

# CS240 Algorithm Design and Analysis: Homework #2

Due on October 24, 2017

## Collecting Toys

There are  $n$  types of toys that you wish to collect. Each time you buy a toy, its type is randomly determined from a uniform distribution (i.e., all possible types have equal probabilities). Let  $p_{i,j}$  be the probability that just after you have bought your  $i^{th}$  toy, you have exactly  $j$  toy types in your collection, for  $i \geq 1$  and  $0 \leq j \leq n$ .

- (a) Find a recursive equation of  $p_{i,j}$  in terms of  $p_{i-1,j}$  and  $p_{i-1,j-1}$  for  $i \geq 2$  and  $1 \leq j \leq n$ .
- (b) Describe how the recursion from (a) can be used to calculate  $p_{i,j}$ .

## Knapsack II

Given  $n$  objects and a knapsack, item  $i$  weighs  $w_i > 0$  kilograms and has value  $v_i$  where  $n > v_i > 0$ . The knapsack has capacity of  $W$  kilograms. The numbers  $n, v_i$  are integers and  $w_i, W$  are real numbers. What is the maximum total value of items that we can fill the knapsack with? Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n^3)$ .

## Counting Friends

There are  $n$  students and each student  $i$  has 2 scores  $x_i, y_i$ . Students  $i, j$  are friends if and only if  $x_i < x_j$  and  $y_i > y_j$ . How many friends are there? Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n \log n)$  time.

## XOR Convolution

Given two arrays  $A = a_0, a_1, \dots, a_{n-1}$  and  $B = b_0, b_1, \dots, b_{n-1}$ , return an array  $C = c_0, c_1, \dots, c_{n-1}$  where  $c_i = \sum_{j \oplus k = i} a_j b_k$ . Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n \log n)$  time.

' $\oplus$ ' is the bitwise XOR operator: [https://en.wikipedia.org/wiki/Bitwise\\_operation#XOR](https://en.wikipedia.org/wiki/Bitwise_operation#XOR)

Hint: Define  $x^i \cdot x^j = x^{i \oplus j}$ , and imitate the Karatsuba algorithm.

## DNA Pattern Recognition

There are four possible bases in a DNA sequence: A, G, C, T. Suppose we have two DNA sequences  $S$  and  $P$  with length  $n$  and  $m$  where  $\sqrt{n} < m < n - \sqrt{n}$ . Design an efficient algorithm to find out the minimum number of bases in  $P$  that we have to change so that  $P$  is a substring of  $S$ . For comparison, our algorithm runs in  $\mathcal{O}(n \log n)$  time.

For instance,  $S = \text{"AGCTAGGCTCT"}$ ,  $P = \text{"AAGTCTC"}$ . The answer is 2. We can change  $P$  to "TAGGCTC".

Hint: An application of FFT.

## 2D Inversions

Given an array of 2D pairs  $A = a_0, a_1, \dots, a_{n-1}$  where  $a_i = (x_i, y_i)$ , define  $a_i > a_j$  as  $x_i > x_j$  and  $y_i > y_j$ .

(a) How many half-inversions are there?  $a_i$  and  $a_j$  are half-inverted if  $i < j$ ,  $x_i > x_j$  and  $y_i \geq y' > y_j$  where  $y'$  is a fixed constant. Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n \log n)$  time.

(b) How many cross-inversions are there?  $a_i$  and  $a_j$  are cross-inverted if  $i < i' \leq j$  and  $a_i > a_j$  where  $i'$  is a fixed constant. Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n \log n)$  time.

(c) How many inversions are there?  $a_i$  and  $a_j$  are inverted if  $i < j$  and  $a_i > a_j$ . Design an efficient algorithm. For comparison, our algorithm runs in  $\mathcal{O}(n \log^2 n)$  time.