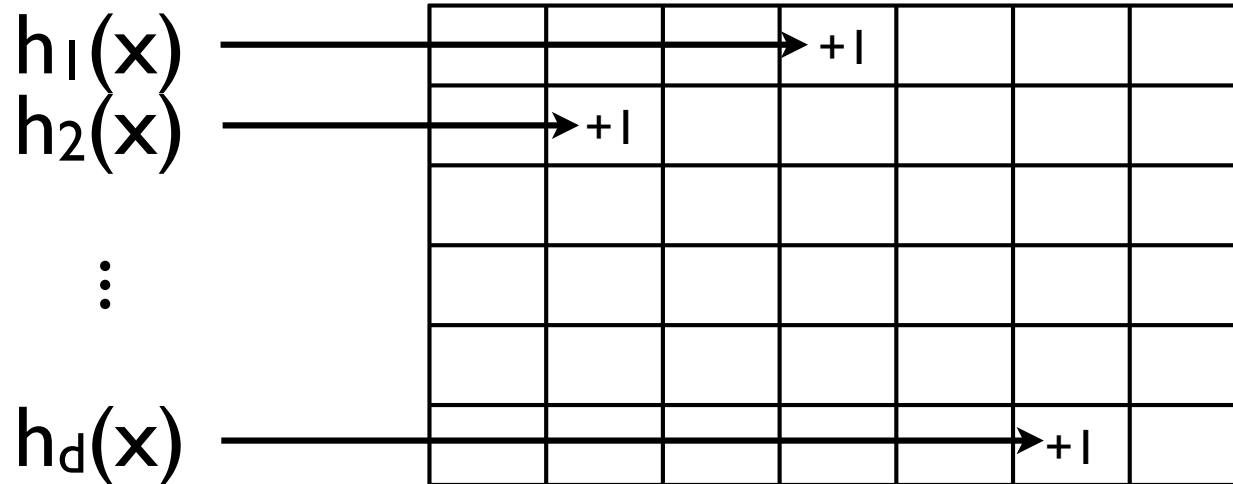
e element in the data

# Count-min sketch: Update

## Image of hash functions

# Compute

**W**



d

# Hash functions

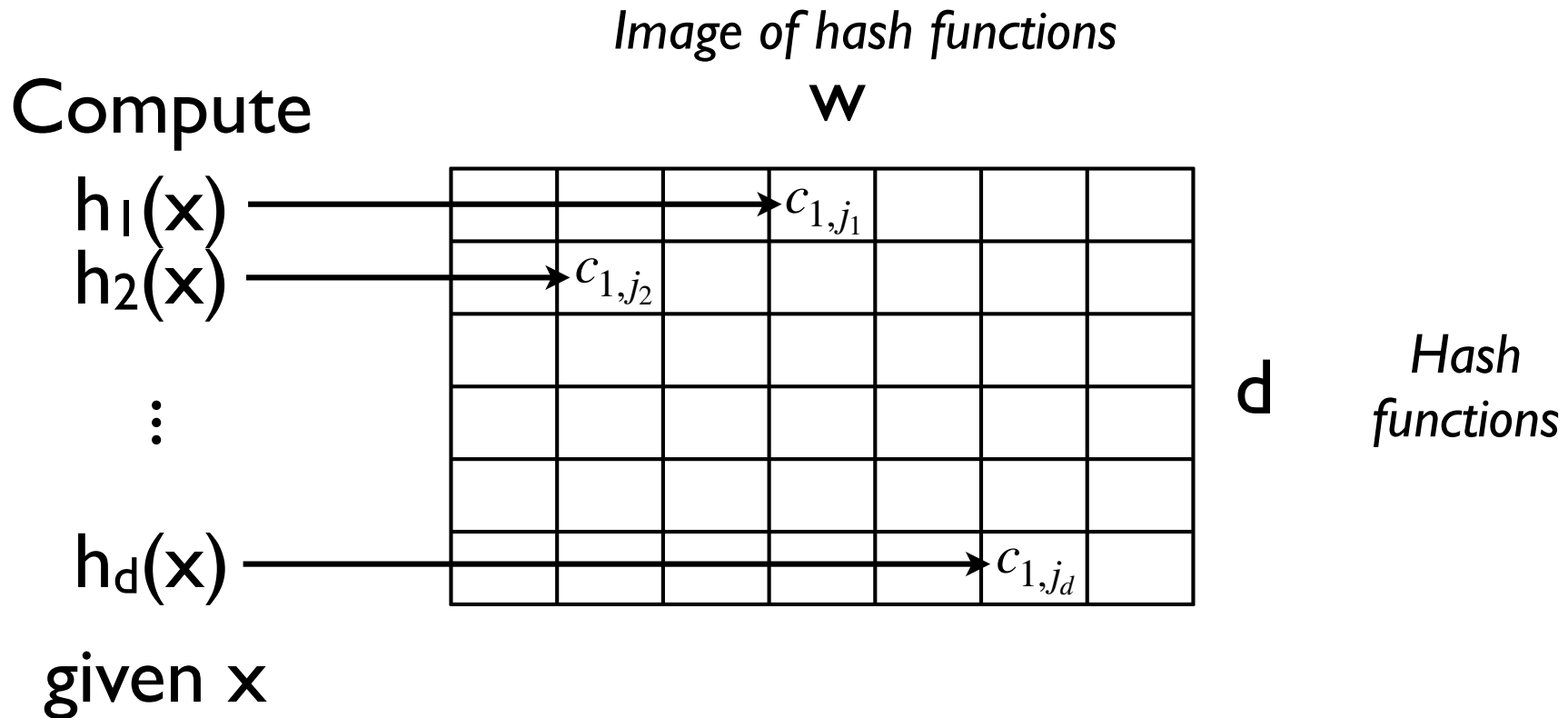
given  $x$

# Increment counters

Count min update can effectively be parallelized.

A	B	C	D	E
True	False			

# Count-min sketch: Query



$$\tilde{f}_x = \min\{c_{1,j_1}, c_{2,j_2}, \dots, c_{d,j_d}\}$$

$$= \min\{c_{1,H_1(x)}, c_{2,H_2(x)}, \dots, c_{d,H_d(x)}\}$$

# Count-min sketch: observations

- For all  $e, i$ :  $c_{i, H_i(x)} \geq f_x$  so  $\tilde{f}_x \geq f_x$
- $d=1, w=n, H_1(x) = x$ : Exact counting using space linear in  $n$
- Space:  $d \times w \times \text{sizeof}(\text{counter})$
- Increasing  $d$ ?
- Decreasing  $w$ ?

# Count-min sketch: analysis

For  $w = 2/\epsilon$  and  $d = \log_2(1/\delta)$ :

$$P[f_x \leq \tilde{f}_x \leq f_x + \epsilon m] \geq 1 - \delta$$

Need 2-way independent hash functions

$$P[h_i(x) = h_i(y)] \leq \frac{1}{w}$$

# Count-min sketch: analysis

For  $w = 2/\epsilon$  and  $d = \log_2(1/\delta)$ :

$$P[f_x \leq \tilde{f}_x \leq f_x + \epsilon m] \geq 1 - \delta$$

Error bound of estimate  
Larger  $w$ , smaller  $\epsilon$

E.g. for error bound of  
 $\epsilon m = 2000$  for  $m = 10^6$   
elements we need  $w = 1,000$   
at  $\epsilon = 0.002$

# Count-min sketch: analysis

For  $w = 2/\epsilon$  and  $d = \log_2(1/\delta)$ :

$$P[f_x \leq \tilde{f}_x \leq f_x + \epsilon m] \geq 1 - \delta$$

Error bound of estimate  
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E.g. for error bound of  
 $\epsilon m = 2000$  for  $m = 10^6$   
elements we need  $w = 1,000$   
at  $\epsilon = 0.002$

Probability of  
staying within  
error bound  
Larger  $d$ ,  
smaller  $\delta$

E.g.  $d=7$  is needed  
for  $\delta = 0.01$

Memory usage:  $w * d * \text{sizeof(counter)} = 1000 * 7 * 4 \text{ bytes} = 28\text{kB}$

# Accelerating computations

## Index data structures

NOTE: The kd-trees + k-means part is for reference only. I mostly skipped it in the lecture. See the original nice paper.

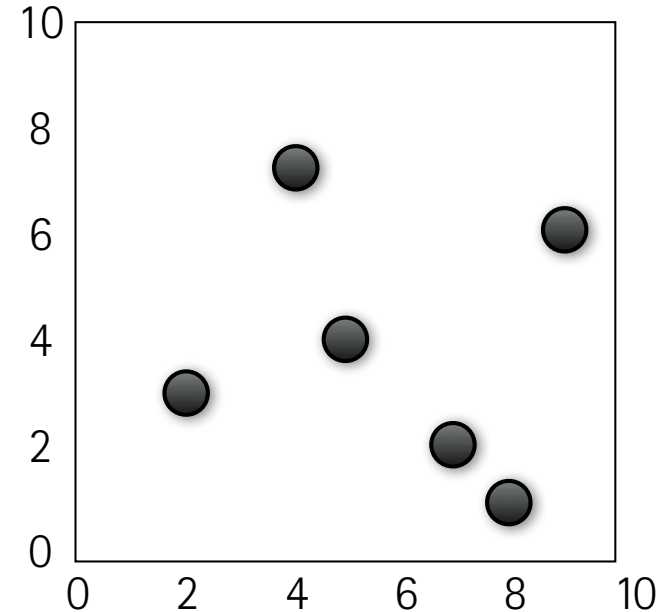
Pelleg, Moore: Accelerating exact k-means algorithms with geometric reasoning. KDD 1999.

# Nearest neighbors

- Given a data base of  $n$  records with coordinates in Euclidean space (e.g.  $(x,z)$  or  $(x,y,z)$ )
- For a query  $q$ , return the nearest neighbor in the database
- *Naive approach:  $O(n)$*
- Application: GIS, computer games, dating websites/apps,...

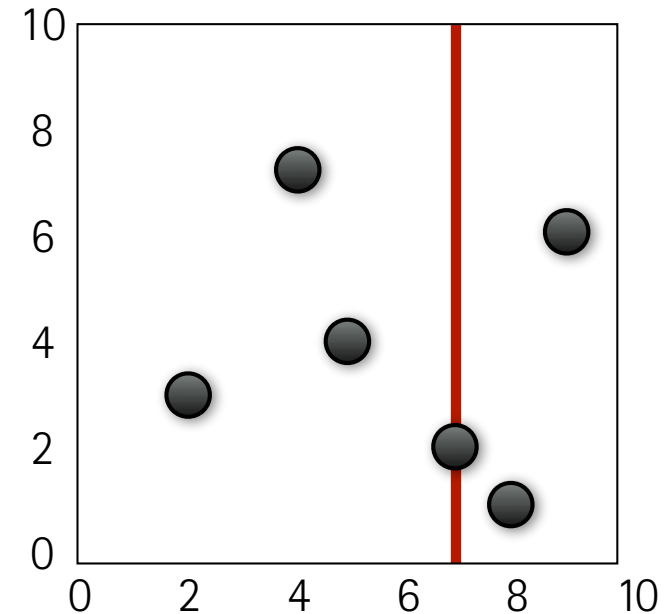
# *kd*-trees

- Spatial index structure
- Balanced binary tree
- Fast nearest neighbor queries (dependent on instances)
- $O(n \log n)$  construction



# *kd*-trees

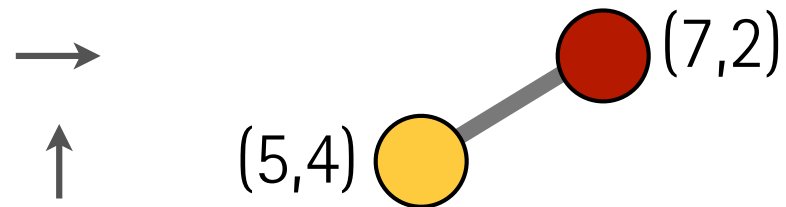
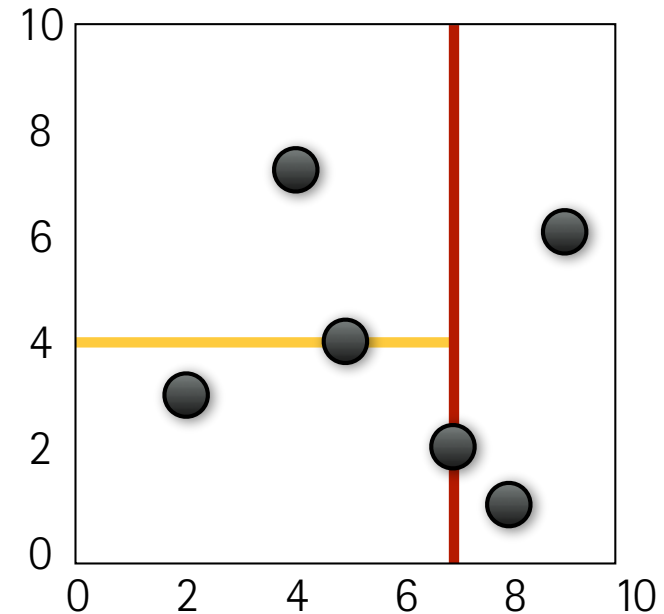
- Spatial index structure
- Balanced binary tree
- $O(\log n)$  nearest neighbor queries (dependent on instances)
- $O(n \log n)$  construction



● (7,2)

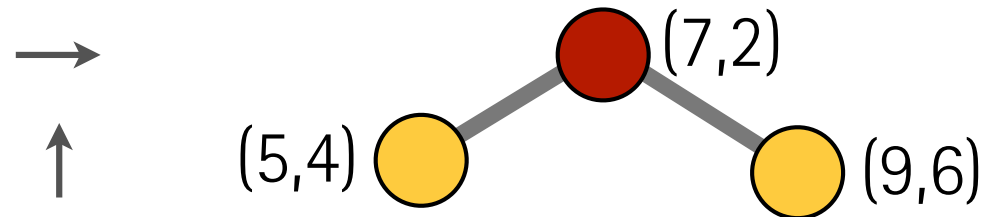
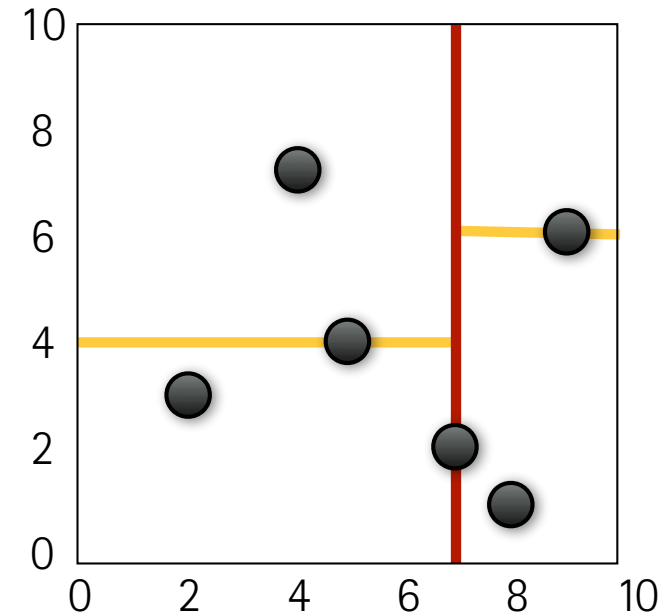
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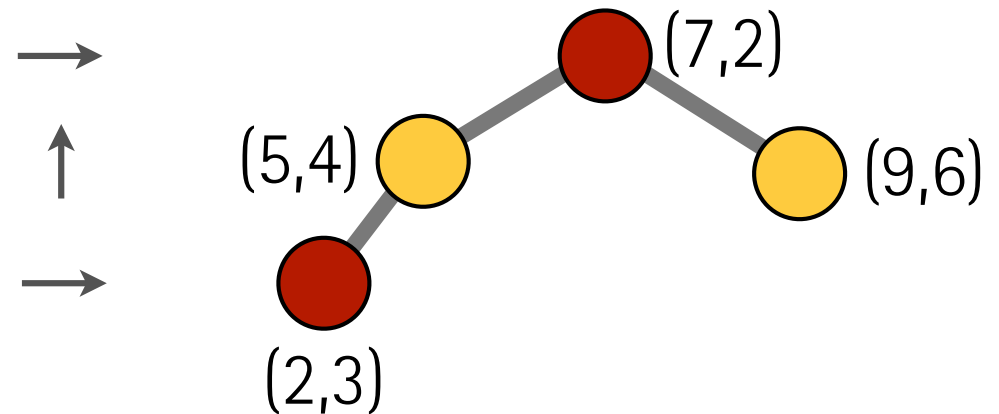
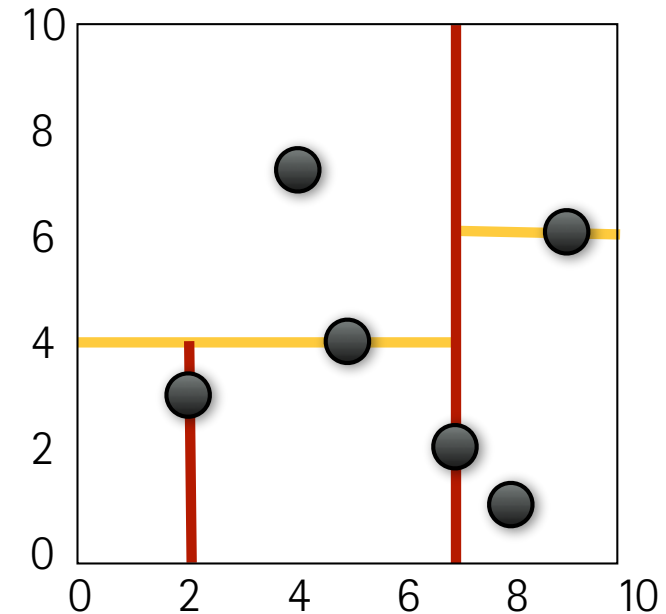
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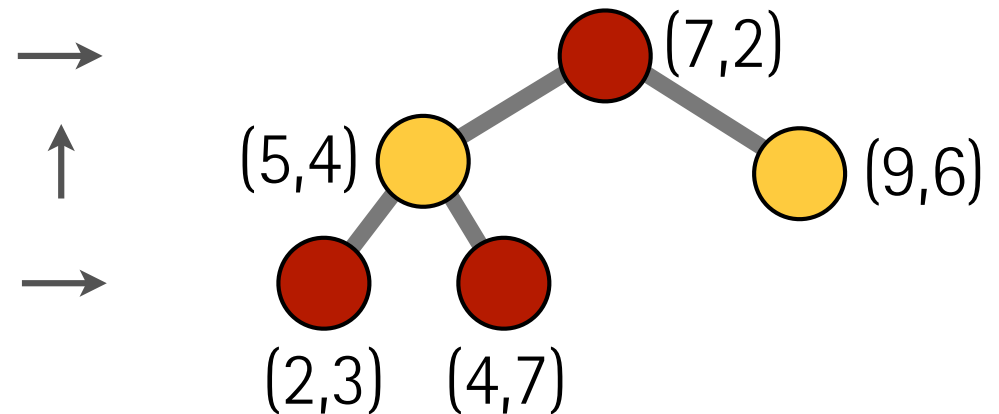
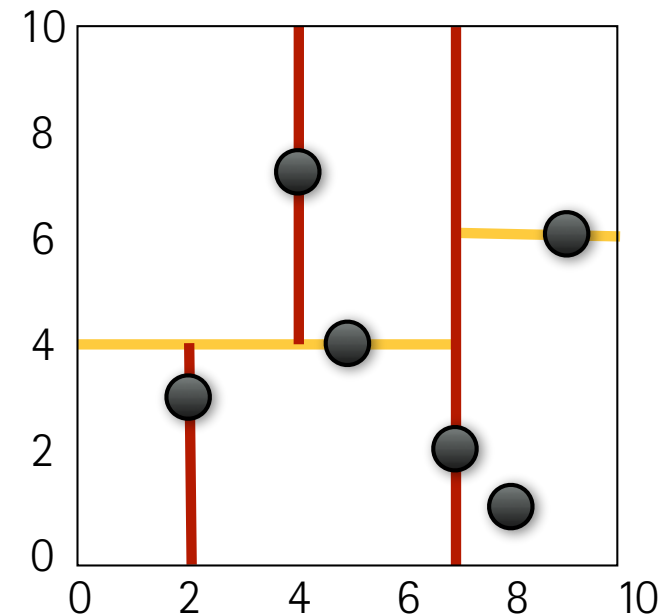
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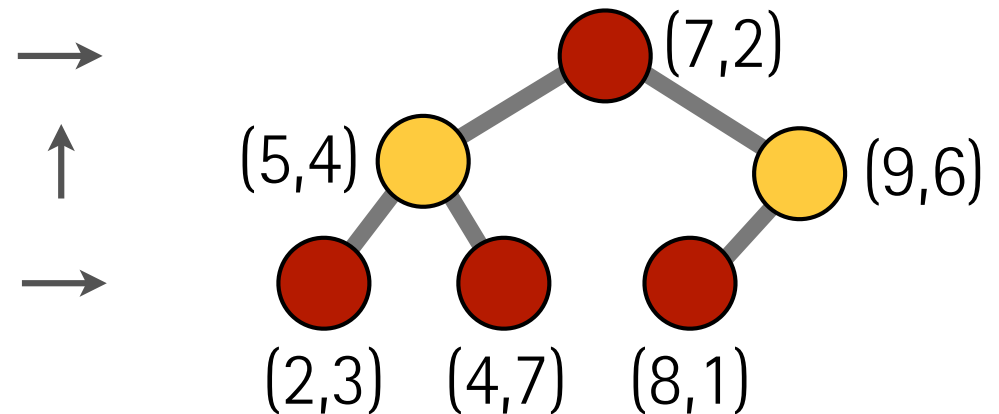
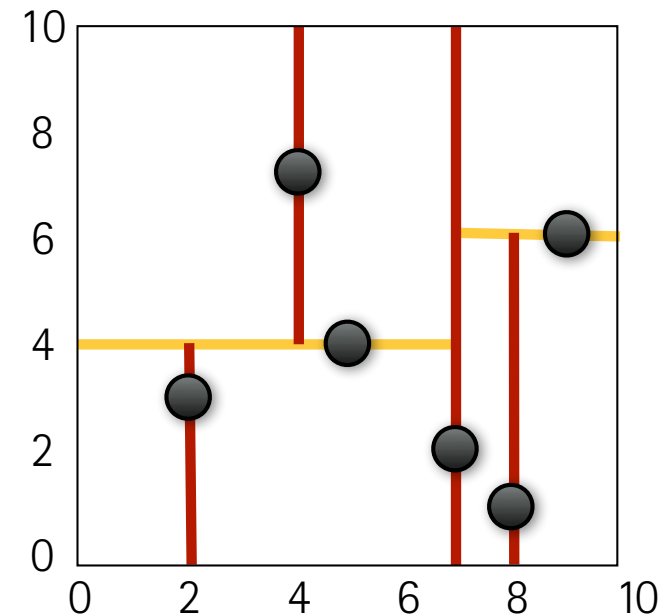
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# *kd*-trees

- Spatial index structure
- Balanced binary tree
- $O(\log n)$  nearest neighbor queries (dependent on instances)
- $O(n \log n)$  construction



# k-means clustering

$$\min_{C_1, C_2, \dots, C_k} \left\{ \sum_{k=1}^K W(C_k) \right\}$$

$$W(C_k) = \frac{1}{|C_k|} \sum_{i, j \in C_k} \|x_i - x_j\|^2$$

$\|x - y\|^2$  Euclidean distance

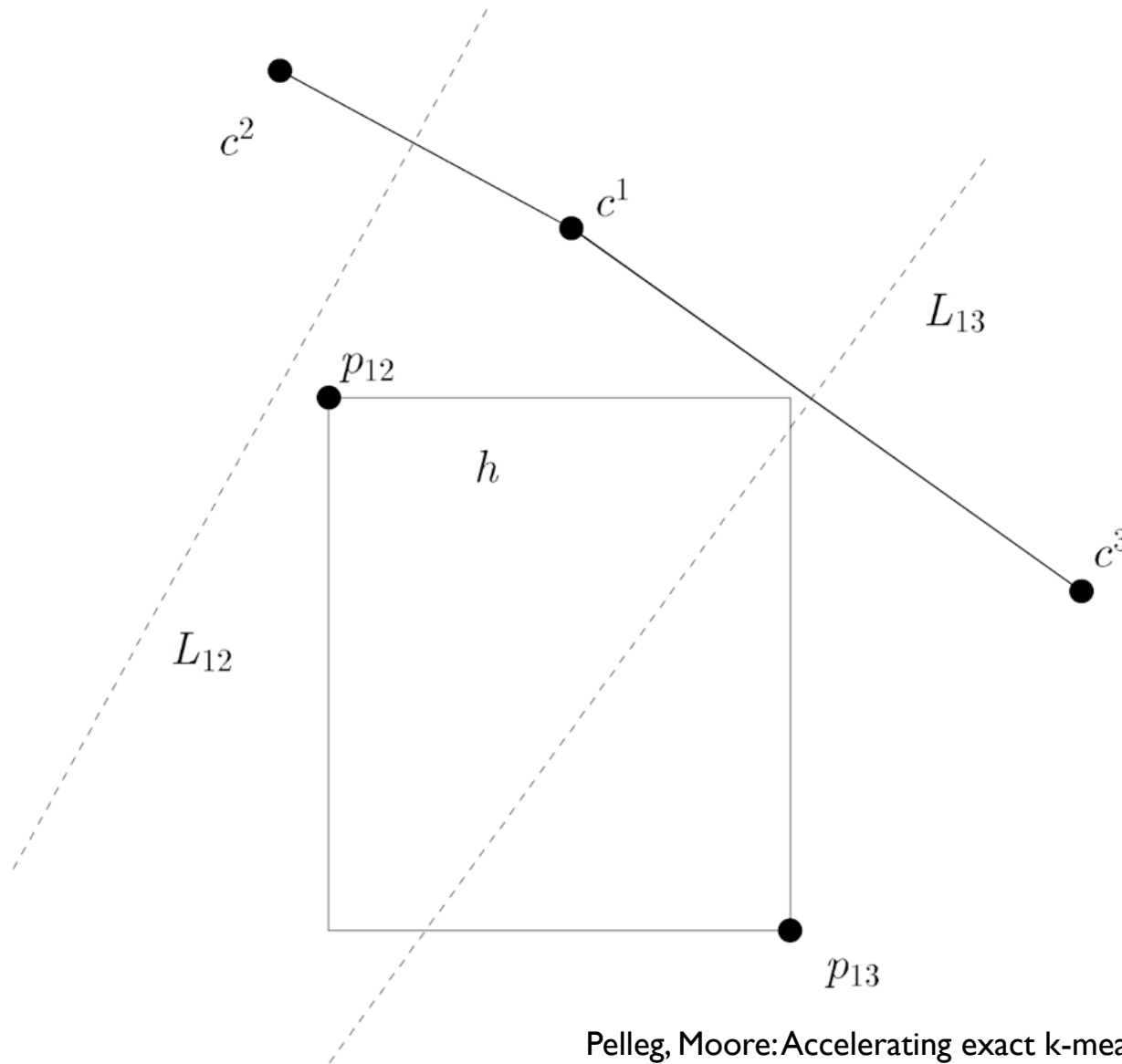
# k-means clustering

- Chose k centroids among data points
- Iterate:
  - assign data points to closest centroid  $O(n \times k)$
  - recompute centroids  $O(n)$

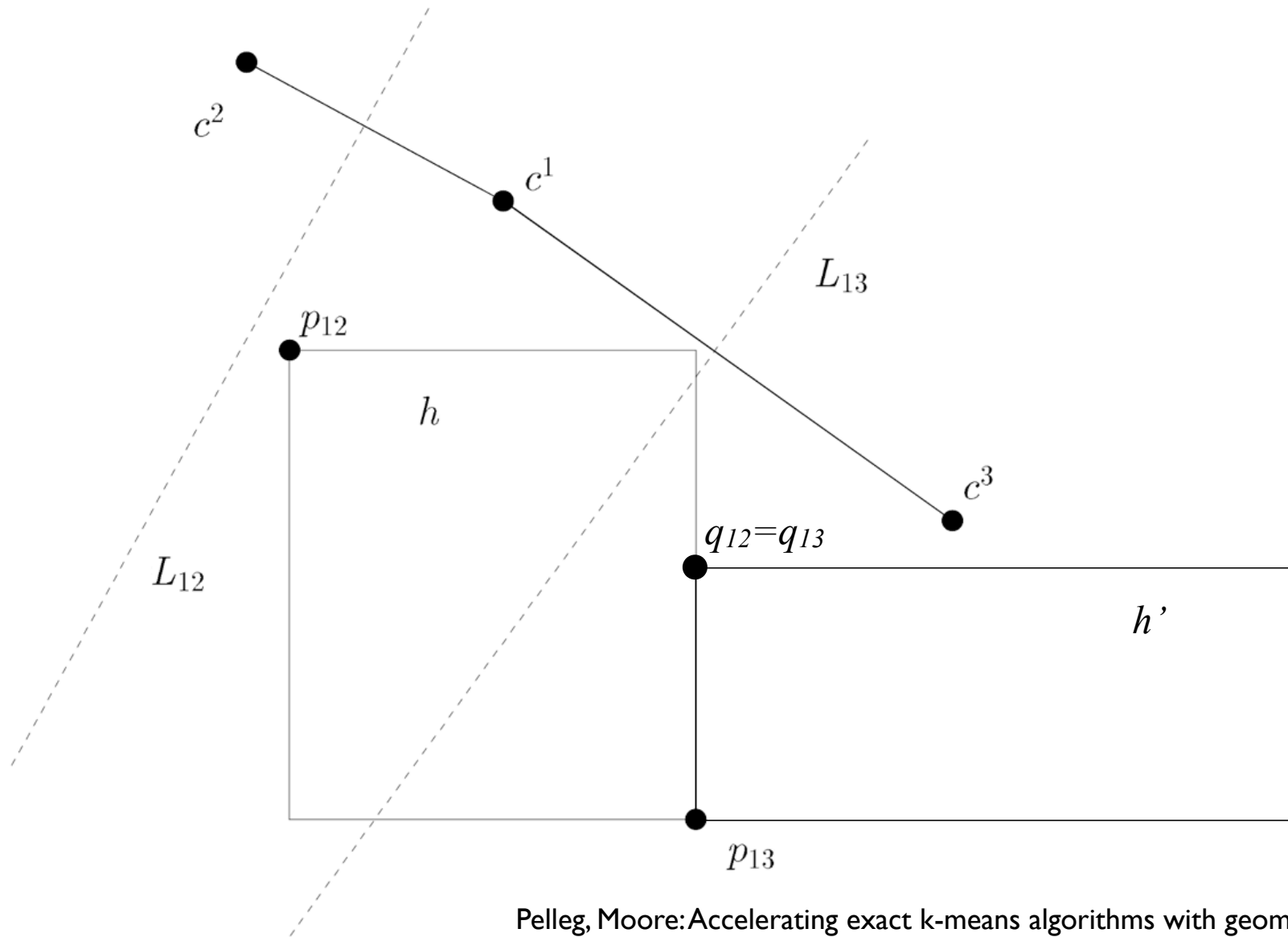
# Accelerating k-means with kd-trees

- Idea: Avoid computing distance between every point and every centroid
- kd-trees partition space into hyper-rectangles

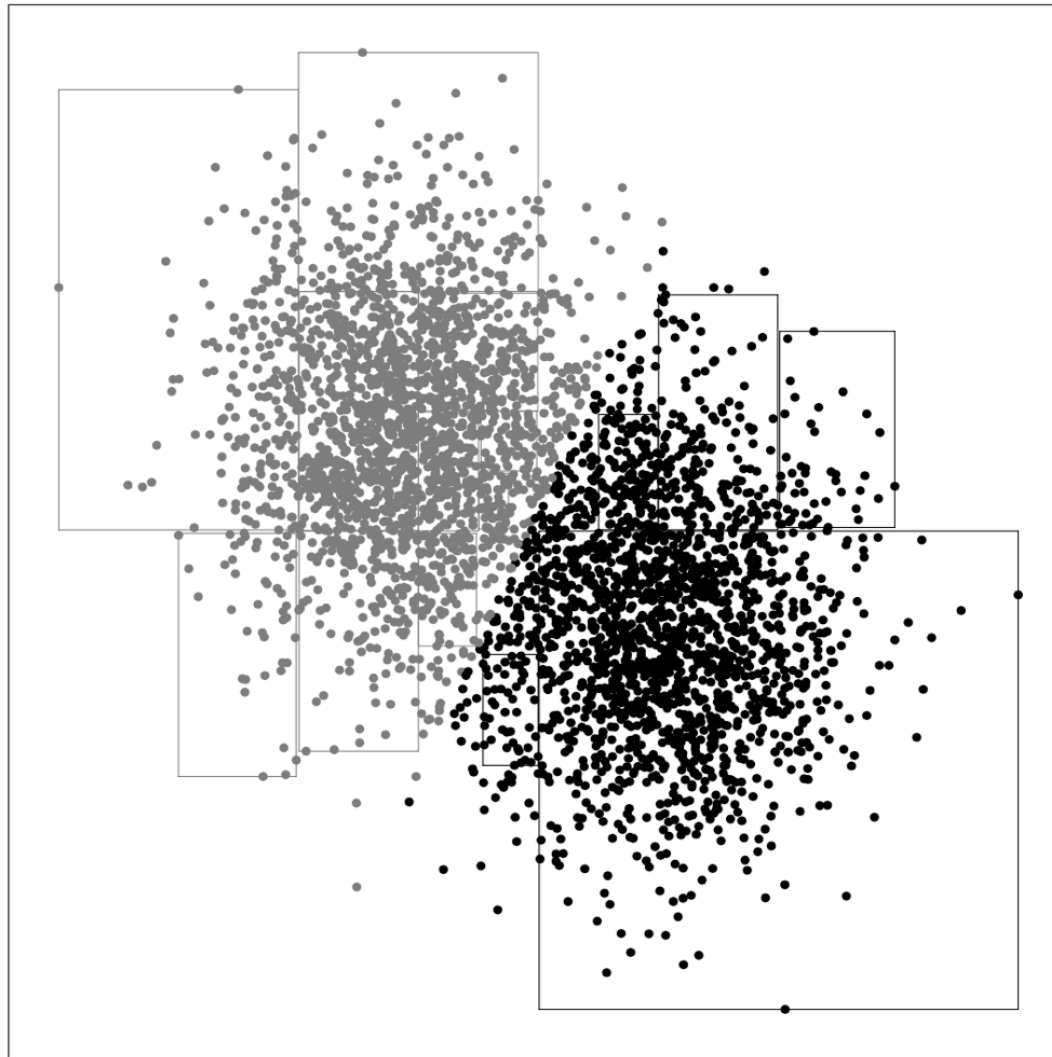
# Accelerating k-means with kd-trees



# Accelerating k-means with kd-trees



# Accelerating k-means with kd-trees



# Accelerating k-means with kd-trees

points	blacklisting	naive	speedup
50000	2.02	52.22	25.9
100000	2.16	134.82	62.3
200000	2.97	223.84	75.3
300000	1.87	328.80	176.3
433208	3.41	465.24	136.6

Table 1: Comparative results on real data.

Run-times of the naive and blacklisting algorithm, in seconds per iteration. Run-times of the naive algorithms also shown as their ratio to the running time of the blacklisting algorithm, and as a function of number of points. Results were obtained on random samples from the 2-D “petro” file using 5000 centers.

# Use in methods

- For dimension up to 10
  - k-means
  - mixture estimation
  - k-nearest neighbor classification
- Active research topic: higher dimensions; specialization for specific combinations of  $n$ ,  $k$ ,  $d$

Elkan, Using the triangle inequality to accelerate k-means, ICML, 2003

Kurban and Dalkilic: A novel approach to optimization of iterative machine learning algorithms: over heap structure. Big Data 2017

# How to apply all of this ...?

Answer: reluctantly

# General approach

- Implement Data Science solutions the framework you are most familiar with (e.g. Python / Pandas) without worrying about efficiency (or parallelism)
- Probably will be okay for  $< 100$  GB on Laptop and  $< 1$  TB of data on desktop

(assuming SSDs / RAID, enough RAM, multi-cores)

# Cost of optimization

- Qualified technical employee: cost to employer 1.5M SEK/year for 1600 hours/year  
⇒ ~1000 SEK/hour
- Most expensive Amazon EC2 on-demand instance is 250 SEK/hour (+storage).
- Not worth to invest an hour, if not saving at least four.
- Q: How frequently does a workload run?

# What if my data is big?

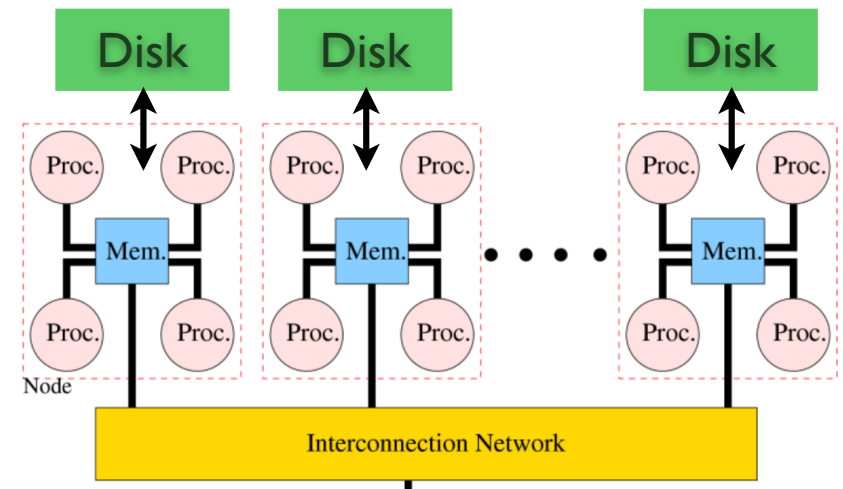
- Bandwidth:
  - Single SSD: 0.5 GB/s
  - Large RAID: 1 GB/s
  - DDR4 RAM > 20 GB/s (peak)
- Reading 1 (resp. 100) TB data needs:
  - 33 min resp. 55h
  - 17 min resp. 28 h
  - ~ 1 min resp. 1:40 h

# Is Input/Output the bottleneck?

- Times below are only a bottleneck if computations are fast
  - 33 min resp. 55h
  - 17 min resp. 28 h
  - ~ 1 min resp resp. 1:40 h
- Alternative: external-memory frameworks and algorithms.
  - E.g. <https://dask.org/> Pandas frames too large for RAM

# What if my data is big?

- Solutions:
  - Up to a point expensive hardware (e.g. RAID with SSDs)
  - Cluster with local disks & HDFS
- $\Rightarrow$  You need to parallelize



# What if my solution is too slow?

- General ideas:
  - Change the problem
  - Refactor
  - Compile
  - Optimize
  - Parallelize

# Change the problem

- E.g. Descriptive statistics with MapReduce: Is the median needed?
- Identifying Duplicates: Are a few false positive duplicates acceptable?
- If a median (or quartiles are needed): are approximate estimates acceptable?
- If a classifier is used: Is a simpler algorithm (e.g. k-nearest neighbor instead of deep learning) acceptable?

# Refactor

- Generally: short Python programs are fast Python programs.
- Use libraries: E.g. numpy and others offering C/C++-speed

```
def nearestCentroid(datum, centroids):  
    # norm(a-b) is Euclidean distance, matrix - vector computes difference  
    # for all rows of matrix  
    dist = np.linalg.norm(centroids - datum, axis=1)  
    return np.argmin(dist), np.min(dist)
```

- Might make some parallelization trivial

```
import mkl  
import numpy as np  
  
mkl.set_num_threads(4)  
np.dot(x,y)
```

# Compile your Python Code

## Cython

<https://cython.org>

```
def primes(int nb_primes):
    cdef int n, i, len_p
    cdef int p[1000]
    if nb_primes > 1000:
        nb_primes = 1000

    len_p = 0 # The current number of elements in p.
    n = 2
    while len_p < nb_primes:
        # Is n prime?
        for i in p[:len_p]:
            if n % i == 0:
                break

        # If no break in the loop, we have a prime.
        else:
            p[len_p] = n
            len_p += 1
            n += 1

    # Let's return the result in a python list:
    result_as_list = [prime for prime in p[:len_p]]
    return result_as_list
```

Some parallelization support OpenMP (not clusters though)  
Allows calling of C libraries, use of C-structs etc.

## Numba

<https://numba.pydata.org/>

```
from numba import jit
import random

@jit(nopython=True)
def monte_carlo_pi(nsamples):
    acc = 0
    for i in range(nsamples):
        x = random.random()
        y = random.random()
        if (x ** 2 + y ** 2) < 1.0:
            acc += 1
    return 4.0 * acc / nsamples

@numba.jit(nopython=True, parallel=True)
def logistic_regression(Y, X, w, iterations):
    for i in range(iterations):
        w -= np.dot(((1.0 /
            (1.0 + np.exp(-Y * np.dot(X, w)
            - 1.0)) * Y), X)
    return w
```

Also parallelizes incl. GPUs (not clusters though)

# Optimize

- Measure running time and identify hot spots
- Better data structures and algorithms usually beats code optimization
  - Constants matter
  - Latency/memory hierarchy matters
  - $\Rightarrow$  Lower computational complexity does not always win
- Sometimes optimizing makes sense

# Parallelize

- Based on structure of workload: data flow, computational effort, hardware ...
- Measure Amdahl's  $f$
- SIMD instructions
- Multi-threading
- Message passing
- MapReduce, Spark, ... and many big data computational frameworks.
- Question: Are there specialized frameworks for *your* problem?
- Avoid oversubscription ...

# Parallelize







- Achieve scaling via:
  - Dedicated hardware: GPU, Tensor Units for deep learning
  - Clusters
  - Clouds ...
  - *Volunteer Clouds (Folding at home...)*

# Outlook

- Very active research field
  - Intel: <https://github.com/IntelPython>,  
<https://www.youtube.com/watch?v=HKjM3peINtw> (SciPy 2018 talk)
  - Amazon–Uber: <https://arrow.apache.org/>;  
see <https://streamdata.io/blog/open-source-apache-big-data-projects/>
  - Tool provider: Anaconda (e.g. Numba) with Intel, Nvidia and AMD

# Q&A from Chat

Q: Where to find hash functions? Defined your own? A: Good hash functions are a science and art in itself. I always took the state-of-the-art for a specific task from the literature. Note that there is a tradeoff between speed and quality.

	<b>Tupelo Honey</b> Cassandra Wilson – Closer To You: The Pop Side
	<b>Axis: Bold As Love</b> Joan Osborne – How Sweet It Is
	<b>Tender Love</b> Me'Shell Ndegéocello – Ventriloquism
	<b>Speak Like A Child</b> The Style Council – Introducing The Style Council
	<b>Gradual Return</b> Trixie Whitley – Fourth Corner
	<b>Everybody Is A Star</b> Joan Osborne – How Sweet It Is