Aim: In this assignment, given an integer k and a set of DNA sequences we ask to find a k-mer pattern that minimizes Total_Distance(pattern,DNA) over all strings of that length under Hamming distance. We call such a k-mer a median string for a set of DNA sequences.

Input: An integer k and a set of DNA sequences with the same length.

Example (input.txt):

```
6
TAAGTCTATACCATCGTAGTCTAATTAACGTTATGGTAGGAT
ATCAAGGACGGAATGACCGCAGAGGCGACGTTAATGCGCCGT
CAGAGACGCCCTAAAGATTGCGGTAGGGTCCCGTTGTTAAAG
AGACTTGAGTGGGTGCTTGATGGGAGTGTATTAAGGGCATGT
ATAAGTGTTGCTGGGTCTAAGGCATTAAAGCTGAGTCAATAG
TTACATTGCAGATTAACGAGATCTGAAATTAAGGGAGAGATT
CCCAGAGTGGCCTAGTACTTAAGGGCACCCACGCCGCAGGCG
GCCCTACGCCCGTTAATGGTTCGAGTGCTATTCACTAACACA
TTAACGGACGTTTAGTGTGGATTATAGGTGAAGGGTCTGCGC
CACTCCAAGGCAGGGAACATATGTGTTGTTACTATCTTAACG
```

Output: A k-mer v that minimizes $Total\_distance(v,\text{DNA})$ over all k-mers. (If multiple k-mers exist, you may return any of them.)

Example (output.txt): Here is one of the possible answers: TTAACG

Notes:
- Your code must be written by yourself. Sufficient evidence of plagiarism will be treated the same as for plagiarism or cheating.
- Non-compiling submissions will not be evaluated.
- Your code must be complete.
- Do not submit the program binary. You must submit the following items:
    - All of the source files
    - A script to compile the source code and produce the binary (Makefile).
    - A README.txt file that describes how the compilation progress works.
- Submit your answers to Fatma Kahveci at ' fatma.balci@bilkent.edu.tr '.
- Use ' CS481 Assignment-1 ' in the subject line of your e-mail.
- Zip your files and send them in only one zipped file. File name format='surname_name_hw1.zip'
- C / C++ will be used as programming language.
- All submissions must be made by 23:59, October 10, 2017.
- The fastest wins. **Bonus** will be given for the fastest code.