

Randomized algorithms 2

Bloom filters, string matching

CS240

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Approximate sets

- A Bloom filter is a data structure that can implement a set.
 - It only keeps track of which keys are present, not any values associated to keys.
 - It supports insert and find operations.
 - It doesn't support delete operations.
- Bloom filters use less memory than hash tables or other ways of implementing sets.
- However, Bloom filters are approximate.
 - It can produce false positives: it says an element is present even though it's not.
 - We can bound the probability of false positives.
 - But it doesn't produce false negatives: if it says an element isn't present, then it's not.



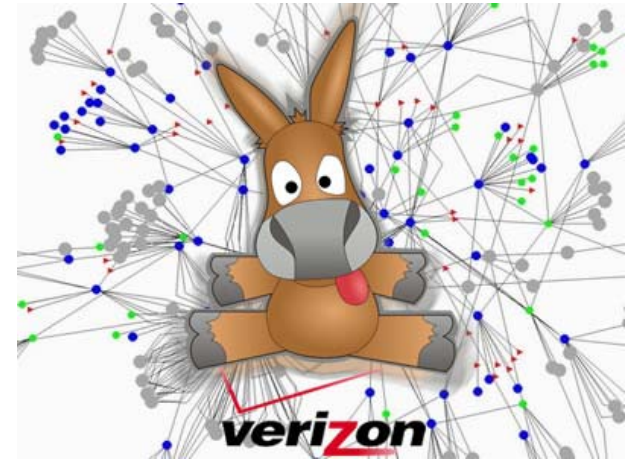
Bloom filter applications

- Suppose we have a big database, and querying it to check if an item is present is expensive.
- We store the set of items in the database using a Bloom filter.
 - This tells us whether an item is in database or not.
- If filter says an item's not present, it's definitely not in the database.
 - So no need to do an expensive query.
- If filter says an item is present, then either item is present, or there's false positive.
 - When we query the database, there's a small probability we waste time querying for a nonexistent item.
- Overall we save time by checking Bloom filter first before querying database.



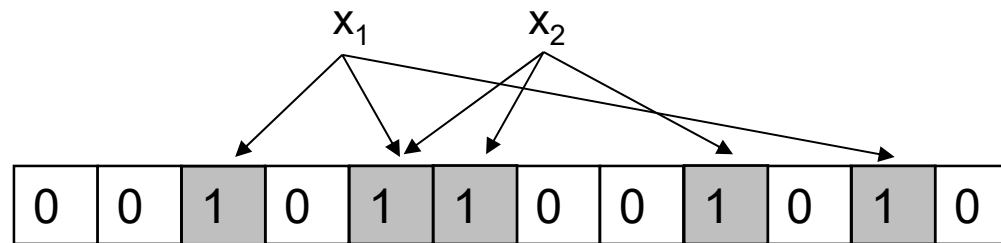
Bloom filter applications

- Consider a P2P network, where each node stores some files.
- If you want to get a file, you need to know which nodes have it.
- Keeping a list of all items stored at each node is too expensive.
- Instead, for every other node, keep a Bloom filter of its files.
- If filter says no for a node, it definitely doesn't have the file.
- If filter says yes, then either node has the file, or there's false positive and we make a useless request.
- Overall we save space, and also won't waste much communication because we rarely make useless requests.



Bloom filters

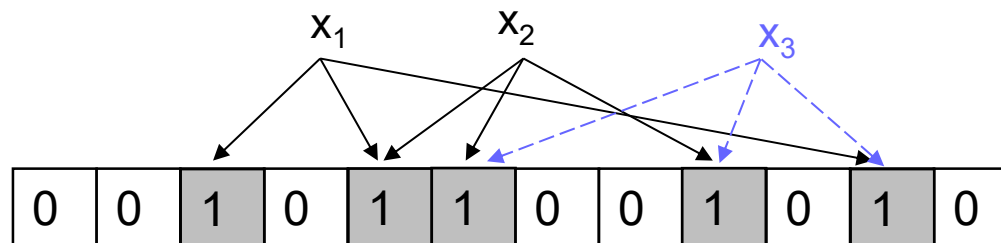
- A Bloom filter consists of
 - An array A of size m , initially all 0's.
 - k independent hash functions h_1, \dots, h_k , each mapping from keys to $\{1, \dots, m\}$.
- To store key x
 - Set $A[h_1(x)], A[h_2(x)], \dots, A[h_k(x)]$ all to 1.
 - Some locations can get set to 1 multiple times; that's fine.
- To check if key x is in the set
 - Read array locations $A[h_1(x)], A[h_2(x)], \dots, A[h_k(x)]$.
 - If all the values are 1, output "x is in set".
 - Otherwise output "x is not in set".



A Bloom filter with $k=3$ hash functions storing 2 items.

Correctness

- Let's look at the correctness of the search function.
- If search for x returns no, then at least one of $A[h_1(x)], \dots, A[h_k(x)]$ equals 0.
 - So x cannot be in the set, because if x had been inserted into the set, then we would have $A[h_1(x)] = \dots = A[h_k(x)] = 1$.
 - So there are no false negatives.
- If search for x returns yes, then $A[h_1(x)] = \dots = A[h_k(x)] = 1$.
 - So either x was inserted into the set.
 - Or we inserted some keys that hashed to the same k locations as x .
 - So it looks as if x was inserted, even though it wasn't.
 - This is a false positive. We'll bound the probability this happens.





False positive probability 1

- False positive probability depends on k (number of hash functions), m (size of table) and n (number of keys inserted).
- Assume hash functions hash keys to random locations.
- When inserting one key, we set k random locations to 1.
- Fix any position i . Probability i is set to 1 by a hash function is $1/m$, so probability i stays 0 is $1 - 1/m$.
 - After k hashes, probability i still 0 is $(1 - 1/m)^k$.
 - To insert n items, we used nk hashes. So probability i still 0 after all these is $p = (1 - 1/m)^{nk}$.
- We now use an approximation $\left(1 - \frac{1}{m}\right)^{nk} \approx e^{-\frac{nk}{m}}$.

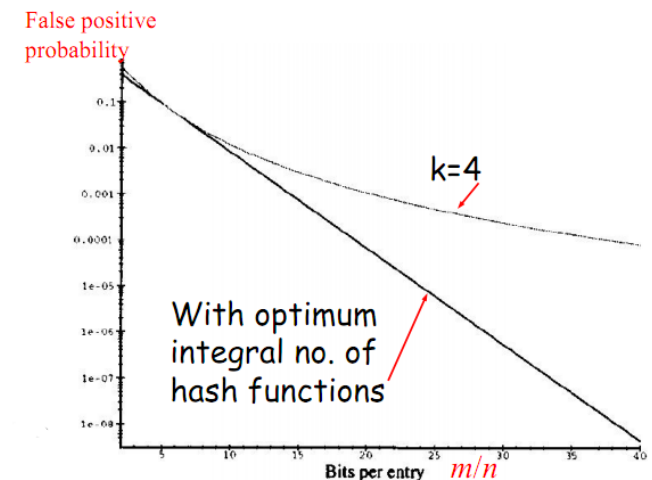


False positive probability 2

- So probability any position i is 1 after n keys inserted is $1 - p \approx 1 - e^{-\frac{nk}{m}}$.
- Since there are m positions in the array, assume there are $(1-p)m$ positions that are 1.
 - This isn't quite correct. The actual number of 1's in the array is a random variable, whose expectation is $(1-p)m$.
 - However, we can make the argument rigorous by showing that the actual number of 1's is $(1 - p)m \pm \sqrt{m \log m}$ with high probability.
- We only get a false positive if when we check k random locations, they're all 1.
 - Probability is $f = (1 - p)^k \approx \left(1 - e^{-\frac{nk}{m}}\right)^k$.

False positive probability 3

- Notice the false prob. $\left(1 - e^{-\frac{nk}{m}}\right)^k$ is a function of k , the number of hash functions we use.
- We find k to minimize the false positive prob. by differentiating f wrt k and solving.
- The optimum k is $\frac{m \ln(2)}{n}$, which leads to $f = \left(\frac{1}{2}\right)^k \approx 0.6185^{\frac{m}{n}}$.
 - Notice that m/n is the average number of bits per item. So error rate decreases exponentially in space usage.





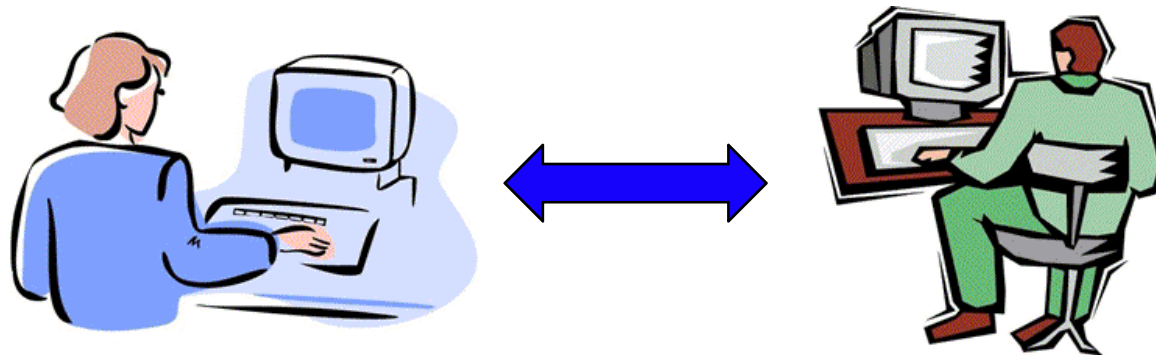
Improvements

- Right now Bloom filters can't handle deletes.
 - Say keys k_1 , k_2 hash to two overlapping sets of locations. If you delete k_1 by setting some of its locations to 0, you could also delete k_2 .
- Deletes can be done by storing a count of how many keys hashed to that location, and inc / dec the counts when inserting or deleting.
 - But this uses more memory.
 - Also, what if the counts overflow?
- **Neat trick** Given Bloom filters for sets S_1 , S_2 , we can create Bloom filter for $S_1 \cap S_2$ and $S_1 \cup S_2$ just by bitwise ANDing or ORing S_1 and S_2 's filters.
 - ORing gives the exact Bloom filter for $S_1 \cup S_2$, while ANDing gives approximately the Bloom filter for $S_1 \cap S_2$.



String equality and fingerprinting

- Alice and Bob both have copies of a database.
- They want to keep the database consistent, so they want to check if their copies are the same.
 - If you think of the databases as strings, they want to check if their strings are equal.
- But transferring the entire database is expensive.
- Instead, they calculate a small value called a fingerprint of their databases.
 - If the fingerprints are the different, then their databases are definitely different.
 - If the fingerprints are the same, then the databases are probably the same; but there's a small probability they're actually different.
- Transferring the fingerprint is much cheaper than the database.





Fingerprinting

- Let Alice and Bob's databases be the bit sequences (a_1, \dots, a_n) and (b_1, \dots, b_n) .
- View these as n -bit integers $a = \sum_{i=1}^n a_i * 2^{i-1}$ and $b = \sum_{i=1}^n b_i * 2^{i-1}$.
- The fingerprint $F(a) = a \bmod p$, for a specially chosen prime number p .
 - Alice transfers $F(a)$ to Bob, and Bob compares it to his fingerprint $F(b) = b \bmod p$.
 - Since $F(a) < p$, transferring the fingerprint only takes $O(\log p)$ bits, instead of n .



Correctness

- No false negatives.
 - If $F(a) \neq F(b)$, then $a \neq b$.
- False positives are possible.
 - If $F(a) = F(b)$, then $a \bmod p = b \bmod p$.
 - So either $a = b$, or $a \neq b$ but p divides $(a - b)$.
- We can't avoid false negatives. 🗨️ But we can minimize the probability it occurs.
- Pick a random p .
 - If $a \neq b$, then probably p doesn't divide $(a - b)$, so probably $F(a) \neq F(b)$ and we'll detect a and b are different.
 - Bigger p decreases false positive probability.
 - But we don't want to make p too big, since we have to transfer $O(\log p)$ bits.



Correctness

- To analyze the false positive probability, we use two facts from number theory.
- **Lemma** Any number t has at most $\log_2(t)$ distinct prime divisors.
- **Proof** Each divisor is ≥ 2 , and their product is $\leq t$. If there were more than $\log_2(t)$ divisors, their product would be $> 2^{\log_2(t)} = t$, contradiction.
- Recall $a = \sum_{i=1}^n a_i \cdot 2^{i-1}$ and $b = \sum_{i=1}^n b_i \cdot 2^{i-1}$.
- So $a - b < 2^n$, and so $a - b$ has at most n distinct prime divisors.



Correctness

- **Prime Number Theorem** Given any number t , the number of primes smaller than t is $\sim t / \ln(t)$.
- The PNT allows us to efficiently generate a random prime.
 - Picking a number less than t at random, it has a $1/\ln(t)$ probability of being prime.
 - We can check if a number is prime using the Rabin-Miller primality test.
 - If number is prime, it always passes the test.
 - If number is composite, there's small probability it's declared a prime.
 - Run the test few more times to exponentially decrease false positive probability.
 - So with high probability, we can tell if a number is prime.



Correctness

- Let $t = n^2 \ln(n)$. The number of primes less than t is $\approx \frac{t}{\ln(t)} = \frac{n^2 \ln(n)}{2 \ln(n) + \ln \ln(n)} = O(n^2)$.
- Pick a random prime p less than t .
- We get a false positive if $a \neq b$ but p divides $(a-b)$.
 - We saw earlier that $a-b$ has $< n$ prime divisors, and p must be one of these.
 - But p is randomly chosen from $O(n^2)$ primes less than t .
 - So false positive probability $\leq n/O(n^2) = O(1/n)$.
- We transfer $\log(p) \leq \log(t) = O(\log n)$ bits.
- Transferring $O(\log n)$ bits gets $O(1/n)$ probability of error. If we want perfect accuracy, we need to transfer the entire database, $O(n)$ bits.



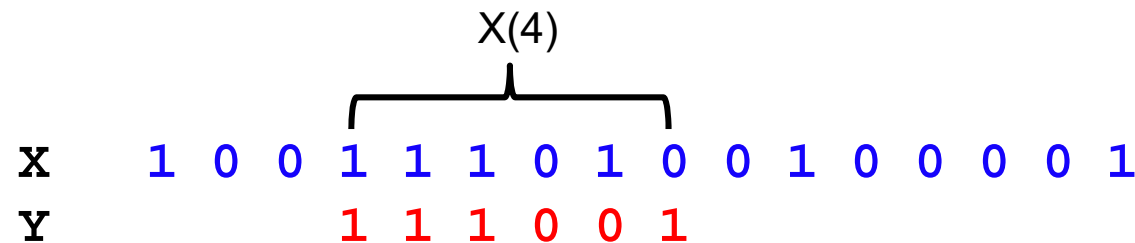
String matching

- In the previous problem, we checked whether two strings are equal.
- We now want to see if one string X contains the other Y . I.e. we want to match Y to a part of X .
- Let X and Y be binary strings with length n and m , resp., where $n \geq m$.
- We'll look at a simple randomized $O(n+m)$ time string matching algorithm Rabin-Karp.

x	1	0	0	1	1	1	0	1	0	0	1	0	0	0	0	1
y				1	1	1	0	0	1							

String matching

- Let $X = x_1x_2\dots x_n$, and define $X(j) = x_jx_{j+1}\dots x_{j+m-1}$.
 - $X(j)$ has the same length as Y .
 - It represents a potential match for Y starting at the j 'th bit of X .
- Y matches X if there exists $1 \leq j \leq n-m+1$ s.t. $X(j) = Y$.
- We just saw a way to test string equality using fingerprints.
- We first give a $O(n+m)$ time Monte Carlo string matching algorithm.
 - There's small probability it says Y matches X even when it doesn't.
- Then we convert it to an expected $O(n+m)$ time Las Vegas algorithm, which always gives correct answer.





Monte Carlo string matching

- ❖ Choose a random prime p .
 - ❖ We'll determine how big p should be later.
- ❖ For every $1 \leq j \leq n-m+1$.
 - ❖ View $X(j)$ and Y as m -bit numbers.
 - ❖ Compute $F(X(j)) = X(j) \bmod p$ and $F(Y) = Y \bmod p$.
 - ❖ If $F(X(j)) \neq F(Y)$, go to next j .
 - ❖ If $F(X(j)) = F(Y)$, output "Y matches X at bit j ".
- ❖ Output "Y doesn't match X".



Correctness

- Consider $X(j)$ and Y , for some j .
- If $F(X(j)) \neq F(Y)$, then $X(j) \neq Y$ and there's no match at X 's j 'th bit.
 - So no false negatives.
- If $F(X(j)) = F(Y)$, then either $X(j) = Y$, or $X(j) \neq Y$ but p divides $X(j) - Y$.
 - So there could be false positives.
 - Let's bound this probability.
- $X(j) - Y$ is an m -bit number, so by the lemma, it has $\leq m$ distinct prime factors.
- Let $t = n^2 m \log(n^2 m)$, and let p be a random prime $\leq t$.
 - There are $\sim n^2 m$ primes $\leq t$, by the PNT.

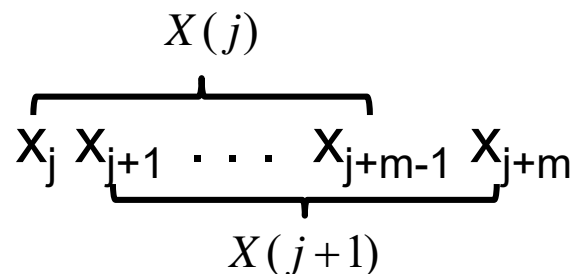


Correctness

- We only get a false positive if p is one of the $\leq m$ factors of $X(j)-Y$.
- So we get a false match between $X(j)$ and Y with probability $\leq m/n^2m = 1/n^2$.
- Now, we falsely match X to Y if there is any $1 \leq j \leq n-m+1$ s.t. $X(j) \neq Y$ but $F(X(j)) = F(Y)$.
 - For each j , this event has probability $\leq 1/n^2$.
 - So the probability this happens at any of the $n-m+1$ j 's is $\leq (n-m+1)/n^2 = O(1/n)$.
 - This is called the union bound.
 - If $\Pr[E_i] = p_i$ for $1 \leq i \leq k$, then $\Pr[E_1 \cup \dots \cup E_k] \leq p_1 + \dots + p_k$.
- Putting it together, if Y matches X somewhere, then this algorithm finds the match. If Y doesn't match X , this algorithm says Y matches X with probability $O(1/n)$.

Running time

- We said this algorithm runs in $O(n+m)$ time. But computing $F(X(j)) = \left(\sum_{i=j}^{j+m-1} x_i 2^{i-1}\right) \bmod p$ takes $O(m)$ time, and we have to do this for $n-m+1$ j 's, which makes the running time $O(mn)$!
- However, there's a trick to computing $F(X(j+1))$ quickly once you've computed $F(X(j))$.
 - $X(j+1)$ and $X(j)$ differ only in bits x_j and x_{j+m} .
 - So $F(X(j+1)) = (2 * (F(X(j)) - 2^{m-1}x_j) + x_{j+m}) \bmod p$.
 - So computing $F(X(j+1))$ given $F(X(j))$ takes $O(1)$ time.
- So computing $F(X(1)), \dots, F(X(n-m+1))$ takes $O(n+m)$ time.
- Computing $F(Y)$ takes $O(m)$ time.
- So altogether the algorithm takes $O(n+m)$ time.





A Las Vegas algorithm

- We now modify the previous algorithm so it always produces the right answer.
- ❖ Run the Monte Carlo algorithm.
- ❖ If it never produces a match, output “Y doesn’t match X”.
- ❖ If it ever outputs a match, say between $X(j)$ and Y , then check $X(j)=Y$ in $O(m)$ time.
- ❖ If $X(j)=Y$, output “Y matches X at bit j”.
- ❖ If $X(j) \neq Y$, start over and run the brute force $O(mn)$ time to match Y to X .



Correctness

- Since the Monte Carlo algorithm only produced false positives and this algorithm checks them using brute force, it always produces the right answer.
- The expected running time is $\Pr[\text{no false positives}] \cdot (\text{running time if no false positives}) + \Pr[\text{there is false positive}] \cdot (\text{running time when there's false positive})$.
 - The first term is $\leq (1 - 1/n)(n+m)$.
 - The second term is $\leq 1/n \cdot O(mn) = O(m)$.
 - So the total expected running time is $O(n+m)$.