RANGE UPDATES

Consider an array C of n integers, initially all equal to zero. We want to support the following operations:

- update(i, j, c), where $0 \leq i \leq j \leq n \leq 1$ and c is an integer: it changes C such that $C[k] := C[k] + c$ for every $i \leq k \leq j$.
- query(i), where $0 \leq i \leq n \leq 1$: it returns the values of$C[i]$.
- sum(i, j), where $0 \leq i \leq j \leq n \leq 1$: it returns $\sum_{k=i}^{j} C[k]$

Design a data structure that uses O(n) space and implements each operation above in O(log n) time. Note that query(i) = sum(i, i) but it helps to reason. [Hint to further save space: use an implicit tree such as the Fenwick tree (see Wikipedia).]

SOLUTION WITH RANGE TREE

Given the problem, in which we want to efficiently (log. time, and linear space) work with values stored in an array contained within an arbitrary range $[1...n]$, we need to implement:

- Updating a portion of the range by adding a value c: Update(i, j, c).
- Querrying the value on a given index: Query(i).
- Obtaining the sum of all elements within a range: Sum(i, j).

A possible solution is to model the range as trees, with branches partitioning the overall ranges in smaller ones to efficiently operate on them. Leaves store discrete indices while their parents represent the index ranges contained under them. A tree for $n = 8$, with indices $[0...7]$ is shown below:

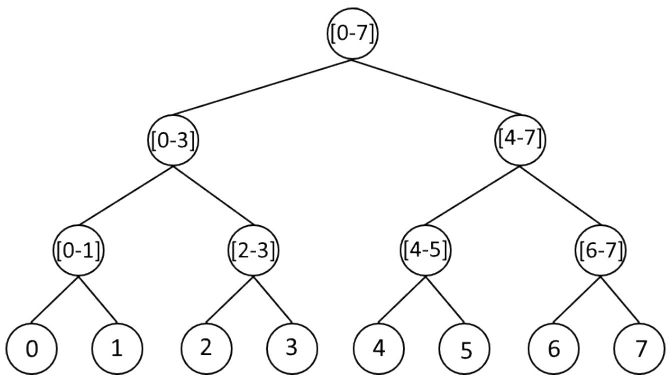


Figure 1: Tree for N=8

Space-wise, this means that for an array of length n, we will at most require $\sum\limits_{i=0}^{\infty} \frac{n}{2^i}$ nodes in the tree, as $\frac{n}{2}$ parents will be needed for the n leaves, $\frac{n}{4}$ for those parents and so on. This geometric series converges to $2n$, leaving us a space complexity bound of $O(n)$.

The implementation of 1-value query is simple: we use the intervals to binary-search our target node. In doing so, we traverse only one tree branch, with time complexity $O(log\ n)$.

Updating and range-summing, on the other hand, are trickier. For them to be efficient, we need to process a whole interval in $O(log\ n)$. To do so, we perform the same binary-search process as before, stopping when the current interval matches the interval of the node. Otherwise we further splitting the interval towards their sub-trees. On a given tree, such splitting will happen at most on $log(n) - 1$ times on both interval extreme, when the range covers all but there is an extreme of the interval that is not fully included. When the intervals match, the marking operation will be applied.

Finally, to efficiently implement both range operations, branch nodes that represent intervals will require two variables: the amount that is added in common to all of their successors and the total sum of their values. That way, operations onto a given node will remain $O(1)$, with our previous analysis being applicable translating into a time complexity bounded by $O(log\ n)$.

SOLUTION WITH BIT TREE
The solution can be implemented using a Segment tree or a Fenwick Tree. Both allowed the aforementioned operation in O(log n). Here we will present a solution that use Fenwick Trees also called Binary Indexed Tree (BIT).
Let's start with some considerations:

- integer can be represented as sum of powers of two. Therefore, I can represent the sum operation as sum of sets of sub-sums.

- each index, if it is a power of 2, will store the sum of all elements before that, and we will apply this repetitively so as to get what each index will store. Let's see an example:
  Suppose, we have an array of 16 elements, $[1 \ldots 16]$. Powers of 2 are the index: 1, 2, 4, 8, 16. These index will store sum of all elements before them. Now, we divide this array in two halves: we get $[1 \ldots 8]$ and $[9 \ldots 16]$, and so on.
  Let's have the following array:

  $$\begin{aligned} A &= [1,2,3,4,5,6,7,8] \\ BIT &= [0,0,0,0,0,0,0,0] \end{aligned} \tag{1}$$

  Let take the power 2 index (i.e. 1,2,4,8), and we store in BIT the value of the sum of the previous element. Then we have:

  $$BIT = [1,3,0,10,0,0,0,36]$$

  Now we divide the array in two: $A_1 = [1,2,3,4]$ and $A_2 = [5,6,7,8]$. Then we take the power 2 index of A_1 and A_2 (i.e. 1,2,4), and we update the value of BIT where there index that are not updated yet. Then we have:

  $$BIT = [1,3,0,10,5,11,0,36]$$

  Following the same procedure, the value doesn't change at any index if it has been already filled. Then we will the following.

  $$BIT = [1,3,3,10,5,11,7,36]$$

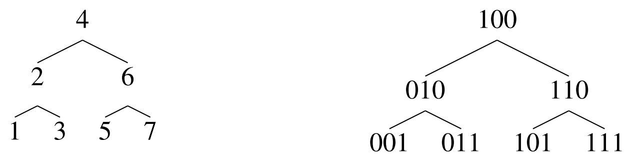
  If we consider our array as a binary tree, and we change the value of each node by adding the sum of nodes in its left sub-tree, we will obtain the same result.

- Now let's see how to implement sum(i, j). The idea is to keep a variable ans initialized to 0. Follow the path from $root$ to the $index$ node. Whenever we need to follow a right link, add the value of current node to ans, and once we reach the node with the searched index we add that value too. To get the sum of elements in range i to j, we get the sum from 0 to j and we subtract the sum from 0 to (i-1).

- Now let's see how to implement update(i, j, c). For now we focus on just the update of a single index. If we want to increment the value at index k by say c. Follow the path from root to the index node k. Whenever we need to follow a left link, add the value of c to current node. Once we reach the node, add c to that node too. This is because we will need to update the set of nodes in the tree that include that node in its left sub-tree, so that it will be consistent with our sum operation.

To implement this kind of idea we need to exploit some properties of the binary numbers. Since for the sum function we need the right-path we exploit the following fact: given an index if we reset the right-most

SET-bit we will go up to the least node that took a RIGHT path. For example:



$$5 \longrightarrow 101 \longrightarrow 100 \longrightarrow 4$$
$$7 \longrightarrow 111 \longrightarrow 110(6) \longrightarrow 100 \longrightarrow 4$$
$$3 \longrightarrow 011 \longrightarrow 010 \longrightarrow 2$$

To implement this concept in to an algorithm we use the following formula $i - (i\ AND(-i))$, where i is the current index and $(-i)$ mean the 2's complement of i.

```
function GETSUM($index$)
    $ans \leftarrow 0$
    while $index\ > 0$ do
        $ans \leftarrow ans + BIT[index]$
        $index \leftarrow index - (index\ AND(-index))$
    end while
    return $ans$
end function
```

Now we should try to do the same for the updating function. Now given an index we should search the least node that took the LEFT path. Here, instead of stripping off the least-significant 1 bit (i.e. subtracting), we now add it on at each stage to get the next entry to adjust. Therefore we simply have:

```
function UPDATE($index$,$val$)
    while $index\ < length\_of\_array$ do
        $BIT[index] \leftarrow BIT[index] + val$
        $index \leftarrow index + (index\ AND(-index))$
    end while
    return $ans$
end function
```

Notice that getSum and update work in O(log n), where n is the length of the input. However, the update function modify one element at the time, then we still need to find a way to do a range update in O(log n). The idea is to keep two BIT (i.e. BIT1 and BIT2) and then modify the functions to sum and update a range.

Let's start with the update function update(i, j, c). When we update BIT1 we will use the previous update as follow:

$$\begin{aligned} update(i, c) &\qquad \textit{\#in BT1} \\ update(j + 1, -c) &\qquad \textit{\#in BT1} \end{aligned}$$

The idea is that the $update(i, c)$ will affect all $i' \leq i$, i.e all the left subtree where we store the partial sum of the sub-interval. To limit the effect to a given range $[i, ..., j]$, we subtract $-c$ from all $i' > j$ by performing the operation $update(j + 1, -c)$. Now, if we use the getSum function as it is, we will have a wrong result. Indeed we should find a way to tell how much the results have to be adjust, here comes the second BIT (i.e BT2). Consider a range $update(i, j, c)$ and let all the elements at the beginning were 0. Now, let consider a getSum(p) for a generic p, then we have:

$$\begin{aligned} &1 \leq p < i \longrightarrow 0 \\ &i \leq p \leq j \longrightarrow c * (p - (i - 1)) \\ &j < p \leq N \longrightarrow c * (j - (i - 1)) \end{aligned}$$

Thus, for a given index p, expanding those formula we obtain the term needed to adjust the prefixed sum. Indeed we find a term X in this way:

$$\begin{aligned}
&1 \leq p < i \longrightarrow 0 \longrightarrow X = 0 \\
&i \leq p \leq j \longrightarrow c * p - c * (i-1) \longrightarrow X = c * (i-1) \\
&j < p \leq N \longrightarrow c * j - c * (i-1) \longrightarrow X = -c * j + c * (i-1)
\end{aligned}$$

This extra factor keep track of the adjustment needed to obtain the correct sum. To maintain this extra factor X, we use another BIT(i.e BT2) then we have:

$$\begin{aligned}
update(i, c * (i-1)) &\qquad \textit{\#in BT2} \\
update(j+1, -c * j) &\qquad \textit{\#in BT2}
\end{aligned}$$

Notice $c * (i-1)$ it's not there because it has been included in the previous update. Indeed to obtain a correct range sum we have to do the following:

$$getSum(p) = getSum(BIT1, p) * p - getSum(BIT2, p)$$

Finally we have the function requested in the exercise:

- $update(i, j, c)$ is equivalent to the following function:
  - $update(BIT1, i, c)$
  - $update(BIT1, j+1, -c)$
  - $update(BIT2, i, c * (i-1))$
  - $update(BIT2, j+1, -c * j)$
- $query(i) = getSum(i) - getSum(i-1)$
- $sum(i, j) = getSum(j) - getSum(i-1)$

Both sum, query and update work in O(4 log(n)). This because: the tree is always balanced and the two function they simply take a path in the tree. Furthermore, this algorithm take just O(2 n) space since it's just storing a flat array.[1]

[1] Some references: LINK1, LINK2, LINK3, LINK4 and LINK5

Depth of a node in a random search tree

A random search tree for a set S can be defined as follows: if S is empty, then the null tree is a random search tree; otherwise, choose uniformly at random a key $k \in S$: the random search tree is obtained by picking k as root, and the random search trees on $L = \{x \in S : x < k\}$ and $R = \{x \in S : x > k\}$ become, respectively, the left and right subtree of the root k. Consider the randomized QuickSort discussed in class and analyzed with indicator variables [CLRS 7.3], and observe that the random selection of the pivots follows the above process, thus producing a random search tree of n nodes. Using a variation of the analysis with indicator variables, prove that the expected depth of a node (i.e. the random variable representing the distance of the node from the root) is nearly 2 $ln\ n$.
Prove that the probability that the expected depth of a node exceeds $c\ 2\ ln\ n$ is small for any given constant $c > 1$. [Note: the latter point can be solved after we see Chernoff's bounds.[1]]

SOLUTION
To give an estimation on the depth of a given node, i, we would need to consider how many of the other nodes are its ancestors. For this, an indicator variable can be defined as follows:

$$X_{ij} = \begin{cases} 1 & \text{IF } j \text{ IS AN ANCESTOR OF } i, \\ 0 & otherwise \end{cases}$$

With this indicator variable, analysis can be performed taking the indices as those of the sorted set when in order: $z_1, z_2, ..., z_n$. For two arbitrary indices z_i, z_j only three possible scenarios apply:

1. z_i was selected as a key on the tree before z_j, so z_j is a successor of z_i and thus $X_{ij} = 0$.
2. Neither z_i nor z_j were selected as a key on the tree before, so a key in the range $(i, ..., j)$ or $(j, ..., i)$ effectively splits the range and thus $X_{ij} = 0$.
3. z_j was selected as a key on the tree before z_i, so z_i will eventually be found and selected as a key preceded by z_j and thus $X_{ij} = 1$.

With this analysis in mind, the expectation of the indicator variable can be computed as follows:

$$E[\sum_{\substack{j=1 \\ j \neq i}}^{n} X_{ij}] = \sum_{\substack{j=1 \\ j \neq i}}^{n} P(X_{ij} = 1) = ...$$

Given the previous analysis, the probability of X_{ij} in the interval containing z_i and z_j on both extremes is that of the only case in which z_j may be an ancestor of z_i over the total amount of cases. In this case that means the number of elements in the range:

$$... = \sum_{\substack{j=1 \\ j \neq i}}^{n} \frac{1}{|j - i| + 1} = ...$$

To explicitly take into account the two orderings between z_i and z_j, we split the computation in two terms. The result resembles two instances of the harmonic series, which are then approximated to $ln(n)$:

$$... = \sum_{j=1}^{i-1} \frac{1}{i - j + 1} + \sum_{j=i+1}^{n} \frac{1}{j - i + 1} < ln(n) + ln(n) = 2ln(n)$$

Finally, the depth of a node in a random search tree is expected to be $2ln(n)$. A variation on the same analysis can be performed to estimate the size of the subtree spanning from a given node. In this case, a similar indicator variable is defined with slightly different semantics:

$$X_{ij} = \begin{cases} 1 & \text{IF } j \text{ IS AN SUCCESSOR OF } i, \\ 0 & otherwise \end{cases}$$

The analysis and computations to be performed afterwards will follow the same structure as before, producing in the same expectancy results for the predicate.

[1] Chernoff's bound

SECOND SOLUTION

Let's start with some key observations: the comparisons are just made with the chosen root k, any two elements are compared at most once, and every time a node is compared with the root k, it will increase its depth in the tree. Let denote with $n_1, \ldots, n_k$ the node of a BST (Binary Search Tree), where an $n_t \leq n_p \forall t \leq p$. Let's fix a generic node n_i then we have:

$$X_j = \begin{cases} 1 & \text{NODE } n_i \text{ IS A DESCENDENT OF } n_j \\ 0 & \text{OTHERWISE} \end{cases}$$

Therefore $X = \sum_{j=i}^{n} X_j$ is the hight (or the depth) of a generic node n_1. Therefore now we need to calculate the $E[X]$ (its expected value). Since the expected value is linear we have that $E[X] = \sum_{j=i}^{n} E[X_j]$, and since we know that $E[X_j] = P[X_j = 1]$ we should approximate the latter probability. Since a couple of element can be compared at most once and every comparison means a comparison with the root (an increasing of the depth), we can can assume that: if n_i is in the left(right) subtree of n_j it means that there are at most $j-i+1$ elements in the left(right) subtree. Since the subtree has $j-i+1$ elements, and because root are chosen randomly and independently, the probability that any given element is the first one chosen as a root is $\frac{1}{j-i+1}$.Therefore we have:

$$\begin{aligned} P(X_j = 1) =& P[n_i \text{ IS A DESCENDENT OF } n_j] \\ \leq& P[n_i \text{ IS IN THE LEFT SUBTREE } n_i \text{ IS IN THE RIGHT SUBTREE}] \\ =& \frac{1}{\text{NUMBER OF NODE IN THE LEFT SUBTREE}} + \frac{1}{\text{NUMBER OF NODE IN THE RIGHT SUBTREE}} \\ \leq& \frac{2}{j-i+1} \end{aligned}$$

Therefore we have $E[X] = \sum_{j=i}^{n} \frac{2}{j-i+1}$, if we change of variables[2] $k = j - i$ and we bound the harmonic series we have:

$$\sum_{k=1}^{n-i} \frac{2}{k+1} < \sum_{k=1}^{n} \frac{2}{k} = 2ln(n)$$

Let's write down the Chernoff Bound:

Theorem 1 *(Chernoff Bounds). Let $X = \sum_{i=1}^{n} X_i$, where $X_i = 1$ with probability p_i and $X_i = 0$ with probability $1 - p_i$, and all X_i are independent. Let $\mu = E(X) = \sum_{i=1}^{n} p_i$[3]. Then*

$$\begin{aligned} &(i)\textbf{\textit{Upper Tail:}} P(X \geq (1+\delta)\mu) \leq e^{-\frac{\delta^2}{2+\delta}\mu} && \textit{for all } \delta > 0 \\ &(ii)\textbf{\textit{Lower Tail:}} P(X \leq (1-\delta)\mu) \leq e^{-\frac{\mu\delta^2}{2}} && \textit{for all } 0 < \delta < 1 \end{aligned}$$

Therefore we have:

$$\begin{aligned} P(X \geq (1+c)2ln(n)) \leq& e^{-\frac{c^2}{2+c}2ln(n)} \\ =& \frac{1}{e^{\frac{c^2}{2+c}2ln(n)}} \\ =& \frac{1}{n^{\frac{2c^2}{2+c}}} \\ =& \frac{1}{n^c} \text{WITH } c > 2 \end{aligned}$$

[2]LINK1
[3]Indicator variable

Karp-Rabin fingerprinting on strings

Given a string $S = S[0 \dots n-1]$, and two positions $0 \leq i < j \leq n-1$, the longest common extension $lce_S(i,j)$ is the length of the maximal run of matching characters from those positions, namely: if $S[i]! = S[j]$ then $lce_S(i,j) = 0$; otherwise, $lce_S(i,j) = max\{l \geq 1 : S[i \dots i+l-1] = S[j \dots j+l-1]\}$. For example, if $S = abracadabra$, then $lce_S(1,2) = 0$, $lce_S(0,3) = 1$, and $lce_S(0,7) = 4$. Given S in advance for preprocessing, build a data structure for S based on the Karp-Rabin fingerprinting, in O(n log n) time, so that it supports subsequent online queries of the following two types:

- $lce_S(i,j)$: it computes the longest common extension at positions i and j in O(log n) time.
- $equalS(i,j,l)$: it checks if $S[i \dots i+l-1] = S[j \dots j+l-1]$ in constant time.

Analyze the cost and the error probability. The space occupied by the data structure can be O(n log n) but it is possible to use O(n) space. [Note: in this exercise, a onetime preprocessing is performed, and then many online queries are to be answered on the fly.]

SOLUTION
Consider a string S of length n, we call $S[i]$ the i-th element in S starting from 0, and $S[i,l]$ the substring of S with length l starting at i (i.e. $S[i] \cdot S[i+1] \dots S[i+l-1]$, where $\cdot$ is the string concatenation). The idea is to build an array R with the same length of the string S such that for each index i we have that $R[i]$ contains the prefix of S of length $i+1$. $R[0]$ contains the first word of S, $R[1]$ contains the concatenation of the first two wolds of S etc. In general we will have that $R[i] = S[0, i+1]$. This representation has of course the problem to be too much expensive, but we will see later how to really implement the data structure, first have a look at how it works for checking the equality of two substring and for finding the lce_S of two indexes.

Given a pair of indexes i and j, and a length l we want to check whether $S[i,l] = S[j,l]$, looking at R. Considering that $\forall i, l. R[i+l] = S[0,i] \cdot S[i+1,l] = R[i] \cdot S[i+1,l]$, we can prove that

$$\forall i, l \,.\, S[i,l] = R[i+l-1] - R[i-1]$$

where we denote by $\alpha - \beta$ the string α without the prefix β (i.e. $\alpha\gamma - \alpha = \gamma$). Now we can simply check whether $s[i,l] = s[j,l]$ by comparing $R[i+l-1] - R[i-1]$ and $R[j+l-1] - R[j-1]$. The problem of finding the longest common extension is quite simple, it is sufficient to use some form of binary search, exploiting the array R. We use a recursive function in order to find the $lce_S(i,j)$, the input are i, j, the string S and its length n. We consider to have a function $is\_equal(A,x,y,l)$ such that return true if $A[x,l] = A[y,l]$. The main difference between this algorithm and a binary search is that we will continue calling recursively the function with a string of halved length regardless of the result of the equality check.

```
function LCE($S$,$i$,$j$,$n$)
    if $n = 1$ then
        if $is\_equal(S, i, j, l)$ then
            return $1$
        else
            return $0$
        end if
    end if
    $l = n/2$
    if $is\_equal(S, i, j, l)$ then
        return $l +$ LCE($S$,$i+l$,$j+l$,$n-l$)
    else
        return LCE($S$,$i$,$j$,$l$)
    end if
end function
```

Note that assuming the is_equal function to have constant cost we have that the cost of lce is $O(log(n))$ since at each iteration only a recursive call is reached and the length of the input is halved each time.

In the real implementation, we will use an array H which is the hash fingerprint of R. For each index i $H[i] = h(R[i]) = R[i] \; mod \; p$, of course we don't really built the array R, then we can simply fill $H[i]$ with $S[0,i+1] \; mod \; p$. An implicit assumption in this step (and in Karp-Rabin fingerprint in fact) is to

see each string as a number, in particular we see S as the representation of an integer number with base b (depending on the number of possible word in the alphabet). In the following we will call S the string and $(S)_b$ the number for which S is the representation in base b. We will also distinguish between $S[i]$ the word in position i of S and $S[i]_b$ the number between 0 and $b-1$ which represents. Note that we have to redefine h as $h(\alpha) = (\alpha)_b \; mod \, p$.
Then the number $(S)_b$ will be $S[0]_b \times b^{n-1} + S[1]_b \times b^{n-2} \cdots + S[n-1]_b \times b^0$. With this representation we have the beautiful feature that $(S[0, i+l])_b = (S[0, i] \cdot S[i, l])_b = (S[0, i])_b \times b^l + (S[i, l])_b$, that we can exploit to prove $h(S[i, l]) = H[i + l - 1] - H[i - 1] \times b^l \; mod \, p$.

$$\begin{aligned}
H[i+l-1] = {} & h(R[i+l-1]) \\
& h(S[0, i+l]) \\
& (S[0, i+l])_b \; mod \, p \\
& (S[0, i])_b \times b^l + (S[i, l])_b \; mod \, p \\
& ((S[0, i])_b \; mod \, p) \times b^l + ((S[i, l])_b \; mod \, p) \; mod \, p \\
& h(S[0, i]) \times b^l + h(S[i, l]) \; mod \, p \\
& h(R[i-1]) \times b^l + h(S[i, l]) \; mod \, p \\
& H[i-1] \times b^l + h(S[i, l]) \; mod \, p
\end{aligned}$$

This way the cost of compare two arbitrary substring of the same length $S[i, l]$ and $S[j, l]$ is the cost of acceding to four elements of H plus a constant number of arithmetic operations, i.e. $O(1)$. Since we have found a good approximation of the procedure is_equal, we can compute lce_S with the algorithm shown before in $O(log \; n)$ time.
The space occupied by the data structure is quasi $O(n)$ where n is the length of S. Actually the size of the input in bit is n times the size of the word (i.e. $n \times log \; b$) and the size of the output is n times the size of an element of H (i.e. $n \times log \; p$). Note that we can consider the use of R as a particular case in which p is equal to b^{n+1} (the maximum number that a string of length n with alphabet of size b can represent plus one), in this case the modulus in h is redundant and we have a data structure of size $O(n^2)$.
It is not difficult to see that we can use the compositional property of the h function in order to achieve a cost of $O(n)$ to fill H. The code speaks for itself probably, the idea is to compute $H[0]$ as $S[0] \; mod \, p$, $H[1]$ as $S[1] + S[0] \times b \; mod \, p$ etc. We use only a constant number of operations for each word in S.

```
$H[0] = S[0] mod p$
**for** $i \in \{1, \ldots n-1\}$ **do**
    $H[i] = H[i-1] \times b + S[i] \; mod \, p$
**end for**
```

We take p as a random prime number $p \in [2, \cdots, \tau]$, where $\tau > n$. Let's have a look at the collision cases: we have a collision when $S[i, l] \neq S[j, l]$ but $h(S[i, l]) = h(S[j, l])$. This is the same as

$$\begin{aligned}
& H[i+l-1] - H[i-1] \times b^l \; mod \, p = H[j+l-1] - H[j-1] \times b^l \; mod \, p \\
& H[i+l-1] - H[i-1] \times b^l - (H[j+l-1] - H[j-1] \times b^l) \; mod \, p = 0 \\
& h(S[i, l]) - h(S[j, l]) \; mod \, p = 0 \\
& ((S[i, l])_b \; mod \, p) - (S[j, l])_b \; mod \, p) \; mod \, p = 0 \\
& (S[i, l])_b - (S[j, l])_b \; mod \, p = 0 \\
& p \; divides \; (S[i, l])_b - (S[j, l])_b
\end{aligned}$$

We define $c = (S[i, l])_b - (S[j, l])_b$, we want to count how many bad choices we have for p (how many choices for p such that p divides c). Note that as $(S)_b$ also c is a number representable with a string of length n with alphabet of size b; then $0 \leq c \leq b^n$. Let k be the number of prime number dividing c, then $c = p_1^{i_1} \times p_2^{i_2} \times \cdots \times p_k^{i_k}$ and, since p_x is grater or equal than 2 and i_x is greater or equal than 1 for all x, we can say that $c \geq 2^k$ (as seen in class). Finally $2^k \leq c \leq b^n \leq b^{n \times log \; b}$, and $k \leq n \times log \; b$.Since the possible choices for a prime number in the interval $[2, \cdots, \tau]$ are approximately $\frac{\tau}{ln(\tau)}$, the probability of error is less or equal to $\frac{\#\text{BAD PRIMES}}{\#\text{PRIMES}} = \frac{n \times log \; b}{\frac{\tau}{ln(\tau)}}$. If we choose $\tau \approx n^{a+1} ln(n)$ then we have that the probability of error is less or equal than $\frac{log \; b}{n^a}$.

SOLUTION in O(N LOG N) works for every kind of hash function
The proposed data structure that maintain a series of trees. At each level we encode power of two elements (THIS IS IMPOSSIBLE TO EXPLAIN... LOOK THE CODE). The space occupied by this data structure is $O(nlog(n))$ where n is the length of the input array.

```
function CreateTree($S$,$n$,$p$)
    $A \leftarrow NEW\ Array[log_2(n)+1]$
    $TEMP \leftarrow NEW\ Array[n]$
    for $i\ IN\ (0,n)$ do
        $TEMP[i] \leftarrow S[i]\ mod\ p$
    end for
    $A[0] \leftarrow TEMP$
    for $i\ IN\ (1,log_2(n))$ do
        $TEMP \leftarrow NEW\ Array[n-i]$
        for $j\ IN\ (0,n-i)$ do
            $TEMP[j] \leftarrow A[i-1][j] + A[i-1][j+2^{i-1}]\ mod\ p$
        end for
        $A[i] \leftarrow TEMP$
    end for
    return $A$
end function
```

Now to have $lce_S(i,j)$ we build the implement the following procedure, where $h = \lfloor log_2(n-j) \rfloor$

```
function LCE($i$,$j$,$h$)
    if $A[h][i] == A[h][j]$ then
        return $2^h$
    else
        if $h \neq 0$ then
            return 0
        else
            return LCE($i, j, h-1$)+LCE($i+2^{h-1}, j+2^{h-1}, h-1$)
        end if
    end if
end function
```

Notice that, this procedure work in $O(log(n))$ since the array is length is at most log(n) and we are doing two recursive call with an array one unit smaller each time. Finally to obtain $equalS(i,j,l)$ in cost $O(1)$ we simply check whether $A[\lceil log_2(l) \rceil)][i] == A[\lceil log_2(l) \rceil][j]$ is true.
Notice that all this algorithm work for arrays in which their length n is a power of two. If we have an array that is not of the latter length, we are doing the following: create the same data structure as before but the part of the array that is not in the tree, that it's at most long $2^{i+1} - 2^i - 1$ where $i = \lfloor log_2(n) \rfloor$, is store in simple array. In this case whether we need to check if $A[\lfloor log_2(n-j) \rfloor]][i] == A[\lfloor log_2(n-j) \rfloor]][j]$, i.e. the longest possible string, we need also to check, manually, whether there is a matching in the array. Last but not least, the calculation of the error probability is exactly the same to the one analysed during the course.

Hashing sets

Your company has a database $S \in U$ of keys. For this database, it uses a randomly chosen hash function h from a universal family H (as seen in class); it also keeps a bit vector B_S of m entries, initialized to zeroes, which are then set $B_S[h(k)] = 1$ for every $k \in S$ (note that collisions may happen). Unfortunately, the database S has been lost, thus only B_S and h are known, and the rest is no more accessible. Now, given $k \in U$, how can you establish if k was in S or not? What is the probability of error? [Note: you are not choosing k and S randomly as the they are both given... randomization here is in the choice of $h \in H$ performed when building B_S] Under the hypothesis that $m \geq c|S|$ for some $c > 1$, find the expected number of $1s$ in B_S under a uniform choice at random of $h \in H$.

SOLUTION

a) To check whether $k \in U$ belong to S, we simply check $B_S[h(k)] = 1$. The probability of error is equal to $P(error) = 1 - (1 - \frac{1}{m})^{|S|}$. This problem is similar to the "Birthday paradox" (i.e. fixed a day how many people are born on the same day). In word: the probability of a collision is $\frac{1}{m}$, thus the probability to do not have a collision is $(1 - \frac{1}{m})$. If we have $|S|$ key the probability do not have any collision is $(1 - \frac{1}{m})^{|S|}$. Therefore the probability to have a collision is: $1 - (1 - \frac{1}{m})^{|S|}$. That is, the probability that there is at least one collision within the key of S, that is the probability that $\exists j \in S : h(k) = h(j)$ but $j \neq k$ with $k \in U$.

b) To estimate the size of S, we first create an indicator variable $X = \sum_{i=0}^{m-1} X_i$ where

$$X_i = \begin{cases} 1 & \text{IF } B_S[i] = 1 \\ 0 & \text{OTHERWISE} \end{cases}$$

Than the expectation $E[X]$ represents the expected number of 1 in the B_s table. To calculate the expectation we need to estimate the $P(B_S[h(k)] = 1)$, that, by the point a), is $1 - (1 - \frac{1}{m})^{|S|}$. Since we do not know $|S|$ we use the hypothesis, that is $|S| \leq \frac{m}{c}$. Therefore we have:

$$P(B_S[h(k)] = 1) = 1 - (1 - \frac{1}{m})^{|S|} \leq 1 - (1 - \frac{1}{m})^{\frac{m}{c}}$$

Hence we have $E[X] = \sum_{i=0}^{m-1} 1 - (1 - \frac{1}{m})^{\frac{m}{c}} = m - m(1 - \frac{1}{m})^{\frac{m}{c}}$. Now we have got a bound for $|S|$: $E[X] \leq |S| \leq \frac{m}{c}$.

Family of uniform hash functions

The notion of pairwise independence says that, for any $x1 \neq x2$ and $c1, c2 \in Z_p$, we have that

$$\Pr_{h\in\mathcal{H}}[h(x_1) = c_1 \wedge h(x_2) = c_2] = \Pr_{h\in\mathcal{H}}[h(x_1) = c_1] \times \Pr_{h\in\mathcal{H}}[h(x_2) = c_2]$$

In other words, the joint probability is the product of the two individual probabilities. Show that the family of hash functions $H = \{h_{ab}(x) = ((ax+b)\ mod\, p)\ mod\, m\ : a \in Z_p^*, b \in Z_p\}$ (seen in class) is "pairwise independent", where p is a sufficiently large prime number $(m+1 \leq p \leq 2m)$.

SOLUTION
Each probability from the right hand side of the equation are equal to $\frac{1}{m}$, simply because there are m buckets chosen uniformly (Universal hash function). Therefore, in the right hand side we have a probability equal to $\frac{1}{m^2}$.
On the left side of the equation, we will first count all the possible solutions (x_1, x_2), and then we will count only the good solutions (that is, the solutions x_1 and x_2 that match, respectively, c_1 and c_2).
$h(x_1)$ and $h(x_2)$ can be rewrite with their expression, such as:

$$\left.\begin{array}{l} h(x_1) = (a \cdot x_1 + b \bmod p) \bmod m \\ h(x_2) = (a \cdot x_2 + b \bmod p) \bmod m \end{array}\right\} x_1 \neq x_2$$

Now, let's consider the inner modulo p expressions as $r = a \cdot x_1 + b \bmod p$ and $s = a \cdot x_2 + b \bmod p$, since p is prime and there is a linear transformation). Thus we can rewrite the original expression as: $Pr[r \bmod m = c_1 \wedge s \bmod m = c_2]$. Since $a \in [1 \ldots p-1] = \mathbb{Z}_p^*$ and $b \in [0 \ldots p-1] = \mathbb{Z}_p$, and both a and b are fixed for r and s, then there are $p\cdot(p-1)$ possible different combination for x_1 and x_2 $(x_1 \neq x_2)$.

Now, we focus on the "good" solutions. When p is sufficiently larger than m, the number of x_i that will match a given value c_i are $\frac{p}{m}$, as we have seen in class. However, we need to take in account modular arithmetic: not every values of m is going to be a multiple of p. Adding this to the analysis, the number of matches are bound by considering the round-to-floor and round-to-ceil limits:

$$\left\lfloor \frac{p}{m} \right\rfloor \leq \text{\# OF } x_i \text{ MATCHING } c_i \leq \left\lceil \frac{p}{m} \right\rceil$$

Since we have both c_1 and c_2, we need to consider their joint probability (i.g. multiplication), and then we can be bound it by combining both pieces of the analysis (dividing "good" solutions by all possible combination), giving us an approximation to the expected $\frac{1}{m^2}$:

$$\frac{1}{p\cdot(p-1)}\left(\left\lfloor \frac{p}{m} \right\rfloor\right)^2 \leq Pr[r \bmod m = c_1 \wedge s \bmod m = c_2] \leq \frac{1}{p\cdot(p-1)}\left(\left\lceil \frac{p}{m} \right\rceil\right)^2$$

It must be noted that the $\frac{1}{m^2}$ result may not be fully reached since that all the possible values a are $p-1$, which make it impossible to remove the $\frac{p}{p-1}$ term. The only possibility is when $a = 0$ that would not make any sense algorithmically speaking. Therefore the result can only be approximated.

Deterministic data streaming

Consider a stream of n items, where items can appear more than once in the stream. The problem is to find the most frequently appearing item in the stream (where ties broken arbitrarily if more than one item satisfies the latter). Suppose that only k items can be stored, one item per memory cell, where the available storage is $k + O(1)$ memory cells. Show that the problem cannot be solved deterministically under the following rules: the algorithm can access only $O(log^c n)$ bits for each of the k items that it can store, and can read the next item of the stream; you, the adversary, have access to all the stream, and the content of the k items stored by the algorithm, and can decide what is the next item that the algorithm reads (please note that you cannot change the past, namely, the items already read by the algorithm) . Hint: it is an adversarial argument based on the k items chosen by the hypothetical deterministic streaming algorithm, and the fact that there can be a tie on $> k$ items till the last minute.

Show that the problem cannot be solved deterministically under the following rules: the algorithm can only use b bits, and read the next item of the stream, one item at a time. You, the adversary, have access to all the stream, and the content of the b bits stored by the algorithm: you cannot change those b bits and the past, namely, the items already read by the algorithm, but you can change the future, namely, the next item to be read. Since the algorithm must be correct for any input, you can use any amount of streams to be fed to the algorithm and as many distinct items as you want. [Hint: it is an adversarial argument based on the fact that, for many streams, there can be a tie on the items.]

SOLUTION

Any deterministic algorithm can be described by a deterministic finite state machine, in which every state given an input move deterministically to another state. Suppose to have a streaming of n element, k memory cell to store the frequencies, and θ are the bit necessary to store the algorithm state. Therefore we can have 2^θ possible states.

Let's suppose to input $2^\theta + 1$ times the same element x to the algorithm. Then, it must be the case that the algorithm is going to be in the same state in two different moments (notice that the possible state are 2^θ). Let's call A that particular state, let's use A_i and A_j to denote the two different moments in which we arrive in state A during the execution of the algorithm (without loss of generality we can assume $i < j - 1$, we will later handle the $i = j - 1$ case).

Now let's input to the algorithm an element $y \neq x$ for $(i + 1)$-times, starting from both A_i and A_j. Then let's proof that the algorithm replies in two different ways, depending on whether it starts from A_i or A_j:

Case 1: when we start from A_i, we will end up in this situation:
(for simplicity, we'll use a JSON-like syntax for representing the counters)
Counters: $\{x : i, y : i + 1\} \implies$ the algorithm outputs y as the most frequent element.

Case 2: when we start from A_i, we will end up in this situation:
Counters: $\{x : j, y : i + 1\} \implies$ since $j > i + 1$, the algorithm outputs x.

We've seen how, starting from the same state A and with the same input, the algorithm produces different outputs; therefore it cannot be deterministic.

case $i = j - 1$

If i=j-1, then the algorithm contains the transition $(A_i, x) \to A_j = A_{i+1}$. This means that the algorithms remains in state A after receving x. In particular, $A_{i+2} = \delta(\delta(A_i, x), x) = \delta(A_i, x) = A_i$, and thus we can just take $j = i + 2$ and we fall in the previous case $i < j + 1$.

Special case of most frequent item in a stream

Suppose to have a stream of n items, so that one of them occurs $> n/2$ times in the stream. Also, the main memory is limited to keeping just two items and their counters, plus the knowledge of the value of n beforehand. Show how to find deterministically the most frequent item in this scenario. [Hint: since the problem cannot be solved deterministically if the most frequent item occurs $\leq n/2$ times, the fact that the frequency is $> n/2$ should be exploited.]

SOLUTION

This solution works with just one counter. We initialize the counter with zero, then we do the following:

- add the first element of the stream to the counter with value 1
- if the next element is the same of the one stored by the counter, then we increment the counter by 1.
- if the element is different, we decrease the counter by 1, but if the counter become zero then we substitute the counter item with the new element, and we set the counter to zero.

Now, we give a little proof of correctness. Suppose we $x_1, \ldots, x_n$ element in the stream, with their relative frequency $f_1, \ldots, f_n$, and suppose the element element with maximum frequency is x_{i^*}. Therefore by hypothesis we have:

$$\sum_{\forall i, i \neq i^*}^{n} f_i < \frac{n}{2} < f_{i^*}$$

Then by the following mathematical steps we have:

$$\begin{aligned}\sum_{\forall i, i \neq i^*}^{n} f_i &< f_{i^*} \\ \sum_{\forall i, i \neq i^*}^{n} f_i - f_{i^*} &< 0 \\ f_{i^*} - \sum_{\forall i, i \neq i^*}^{n} f_i &> 0\end{aligned}$$

Notice that this inequality is true by hypothesis. Thus the element remaining in the counter must be the one with higher frequency.

Count-min sketch: extension to negative counters

Check the analysis seen in class, and discuss how to allow $F[i]$ to change by arbitrary values read in the stream. Namely, the stream is a sequence of pairs of elements, where the first element indicates the item i whose counter is to be changed, and the second element is the amount v of that change (v can vary in each pair). In this way, the operation on the counter becomes $F[i] = F[i] + v$, where the increment and decrement can be now seen as $(i, 1)$ and $(i, -1)$.

SOLUTION

The frequency of the item i is represented by $\hat{F}[i] \to T[j, h_j(i)] = F[i] + X_{ji}$, where X_{ji} represent the garbage introduced by the other counters. If we just increment the counter X_{ji} is going to be positive, and then we can take the $min_j T[j, h_j(i)]$ to approximate $F[i]$. Instead, if we have also decrement, it could happen that $X_{ij} < 0$ therefore the method for the min is not going to work. In this case, we consider the absolute value of X_{ji}(i.e. $|X_{ji}|$) and we use $median_j T[j, h_j(i)]$ to approximate $F[i]$. Now let's proof that, with probability $1 - \delta^{1/4}$ holds:

$$F[i] - 3\epsilon\|F\| \leq \hat{F}[i] \leq F[i] + 3\epsilon\|F\|$$

First, let's do some consideration. The value of $\hat{F}[i] = median_j T[j, h_j(i)]$, and $T[j, h_j(i)] = F[i] + |X_{ji}|$. The first inequality(i.e. $F[i] \leq \hat{F}[i]$) holds because we took the absolute value of X_{ji}. Now we shall prove that $Pr[|X_{ji}| > 3\epsilon\|F\|] \leq 1/8$. Taken j such that $\hat{F}[i] = median_j T[j, h_j(i)] = F[i] + |X_{ji}|$, then we have:

$$\begin{aligned}
Pr[F[i] - 3\epsilon\|F\| \leq \hat{F}[i] \leq F[i] + 3\epsilon\|F\|]\\
Pr[F[i] - 3\epsilon\|F\| \leq F[i] + |X_{ji}| \leq F[i] + 3\epsilon\|F\|]\\
Pr[-3\epsilon\|F\| \leq |X_{ji}| \leq 3\epsilon\|F\|]\\
Pr[|X_{ji}| \leq 3\epsilon\|F\|]
\end{aligned}$$

From what we have seen in class and by the property of the absolute value, we have $E[|X_{ji}|] \leq E[X_{ji}] = \frac{\epsilon}{e}\|F\|$. Then we can apply the Markov inequality and since universal hash functions are pairwise independent, we have:

$$Pr[|X_{ji}| > 3\epsilon\|F\|] < \frac{E[|X_{ji}|]}{3\epsilon\|F\|} \leq \frac{\frac{\epsilon}{e}\|F\|}{3\epsilon\|F\|} = \frac{1}{3e} < \frac{1}{8}$$

Let's now define the indicator variable $Y = \sum_{j=0}^{r} Y_j$ which tell us the number of elements i (columns of the sketch) that have a garbage $|X_{ji}|$ greater than $3\epsilon\|F\|$.

$$Y_j = \begin{cases} 1 & \text{IF } |X_{ji}| > 3\epsilon\|F\| \text{ WITH } p < \frac{1}{8} \\ 0 & \text{OTHERWISE} \end{cases}$$

The median of $\hat{F}[i]$ is going to be a good approximation if we haven't got more than $\frac{r}{2}$ rows such that $|X_{ji}| > 3\epsilon\|F\|$ (that is we want $Y < \frac{r}{2}$).
Therefore, to calculate the probability of error, we calculate the probability of $Pr[Y \geq \frac{t}{2}]$. Here, we can use the Chernoff's Bound With: $(1+\lambda)\mu = \frac{t}{2}$, $\mu = E[Y] = rp$.

$$\Pr[Y \geq (1+\lambda)\mu] < \left[\frac{e^{\lambda}}{(1+\lambda)^{1+\lambda}}\right]^{\mu} = \left[\frac{e}{e}\frac{e^{\lambda}}{(1+\lambda)^{1+\lambda}}\right]^{\mu} = \frac{1}{e^{\mu}}\left[\frac{e}{(1+\lambda)}\right]^{(1+\lambda)\mu} = \frac{1}{e^{rp}}\left[\frac{1}{(1+\lambda)}e\right]^{\frac{r}{2}} = \frac{1}{e^{rp}}\left[2pe\right]^{\frac{r}{2}}$$

Now we need to prove that $\frac{1}{e^{rp}}[2pe]^{\frac{r}{2}} \leq \delta^{\frac{1}{4}} = \frac{1}{2^{\frac{r}{4}}}$. If we use the reciprocal we have:

$$2^{\frac{r}{4}} \leq \frac{e^{rp}}{[2pe]^{\frac{r}{2}}} \leq \frac{1}{[2pe]^{\frac{r}{2}}}$$

$$2^{\frac{1}{4}} \leq \frac{1}{\sqrt{2pe}}$$

Since $e^{rp} \geq 1$. Then, we take $\frac{1}{2pe} > \sqrt{2}$, that is possible just if $p < \frac{1}{2\sqrt{2}e}$, indeed $p = \frac{1}{8}$.

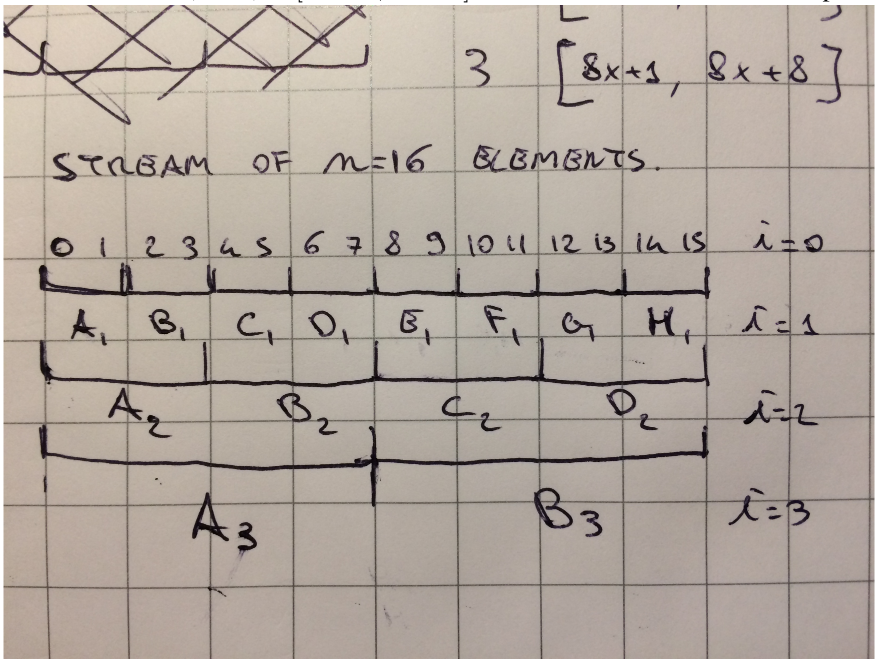
Count-min sketch: range queries

Show and analyse the application of count-min sketch to range queries (i,j) for computing $\sum_{k=i}^{j} F[k]$. Hint: reduce the latter query to the estimate of just $t \leq 2\ log\ n$ counters $c_1, c_2, ..., c_t$. Note that in order to obtain a probability at most δ of error (i.e. that $\sum_{l=1}^{t} c_l > \sum_{k=i}^{j} F[k] + 2\epsilon\ log\ n||F||$), it does not suffices to say that it is at most δ the probability of error of each counter c_l: while each counter is still the actual wanted value plus the residual as before, it is better to consider the sum V of these t wanted values and the sum X of these residuals, and apply Markov's inequality to V and X rather than on the individual counters.

SOLUTION

We use the Dyadic Interval: a dyadic interval is a range of the form $[x2^i + 1...(x+1)2^i]$ for parameters x and i. Each point in the range $[1 \ldots n]$ is a member of $log_2 n$ dyadic intervals, one for each i in the range $0 \ldots log_2(n) - 1$ (think it as a tree, where we split the interval in 2 at each level).

An example: let's say I have a stream of $N = 16$ different items, this means I need to use $logN = 4$ CMSs, one for each $i \in \{0,1,2,3\}$. So the first CMS ($i = 0$) will correspond to the interval $[x+1, x+1]$, the second CMS ($i = 1$) to $[2x+1, 2x+2]$ and so on. The elements will be partioned like in the picture:



The sketch corresponding to ($i = 3$) will count occurences of A_3 and B_3 (will count an A_3 every time a number in $\{0,1,2,3,4,5,6,7\}$ arrives, and a B_3 when a $\{8,9,10,11,12,13,14,15\}$ arrives.); the ($i = 2$) sketch will count A_2,B_2, C_2, D_2 and so on. Then for each arbitrary interval (a,b) we just need to sum the corresponding dyadic intervals that makes it. (e.g. if I receive a query for $(7,13)$, then i can just sum up the occurences of C_2, G_1 and "7").

A count-min sketch table is kept for each set of dyadic intervals of length 2^i, one for each level in the tree (one for each value of i). Thus we have $log_2 n$ vectors $\widetilde{F_i}$ and, in line of principle, $log_2 n$ vectors F_i.

You can see this as associating each new sketch to a reencoding of the original stream, where you have partitioned the alphabet in 2^i subsets of symbols and represented each of them with a single new symbol. Say: ABCD as alphabet, map AB $\rightarrow$ E, CD $\rightarrow$ F; each time you witness A *or* B you count an occurrence of E, each time you witness C *or* D you count an occurrence of F.

Witnessing a new element in the stream will therefore trigger an update to all the $log_2 n$ tables.

The idea for a range query is to partition the range into dyadic intervals (of a number of sizes, in general, thus from a number of CMS tables) and return as result the sum of the values stored in the CMS tables for the corresponding intervals [see this link for further reference].

It can be shown[1] that any range will be split at most into $2log_2 n$ dyadic intervals.

Therefore for each query we access $t \leq 2\ log\ n$ counters $c_1, c_2, ..., c_t$. We then, want to proof $Pr[\sum_{l=1}^{t} c_l > \sum_{k=i}^{j} F[k] + 2\epsilon\ log\ n||F||] < \delta$.

Firstly, we notice that each counter c_i represents an interval $[a, b]$ and it value is $\sum_{k=a}^{b}(F[k]) + X_i$, where X_i is the rubbish of that particular interval. Then, give an interval $[l, r]$, and the counters we have $\sum_{i=1}^{t} c_i = \sum_{k=l}^{r} F[k] + X$, where X is the total error (notice that this works because the interval are disjoint). Then we substitute to the previous equation and we have:

$$Pr[\sum_{l=1}^{t} c_l > \sum_{k=l}^{r} F[k] + 2\epsilon\ log\ n||F||] < \delta$$
$$Pr[\sum_{k=l}^{r} F[k] + X > \sum_{k=l}^{r} F[k] + 2\epsilon\ log\ n||F||] < \delta$$
$$Pr[X > 2\epsilon\ log\ n||F||] < \delta$$

Now, we apply Markov inequality and by the linearity of the expectation we have:

$$Pr[X > 2\epsilon\ log\ n||F||] \leq \frac{E[X]}{2\epsilon\ log\ n||F||} \leq \frac{\sum_{i}^{2log_2(n)} E[X_i]}{2\epsilon\ log\ n||F||}$$

Now, let $d(i)$ be the depth in the tree to which the dyadic interval i belongs (identifying its CMS table). We see that $\forall i.E[X_i] < \frac{\epsilon}{e}||F_{d(i)}||_1$, but $\forall x, y.||F_x||_1 = ||F_y||_1 = ||F||_1 \implies E[X_i] < \frac{\epsilon}{e}||F||_1$.
(by definition $||A||_1 = \sum_{h=1}^{n} |A[h]|$, that is in our case we sum the frequencies of symbols, which sum up to the same total amount no matter how we group them with a reencoding)

Thus we have
$$\frac{\sum_{i}^{2log_2(n)} E[X_i]}{2\epsilon\ log\ n||F||} \leq \frac{2\frac{\epsilon}{e}log\ n||F||}{2\epsilon\ log\ n||F||} = \frac{1}{e}$$

This is the probability of error (that the sum of garbage is more the $2\epsilon\ log\ n||F||$) in row j (the min, potentially distinct for each table).

Since we choose the row of each table that minimize the sum of the counter (by definition), then there must be an error in all the row r. Thus we have $\frac{1}{e^r} = \delta$ since $r = ln(\frac{1}{\delta})$.

A little example: suppose we have $n = 16$ (item), then a range $[1 \dots 16]$. Thus, we query $(8, 12)$, this interval is fully included, then we split in $[1 \dots 8]$ and $[9 \dots 16]$ (we go down in the tree). $[1 \dots 8]$ is still too big then we split in $[1 \dots 4]$ and $[5 \dots 8]$, $[1 \dots 4]$ is not included then we take it off. $[5 \dots 8]$ for the same reason we split it in $[5 \dots 6]$ and $[7 \dots 8]$ and so on.

[1] First, note that:

- No three intervals of the same length can be contained in the partition of the same query, otherwise you could merge two of them;
- If there are two consecutive intervals of the same length, they must belong to two different larger "parent" intervals (otherwise you could replace them with their parent), i.e. their union cannot belong to the dyadic partition.

Thus, there are at most 2 intervals of each possible size in the partition. As the sizes are $log_2 n$ in all, the partition is made up of at most $2log_2 n$ intervals.

Space-efficient perfect hash

Consider the two-level perfect hash tables presented in [CLRS] and discussed in class. As already discussed, for a given set of n keys from the universe U, a random universal hash function $h : U \to [m]$ is employed where $m = n$, thus creating n buckets of size $n_j \geq 0$, where $\sum_{j=0}^{n-1} nj = n$. Each bucket j uses a random universal hash function $h_j : U \to [m]$ with $m = n_j^2$. Key x is thus stored in position $h_j(x)$ of the table for bucket j, where $j = h(x)$.

This problem asks to replace each such table by a bitvector of length $n = n_j^2$, initialized to all 0s, where key x is discarded and, in its place, a bit 1 is set in position $h_j(x)$ (a similar thing was proposed in Problem 4 and thus we can have a one-side error). Design a space-efficient implementation of this variation of perfect hash, using a couple of tips. First, it can be convenient to represent the value of the table size in unary (i.e., x zeroes followed by one for size x, so 000001 represents x = 5 and 1 represents x = 0). Second, it can be useful to employ a rank-select data structure that, given any bit vector B of b bits, uses additional o(b) bits to support in O(1) time the following operations on B:

- $rank_1(i)$: return the number of 1s appearing in the first i bits of B.
- $select_1(j)$: return the position i of the jth 1, if any, appearing in B (i.e. B[i] = 1 and $rank_1(i) = j$).

Operations $rank_0(i)$ and $select_0(j)$ can be defined in the same way as above. Also, note that o(b) stands for any asymptotic cost that is smaller than $\Theta(b)$ for $b \to \inf$.

SOLUTION

The solution uses five data structures:

`H` is the Header table, it substitute the first level hash table and is memorized using a rank-select data structure;

`T` is the bitvector in which we will sore the bits for the presence/absence of the elements, it plays the role of all the second level tables;

`A` is the table that store the a parameters for the hash functions of the second level;

`B` is the table that store the b parameters for the hash functions of the second level;

`P` is the table that store the p parameters for the hash functions of the second level.

Before continue we make some observations:

1. $\sum_{j=1}^{n} n_j = n$, where n_j is the number of elements in the bucket j (called B_j from now on), as seen in class since by definition n is the number of elements to be stored;
2. in each bucket B_j we use an universal hash function h_j with $m = n_j^2$, and we have already proved that it's perfect (no collision) with probability $\geq \frac{1}{2}$;
3. given that $E[\sum_{j=1}^{n} n_j^2] < 2n$ and so by *Markov's inequality* that $Pr[\sum_{j=1}^{n} n_j^2 \geq 4n] < 1/2$, we know that $\sum_{j=1}^{n} n_j^2 \leq 4n$ with probability greater or equal to 1/2;
4. p, the parameter of the family of hash functions for the first level of hashing is a prime number greater than n, so for the *Bertrand's postulate* we know that we can choose a $p < 2n$ and we need less than $log_2 2n = log_2 2 + log_2 n = 1 + log_2 n$ to store it;
5. we take a and b (the parameters of the hash function in the first level) from $\mathbb{Z}_p$ and, since we know that we can choose a $p < 2n$, we need less than $log_2 2n = 1 + log_2 n$ bits for each one of them;
6. for each bucket B_j we choose randomly the parameters a_j and b_j of the hash function from $\mathbb{Z}_{p_j}$, with $p_j > n_j^2$ prime number (greater than the size of the bitvector), since we can choose $p_j < 2n_j^2$, the number of bits needed for each one of the two is less then $log_2 2{n_j}^2 = 1 + log_2 {n_j}^2$, the same number of bits are needed also for storing p_j itself.

Now we can speak more precisely about H and T.

H is simply the concatenation of the unary representation of n_1^2, n_2^2 ... n_n^2, so essentially n_1^2 times 0, followed by a 1 bit, then n_2^2 times 0, followed by a 1 bit, etc. We will use an additional amount of bits because of the rank-select data structure.

The table T is the concatenation of the bit vector of each bucket: the one for B_1 followed by the one for B_2, and so on, until B_n. Notice that the length of those buckets (and respectively of the vectors) can be different one from each other. For each bucket B_j we will call its bitvector Bv_j, we recall that the size of B_j is n_j and the size of Bv_j is n_j^2. We have

$$\begin{aligned} H &= (n_1^2)_1 \,|(n_2^2)_1 \mid \dots \mid (n_n^2)_1 \\ T &= Bv_1 \,|Bv_2 \mid \dots \mid Bv_n \end{aligned}$$

where $(\_)_1$ means the unary notation.

So we have that initially T is the concatenation of n_1^2 bits at 0, n_2^2 bits at 0 etc... Notice that in H we can consider the 1 bits as separator between the information about one bucket and the others, but we don't have anything similar in T: since we have concatenate all the bitvectors, we need some way to retrieve the range of any bitvector. To do so, we use the length of the bitvectors, contained in the header H.

The procedure for setting to 1 the bits relative to a given key x, and for looking whether the key is in S or not is the following:

$$\begin{aligned} j &= h_{abpn}(x) \\ k &= H.select_1(j-1) \ \# \text{ POSITION OF THE } j-1_{th} \ 1 \\ \texttt{base} &= H.rank_0(k) \ \# \text{ NUMBER OF 0S BEFORE THE INDEX } k \\ a' &= A[j] \\ b' &= B[j] \\ p' &= P[j] \\ m' &= H.select_1(j) - H.select_1(j-1) - 1 \\ \texttt{offset} &= h_{a'b'p'm'}(x) \\ T[\texttt{base}+\texttt{offset}] &= 1 \ // \ return\ T[\texttt{base}+\texttt{offset}] \end{aligned}$$

where a and b are the parameters of the hash function in the first level, and the last operation is $T[\texttt{base}+\texttt{offset}] = 1$ if we are filling the table (creation phase), and $return\ T[\texttt{base}+\texttt{offset}]$ if we are querying the hash table for key x. Notice that by definition of H, m' is the number of 0s between the $j-1_{th}$ and the j_{th} 1 and so it is n_j^2. Notice also that we can calculate base as $k-j$ since all but j bits are at 0 from the position 0 to the position k. We used the notation $h_{abpm}(x)$ for $((ax+b)\ mod\ p)\ mod\ m$.

If we are querying the table and the value returned is 0 then the element is not present, instead if it is 1 we say that the element is present, with a probability of error (one side error as usual).

The space occupied by the data structures used here is the following:

H : the number of $0s = \sum_{j=1}^n n_j^2$ plus the number of $1s = \#\text{BUCKETS} = n$ plus the extra space for the rank-select data structure, so totally $\sum_{j=1}^n n_j^2 + n + o(\sum_{j=1}^n n_j^2 + n) \le 4n+n+o(4n+n) = 5n+o(n)$ with probability grater or equal 1/2;

T : the same number of $0s$ in H, $\sum_{j=1}^n n_j^2 \le 4n$ whit probability grater or equal to 1/2;

A : one array of n elements, each one needs less than $1 + log_2 {n_j}^2$ bits, then the total number of bits is less than $\sum_{j=1}^n (1+log_2{n_j}^2) = n + \sum_{j=1}^n (2log_2 n_j) = n + 2\sum_{j=1}^n (log_2 n_j) < n + 2\sum_{j=1}^n n_j = n + 2n = 3n$;

B : by the same reasoning made for A we have less than $3n$ bits.

P : by the same reasoning made for A we have less than $3n$ bits.

Considering the space needed for a, b and p of the first level hash function, the total space used is less than: $5n + 4n + 3n + 3n + 3n + 3(1 + log_2 n) + o(n) = 18n + o(n)$.

Notice that if we use $p_j = p$ for each bucket B_j, than the size of A is $nlog_2 2n = n(1+log_2 n) = n + nlog_2 n$, which is a problem since $nlog_2 n \notin o(n)$

Bloom filters vs. space-efficient perfect hash

Recall that classic Bloom filters use roughly $1.44 log_2(1/f)$ bits per key, as seen in class (where $f = (1-p)^k$ is the failure probability minimized for $p \approx e^{-\frac{kn}{m}=1/2}$). The problem asks to extend the implementation required in Problem 10 by employing an additional random universal hash function $s : U \to [m]$ with $m = \lceil \frac{1}{f} \rceil$, called signature, so that s(x) is also stored (in place of x, which is discarded). The resulting space-efficient perfect hash table T has now a one-side error with failure probability of roughly f, as in Bloom filters: say why. Design a space-efficient efficient implementation of T, and compare the number of bits per key required by T with that required by Bloom filters.

SOLUTION

The probability of error in the first data structure (the bit perfect min hash) is $\frac{1}{m}$ for the external table. Instead we approximate the error in each bucket with 1, this because the length of each bucket is not know apriori, and thus we can just have an expectation.Now the addiction of the hash table s, which has got m elements, introduce another probability of a collision which is $\frac{1}{m}$.
Wrapping all we have $Pr[error] = \frac{1}{m} * \frac{1}{m} = 2 * f'$ since $m = \frac{1}{f'}$. So to obtain the same probability of error we should have $f' = \frac{f}{2}$.

We consider first of all to have the same data structure of EX10. Therefore, we have H, T, A, B, P, and then till now if we have n keys we occupy a space equal to $18n + o(n)$ bits. Now we add another data structure T' where we store the hash generated by s. T' has got n slots, as the number of keys, in which every element occupy $log_2(m) = log_2(1/f)$ bits, since $s : U \to [m]$ with $m = \lceil \frac{1}{f} \rceil$. Now, since this data structure is static, ones we build the H, T, A, B, P we can insert each $s(k)$ in T' in the same position as it is in T. For example, the first element of bucket 1 (if it exist) is going to be the fist element of T', and so on. Then now to find the position of the hash in T' given a key k we use $rank_1(\text{BASE} + \text{OFFSET})$, where $\text{BASE} + \text{OFFSET}$ is the position calculate to check the if there is a 1 in T ($T[\text{BASE} + \text{OFFSET}]$, look EX10).

Now we need to check how many bits are used for each key. T' uses $log_2(1/f)$ bit per key as explained before, and, by the previous analysis, we have 18 bit for each key + o(1)($18n + o(n)$). Therefore, we have roughly $log_2(1/f) + 18$ per key, instead Bloom filters use roughly $1.44 log_2(1/f)$. Let's compare them, to see which is more convenient:

$$\begin{aligned} log_2(1/f) + 18 &< 1.44 log_2(1/f) \\ -log_2(f) + 18 &< -1.44 log_2(f) \\ -log_2(f) + 1.44 log_2(f) &< -18) \\ log_2(f) &< -\frac{18}{0.44}) \\ f &< \frac{1}{2^{\frac{18}{0.44}}} \end{aligned}$$

Then perfect hash is convenient for f less than $\approx 4.84 \times 10^{-13}$.

MinHash sketches

As discussed in class, for a min-wise independent family H, we can associate a sketch

$$s(X) = \langle min\ h_1(X), min\ h_2(X), \dots min\ h_k(X)\rangle$$

with each set X in the given data collection, where $h_1, h_2, \dots, h_k$ are independently chosen at random from H. Consider now any two sets A and B, with their sketches $s(A)$ and $s(B)$. Can you compute a sketch for $A \cup B$ using just $s(A)$ and $s(B)$ in $O(k)$ time? Can you prove that it is equivalent to compute $s(A \cup B)$ from scratch directly from $A \cup B$?

SOLUTION

We have the two sketches of A and B:

$$s(A) = \langle min\ h_1(A), min\ h_2(A), \dots min\ h_k(A)\rangle$$
$$s(B) = \langle min\ h_1(B), min\ h_2(B), \dots min\ h_k(B)\rangle$$

We want to compute the sketch for $A \cup B$:

$$s(A \cup B) = \langle min\ h_1(A \cup B), min\ h_2(A \cup B), \dots min\ h_k(A \cup B)\rangle$$

For each $i \in 1, 2, \dots k$ we will take $min\ \{\ min\ h_i(A),\ min\ h_i(B)\ \}$ as $min\ h_i(A \cup B)$. This procedure require a constant number of operation (exactly one min) and must be repeated k times, so the time needed is $O(k)$.

In order to prove that what we obtain is exactly the sketch of $A \cup B$ we exploit the following lemma.

Lemma 1. *For each $i \in \{1, 2, \dots k\}$ it holds $h_i(A \cup B) = h_i(A) \cup h_i(B)$.*

Proof. take any x, then all the following are equivalent:

$$x \in h_i(A \cup B)$$
$$\exists y \in A \cup B\ .\ h_i(y) = x$$
$$\exists y \in A\ .\ h_i(y) = x \quad OR\ \ \exists y \in B\ .\ h_i(y) = x$$
$$x \in h_i(A) \qquad OR \qquad x \in h_i(B)$$
$$x \in h_i(A) \cup h_i(B)$$

□

Finally.

Theorem 2. *For each $i \in \{1, 2, \dots k\}$ it holds $min\ h_i(A \cup B) = min\ \{\ min\ h_i(A),\ min\ h_i(B)\ \}$.*

Proof. take any $i \in \{1, 2, \dots k\}$, then

$$min\ h_i(A \cup B) = \qquad [using\ lemma 1]$$
$$min\ (h_i(A) \cup h_i(B)) = \qquad [trivial\ property\ of\ min]$$
$$min\ \{min\ h_i(A),\ min\ h_i(B)\}$$

□

Randomized min-cut algorithm

Consider the randomized min-cut algorithm discussed in class. We have seen that its probability of success is at least $1/\binom{n}{2}$, where n is the number of its vertices.

- Describe how to implement the algorithm when the graph is represented by adjacency lists, and analyze its running time. In particular, a contraction step can be done in $O(n)$ time.
- A weighted graph has a weight $w(e)$ on each edge e, which is a positive real number. The min-cut in this case is meant to be min-weighted cut, where the sum of the weights in the cut edges is minimum. Describe how to extend the algorithm to weighted graphs, and show that the probability of success is still $\geq 1/\binom{n}{2}$. [hint: define the weighted degree of a node]
- Show that running the algorithm multiple times independently at random, and taking the minimum among the min-cuts thus produced, the probability of success can be made at least $1 - 1/n^c$ or a constant $c > 0$ (hence, with high probability).

SOLUTION

First Point

We shall keep nodes in an array. We expect to run $N-2$ contractions, spawning a new node for each of them, thus the array shall be of length $2N-2$, the last $N-2$ elements initially NULL.

Nodes will be annotated with their *degree* and a *container* field with the ID of the node they're currently "contained" in (initially themselves, then the nodes they get contracted into).

An edge (i, j) shall be a vector of three elements $< dest, mult, reverse >$:

- *dest*: the node ID of the destination (i.e. j);
- *mult*: recall we're in a multigraph, so there can be many edges $(i, j)_k$. We represent them as a single edge annotated with a *multiplicity* value, i.e. $(i, j).mult = |\{(i, j)_k\}|$.

  This way, each adjacency list contains $O(N)$ elements;
- *reverse*: as we're in an undirected graph, for each edge (i, j) there is the reverse (j, i). In *reverse* we store a pointer to (j, i), as we'll need it for bookkeeping during contraction operations.

Adjacency lists shall be doubly linked and sorted on *dest* fields.

Random choice of edge

Let N be the initial number of nodes, n be the number of remaining unique nodes.

Let M be the initial number of edges, m be the number of remaining edges.

Let $\delta(i)$ be the degree of node i (NB: contracted nodes will have degree 0). Then:

```
function ChooseEdge
    $r \leftarrow rand(0, 2m-1)$                          ▷ note $\sum_{i=1}^{n} \delta(i) = 2m$
    $i \leftarrow 0$
    while $nodes[i].degree < r$ do                 ▷ note we'll never reach the NULL tail of $nodes[]$
        $r \leftarrow r - nodes[i].degree$
        $i \leftarrow i + 1$
    end while
    $j \leftarrow 0$
    while $nodes[i].adj[j].mult < r$ do
        $r \leftarrow r - nodes[i].adj[j].mult$
        $j \leftarrow j + 1$
    end while
    return $(i,\ j)$

end function
```

You can think of what we're doing as having concatenated the adjacency lists and then crawled through them to edge r. This would require $O(n^2)$ steps done naively, but saving the degree of the node (the length of the adjacency list) allows us to skip to the next node in one step (a sort of skip-pointer).

In fact, what we do is crawl the list of nodes ($O(n)$) and then one adjacency list ($O(n)$ again).

This procedures results in a random uniform choice of the edge. In fact, the chance that a specific (directed!) edge $(i,j)_k$ is chosen ends up being:

$$P_r[(i,j_k)] = \frac{\delta(i)}{2\times m} \times \frac{mult(i,j)}{\delta(i)} \times \frac{1}{mult(i,j)} = \frac{1}{2\times m}$$

where

$$\frac{\delta(i)}{2\times m} = P_r[node\ i\ is\ chosen]$$

$$\frac{mult(i,j)}{\delta(i)} = P_r[\{(i,j)_k\}|\ node\ i]$$

$$\frac{1}{mult(i,j)} = P_r[(i,j)_k|\ \{(i,j)_k\}]$$

$\{(i,j)_k\}$ is the set of all edges going from i to j

$mult(i,j) = |\{(i,j)_k\}|$ is the multiplicity of edge (i,j)

Thus, the probability that an (undirected!) edge $(i,j)_k$ is chosen results

$$\frac{1}{2m} + \frac{1}{2m} = \frac{1}{m}$$

Contraction

General idea for contracting over edge (i,j):

- Spawn a new node that will represent i and j contracted;
- Update the *container* field of nodes "contained" in i or j;
- Crawl through i and j's adjacency lists: nodes pointed by one but not the other get appended to the new node's list; nodes pointed by both are also appended, but their multiplicity is the sum of the old egdes' multiplicity.

  This can be done in linear time w.r.t. the length of the adjacency lists ($O(N)$) because they're sorted, so we proceed as in a *merge* operation of a MergeSort.

  In all cases, we take advantage of $(i,j).reverse$ to update the adjacency list of the pointed node with the new node. As the lists are doubly linked and assuming a pointer to the last element is kept, this can be done in $O(1)$ time.

```
**function** CONTRACT(i, j)
    $nID \leftarrow$ position of next NULL element in the tail of $nodes[]$
    $nodes[n] \leftarrow new\ Node()$
    **for** $x$ in $nodes$ **do**
        **if** $x.container = i \vee x.container = j$ **then**
            $x.container \leftarrow nID$
        **end if**
    **end for**
    $it_i \leftarrow$ iterator over $nodes[i].adj$
    $it_j \leftarrow$ iterator over $nodes[j].adj$
    **while** $it_i.hasNext()$ and $it_j.hasNext()$ **do**
        **if** $it_i.dest = j$ **then**
            $it_i.next()$
        **else if** $it_j.dest = i$ **then**
```

```
            $it_j.next()$
        else if $it_i.dest = it_j.dest$ then
            /* create a pair of edges, one the reverse of the other */
            /* constructor takes, in order, $dest$, $mult$, $reverse$ */
            /* also passing $e$ to its own constructor is questionable but this is just pseudocode */
            $e \leftarrow new\ Edge(it_i.dest, it_i.mult + it_j.mult, new\ Edge(nID, it_i.mult + it_j.mult, e))$
            /* remove old edges from the destination's adjacency list */
            $it_i.reverse.remove()$
            $it_j.reverse.remove()$
            /* put reverse in destinations; note $nID$ is highest so it goes to the tail*/
            $nodes[e.dest].adj.append(e.reverse)$
            /* put $e$ at the tail of $nodes[nID].adj$ */
            $nodes[nID].adj.append(e)$
            $it_i.next()$
            $it_j.next()$
            /* increment $nodes[nID]$'s degree by $e.mult$ */
            $nodes[nID].degree \leftarrow nodes[nID].degree + e.mult$
        else if $it_i.dest < it_j.dest$ then
            $e \leftarrow new\ Edge(it_i.dest, it_i.mult, new\ Edge(nID, it_i.mult, e))$
            $it_i.reverse.remove()$
            $nodes[e.dest].adj.append(e.reverse)$
            $nodes[nID].adj.append(e)$
            $it_i.next()$
            $nodes[nID].degree \leftarrow nodes[nID].degree + e.mult$
        else                                                    ▷ $it_j.dest < it_i.dest$
            $e \leftarrow new\ Edge(it_j.dest, it_j.mult, new\ Edge(nID, it_j.mult, e))$
            $it_j.reverse.remove()$
            $nodes[e.dest].adj.append(e.reverse)$
            $nodes[nID].adj.append(e)$
            $it_j.next()$
            $nodes[nID].degree \leftarrow nodes[nID].degree + e.mult$
        end if
    end while
    Process leftovers from either $i$ or $j$'s adjacency lists, if there are any, in a similar fashion.
    $nodes[i].degree \leftarrow 0$       ▷ degrees of $i$ and $j$ are put to 0 for ChooseEdge's conveniency
    $nodes[j].degree \leftarrow 0$       ▷ we could also detach the adjacency lists if we liked, but it's not necessary
end function
```

Computing the cut

After running $N - 2$ contractions, you'll end up with two nodes hl_1 and hl_2 (highlanders) left over in the graph.

The size of the cut will be $hl_1.degree = hl_2.degree.$

The *container* field of the first N elements of *nodes* will be either hl_1 or hl_2.

The two classes of nodes will thus define the cut. Should you need the actual edges making up the cut, you'll crawl through the original graph and output edges connecting nodes of the two classes ($O(N^2)$).

Second Point

In the algorithm we change the way we choose an edge to contract: edges with high weight will have a greater probability to be chosen with respect to others with lower weight. We define $weight : E \longrightarrow \mathbb{R}$ as the function that associate the weight to a given edge. We will use the *weight* function also on subsets of E, intending for $weight(X)$ with $X \subseteq E$ the sum of the weight of all the edges in X.

$$weight(X) = \sum_{e \in X} weight(e) \qquad\qquad where\ X \subseteq E$$

As seen in class, the *min cut* is not unique, nevertheless the sum of weights in all *min_cuts* is the same, than with a notation abuse we will call it $weight(min\_cut)$. For each edge $x \in E$ the probability to be choose for a contraction is given by its weights normalized with the total sum of the weights of all the edges of the graph.

$$Pr[extract\ x] = \frac{weight(x)}{weight(E)}$$

Now the probability of making an error, when extracting an edge at random, is the probability of extracting one of the "bad" edges, i.e. edges such that their contraction cause a variation in $weight(min\_cut)$. We name BAD the set of "bad" edges.

$$Pr[error] = \sum_{e \in BAD} Pr[extract\ e] = \sum_{e \in BAD} \frac{weight(e)}{weight(E)} = \frac{weight(BAD)}{weight(E)} \tag{1}$$

As usual bad edges are those belonging to every *min cut*, so the total weight of bad edges is less or equal to the weight of *min cut*.

$$weight(BAD) \leq weight(min\_cut) \tag{2}$$

Given a node v, we define $star(v)$ as the set of all the edges touching v. For the same reasons explained in class, for each node v the weight of *min cut* must be less or equal to the sum of the weights of the edges touching v. This is because otherwise we would have a cut, $star(n)$, with weight less than *min cut*, which is absurd.

$$\forall\ v \in V\ .\ weight(min\_cut) \leq weight(star(v)) \tag{3}$$

We can reformulate the *handshaking lemma* for weighted graph in the following way, in which $weight(star(v))$ is something like the "weighted degree" of the node v.

$$weight(E) = \frac{\sum_{v \in V} weight(star(v))}{2} \tag{4}$$

Now we can derive:

$$\begin{aligned} weight(E) &= \frac{\sum_{v \in V} weight(star(v))}{2} && \text{(from 4)} \\ &\geq \frac{|V| weight(min\_cut)}{2} && \text{(from 3)} \end{aligned}$$

$$weight(min\_cut) \leq \frac{2\ weight(E)}{|V|} \tag{5}$$

Finally we have all the ingredients for the proof:

Theorem 1. *Selecting the edges for the contraction according to the probability described, each time we choose an edge the probability of choosing a "bad" edge is less or equal than* $2/|V|$.

$$Pr[error] \leq \frac{2}{|V|}$$

Proof.

$$\begin{aligned} Pr[error] &= \frac{weight(BAD)}{weight(E)} && \text{(from 1)} \\ &\leq \frac{weight(min\_cut)}{weight(E)} && \text{(from 2)} \\ &\leq \frac{\frac{2\ weight(E)}{|V|}}{weight(E)} && \text{(from 5)} \\ &= \frac{2\ weight(E)}{|V| weight(E)} = \frac{2}{|V|} \end{aligned}$$

□

The probability of making an error when selecting an edge is the same as for the case of a normal graph seen in class, so the probability of success for the algorithm (i.e. the probability of choosing well all the times) is still $\geq 1/\binom{n}{2}$.

Third Point

We know that $P(n) \geq 1/\binom{n}{2}$ is the probability of choose well for N times. We have seen also that the probability of error is $\leq (1 - 1/\binom{n}{2})$. Then the probability of having an error each time in N repetitions of the algorithm is

$$leq(1 - \frac{1}{\binom{n}{2}})^N \approx e^{-\frac{2N}{n(n-1)}}$$

Given a c we want the probability of success to be $\geq 1 - 1/n^c$. This is equivalent to ask that the probability of error is $\leq 1/n^c$. Making some calculations:

$$\begin{aligned} \frac{1}{e^{\frac{2N}{n(n-1)}}} = e^{-\frac{2N}{n(n-1)}} &\leq \frac{1}{n^c} \\ n^c &\leq e^{\frac{2N}{n(n-1)}} \\ ln(n^c) &\leq ln(e^{\frac{2N}{n(n-1)}}) = \frac{2N}{n(n-1)} \\ N \geq \frac{n(n-1)ln(n^c)}{2} \end{aligned}$$

So, for each given c, to make the probability of success at least $1 - 1/n^c$ is sufficient to take N grater or equal than $\frac{1}{2}n(n-1)ln(n^c)$.

External memory implicit searching

Given a static input array A of N keys in the EMM (external memory or cache-aware model), describe how to organize the keys inside A by suitably permuting them during a preprocessing step, so that any subsequent search of a key requires $O(log_B N)$ block transfers using just $O(1)$ memory words of auxiliary storage (besides those necessary to store A). Clearly, the CPU complexity should remain $O(logN)$. Discuss the I/O complexity of the above preprocessing, assuming that it can uses $O(N/B)$ blocks of auxiliary storage. (Note that the additional $O(N/B)$ blocks are employed only during the preprocessing; after that, they are discarded as the search is implicit and thus just O(1) words can be employed.)

SOLUTION

We start with a sorted array A (we can sort it otherwise). First we will build a k-way search tree with exactly the same elements of A (no duplication) i.e. a B-tree. Second we will describe how to store the tree implicitly in an array. Finally we will say how to find the children of a given node without explicit pointers (smell like heap spirit).

Given the block size B, the arity of the tree must be $k = B + 1$. For the construction of the k-way search tree first we need to calculate the height. A complete k-ary tree of height h has 1 node for the first level plus k for the second, plus the square of k for the third etc [1].

$$\begin{aligned} nodes(h) &= \sum_{i=0}^{h} k^i \\ &= k^0 + k^1 + k^2 \cdots + k^h \\ &= \frac{k^{h+1} - 1}{k - 1} \end{aligned}$$

Using

$$(k^0 + k^1 + k^2 \cdots + k^h)(k-1) = (k^1 + k^2 + k^3 \cdots + k^h + k^{h+1}) - (k^0 + k^1 + k^2 \cdots + k^h) = k^h - 1$$

And since each node contains B elements of the array

$$elements(h) = B\frac{k^{h+1} - 1}{k - 1}$$

But in the tree we are going to build we assume that $k - 1 = B$, then

$$elements(h) = B\frac{k^{h+1} - 1}{k - 1} = k^{h+1} - 1$$

The inverse gives us the formula for the height given the number of elements N

$$height(n) = \lceil \log_k(N + 1) - 1 \rceil$$

Before starting the construction of the tree we need one more information about the structure it should have. For reasons that will be clarified later we want a complete tree i.e. one such that every level, except possibly the last, is completely filled, and all nodes in the last level are as far left as possible. Given this shape we want to know how many elements are there in the last level nodes (we name their number L). The calculation is simple since we know the dept of the last level and the number of elements in all the other levels.

$$\begin{aligned} L\ [\textit{last\_level\_elements(N, h)}] &= N - elements(h-1) \\ &= N - (k^h - 1) \end{aligned}$$

[1]Note that we count the height of a tree assuming that a single node tree has height zero, not one.

Now we build the tree, selecting the elements to insert in each node of the tree (B elements for node since every node must be contained in a memory block). We will proceed level by level, from the last to the root (see 1).

For the last level we need exactly L elements, we traverse the sorted array A from left to right selecting B elements and then skipping the next, then taking the B following, then skipping the next and so on, until we select L elements. This way we build the L/B blocks (i.e. nodes) for the last level. It is possible that the last block selected this way remain half empty, we pad with ∞ in that case. Selected elements must be removed from the array.

For the next level the procedure is the same, we scan the remaining array left to right and select blocks of B consecutive elements, than skip the following one and continue, we continue until the end of the array. The procedure is exactly the same for each level until the root, for which we put the remaining B elements.

We number the nodes of the obtained tree level by level, from root to leaves, and left to right. We use this numbering for storing the tree in implicit way (as is usual for heap data structure), with the advantage that pointers are not needed this way. Since we don't use pointers, we must show, given the index of an element, how to find the node which it belongs to and the indexes of the children of the node.

The first problem is trivial: since the number of elements in each node is exactly the block size, the node containing the element at index i is the n-th, with $n = \lfloor i/B \rfloor$ i.e. the block containing i. In the following we call i the index of the element and n the index of the node containing the element.

The problem of finding the children of a given node can be solved in a very elegant way. It comes out that the children of the node n are the nodes $kn + 1$, $kn + 2$, $kn + 3$... $kn + k$. The idea is the following.

Consider that the numbering is such that the index of a node is the number of nodes preceding it in a level by level scan. We call $prec$ the set of preceding nodes of our node n. You can see that multiplying the index by k is equal to taking as number of preceding nodes the number of all the children of the nodes in $prec$, this way we loose the root, but we reach exactly the first child of n. This is because we have the same elements that are in $prec$, all but the root, plus the whole level of n, plus k nodes for each node at the left side of n (see figure 2). We add 1 for the root and we are done.

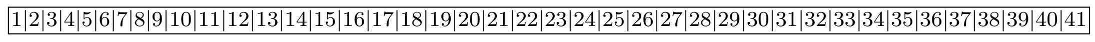
Note that we can do this because the tree is complete. Since we want the indexes of the first element of those nodes we have to multiply those numbers by B, obtaining: $B(kn + 1)$ for the first child, $B(kn + 2)$ for the second, $B(kn + 3)$ for the third etc, until $B(kn + k)$ for the k-th child.

The way we traverse the tree for finding an element e is the usual one.

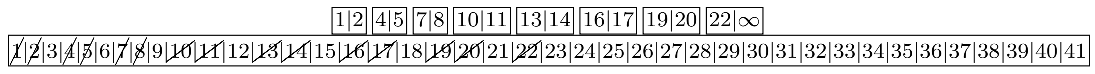
```
function FIND(e)
    $n \leftarrow 0$                                                    ▷ we start from the root
    while $n < sizeofthearray$ do
        load the block in position $n$
        if $e$ is in the block in position $j$ then
            return $n + j$
        else
            find the position $j$ of the first element in the block grater than $e$, if none $j = B + 1$
            $n \leftarrow B * (k * n + j)$
        end if
    end while
    return $-1$
end function
```

The cost of searching is of course $O(\log_B N)$ because at each iteration we divide the tree in which we search by B. The data structure we build occupy exactly the same number of block occupied by A the original array, i.e. $\lceil (N/B) \rceil$ since we store each value only once and all block but one are completely full.

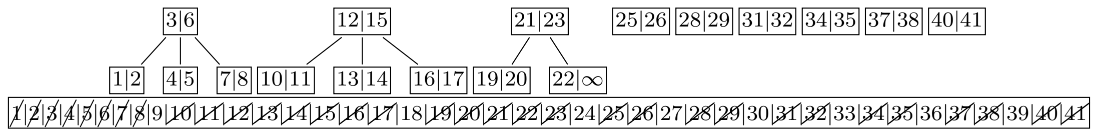
What remain is to discuss the I/O complexity of the construction phase and to show that it doesn't need more than $O(N/B)$ auxiliary storage. For each level of the tree, while building it we must scan the array of remaining elements A block by block, one block is sufficient for this in main memory since when we pass to the next block we don't need the old anymore. We also build the node of each level of the tree in order, from left to right, then we need one block of memory for this, when the node is complete we store it in external memory and start building the next. While building the node of a given level of the tree we also build the new A array for the next iteration, inserting the unused element of the actual A; also this array is build left to right one block at the time, so it require only one block. The procedure require memory size $M \geq 3B + O(1)$.



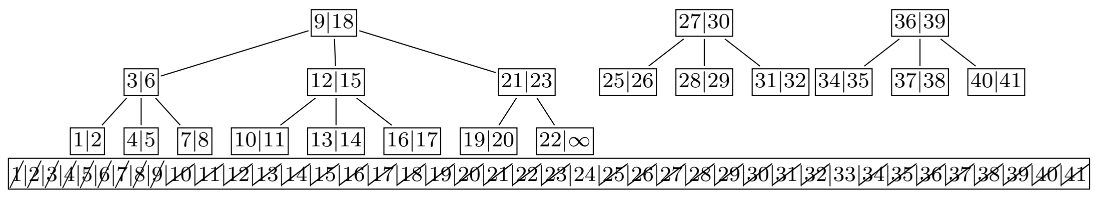
(a) nodes $N = 41$, $B = 2$, $k = 3$, $h = 3$, $L = 15$



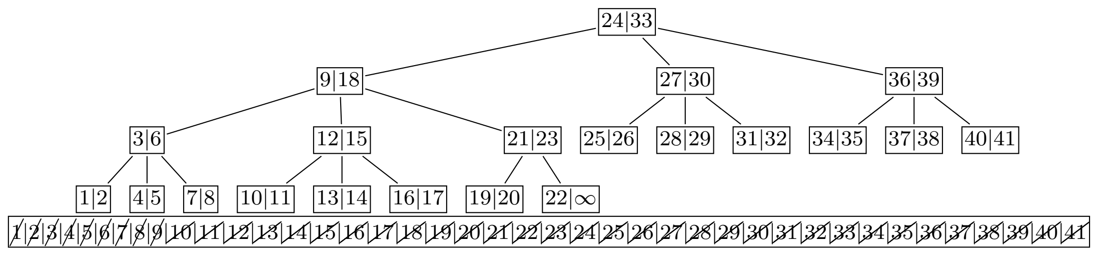
(b) level $i = 3$



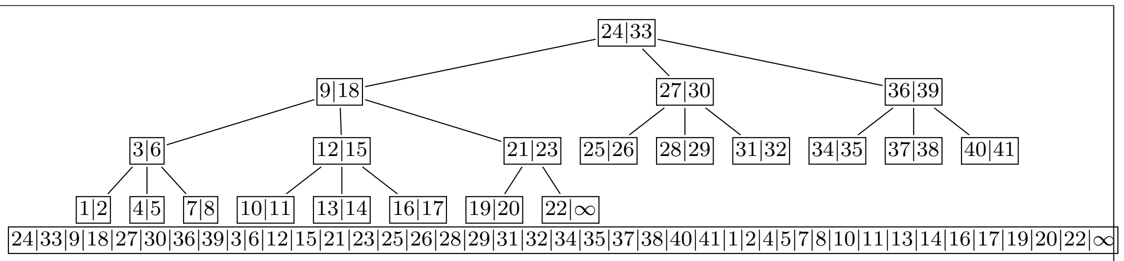
(c) level $i = 2$



(d) level $i = 1$

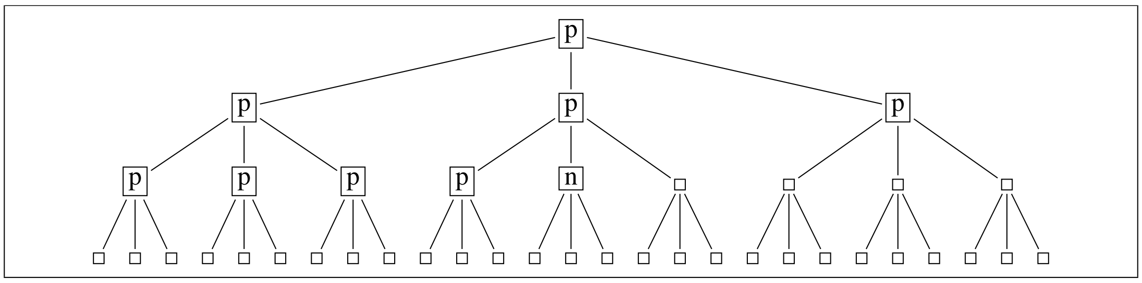


(e) level $i = 0$

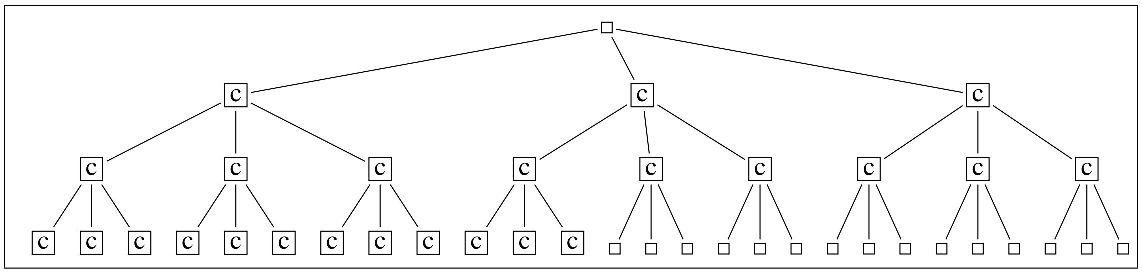


(f) implicit tree representation

Figure 1: tree construction



(a) given node is n, p are elements of prec



(b) given node is n, c are children of elements of prec

Figure 2: number of nodes preceding the children of node n

Note that even if we don't build the nodes of the tree in the exact order we have to store them, for every node, when we build it, we know exactly where to place it since we know the level and the number of previous node in the level. Then we can transform the sorted array A in the implicit tree version without storing in external memory any intermediate form. In external memory we need extra $\lceil N/B \rceil$ blocks for containing the tree we are building (additional with respect to the $\lceil N/B \rceil$ that we need for the original A and that we can continue to use for the array of remaining elements). At the end of the building we remove the space reserved for A and we remain with exactly $\lceil N/B \rceil$.

The I/O cost of the construction phase is then the cost of the creation of the k-ary search tree. For each level we read from memory what remain of the array A and write the exact same number of block in external memory in the form of nodes of the tree or in the form of the new remaining array A.

So the total cost is two times the sum of the length of A divided by the size of the block, for each level. The first iteration is somehow nonstandard, but for all the others we have that the dimension of A decrease and become exactly $|A|/k^i$ (where we indicate the length of A as $|A| = \lceil N/B \rceil$ and i is the depth of a generic level in the tree). We take $\lceil N/B \rceil$ as an upper bound of the cost of the first iteration. Knowing that the length of A at the beginning of the second iteration is less or equal than N, and that we stop the algorithm when $|A| \leq B$ the total I/O cost is less or equal than

$$\lceil N/B \rceil + 2 \times \sum_{i=0}^{\infty} \frac{N}{Bk^i} = \lceil N/B \rceil + 2N/B \times \sum_{i=0}^{\infty} \frac{1}{k^i} = \lceil N/B \rceil + 2N/B \times \frac{k}{k-1}$$

The last step is given by the rules of geometric series, if x is between 0 and 1 then $\sum_{t=0}^{\infty} x^t = \frac{1}{1-x}$. For concluding, if $k \geq 2$ then the I/O complexity is less or equal than $5N/B$.

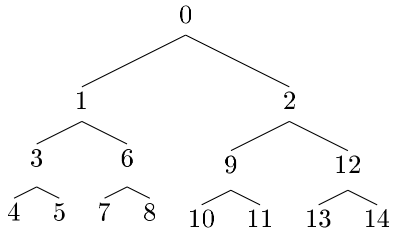
Implicit navigation in vEB layout

Consider $N = 2h - 1$ keys where h is a power of 2, and the implicit cache-oblivious vEB layout of their corresponding complete binary tree, where the keys are suitably permuted and stored in an array of length N without using pointers (as it happens in the classical implicit binary heap but the rule here is different). The root is in the first position of the array. Find a rule that, given the position of the current node, it is possible to locate in the array the positions of its left and right children. Discuss how to apply this layout to obtain (a) a static binary search tree and (b) a heap data structure, discussing the cache complexity

SOLUTION

Assumptions

Suppose you have a binary vEB tree T stored in an array `T[]` in external memory, as seen in class, ordered as in the tree's induced "fractal" numbering, starting from 0:



This is the same order in which elements are stored in `T[]`

Let the tree be complete and let its height, `H`, be a power of two. Also suppose you can store `H` locally.

N.B. In the code that follows, all division signs (/) represent integer division (div).

ZoomSequence

The following function generates a sequence zs of indexes of *nested* subtrees of T that uniquely identifies the position of node `target` in both T and `T[]`.

Starting from T, the decomposition will split a generic binary vEB tree A of height h into a *top tree* of index 0 and height $\frac{h}{2}$ and $2^{\frac{h}{2}}$ *bottom trees* (two per leaf of the top tree) of indexes $1 \ldots 2^{\frac{h}{2}}$ and again height $2^{\frac{h}{2}}$.

An element zs_i will thus correspond to the index of a subtree of height $2^{\frac{H}{2^{i+1}}}$, nested into the subtree identified by zs_{i-1} (or T for zs_0).

Note that the sequence zs contains exactly $log_2(H)$ entries.

```
ZoomSequence(target, H)
  let zs = Sequence.Empty; /* empty ordered list, first element will have index 0 */
  let h = H, i = target, blocksize = 0;
  while (h > 1)
    blocksize = 2^(h/2) -1;
    zs.Enqueue(i/blocksize);
    i = i mod blocksize;
    h = h/2;
  end
  return zs;
end
```

Note that this requires no accesses to the tree, generating no cachefaults.

GetChildren

The following (absolutely horrific...) function returns the *tree node* indexes of the left and right children of tree node `i`. These can be fed to `GetElement` to obtain the contents of the actual nodes.

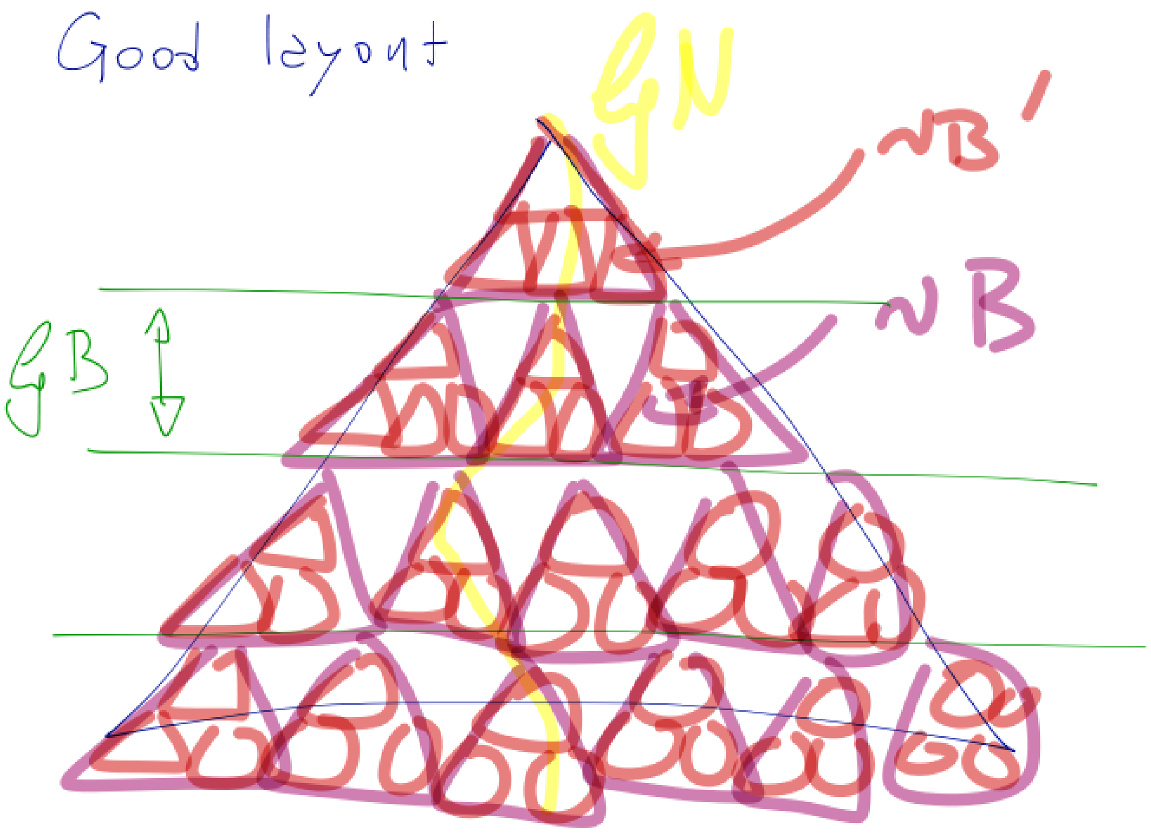
The basic idea is to traverse zs looking for the largest j such that $zs_j = 0$, which identifies the biggest vEB subtree that i is a leaf of (it is T if there is no such j, which means i has no children).

Then it is a matter of going up one level from that, and moving ahead by an appropriate amount of subtrees of height $\frac{H}{2^{j+1}}$.

```
GetChildren(i)
  if (i mod 3 = 0) then /* subtrees of height 2 are stored consecutively */
    return <i+1, i+2>; /* note that such children nodes necessarily exist
      because T is a complete tree */
  end
  let zs = ZoomSequence(i, H);
  let idx0 = zs.FirstIndexOf(0);  /* index of the first occurrence of 0 in zs
    or -1 if no such element exists */
  if (idx0 = -1) then /* i is a leaf of T, so it has no children */
    return <-1, -1>
  end
  /* from here on out we're sure we're not a leaf of T itself */
  let h = H, blocksize = 0;
  let k = H/2^(idx0+1); /* height of the biggest tree i is a leaf of */
  let off = 0; /* will be the index of the root of the tree immediately
    encompassing the biggest tree i is a leaf of */
  for i = 0 to idx0-1 do
    blocksize = 2^(h/2)-1;
    off = off + zs.Get(i)*blocksize;
    h = h/2;
  end
  h = H;
  let leafidx = 0; /* leafidx will be s.t. i is the leafidx-th leaf
    of the tree of height k, starting from 0 */
  for i = idx0+1 to zs.Length do /* stuff following last zero element in zs */
    leafidx = (zs.Get(i)-1);
    h = h/2;
  end
  let left = off + (2^k -1)*(2*leafidx +1); /* 2 children per leaf of top tree
    +1 because of top tree */
  let right = off + (2^k -1)*(2*leafidx +2); /* +2 because of top tree and left child */
  return <left, right>;
end
```

Again, the function never accessed the tree itself, generating no cachefaults.

Binary Search Tree



As is quite evident from Professor Grossi's very excellent picture, given any block size B (which we can reasonably assume to be a power of two), a block will be able to hold a subtree of height $log_2(B)$.

For a binary vEB tree T made up of N nodes, a single lookup will traverse $H = log_2(N)$ nodes. Such nodes residing into blocked memory, we will observe a total of

$$O\left(\frac{log_2(N)}{log_2(B)}\right) = O(log_B(N))$$

cachefaults.

1-D range query

Describe how to efficiently perform one-dimensional range queries for the data structures described in Problems 14 and 15. Given two keys $k_1 \leq k_2$, a range query asks to report all the keys k such that $k_1 \leq k \leq k_2$. Give an analysis of the cost of the proposed algorithm, asking yourself whether it is output-sensitive, namely, it takes $O(log_B N + R/B)$ block transfers where R is the number of reported keys.

SOLUTION

The main idea in this exercise is to exploit the fact that keys at each level are stored sequentially, and they are sorted since we have a binary search tree[1]. Therefore, we can query the two keys k_1, k_2 using a simple binary search, and take all the keys that are in this range. Let's go in details for both data structures.

Problem 14 In this case the tree has been stored in an array, in which every layer of the tree is stored sequentially. For example for a binary tree we have:

$$[root, L_1, R_1, L_{11}, R_{11}, L_{21}, R_{22}, ...]$$

Therefore, the algorithm is going to search simultaneously the two keys k_1, k_2, and thus at each level is going through each layer. Here is going to find two position t_1, t_2 (in the case are not directly the keys) in which the algorithm is going to land, then all the keys we will find in the middle of t_1, t_2 are in the range k_1, k_2.

Problem 15 Here is a bit less intuitive but we exploit the same fact. Ones we have store implicitly the tree we are going to have a recursive layout of the tree, as shown in the picture below.

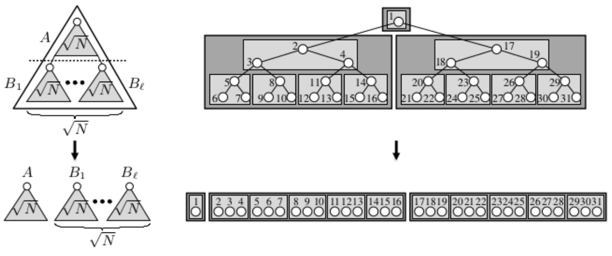


FIG. 2.1. *The van Emde Boas layout. Left: in general; right: of a tree of height 5.*

Therefore at each splitting we are going to land (in the worst case) in two different blocks, and then we get all the keys that are between k_1, k_2 until we reach the keys in them self. At this point we get all the blocks that are in the middle.

Notice that at certain point, in both cases we are going to end up with a sequence of key (R) stored sequentially. Therefore, we are going to have $2log_B N$ access for two binary search and another $O(\frac{R}{B})$ to return the keys.

[1]Notice that in both exercise we have provided a way to access the left and the right child

External memory mergesort

In the external-memory model (hereafter EM model), show how to implement the k-way merge (where $(k+1)B \leq M$), namely, how to simultaneously merge k sorted sequences of total length N, with an I/O cost of $O(N/B)$ where B is the block transfer size. Also, try to minimize and analyze the CPU time cost.

SOLUTION

The classical external sorting algorithm, called merge-sort, consists of two phases:

1. **The sort phase**. M ($k * B$) element are read into the memory, sorted, and written to the disk. This creates $n = \lceil N/M \rceil$ sorted subset of records, called runs, stored in separate auxiliary files, numbered from 1 to n. The runs have all the same number of elements, M, except the last.

2. **The merge phase** consists of multiple merge passes. Since we have $(k+1)B \leq M$ then $k \leq \frac{M}{B} - 1$, hence in RAM we keep k buffer of size B plus one for the output. The merge is done transferring k blocks, of size B, in main memory from the first k runs. Since each run is sorted, we keep the minimum from each run, and we store it to an other block (notice that we delete the element in the input buffer and we create a copy in the output ones). When we full fill the latter block we transfer it in external memory. At the end of a merge pass, the number of runs becomes $n = \lceil n/k \rceil$. A merge pass is repeated until n > 1. Notice that we could add some implementation details such as a counter to keep track of how many element are still in the buffer.

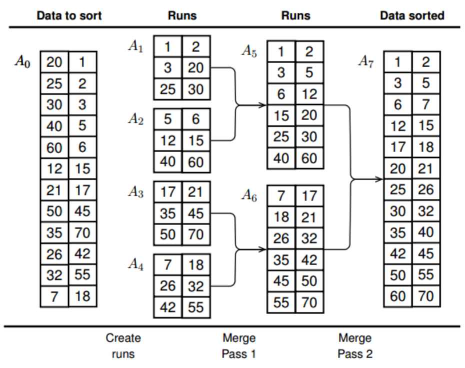


Figure 1: Let us show how to sort the file A_0 containing 12 pages, with file and buffer pages capacity of 2 records[**IT'S AN EXAMPLE** no need to consider the records], B = 3 and 2-merge passes.

- The initial sort phase creates the runs A_1, A_2, A_3 and A_4.
- The first merge pass creates the runs A_5 and A_6 by merging A_1, A_2 and A_3,A_4.
- The second merge pass creates the sorted data A_7 by merging A_5, A_6.

At each iteration of merge we read $\lceil \frac{N}{B} \rceil$ block and the same for the writing. Therefore we have $O(\frac{N}{B})$ I/O operation. So since each merge phase reduce by k the number of runs, we have a total I/O cost equal to $O(\frac{N}{B} + \frac{N}{B} log_{\frac{M}{B}-1}(\frac{N}{B}))$

The bottle neck in CPU cost is to search of the min key in the k runs. Indeed if we do a linear search we pay $O(k)$ at each element, then a total of $O(Nk)$. Instead, if we use an MinHeap (priority queue), we pay $O(log\ k)$ to insert an element in the Heap and O(1) to retrieve the min. To do so we should modified a bit an implementation detail, since each time we insert the head (the currently min element of the block) of each block B. To do so, we insert in the min heap a pair $< key, \#block >$, where key is the value which the heap keep sorted, and $\#block$ keep track which to the position of the element in the block. To keep updated the latter, we set it to B when we upload a new block, and we decrease it each time when we insert an element of the block to heap. This allowed us also to know when we need a new block from the run.

Therefore the total cost in $O(Nlog\ k)$ for each merge phase. Since we have $log_k \frac{N}{B}$ phase we have the following:

$$COST = Nlog(k) * log_k(\frac{N}{B}) = Nlog_(k) * \frac{log_2(\frac{N}{B})}{log_2(k)} = N * log_2(\frac{N}{B}) \in O(Nlog_2 N)$$

External memory (EM) permuting

Given two input arrays A and π, where A contains N elements and π contains a permutation of $\{1, ..., N\}$, describe and analyze an optimal external-memory algorithm for producing an output array C of N elements such that $C[i] = A[\pi[i]]$ for $1 \leq i \leq N$.

SOLUTION

The algorithm is divided in 5 parts:

Pairs$_\pi$ In this phase we create couples $(\pi[i], i)$ for each $0 \leq i \leq N-1$ and we put them in an array called P. To do so we need to read and write all the elements, therefore we pay $O(\frac{N}{B})$ IOs (actually it should be more or less $4\frac{N}{B} + o(1)$).

Sort$_P$ In this phase we sort P in lexicographic order, using a K-way merge sort. This costs $O(sort(N))$ IOs, that is $O(\frac{N}{B} log_B \frac{N}{B})$.

So, let P' be the (sorted) array projected on the second component only. You see this way $\forall i.P'[i] = \pi^{-1}(i)$, that is P' maps the reverse permutation of $\pi : \forall\ 0 \leq i \leq N-1. i \xrightarrow{\pi(i)} x \xrightarrow{P'(x)} i$ (note i and x are indices, not values).

Pairs$_A$ In this phase we create couples $(P'[i], A[i])$ for each $0 \leq i \leq N-1$ and we put them in an array called B. Again, this costs $O(\frac{N}{B})$.

Sort$_B$ In this phase we sort B in lexicographic order. Again, with a K-way merge sort this costs $O(\frac{N}{B} log_B \frac{N}{B})$.

So, let B' be the (sorted) array projected on the second component only. You see this way $\forall\ 0 \leq i \leq N-1. B'[i] = A[\pi[i]]$, that is to say $B' = C$.

Therefore the cost is dominated by (twice) sorting pairs. For completeness we have a simple example:

$$\begin{aligned}
A &= [1, 3, 4, 0, 2] \\
\pi &= [3, 4, 0, 2, 1] \\
P &= [(3, 0), (4, 1), (0, 2), (2, 3), (1, 4)] \\
P' &= [(0, 2), (1, 4), (2, 3), (3, 0), (4, 1)] \\
B &= [(2, 1), (4, 3), (3, 4), (0, 0), (1, 2))] \\
B' &= [(0, 0), (1, 2), (2, 1), (3, 4), (4, 3)] \\
C &= [0, 2, 1, 4, 3]
\end{aligned}$$

Wrong greedy for minimum vertex cove

Find an example of (family of) graphs for which the following greedy approach fails to give a 2-approximation for the minimum vertex cover problem (and prove why this is so). Start out with an empty $\tilde{S}$. Choose each time a vertex v with the largest number of incident edges in the current graph. Add v to $\tilde{S}$ and remove its incident edges. Repeat the process on the resulting graph as long as there are edges in it. Return $|\tilde{S}|$ as the approximation of the minimal size of a vertex cover for the original input graph.

Generalize your argument to show that the above greedy algorithm cannot actually provide an r-approximation for any given constant $r > 1$.

Solution

We will use a partitioned graph $G = (V, E)$. The set of vertices V is divided in two partitions A and B. The graph is such that all the edges connect two vertices one from A and one from B (i.e. we don't allow intra-partition edges).

In this way we can see that the degree of A and B are the same (we define the degree of a set of vertices to be the sum of the degrees of the vertices), they are exactly $|E|$. We name $n = |B|$ and $m = |A|$. Note that if every node is touched by at least one edge (it will be the case for our graph), then one minimum vertex cover is exactly A or B depending on which is the minimum between m and n.

We will build the graph in a way such that the minimum vertex cover is B (i.e. $m > n$), but the greedy algorithm can choose all the nodes of A as minimum vertex cover, and we will show that m can be strictly greater than $2n$ if n is sufficiently large.

The idea is to fix n and then build the graph having m depending somehow on n, such that the m node of A can be chosen by the algorithm.

The construction works this way:

1. set $i = 1$, $A = \{\}$
2. create $\lfloor n/i \rfloor$ new nodes with degree i
3. insert the nodes obtained in A
4. connect each edge of those nodes to a *different* node in B (e.g. with a round robin policy[1])
5. increase i, if it is not greater than n then go to 1. else you are done

Following this construction the following facts are true:

fact 1 At the i-th iteration we add a total number of new edges *less or equal* than n, each one connected to a different node in B.

fatc 2 Since we distribute the edges in a uniform way on the nodes in B, the degree of a node in B at iteration i will be less or equal than i (i.e. for each iteration we add zero or one edge to each node in B)

fact 3 A node created at iteartion i has exactly degree i.

Now let's study what happends when we run the greedy algorithm on the graph obtained in the proposed way.

At the very beginning the graph is the one obtained after the n-th iteration of the construction algorithm. The greedy algorithm will select a node between one of the nodes in B (each of them has degree less or equal than n for **fact2**) or the last node inserted in A, which has degree n exactly (for **fact3**). If the greedy algorithm select this last node from A the algorithm will remove all the edges touching this node (and the node itself) and so each node in B will have its degree

[1]this roundrobin policy is to be considered over the whole execution of the algorithm, i.e. at iteration i we will start connecting the new edges to the node in B "immediatly after" the lastone connected at the $i - 1$ iteration.

decreased by 1. The remaining graph will be the one obtained after the $(n-1)$-th iteration of the construction!

By construction we know that at iteration $n-1$ we have $\lfloor n/n-1 \rfloor$ nodes in A each of which with degree $n-1$. From **fact2** we also know that at the $(n-1)$-th iteration the maximum degree of the nodes in B is *at most* $n-1$.

We are in the same situation of the very beginning and the greedy algorithm can choose again a node in A. This time we can know that the greedy algorithm can choose from A not only one time, but $\lfloor n/n-1 \rfloor$ times, and choosing all the nodes from A (removing those nodes and edges) will cause the graph to return in the state it was at iteration $n-2$ of the building algorithm.

With the same reasoning of above we can observe that at any iteration of the greedy algorithm the graph will have a node in A which has degree greater or equal than the degree of each node in B, hence legal to be chosen[2].

Therefore the greedy algorithm running on a graph constructed as described above can return $m = |A|$ as approximation of the MVC of that graph, i.e. there exists a sequence of choices that will select all the nodes in A. If $m > 2n$ the result will not be a 2-approximation of MVC. We can see that this happens with $n \geq 6$

Infact we can see that with our construction A will have $m = 6 + \frac{6}{2} + \frac{6}{3} + \lfloor \frac{6}{4} \rfloor + \lfloor \frac{6}{5} \rfloor + 1 = 14$ nodes and so the greedy algorithm can return 14 that is not a 2 approximation of the MVC problem.

Generalization

We want to show that for any $r > 1$ there exist a graph such that the greedy algorithm will not provide an r-approximation running on it.

What we have defined is a sort of class of graph that depends only on the parameter n of nodes in B. We have seen before that for $n = 6$ the graph obtained is not good for a 2-approximation using the greedy algorithm.

We can generalize the solution showing that for any $r > 1$ it is sufficient to take an n big enough to have a graph for which the greedy algorithm can fail in providing a valid r-approximation.

Using our construction algorithm, given n (which is the correct size of the MVC), the number of nodes in A will be

$$m = \sum_{i=1}^{n} \lfloor n/i \rfloor$$

so we want to show that

$$\sum_{i=1}^{n} \lfloor n/i \rfloor > rn$$

We can observe that[3]

$$\sum_{i=1}^{n} \lfloor \frac{n}{i} \rfloor > \sum_{i=1}^{n} (\frac{n}{i} - 1) = n \sum_{i=1}^{n} \frac{1}{i} - n = n(-1 + \sum_{i=1}^{n} \frac{1}{n}) > n(\ln(n+1) - 1) \approx n(\ln(n))$$

Since $nlogn$ grows faster than rn, for any given $r > 1$, there will always be a value of n that cause the greedy algorithm to provide a value $m = \sum_{i=1}^{n} \lfloor n/i \rfloor > rn$ that is not an r-approximation.

[2]of course the greedy algorithm could select a note in B as well, but this will not affect our argument because we are trying to prove that there is a sequence of possible wrong choices.

[3]remember that $\sum_{i=1}^{n} \frac{1}{n}$ is the nth partial sum of the diverging harmonic series, and that it holds

$$\sum_{i=1}^{n} \frac{1}{n} > ln(n+1)$$

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