2.3 Problem 3

Step 1

Genetic Linkage Map

In this problem you are given 10 different tests for the proposed problem in 10 different tabs. You should submit only answers in plain text format. Depending on the quality of your answer you will be given some fraction of points on the corresponding test (the exact formulas are given for each test in the corresponding step). Note, that in first 3 tests your solution should be exact, otherwise, none of the points will be awarded.

The points are distributed as follows: for tests 1-3 we give 100 points each, for tests 4-9 we give 200 points each and for test 10 we give 300 points. There is no limit on time nor memory. You are only limited by the performance of your computer and the duration of the contest.

All tests are artificially generated. The generation method is described in the problem description.

You can download an archive as two-part zip-archive using the following two links:
https://stepik.org/media/attachments/lesson/40779/tests.zip.001
https://stepik.org/media/attachments/lesson/40779/tests.zip.002

Step 2

Genetic Linkage Map

In this problem your task will be to restore genetic map from genetic linkage experiments data.

Here we consider a diploid organism. The organism contains two sets of homologous chromosomes, where chromosomes in a homolohous pair contain the same set of genes in the same positions. In this problem a simplified case is considered where each gene on each chromosome can be present as one of the two alleles: either dominant or reccessive. For a gene *A* a capital letter *A* denotes the dominant allele and a small letter *a* denotes a recessive one. How a gene will translate to phenotype depends on which alleles of this gene are present in the genome. If at least one of the chromosomes contain a dominant allele for a gene then there will be one phenotypic trait, and if both genes are present in the reccessive form there will be another phenotypic trait. Before sequencing technologies appeared, only phenotipic traits could be observed, from which the genotype — which alleles a present in the genome — can be inferred only partially.

To restore a genetic map of genes relative location we will do crossing experiments. Let us consider a so-called F1 generation obtained by crossing two pure lines of only dominant alleles and only recessive allels for two genes A and B: *AABB* and *aabb* cross. All organisms in this generation have identical genotypes *AB/ab*, meaning that one of the chromsomes contains both dominant alleles and the other contains both recessive alleles.

Crossing orgasnisms from F1 generation results in F2 generation. There a crossover process start to manifest itself. At one of the phases of meyosis pairs of chromosomes become co-located and can exchange some of their homologous regions. Then the cell divides into two haploid cells, each containing only one of the chrosomes in pair. An organism from the F2 generation is developed from two haploid cells: one from each parent.

Let us consider genes *A* and *B* from the same type of chromosomes and let us use the following notation:

- *A_B_* — for an organism with dominant phenotypes for both genes A and B.
- *A_bb* — for an organism with a dominant phenotype for gene A and a recessive phenotype for gene B.
- *aaB_* — for an organism with a recessive phenotype for gene A and a dominant phenotype for gene B.
- *aabb* — for an organism with recessive phenotypes for both genes A and B.

The F2 generation may contain organisms of all four types. Organisms *A_bb* и *aaB_* appear beacause of the crossover process. The relative abundances of the organism types depends on how close genes *A* and *B* located on the cromosome. If the genes are far away they are inherited almost indepently and the ratio of *A_B_, A_bb, aaB_, aabb* will be close to 9:3:3:1. If the genes are very close to each orther they will rarely be split and the ratio will be close to 3:0:0:1.

Using a simplified model we generated a number of organisms from the F2 generation for each pair of genes. You task is to restore an order of the genes on the chromosomes using the counts of how many of each organism type appeared.

Description of the simulation

Let us consider a chromosome of length L with $p(A)$ denoting position of gene A (sizes of genes are infinitely small). It was assumed that there is always a gene with position 0 and a gene with position L. A one-point crossover with probability 0.5 is modeled. That means that the probability of crossover between genes A and B is $P_{cross}(A, B) = 0.5 \cdot \frac{|p(B) - p(A)|}{len}$.

For each pair of genes *A* and *B* independently, organisms from the F2 generation were generated according to this model. More precisely:

- With probability $\frac{3}{4} \cdot (1 - P_{cross}(A, B))^2 + P_{cross}(A, B) \cdot (1 - P_{cross}(A, B)) + \frac{1}{2} \cdot P_{cross}(A, B)^2$ an organism *A_B_* is generated. We denote their count as $H_{11,A,B}$.
- With equal probabilities $\frac{1}{2} \cdot (1 - P_{cross}(A, B)) \cdot P_{cross}(A, B) + \frac{1}{4} \cdot P_{cross}(A, B)^2$ organisms *A_bb* and *aaB_* are generated, their counts are $H_{10,A,B}$ и $H_{01,A,B}$ respectively.
- With probability $\frac{1}{4} \cdot (1 - P_{cross}(A, B))^2$ an organism *aabb* is generated, their count is $H_{00,A,B}$.

In this problem your task is to recover the order of genes from the values $H_{00,A,B}, H_{01,A,B}, H_{10,A,B}, H_{11,A,B}$ for each pair of genes. There will be 10 test files with results of 10 simulations of F2 generation. You need to submit 10 files with gene orders.

Input Format

The first line of the input file contains an integer T — a number of different chromosomes in the test. Next goes description of the generation results seperetely for each chromosome.

The description starts with an integer n — a number of the genes on the chromosome. The next n lines contain n numbers each: the values of $H_{00,A,B}$. Genes are numbered from 1 to n, j-th number in i-th line contains value $H_{00,i,j}$. All values $H_{00,i,i}$ are equal to zero. Next, separated by blank lines, in a similar format follow values for $H_{01,A,B}, H_{10,A,B}$ and $H_{11,A,B}$. It is guaranteed that $H_{00,A,B} = H_{00,B,A}, H_{01,A,B} = H_{10,B,A}, H_{11,A,B} = H_{11,B,A}$.

Output Format

Output file should contain T lines. Each line should contain all genes in the order of their positions in the corresponding chromosome separated by spaces.

Examples

Sample Input

```
1
3
0 64 121
64 0 87
121 87 0

0 222 62
211 0 89
52 100 0

0 211 52
222 0 100
62 89 0

0 636 485
636 0 447
485 447 0
```

Sample Output

```
1 2 0
```

Scoring

When the submitted gene ordering is compared with the true ordering a number of inversions is counted, that is a number of pairs of genes *A* and *B* such that gene *A* goes before gene *B* in the true order but *A* goes after *B* in the submission. Moreover, the submitted gene ordering is compared with reverse true ordering. A minimum of the two inversions numbers is selected.

Score for each submission is counted as the average number of inversions for all the chromosomes in the test. Scoring formula for each test is present in the corresponding step.

Step 3

Genetic Linkage Map (Test #1)

Upload your result on the test #1.

Download the test at https://stepik.org/media/attachments/lesson/40779/1.in.zip.

You will receive 100 points if you return exactly correct order of genes for all test cases, otherwise, you will receive 0 points.

To solve this problem please visit https://stepik.org/lesson/40779/step/3

Step 4

Genetic Linkage Map (Test #2)

Upload your result on the test #2.

Download the test at https://stepik.org/media/attachments/lesson/40779/2.in.zip.

You will receive 100 points if you return exactly correct order of genes for all test cases, otherwise, you will receive 0 points.

To solve this problem please visit https://stepik.org/lesson/40779/step/4

Step 5

Genetic Linkage Map (Test #3)

Upload your result on the test #3.

Download the test at https://stepik.org/media/attachments/lesson/40779/3.in.zip.

You will receive 100 points if you return exactly correct order of genes for all test cases, otherwise you will receive 0 points.

To solve this problem please visit https://stepik.org/lesson/40779/step/5

Step 6

Genetic Linkage Map (Test #4)

Upload your result on the test #4.

Download the test at https://stepik.org/media/attachments/lesson/40779/4.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \geq \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \leq ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 170 \cdot (1 - \frac{ANS - C}{B - C}) -$ if $ANS < B$

For this test : $B = 6$.

To solve this problem please visit https://stepik.org/lesson/40779/step/6

Step 7

Genetic Linkage Map (Test #5)

Upload your result on the test #5.

Download the test at https://stepik.org/media/attachments/lesson/40779/5.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \geq \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \leq ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 170 \cdot (1 - \frac{ANS - C}{B - C}) -$ if $C \leq ANS < B$
- $200 -$ otherwise

For this test : $B = 8, C = 2$.

Step 8

Genetic Linkage Map (Test #6)

Upload your result on the test #6.

Download the test at https://stepik.org/media/attachments/lesson/40779/6.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \geq \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \leq ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 170 \cdot (1 - \frac{ANS - C}{B - C}) -$ if $C \leq ANS < B$
- $200 -$ otherwise

For this test : $B = 12, C = 4$.

Step 9

Genetic Linkage Map (Test #7)

Upload your result on the test #7.

Download the test at https://stepik.org/media/attachments/lesson/40779/7.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \geq \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \leq ANS < \frac{1}{4} \cdot n \cdot (n-1)$

- $30 + 170 \cdot (1 - \frac{ANS-C}{B-C}) -$ if $C \le ANS < B$
- $200 -$ otherwise

For this test : $B = 100, C = 15$.

Step 10

Genetic Linkage Map (Test #8)

Upload your result on the test #8.

Download the test at https://stepik.org/media/attachments/lesson/40779/8.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \ge \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \le ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 170 \cdot (1 - \frac{ANS-C}{B-C}) -$ if $C \le ANS < B$
- $200 -$ otherwise

For this test : $B = 160, C = 80$.

Step 11

Genetic Linkage Map (Test #9)

Upload your result on the test #9.

Download the test at https://stepik.org/media/attachments/lesson/40779/9.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \ge \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \le ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 170 \cdot (1 - \frac{ANS-C}{B-C}) -$ if $C \le ANS < B$
- $200 -$ otherwise

For this test : $B = 100, C = 30$.

Genetic Linkage Map (Test #10)

Upload your result on the test #10.

Download the test at https://stepik.org/media/attachments/lesson/40779/10.in.zip.

Let ANS be the mean number of inversions per test case in your answer, then your score will be calculated by the following expression:

- $0 -$ if $ANS \geq \frac{1}{4} \cdot n \cdot (n-1)$, where n is number of genes in each test case
- $30 \cdot (\frac{\frac{1}{4} \cdot n \cdot (n-1) - ANS}{\frac{1}{4} \cdot n \cdot (n-1) - B}) -$ if $B \leq ANS < \frac{1}{4} \cdot n \cdot (n-1)$
- $30 + 270 \cdot (1 - \frac{ANS-C}{B-C}) -$ if $ANS < B$

For this test : $B = 2000$.

To solve this problem please visit https://stepik.org/lesson/40779/step/12