

Biologists use a sequence of letters **A**, **C**, **T**, and **G** to model a genome. A gene is a substring of a genome that starts after a triplet **ATG** and ends before a triplet **TAG**, **TAA**, or **TGA**. Furthermore, the length of a gene string is a multiple of 3 and the gene does not contain any of the triplets **ATG**, **TAG**, **TAA**, and **TGA**. Write a program that reads a text file containing a genome in each line and write all genes in the genome line wise as follows. If no gene is found in the input sequence, displays no gene. File names are given as command line arguments. Here is a sample output:

Input File

```
TTATGTTTTAAGGATGGGGCGTTAGTT
TTATGGGGGTAAGGATGGGGCGTTAGTT
```

Output File

```
Line 1
TTT
GGGCGT
Line 2
GGGGG
GGGCGT
End
```