

## 2E Implement GreedyMotifSearch with Pseudocounts

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### Greedy Motif Search with Pseudocounts Problem

Implement GreedyMotifSearch with pseudocounts.

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

**Output:** A collection of strings resulting from running GREEDYMOTIFSEARCH( $Dna, k, t$ ) with pseudocounts.

The diagram illustrates the iterative update of a profile matrix during the Greedy Motif Search process. It consists of two tables separated by a right-pointing arrow. The left table shows initial pseudocounts (red values) for four DNA bases (A, C, G, T) across six positions. The right table shows the updated profile (blue values) after one iteration, where the counts have been normalized and adjusted based on the current motif found.

A	6/10	1/10	2/10	0/10	1/10
C	2/10	1/10	4/10	0/10	7/10
G	0/10	0/10	2/10	2/10	0/10
T	2/10	8/10	2/10	8/10	2/10

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A	7/14	2/14	3/14	1/14	2/14
C	3/14	2/14	5/14	1/14	8/14
G	1/14	1/14	3/14	3/14	1/14
T	3/14	9/14	3/14	9/14	3/14

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### Formatting

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

**Output:** A space-separated list of strings containing a collection of strings resulting from running GREEDYMOTIFSEARCH( $Dna, k, t$ ) with pseudocounts (If at any step you find more than one *Profile*-most probable  $k$ -mer in a given string, use the one occurring first).

### Constraints

- The integer  $k$  will be between 1 and  $10^2$ .
- The integer  $t$  will be between 1 and  $10^2$ .
- 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  $10^2$ .
- Each string in  $Dna$  will be a DNA string.

## Test Cases

### Case 1

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

**Input:**

3 5

GGCGTTCAGGCA AAGAATCAGTCA CAAGGAGTCGC CACGTCAATCAC CAATAATATTG

**Output:**

TTC ATC TTC ATC TTC

### Case 2

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**Description:** A larger dataset of the same size as that provided by the randomized autograder.