## **Randomized Motif Search**

**Input**: Integers k and t, followed by a collection of strings Dna. **Output**: A collection BestMotifs resulting from running RandomizedMotifSearch(Dna, k, t) 1,000 times. Remember to use pseudocounts!

# Pseudocode

```
RandomizedMotifSearch(Dna, k, t):

Motifs ← empty list

for each sequence seq in Dna

add randomly selected k-mer from seq to Motifs

BestMotifs ← Motifs

while forever

Profile ← Profile(Motifs)

Motifs ← Motifs(Profile, Dna)

if Score(Motifs) < Score(BestMotifs)

BestMotifs ← Motifs

else

return BestMotifs
```

# **SAMPLE DATASET:**

Input:

8 5

CGCCCCTCTCGGGGGGTGTTCAGTAAACGGCCA GGGCGAGGTATGTGTAAGTGCCAAGGTGCCAG TAGTACCGAGACCGAAAGAAGTATACAGGCGT TAGATCAAGTTTCAGGTGCACGTCGGTGAACC AATCCACCAGCTCCACGTGCAATGTTGGCCTA

Output:

TCTCGGGG

**CCAAGGTG** 

**TACAGGCG** 

**TTCAGGTG** 

**TCCACGTG** 

The sample dataset is not actually run on your code.

# **TEST DATASET 1:**

Input:

68

AATTGGCACATCATTATCGATAACGATTCGCCGCATTGCC
GGTTAACATCGAATAACTGACACCTGCTCTGGCACCGCTC
AATTGGCGGCGGTATAGCCAGATAGTGCCAATAATTTCCT
GGTTAATGGTGAAGTGTGGGTTATGGGGAAAGGCAGACTG
AATTGGACGGCAACTACGGTTACAACGCAGCAAGAATATT
GGTTAACTGTTGTTGCTAACACCGTTAAGCGACGGCAACT
AATTGGCCAACGTAGGCGCGGCTTGGCATCTCGGTGTGTG
GGTTAAAAAGGCGCATCTTACTCTTTTCGCTTTCAAAAAAA

Output:

**CGATAA** 

**GGTTAA** 

**GGTATA** 

**GGTTAA** 

GGTTAC

**GGTTAA** 

**GGCCAA** 

**GGTTAA** 

This dataset checks if your code has an off-by-one error at the beginning of each sequence of Dna. Notice that the some of the motifs of the solution occur at the beginning of their respective sequences in Dna, so if your code did not check the first k-mer in each sequence of Dna, it would not find these sequences.

## **TEST DATASET 2:**

Input:

68

Output:

TTAACC

**ATAACT** 

TTAACC

TGAAGT

TTAACC

TTAAGC

TTAACC

**TGAACA** 

This dataset checks if your code has an off-by-one error at the end of each sequence of Dna. Notice that the some of the motifs of the solution occur at the end of their respective sequences in Dna, so if your code did not check the last k-mer in each sequence of Dna, it would not find these sequences.