



A toolkit for DNA sequence analysis and manipulation

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Contents

1	Introduction	2
1.1	Installation	2
1.2	License	2
2	FASTQ tools	4
2.1	Program goose-fastq2fasta	5
2.2	Program goose-fastq2mfasta	6
2.3	Program goose-FastqExcludeN	8
2.4	Program goose-FastqInfo	9
2.5	Program goose-FastqMaximumReadSize	10
3	FASTA tools	12
3.1	Program goose-fasta2seq	12
3.2	Program goose-fastaextract	13
3.3	Program goose-fastaextractbyread	14
3.4	Program goose-fastainfo	16
3.5	Program goose-mutatefasta	17
3.6	Program goose-randfastaextrachars	18
4	Genomic sequence tools	21
5	Amino acid sequence tools	22
5.1	Program goose-AminoAcidToGroup	22
5.2	Program goose-ProteinToPseudoDNA	23
6	General purpose tools	26
6.1	Program goose-reverse	26
	Bibliography	27

Chapter 1

Introduction

Recent advances in DNA sequencing have revolutionized the field of genomics, making it possible for research groups to generate large amounts of sequenced data, very rapidly and at substantially lower cost. Its storage have been made using specific file formats, such as FASTQ and FASTA. Therefore, its analysis and manipulation is crucial [?]. Several frameworks for analysis and manipulation emerged, namely **GALAXY** [?], **GATK** [?], **HTSeq** [?], **MEGA** [?], among others. In the majority, these frameworks require licenses and do not provide a low level access to the information, since they are commonly approached by scripting or interfaces.

We describe **GOOSE**, a (free) novel toolkit for analyzing and manipulating FASTA-FASTQ formats and sequences (DNA, amino acids, text), with many complementary tools. The toolkit is for Linux-based systems, built for fast processing. **GOOSE** supports pipes for easy integration. It includes tools for information display, randomizing, edition, conversion, extraction, searching, calculation and visualization. **GOOSE** is prepared to deal with very large datasets, typically in the scale Gigabytes or Terabytes.

The toolkit is a command line version, using the prefix “goose-” followed by the suffix with the respective name of the program. **GOOSE** is implemented in C language and it is available, under GPLv3, at:

```
https://pratas.github.io/goose
```

1.1 Installation

For **GOOSE** installation, run:

```
git clone https://github.com/pratas/goose.git
cd goose/src/
make
```

1.2 License

The license is **GPLv3**. In resume, everyone is permitted to copy and distribute verbatim copies of this license document, but changing it is not allowed. For details on the license, consult: <http://www.gnu.org/>

[licenses/gpl-3.0.html](#).

Chapter 2

FASTQ tools

Current available tools for FASTQ format analysis and manipulation include:

1. `goose-fastq2fasta`: it converts a FASTQ file format to a pseudo FASTA file.
2. `goose-fastq2mfasta`: it converts a FASTQ file format to a pseudo Multi-FASTA file.
3. `goose-fastqclustreads`
4. `goose-FastqExcludeN`: it discards the FASTQ reads with the minimum number of "N" symbols.
5. `goose-FastqExtractQualityScores`
6. `goose-FastqInfo`: it analyses the basic informations of FASTQ file format.
7. `goose-FastqMaximumReadSize`: it filters the FASTQ reads with the length higher than the value defined.
8. `goose-FastqMinimumLocalQualityScoreForward`
9. `goose-FastqMinimumLocalQualityScoreReverse`
10. `goose-FastqMinimumQualityScore`
11. `goose-FastqMinimumReadSize`
12. `goose-count`
13. `goose-extractreadbypattern`
14. `goose-fastqpack`
15. `goose-fastqsimulation`
16. `goose-FastqSplit`
17. `goose-FastqTrimm`

18. `goose-fastqunpack`
19. `goose-filter`
20. `goose-findnpos`
21. `goose-genrandomdna`
22. `goose-getunique`
23. `goose-info`
24. `goose-mfmotifcoords`
25. `goose-mutatefastq`
26. `goose-newlineonnewx`
27. `goose-period`
28. `goose-permuteseqbyblocks`
29. `goose-randfastqextrachars`
30. `goose-real2binthreshold`
31. `goose-reducematrixbythreshold`
32. `goose-renamehumanheaders`
33. `goose-searchphash`
34. `goose-seq2fasta`
35. `goose-seq2fastq`
36. `goose-SequenceToGroupSequence`
37. `goose-splitreads`
38. `goose-wsearch`

2.1 Program `goose-fastq2fasta`

The `goose-fastq2fasta` converts a FASTQ file format to a pseudo FASTA file. However, it does not align the sequence. Also, it extracts the sequence and adds a pseudo header.

For help type:

```
./goose-fastq2fasta -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-fastq2fasta` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTQ file.

The attribution is given according to:

```
Usage: ./goose-fastq2fasta [options] [--] args]
       or: ./goose-fastq2fasta [options]

It converts a FASTQ file format to a pseudo FASTA file.
It does NOT align the sequence.
It extracts the sequence and adds a pseudo header.

    -h, --help                show this help message and exit

Basic options
    < input.fastq             Input FASTQ file format (stdin)
    > output.fasta            Output FASTA file format (stdout)

Example: ./goose-fastq2fasta < input.fastq > output.fasta
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTTCAGGGATACGACGCTTTGTATTTTAAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIII-I)8I
```

Output

The output of the `goose-fastq2fasta` program is a FASTA file.

An example, for the input, is:

```
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGGTTTTCAAATAGA
GTTTCAGGGATACGACGCTTTGTATTTTAAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
```

2.2 Program `goose-fastq2mfasta`

The `goose-fastq2mfasta` converts a FASTQ file format to a pseudo Multi-FASTA file. However, it does not align the sequence. Also, it extracts the sequence and adds a pseudo header.

For help type:

```
./goose-fastq2mfasta -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-fastq2mfasta` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTQ file.

The attribution is given according to:

```
Usage: ./goose-fastq2mfasta [options] [--] args]
       or: ./goose-fastq2mfasta [options]

It converts a FASTQ file format to a pseudo Multi-FASTA file.
It does NOT align the sequence.
It extracts the sequence and adds each header in a Multi-FASTA format.

        -h, --help                show this help message and exit

Basic options
  < input.fastq                  Input FASTQ file format (stdin)
  > output.mfasta                Output Multi-FASTA file format (stdout)

Example: ./goose-fastq2mfasta < input.fastq > output.mfasta
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIII-I)8I
```

Output

The output of the `goose-fastq2mfasta` program is a Multi-FASTA file.

An example, for the input, is:

```
>SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGGTTTTCAAATAGA
>SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
```


2.3 Program goose-FastqExcludeN

The `goose-FastqExcludeN` discards the FASTQ reads with the minimum number of "N" symbols. Also, if present, it will erase the second header (after +).

For help type:

```
./goose-FastqExcludeN -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-FastqExcludeN` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTQ file.

The attribution is given according to:

```
Usage: ./goose-FastqExcludeN [options] [--] args]
or: ./goose-FastqExcludeN [options]

It discards the FASTQ reads with the minimum number of ''N'' symbols. If present,
it will erase the second header (after +).

    -h, --help                show this help message and exit

Basic options
    -m, --max=<int>          The maximum of of "N" symbols in the read
    < input.fastq            Input FASTQ file format (stdin)
    > output                  Output read information (stdout)

Example: ./goose-FastqExcludeN < input.fastq > output

Output example :
<FASTQ filtered reads>
Total reads      : value
Filtered reads   : value
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIII-1)8I
```

Output

The output of the `goose-FastqExcludeN` program is a set of all the filtered FASTQ reads, followed by the execution report.

Using the max value as 5, an example for this input, is:

[illegible]

2.4 Program goose-FastqInfo

The `goose-FastqInfo` analyses the basic informations of FASTQ file format. For help type:

```
./goose-FastqInfo -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-FastqInfo` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTQ file.

The attribution is given according to:

```
Usage: ./goose-FastqInfo [options] [--] args]
      or: ./goose-FastqInfo [options]

It analyses the basic informations of FASTQ file format.

-h, --help                show this help message and exit

Basic options
  < input.fastq           Input FASTQ file format (stdin)
  > output                 Output read information (stdout)

Example: ./goose-FastqInfo < input.fastq > output

Output example :
Total reads      : value
Max read length : value
Min read length : value
Min QS value    : value
Max QS value    : value
QS range        : value
```

An example on such an input file is:

[illegible]

```

@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII>IIIII-I)8I

```

Output

The output of the `goose-FastqInfo` program is a set of informations related with the file readed. An example, for the input, is:

```

Total reads      : 2
Max read length : 72
Min read length : 72
Min QS value     : 41
Max QS value     : 73
QS range        : 33

```

2.5 Program `goose-FastqMaximumReadSize`

The `goose-FastqMaximumReadSize` filters the FASTQ reads with the length higher than the value defined. For help type:

```

./goose-FastqMaximumReadSize -h

```

In the following subsections, we explain the input and output paramters.

Input parameters

The `goose-FastqMaximumReadSize` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTQ file.

The attribution is given according to:

```

Usage: ./goose-FastqMaximumReadSize [options] [--] args]
or: ./goose-FastqMaximumReadSize [options]

It filters the FASTQ reads with the length higher than the value defined.
If present, it will erase the second header (after +).

    -h, --help                show this help message and exit

Basic options
    -s, --size=<int>          The maximum read length
    < input.fastq             Input FASTQ file format (stdin)
    > output                  Output read information (stdout)

Example: ./goose-FastqMaximumReadSize < input.fastq > output

Output example :
<FASTQ filtered reads>

```

```
Total reads      : value
Filtered reads   : value
```

An example on such an input file is:

[illegible]

Output

The output of the `goose-FastqMaximumReadSize` program is a set of all the filtered FASTQ reads, followed by the execution report.

Using the size value as 60, an example for this input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCACCAAGTTACCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
Total reads      : 2
Filtered reads   : 1
```

Chapter 3

FASTA tools

Current available FASTA tools, for analysis and manipulation, are:

1. `goose-fasta2seq`: it converts a FASTA or Multi-FASTA file format to a seq.
2. `goose-fastaextract`: it extracts sequences from a FASTA file, which the range is defined by the user in the parameters.
3. `goose-fastaextractbyread`: it extracts sequences from each read in a Multi-FASTA file (splited by `\n`), which the range is defined by the user in the parameters.
4. `goose-fastainfo`: it shows the readed information of a FASTA or Multi-FASTA file format.
5. `goose-mutatefasta`: it reates a synthetic mutation of a fasta file given specific rates of editions, deletions and additions.
6. `goose-randfastaextrachars`: it substitutes in the DNA sequence the outside ACGT chars by random ACGT symbols.

3.1 Program `goose-fasta2seq`

The `goose-fasta2seq` converts a FASTA or Multi-FASTA file format to a seq.

For help type:

```
./goose-fasta2seq -h
```

In the following subsections, we explain the input and output paramters.

Input parameters

The `goose-fasta2seq` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTA or Multi-FASTA file.

The attribution is given according to:

```
Usage: ./goose-fasta2seq [options] [--] args]
      or: ./goose-fasta2seq [options]

It converts a FASTA or Multi-FASTA file format to a seq.

      -h, --help                show this help message and exit

Basic options
      < input.fasta             Input FASTA or Multi-FASTA file format (stdin)
      > output.seq              Output sequence file (stdout)

Example: ./goose-fasta2seq < input.fasta > output.seq
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCTGACTTTCTCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `goose-fasta2seq` program is a group sequence.

An example, for the input, is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCTGCAAAATAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

3.2 Program `goose-fastaextract`

The `goose-fastaextract` extracts sequences from a FASTA file, which the range is defined by the user in the parameters.

For help type:

```
./goose-fastextract -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-fastextract` program needs two parameters, which defines the begin and the end of the extraction, and two streams for the computation, namely the input and output standard. The input stream is a FASTA file.

The attribution is given according to:

```
Usage: ./goose-fastextract [options] [--] args]
or: ./goose-fastextract [options]

It extracts sequences from a FASTA file.

    -h, --help            show this help message and exit

Basic options
    -i, --init=<int>      The first position to start the extraction (default 0)
    -e, --end=<int>       The last extract position (default 100)
    < input.fasta         Input FASTA or Multi-FASTA file format (stdin)
    > output.seq          Output sequence file (stdout)

Example: ./goose-fastextract -i <init> -e <end> < input.fasta > output.seq
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `goose-fastextract` program is a group sequence.

An example, using the value 0 as extraction starting point and the 50 as the end, for the provided input, is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGG
```

3.3 Program `goose-fastextractbyread`

The `goose-fastextractbyread` extracts sequences from a FASTA or Multi-FASTA file, which the range is defined by the user in the parameters.

For help type:

```
./goose-fastaextractbyread -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-fastaextractbyread` program needs two parameters, which defines the begin and the end of the extraction, and two streams for the computation, namely the input and output standard. The input stream is a FASTA or Multi-FASTA file.

The attribution is given according to:

```
Usage: ./goose-fastaextractbyread [options] [--] args]
or: ./goose-fastaextractbyread [options]

It extracts sequences from each read in a Multi-FASTA file (splited by \n)

    -h, --help                show this help message and exit

Basic options
    -i, --init=<int>          The first position to start the extraction (default 0)
    -e, --end=<int>           The last extract position (default 100)
    < input.fasta             Input FASTA or Multi-FASTA file format (stdin)
    > output.fasta            Output FASTA or Multi-FASTA file format (stdout)

Example: ./goose-fastaextractbyread -i <init> -e <end> < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCCTCGGGGCCACGGCCCTGGAGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCCTCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGT
GGCCCCACCGCGCGGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCAGGCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `goose-fastaextractbyread` program is FASTA or Multi-FASTA file with the extracted sequences.

An example, using the value 0 as extraction starting point and the 50 as the end, for the provided input, is:


```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGG
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCC
```

3.4 Program goose-fastainfo

The `goose-fastainfo` shows the readed information of a FASTA or Multi-FASTA file format. For help type:

```
./goose-fastainfo -h
```

In the following subsections, we explain the input and output paramters.

Input parameters

The `goose-fastainfo` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTA or Multi-FASTA file.

The attribution is given according to:

```
Usage: ./goose-fastainfo [options] [--] args]
or: ./goose-fastainfo [options]

It shows read information of a FASTA or Multi-FASTA file format.

-h, --help          show this help message and exit

Basic options
< input.fasta      Input FASTA or Multi-FASTA file format (stdin)
> output           Output read information (stdout)

Example: ./goose-fastainfo < input.fasta > output

Output example :
Number of reads      : value
Number of bases      : value
MIN of bases in read : value
MAX of bases in read : value
AVG of bases in read : value
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAACCTCACCCATGAATGCTCAGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
```

```

ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCCTGGAGGGT
GGCCCCACCGCGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGTAGTGGACCTCCCAGGCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA

```

Output

The output of the `goose-fastainfo` program is a set of informations related with the file readed. An example, for the input, is:

```

Number of reads      : 2
Number of bases      : 736
MIN of bases in read : 368
MAX of bases in read : 368
AVG of bases in read : 368.0000

```

3.5 Program `goose-mutatefasta`

The `goose-mutatefasta` creates a synthetic mutation of a fasta file given specific rates of editions, deletions and additions. All these paramenters are defined by the user, and their are optional.

For help type:

```
./goose-mutatefasta -h
```

In the following subsections, we explain the input and output paramters.

Input parameters

The `goose-mutatefasta` program needs two streams for the computation, namely the input and output standard. However, optional settings can be supplied too, such as the starting point to the random generator, and the edition, deletion and insertion rates. Also, the user can choose to use the ACGTN alphabet in the synthetic mutation. The input stream is a FASTA or Multi-FASTA File.

The attribution is given according to:

```

Usage: ./goose-mutatefasta [options] [--] args]
       or: ./goose-mutatefasta [options]

Creates a synthetic mutation of a fasta file given specific rates of editions, deletions and additions

-h, --help                show this help message and exit

Basic options
< input.fasta             Input FASTA or Multi-FASTA file format (stdin)
> output.fasta            Output FASTA or Multi-FASTA file format (stdout)

Optional
-s, --seed=<int>          Starting point to the random generator

```

```

-e, --edit-rate=<dbl>      Defines the edition rate (default 0.0)
-d, --deletion-rate=<dbl>  Defines the deletion rate (default 0.0)
-i, --insertion-rate=<dbl> Defines the insertion rate (default 0.0)
-a, --ACGTN-alphabet       When active, the application uses the ACGTN alphabet

```

Example: `./goose-mutatefasta -s <seed> -e <edit rate> -d <deletion rate> -i <insertion rate> -a <input.fasta>`

An example on such an input file is:

```

>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGT
GGCCCCACGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTG
GTGGTTTGAGTGGACCTCCAGGCCAGTGCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCTGCAAA
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA

```

Output

The output of the `goose-mutatefasta` program is a FASTA or Multi-FASTA file with the synthetic mutation of input file.

Using the seed value as 1 and the edition rate as 0.5, an example for this input, is:

```

>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACGCAACGNATTCCTGCTGATCATANTGTNCCGCNCCCCNGCGACGGGGNCTCNCNNGCACACATNGTACCATTGTCCAC
NCTTNCANGTNANCGCTAGCAGGCTACNGTTTNTCCTCNCCATANNCCAANCNGGCGTNNNTACACTGGCACGTGCAGGCA
TNGGTGCGCNGGNNCTCCGGNAACGGCACCGGAGACGAAGCTCGGNGGNTATACAGGTGTCANGAAACATCCCCGCGNC
GNGTGNCNNGAANCCANAGAGTATCTCACTCACAAACCTGCGTGACANTCTAGAGNANGACCTTACNCACCNTCCCNNT
NNGTACCACACCAATGAACGCTGCAGAAAGTCTGTTTNNAGGNGNGCA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ATTTGAAGGCAANCNGNCCAGNAATNCGGNGGGTGCGCTCNTGTNGGCTACGGNCATCGGGCCCTGCTNTANTAAGCN
TGAACCACCGNTCGNNGCACTTAGCAATNGCGNAANCCGTCGGCACGGCGGAGACNAANCCGCTANTNNTTCCCGCTNA
ATGGNTGTACAAGACCNACTANACCANCCCTCCGTCACCACACTGGAGCGCANGATGGNNGCCTGNCAGNAGCNNTGAG
GCGCTCCNTCTANAAANCCGTGGNCGAGCNCCCTATGGNAGNGTGGGGGTTTTACCGGAAGACCNCTCGNGCCCTATGGG
AGCAATCANANCTAGAAAGCTTACNGATGGTGANGAANTAGACTANG

```

3.6 Program `goose-randfastaextrachars`

The `goose-randfastaextrachars` substitutes in the DNA sequence the outside ACGT chars by random ACGT symbols. It works both in FASTA and Multi-FASTA file formats.

For help type:

```
./goose-randfastaextrachars -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-randfastaextrachars` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTA or Multi-FASTA file.

The attribution is given according to:

```
Usage: ./goose-randfastaextrachars [options] [--] args]
      or: ./goose-randfastaextrachars [options]

It substitutes in the DNA sequence the outside ACGT chars by random ACGT symbols.
It works both in FASTA and Multi-FASTA file formats

      -h, --help                show this help message and exit

Basic options
      < input.fasta             Input FASTA or Multi-FASTA file format (stdin)
      > output.fasta            Output FASTA or Multi-FASTA file format (stdout)

Example: ./goose-randfastaextrachars < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ANAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGNCCCTGGAGGGTCCNCCGCTGCCCTGCTGCCATTGNCNCC
NGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCNGGAAGCGGCAGGAA
GNGGTTTGAGTGACCTCCNGGCCCTCATAGGAGAGGAAGCNGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGNC
GCGAATCCGNGCGCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCENN
TAAANNNTACCCATGAATGCTCAGCAANTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
GCGAATCCGNGCGCGGGACAGAATCTCCTTCTCCACCCCCCENNNTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACC
NGCCCCACCTAAGGAAAAGCAGCCTCCAGGAACGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCNGGAAGCGG
ANAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGNCCCTGGCNCAGGGTCCNCCGCTGCCCTGCTGCCATTGN
GAGGAAGCNGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGNCNGGTTTGAGTGACCTCCNGGCCCTCATAGGA
TCACGCAANTTTAATTACAGACCTGAATAAANNNTACCCATGAATGC
```

Output

The output of the `goose-randfastaextrachars` program is a FASTA or Multi-FASTA file.

An example, for the input, is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ATAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCCCGCTGCCCTGCTGCCATTGTCCCC
TGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCGGGAAGCGGCAGGAA
GAGGTTTGAGTGACCTCCCGGCCCTCATAGGAGAGGAAGCCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGTC
GCGAATCCGGGCGCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCTTG
TAAAAGATCACCCATGAATGCTCAGCAAAATTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
GCGAATCCGTGCGCGGGACAGAATCTCCTTCTCCACCCCCCATCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACC
GGCCCCACCTAAGGAAAAGCAGCCTCCAGGAACGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCGGGAAGCGG
AGAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGTCCCTGGCTCCAGGGTCTCCGCTGCCCTGCTGCCATTGC
```

GAGGAAGCGGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGGCGGGTTTGAGTGGACCTCCTGGCCCCCATAGGA
TCACGCAACTTTAATTACAGACCTGAATAAAATGTCACCCATGAATGC

Chapter 4

Genomic sequence tools

Current available genomic sequence tools, for analysis and manipulation, are:

1. `goose-mutatedna`
2. `goose-randseqextrachars`
3. `goose-geco`
4. `goose-gede`

Chapter 5

Amino acid sequence tools

Current available amino acid sequence tools, for analysis and manipulation, are:

1. `goose-AminoAcidToGroup`: it converts an amino acid sequence to a group sequence.
2. `goose-ProteinToPseudoDNA`: it converts an amino acid (protein) sequence to a pseudo DNA sequence.

5.1 Program `goose-AminoAcidToGroup`

The `goose-AminoAcidToGroup` converts an amino acid sequence to a group sequence.

For help type:

```
./goose-AminoAcidToGroup -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-AminoAcidToGroup` program needs two streams for the computation, namely the input and output standard. The input stream is an amino acid sequence. The attribution is given according to:

```
Usage: ./goose-AminoAcidToGroup [options] [--] args]
or: ./goose-AminoAcidToGroup [options]

It converts a amino acid sequence to a group sequence.

    -h, --help                show this help message and exit

Basic options
    < input.prot              Input amino acid sequence file (stdin)
    > output.group            Output group sequence file (stdout)

Example: ./goose-AminoAcidToGroup < input.prot > output.group
Table:
Prot      Group
R         P
```

```

H   P   Amino acids with electric charged side chains: POSITIVE
K   P
-   -
D   N
E   N   Amino acids with electric charged side chains: NEGATIVE
-   -
S   U
T   U
N   U   Amino acids with electric UNCHARGED side chains
Q   U
-   -
C   S
U   S
G   S   Special cases
P   S
-   -
A   H
V   H
I   H
L   H
M   H   Amino acids with hydrophobic side chains
F   H
Y   H
W   H
-   -
*   *   Others
X   X   Unknown

```

It can be used to group amino acids by properties, such as electric charge (positive and negative), uncharged side chains, hydrophobic side chains and special cases. An example on such an input file is:

```

IPFLLKKQFALADKLVL SKLRQLLGGR IKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPN SIG
TLMPKAEVKIGENNEILVRGGMVMKGYKKPEETAQAFTEDGFLKTGDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE

```

Output

The output of the `goose-AminoAcidToGroup` program is a group sequence.

An example, for the input, is:

```

HSHHHPPUHHHHNPHHHUPHPUHHSSPHPHSSSSHPHNSHHSHHHPHHSHUHPHSHSHUNUHUHUSHPNHUHUSUHS
UHHSPhNHPhSNUUNHHHPSSHHHP SHHPPSNNUHUHHUNNSHHPUSNHSNNHNNUSUHHHUNPHPNHHPUUUSPHHHSUH
HNUPHSPNPHHN UHHHHHNNPHPHUHHHHSSHNUNHNNHPUHUHPHPNPHNHHPUUNHHPHHN

```

5.2 Program `goose-ProteinToPseudoDNA`

The `goose-ProteinToPseudoDNA` converts an amino acid (protein) sequence to a pseudo DNA sequence. For help type:


```
./goose-ProteinToPseudoDNA -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-ProteinToPseudoDNA` program needs two streams for the computation, namely the input and output standard. The input stream is an amino acid sequence. The attribution is given according to:

```
Usage: ./goose-ProteinToPseudoDNA [options] [--] args]
       or: ./goose-ProteinToPseudoDNA [options]

It converts a protein sequence to a pseudo DNA sequence.

       -h, --help           show this help message and exit

Basic options
  < input.prot             Input amino acid sequence file (stdin)
  > output.dna             Output DNA sequence file (stdout)

Example: ./goose-ProteinToPseudoDNA < input.prot > output.dna
Table:
Prot    DNA
A      GCA
C      TGC
D      GAC
E      GAG
F      TTT
G      GGC
H      CAT
I      ATC
K      AAA
L      CTG
M      ATG
N      AAC
P      CCG
Q      CAG
R      CGT
S      TCT
T      ACG
V      GTA
W      TGG
Y      TAC
*      TAG
X      GGG
```

It can be used to generate pseudo-DNA with characteristics passed by amino acid (protein) sequences. An example on such an input file is:

```
IPFLLKKQFALADKLVLSKLRQLLGGRICKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPNSIG
TLMPPKAEVKIGENNEILVRGGMVMKGYKKPEETAQAFTEDGFLKTGDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE
```

Output

The output of the `goose-ProteinToPseudoDNA` program is a DNA sequence.

An example, for the input, is:

```
ATCCCGTTTCTGCTGAAAAACAGTTTGC ACTGGCAGACAAACTGGTACTGTCTAAACTGCGTCAGCTGCTGGGCGGCCG
TATCAAAATGATGCCGTGCGGCGGCGCAAACTGGAGCCGGCAATCGGCCTGTTTTTTCATGCAATCGGCATCAACATCA
AACTGGGCTACGGCATGACGGAGACGACGGCAACGGTATCTTGCTGGCATGACTTTCAGTTTAACCCGAACCTCTATCGGC
ACGCTGATGCCGAAAGCAGAGGTAAAAATCGGCGAGAACACGAGATCCTGGTACGTGGCGGCATGGTAATGAAAGGCTA
CTACAAAAAACCGAGGAGACGGCACAGGCATTTACGGAGGACGGCTTTCTGAAACGGGCGACGCAGGCGAGTTTGACG
AGCAGGGCAACCTGTTTATCACGGACCGTATCAAAGAGCTGATGAAAACGTCTAACGGCAAATACATCGCACCGCAGTAC
ATCGAGTCTAAAATCGGCAAAGACAAATTTATCGAGCAGATCGCAATCATCGCAGACGCAAAAAATACGTATCTGCACT
GATCGTACCGTGCTTTGACTCTCTGGAGGAGTACGCAAAACAGCTGAACATCAAATACCATGACCGTCTGGAGCTGCTGA
AAAACTCTGACATCCTGAAAAATGTTTGAG
```

Chapter 6

General purpose tools

1. `goose-comparativemap`
2. `goose-BruteForceString`
3. `goose-char2line`
4. `goose-sum`
5. `goose-min`
6. `goose-minus`
7. `goose-max`
8. `goose-extract`
9. `goose-segment`
10. `goose-reverse`: it reverses the order of a sequence.

6.1 Program `goose-reverse`

The `goose-reverse` reverses the order of a sequence file.

For help type:

```
./goose-reverse -h
```

In the following subsections, we explain the input and output parameters.

Input parameters

The `goose-reverse` program needs two streams for the computation, namely the input and output standard. The input stream is a sequence file.

The attribution is given according to:

```
Usage: ./goose-reverse [options] [--] args]
or: ./goose-reverse [options]

It reverses the order of a sequence file.

-h, --help          show this help message and exit

Basic options
< input.seq         Input sequence file (stdin)
> output.seq         Output sequence file (stdout)

Example: ./goose-reverse < input.seq > output.seq
```

An example on such an input file is:

```
ACAAGACGGCCTCCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGAACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGTGGCCCCACCGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCTCGCTTGGTGGTTTGAGTGGAACCTCCCAGGCCAGTGCCG
GGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCTCTGCAAAATAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

Output

The output of the **goose-reverse** program is a group sequence.

An example, for the input, is:

```
AAGTCCAGACATTAATTTGAACGCACTCGTAAGTACCCACTCCAAAATAAACGTCTCTCTTCCAGAAGGTCTTCTTCA
AGGACGTCCCGTAAGACAGGGCCGCGCCCTAACGACCCCCCACGCGGAAGGACGGCGGACCGGTGGAGGGCTCGAAGG
AGAGGATACTCCCCGGGCGGTGACCGGACCCTCCAGGTGAGTTTGGTGGTTTCGCTCCTTTCAGTCTCCGACGAAAAGGA
ATAAGGACGGCGAAGGACGTATACGAGCGACAGAGCCGGCCACCCCGGTGGGAGGTCCCCGTCCCGTCGCCACCGGCACC
GGGGCCTCTCGTCGTCGTCCTCCGGCCCCCTGTTACCGTAGAACAAAGTCCAGACATTAATTTGAACGCACTCGTAA
GTACCCACTCCAAAATCGACCCCCCACCTCTTCCAGAAGGTCTTCTTCAAGGACGTCCCGAAACGTCTCTAAGACAGG
GCCGCGCGCCTAAGCGCCGTGACCGGACGAAGGACGGCGGACCGGTGGAGGGCTCGAAGGAGAGGATACTCCCCGGGCCT
CCAGGTGAGTTTGGTGAAGGACGGCGAAGGACGTATACGAGCGACAGAGCCGGGTTCGCTCCTTTTCAGTCTCCGACGAA
AAGGAATCCACCCCGGCCCTGTTACCGTCGTCCCGTCGCCACCTGGGAGGTCCCGGCACCGGGGCCTCTCGTCGTCGTC
GTCTCCGGCAGAACA
```