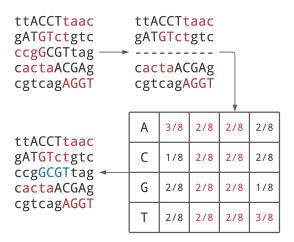
## 2G Implement GibbsSampler

#### Gibbs Sampler Problem

Implement GibbsSampler.

**Input:** A collection of DNA strings *Dna*, and integers *k*, *t*, and *N*.

**Output:** The strings resulting from running GIBBSSAMPLER(Dna, k, t, N) with 20 random starts. Remember to use pseudocounts!



# **Formatting**

**Input:** Space-separated integers k, t, and N, followed by a newline-separated collection of DNA strings Dna.

**Output:** A space-separated list of strings containing the strings resulting from running GIBBSSAMPLER(Dna, k, t, N) with 20 random starts. Remember to use pseudocounts!

#### **Constraints**

- The integer k will be between 1 and  $10^2$ .
- The integer t will be between 1 and  $10^2$ .
- The integer N will be between 1 and  $10^4$ .
- The number of strings in Dna will be between 1 and  $10^2$ .
- The length of each string in Dna will be between 1 and  $10^3$ .
- Each string in *Dna* will be a DNA string.

## **Test Cases**

#### Case 1

**Description:** The sample dataset is not actually run on your code.

## Input:

8 5 100

CGCCCCTCTCGGGGGTGTTCAGTAAACGGCCA GGGCGAGGTATGTGTAAGTGCCAAGGTGCCAG TAGTACCGAGACCGAAAGAAGTATACAGGCGT TAGATCAAGTTTCAGGTGCACGTGCAACC AATCCACCAGCTCCACGTGCAATGTTGGCCTA

### **Output:**

TCTCGGGG CCAAGGTG TACAGGCG TTCAGGTG TCCACGTG

#### Case 2

**Description:** A larger dataset of the same size as that provided by the randomized autograder. Check input/output folders for this dataset.