

# Maxwell Chibuogwu's Bio\_Systems 534 Project

## Finding Open Reading Frames

- NAME

```
orf_finder.py -- Finding the Open Reading Frames (ORFs)
```

- SYNOPSIS

```
orf_finder.py [-h] [-s str] [-m int] [-o outfile] str
```

- DESCRIPTION

This program 'orf\_finder.py' will accept a text(nucleotide) sequence (DNA or RNA) from the command line or a file with sequences. It will then look for potential Open Reading Frames and write them to a named output file in FastA format.

The program will first convert the DNA sequence to RNA. Then, the potential open reading frames would start from the Default 'AUG' codon or any of the specified codons given with '-s' or '--start'. It will also accept a minimum length of ORFs that should be found.

At the end, the ORFs found will be printed in FastA format to a file or to the screen if no 'outfile' is given.

- EXIT STATUS

If no ORFs are found, the program will report 'No ORFs in this sequence'.

- The program should handle a *DNA or RNA sequence* as a text or in a *single file* provided as a positional argument:

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-s | --start: CODON to start reading

-m | --minlength: Minimum ORF length

-o | --outfile: where to write the ORFs

```
$ ./orf_finder.py -h
usage: orf_finder.py [-h]
```

Given no arguments, it should print a short usage statement:

```
$ ./orf_finder.py
usage: orf_finder.py [-h] [-s str] [-m int] [-o outfile] str
orf_finder.py: error: the following arguments are required: str
```

The program should reject a `--minlength` argument less than 20

```
$ ./orf_finder.py input.txt -m 15
usage: orf_finder.py [-h] [-s str] [-m int] [-o outfile] str
orf_finder.py: error: --minlength "15" must be greater than 20.
```