The Genomics Toolkit

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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 [?]. The storage of genomic data is being addressed using specific file formats, such as FASTQ and FASTA. Therefore, its analysis and manipulation is crucial [?]. Many frameworks for analysis and manipulation emerged, namely `GALAXY` [?], `GATK` [?], `HTSeq` [?], `MEGA` [?], among others. Several of these frameworks require licenses, while others do not provide a low level access to the information, since they are commonly approached by scripting or programming laguages not efficient for the purpose. Moreover, several lack on variety, namely the ability to perform multiple tasks using only one toolkit.

We describe `GTO`, a complete toolkit for genomics, namely for FASTA-FASTQ formats and sequences (DNA, amino acids, text), with many complementary tools. The toolkit is for Linux- and Unix-based systems, built for ultra-fast computations. `GTO` supports pipes for easy integration with the sub-programs belonging to `GTO` as well as external tools. `GTO` works as the *LEGOs*, since it allows the construction of multiple pipelines with many combinations.

`GTO` includes tools for information display, randomization, edition, conversion, extraction, search, calculation, and visualization. `GTO` is prepared to deal with very large datasets, typically in the scale Gigabytes or Terabytes (but not limited).

The complete toolkit is an optimized command line version, using the prefix "gto-" followed by the suffix with the respective name of the program. `GTO` is implemented in `C` language and it is available, under the MIT license, at:

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

1.1 Installation

For `GTO` installation, run:

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

```
make
```

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Chapter 2

Amino acid sequence tools

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

1. `gto_amino_acid_to_group`: it converts an amino acid sequence to a group sequence.
2. `gto_amino_acid_to_pseudo_dna`: it converts an amino acid (protein) sequence to a pseudo DNA sequence.

2.1 Program gto_amino_acid_to_group

The `gto_amino_acid_to_group` converts an amino acid sequence to a group sequence.
For help type:

```
./gto_amino_acid_to_group -h
```

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

Input parameters

The `gto_amino_acid_to_group` 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: ./gto_amino_acid_to_group [options] [[--] args]
   or: ./gto_amino_acid_to_group [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: ./gto_amino_acid_to_group < 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:

```
IPFLLKKQFALADKLVLSKLRQLLGGRIKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPNSIG
TLMPKAEVKIGENNEILVRGGMVMKGYYKKPEETAQAFTEDGFLKTGDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE
```

Output

The output of the `gto_amino_acid_to_group` program is a group sequence.
An example, for the input, is:

```
HSHHHPPUHHHHNPHHHUPHPUHHSSPHPHHSSSSHPHNSHHSHHHPHHSHUHPHSHSHUNUUHUHUSHPNHUHUSUUHS
UHHSPHNHPHSNUUNHHHPSSHHHPSHHPPSNNUHUHHUNNSHHPUSNHSNHNNUSUHHHUNPHPNHHPUUUSPHHHSUH
HNUPHSPNPHHNUHHHHHNHPPHHUHHHHSSHNUHNNHHPUHUHPHPNPHNHHPUUNHHPHHN
```

2.2 Program gto_amino_acid_to_pseudo_dna

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

```
./gto_amino_acid_to_pseudo_dna -h
```

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

Input parameters

The `gto_amino_acid_to_pseudo_dna` 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: ./gto_amino_acid_to_pseudo_dna [options] [[--] args]
   or: ./gto_amino_acid_to_pseudo_dna [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: ./gto_amino_acid_to_pseudo_dna < 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:

```
IPFLLKKQFALADKLVLSKLRQLLGGRIKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPNSIG
TLMPKAEVKIGENNEILVRGGMVMKGYYKKPEETAQAFTEDGFLKTGDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE
```

Output

The output of the `gto_amino_acid_to_pseudo_dna` program is a DNA sequence.
An example, for the input, is:

```
ATCCCGTTTCTGCTGAAAAAACAGTTTGCACTGGCAGACAAACTGGTACTGTCTAAACTGCGTCAGCTGCTGGGCGGCCG
TATCAAAATGATGCCGTGCGGCGGCGCAAAACTGGAGCCGGCAATCGGCCTGTTTTTTCATGCAATCGGCATCAACATCA
AACTGGGCTACGGCATGACGGAGACGACGGCAACGGTATCTTGCTGGCATGACTTTCAGTTTAACCCGAACTCTATCGGC
ACGCTGATGCCGAAAGCAGAGGTAAAAATCGGCGAGAACAACGAGATCCTGGTACGTGGCGGCATGGTAATGAAAGGCTA
CTACAAAAAACCGGAGGAGACGGCACAGGCATTTACGGAGGACGGCTTTCTGAAAACGGGCGACGCAGGCGAGTTTGACG
AGCAGGGCAACCTGTTTATCACGGACCGTATCAAAGAGCTGATGAAAACGTCTAACGGCAAATACATCGCACCGCAGTAC
ATCGAGTCTAAAATCGGCAAAGACAAATTTATCGAGCAGATCGCAATCATCGCAGACGCAAAAAAATACGTATCTGCACT
GATCGTACCGTGCTTTGACTCTCTGGAGGAGTACGCAAAACAGCTGAACATCAAATACCATGACCGTCTGGAGCTGCTGA
AAAACTCTGACATCCTGAAAATGTTTGAG
```

Chapter 3

FASTQ tools

Current available tools for FASTQ format analysis and manipulation include:

1. `gto_fastq_to_fasta`: it converts a FASTQ file format to a pseudo FASTA file.
2. `gto_fastq_to_mfasta`: it converts a FASTQ file format to a pseudo Multi-FASTA file.
3. `gto_fastq_exclude_n`: it discards the FASTQ reads with the minimum number of "N" symbols.
4. `gto_fastq_extract_quality_scores`: it extracts all the quality-scores from FASTQ reads.
5. `gto_fastq_info`: it analyses the basic information of FASTQ file format.
6. `gto_fastq_maximum_read_size`: it filters the FASTQ reads with the length higher than the value defined.
7. `gto_fastq_minimum_quality_score`: it discards reads with average quality-score below of the defined.
8. `gto_fastq_minimum_read_size`: it filters the FASTQ reads with the length smaller than the value defined.
9. `gto_fastq_rand_extra_chars`: it substitues in the FASTQ files, the DNA sequence the outside ACGT chars by random ACGT symbols.
10. `gto_fastq_from_seq`: it converts a genomic sequence to pseudo FASTQ file format.
11. `gto_fastq_mutate`: it creates a synthetic mutation of a FASTQ file given specific rates of mutations, deletions and additions.
12. `gto_fastq_split`: it splits Paired End files according to the direction of the strand ('/1' or '/2').
13. `gto_fastq_pack`: it packages each FASTQ read in a single line.
14. `gto_fastq_unpack`: it unpacks the FASTQ reads packaged using the `gto_fastq_pack` tool.

15. `gto_fastq_quality_score_info`: it analyses the quality-scores of a FASTQ file.
16. `gto_fastq_quality_score_min`: it analyses the minimal quality-scores of a FASTQ file.
17. `gto_fastq_quality_score_max`: it analyses the maximal quality-scores of a FASTQ file.
18. `gto_fastq_cut`: it cuts read sequences in a FASTQ file.
19. `gto_fastq_minimum_local_quality_score_forward`: it filters the reads considering the quality score average of a defined window size of bases.
20. `gto_fastq_minimum_local_quality_score_reverse`: it filters the reverse reads, considering the average window size score defined by the bases.

3.1 Program gto_fastq_to_fasta

The `gto_fastq_to_fasta` 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:

```
./gto_fastq_to_fasta -h
```

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

Input parameters

The `gto_fastq_to_fasta` 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: ./gto_fastq_to_fasta [options] [[--] args]
   or: ./gto_fastq_to_fasta [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: ./gto_fastq_to_fasta < 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
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_to_fasta` program a FASTA file.
An example, for the input, is:

```
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
```

3.2 Program gto_fastq_to_mfasta

The `gto_fastq_to_mfasta` onverts 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:

```
./gto_fastq_to_mfasta -h
```

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

Input parameters

The `gto_fastq_to_mfasta` 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: ./gto_fastq_to_mfasta [options] [[--] args]
   or: ./gto_fastq_to_mfasta [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: ./gto_fastq_to_mfasta < 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
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_to_mfasta` program a Multi-FASTA file.
An example, for the input, is:

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

3.3 Program gto_fastq_exclude_n

The `gto_fastq_exclude_n` discards the FASTQ reads with the minimum number of "N" symbols. Also, if present, it will erase the second header (after +).
For help type:

```
./gto_fastq_exclude_n -h
```

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

Input parameters

The `gto_fastq_exclude_n` 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: ./gto_fastq_exclude_n [options] [[--] args]
   or: ./gto_fastq_exclude_n [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.fastq        Output FASTQ file format (stdout)

Example: ./gto_fastq_exclude_n < input.fastq > output.fastq

Console output example :
<FASTQ non-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
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_exclude_n` program is a set of all the filtered FASTQ reads, followed by the execution report. The execution report only appears in the console.
Using the max value as 5, an example for this input, is:

```
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
Total reads    : 2
Filtered reads : 1
```

3.4 Program gto_fastq_extract_quality_scores

The `gto_fastq_extract_quality_scores` extracts all the quality-scores from FASTQ reads.
For help type:

```
./gto_fastq_extract_quality_scores -h
```

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

Input parameters

The `gto_fastq_extract_quality_scores` 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: ./gto_fastq_extract_quality_scores [options] [[--] args]
   or: ./gto_fastq_extract_quality_scores [options]

It extracts all the quality-scores from FASTQ reads.

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

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

Example: ./gto_fastq_extract_quality_scores < input.fastq > output.fastq

Console output example:
<FASTQ quality scores>
Total reads          : value
Total Quality-Scores : value
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_extract_quality_scores` program is a set of all the quality scores from the FASTQ reads, followed by the execution report. The execution report only appears in the console.
An example, for the input, is:

```
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
Total reads          : 2
Total Quality-Scores : 144
```

3.5 Program gto_fastq_info

The `gto_fastq_info` analyses the basic information of FASTQ file format.
For help type:

```
./gto_fastq_info -h
```

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

Input parameters

The `gto_fastq_info` 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: ./gto_fastq_info [options] [[--] args]
   or: ./gto_fastq_info [options]

It analyses the basic information 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: ./gto_fastq_info < 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:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_info` program is a set of information related to the file read.
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
```

3.6 Program gto_fastq_maximum_read_size

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

```
./gto_fastq_maximum_read_size -h
```

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

Input parameters

The `gto_fastq_maximum_read_size` 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: ./gto_fastq_maximum_read_size [options] [[--] args]
   or: ./gto_fastq_maximum_read_size [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.fastq         Output FASTQ file format (stdout)

Example: ./gto_fastq_maximum_read_size -s <size> < input.fastq > output.fastq

Console output example :
<FASTQ non-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=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_maximum_read_size` program is a set of all the filtered FASTQ reads, followed by the execution report. The execution report only appears in the console.
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
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
Total reads    : 2
Filtered reads : 1
```

3.7 Program gto_fastq_minimum_quality_score

The `gto_fastq_minimum_quality_score` discards reads with average quality-score below of the defined. For help type:

```
./gto_fastq_minimum_quality_score -h
```

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

Input parameters

The `gto_fastq_minimum_quality_score` 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: ./gto_fastq_minimum_quality_score [options] [[--] args]
   or: ./gto_fastq_minimum_quality_score [options]

It discards reads with average quality-score below value.

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

Basic options
    -m, --min=<int>        The minimum average quality-score (Value 25 or 30 is commonly used)
    < input.fastq          Input FASTQ file format (stdin)
    > output.fastq         Output FASTQ file format (stdout)

Example: ./gto_fastq_minimum_quality_score -m <min> < input.fastq > output.fastq

Console output example:
<FASTQ non-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
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
```

```
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
54599<>77977==6=?I6IBI::33344235521677999>>><<<<@@A@BBCDGGBFFH>IIIII-I)8I
```

Output

The output of the `gto_fastq_minimum_quality_score` program is a set of all the filtered FASTQ reads, followed by the execution report.
Using the minimum average value as 30, an example for this input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
Total reads    : 2
Filtered reads : 1
```

3.8 Program gto_fastq_minimum_read_size

The `gto_fastq_minimum_read_size` filters the FASTQ reads with the length smaller than the value defined.
For help type:

```
./gto_fastq_minimum_read_size -h
```

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

Input parameters

The `gto_fastq_minimum_read_size` 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: ./gto_fastq_minimum_read_size [options] [[--] args]
   or: ./gto_fastq_minimum_read_size [options]

It filters the FASTQ reads with the length smaller 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 minimum read length
    < input.fastq          Input FASTQ file format (stdin)
    > output.fastq         Output FASTQ file format (stdout)

Example: ./gto_fastq_minimum_read_size -s <size> < input.fastq > output.fastq

Console output example:
<FASTQ non-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=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGG
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_minimum_read_size` program is a set of all the filtered FASTQ reads, followed by the execution report. The execution report only appears in the console.
Using the size value as 65, an example for this input, is:

```
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
Total reads    : 2
Filtered reads : 1
```

3.9 Program gto_fastq_rand_extra_chars

The `gto_fastq_rand_extra_chars` substitues in the FASTQ files, the DNA sequence the outside ACGT chars by random ACGT symbols.
For help type:

```
./gto_fastq_rand_extra_chars -h
```

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

Input parameters

The `gto_fastq_rand_extra_chars` 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: ./gto_fastq_rand_extra_chars [options] [[--] args]
   or: ./gto_fastq_rand_extra_chars [options]

It substitues in the FASTQ files, the DNA sequence the outside ACGT chars by random ACGT symbols.

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

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

Example: ./gto_fastq_rand_extra_chars < input.fastq > output.fastq
```

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
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_rand_extra_chars` program is a FASTQ file.
An example, for the input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GTGTGATGGCCGCTGCCGATGGCGCATAATCCCACCAACATACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGATTGTATTTTAAGAATCTGCAGCAGAAGTCGATGATAATACGCGCCGTTTTATCAG
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

3.10 Program gto_fastq_from_seq

The `gto_fastq_from_seq` converts a genomic sequence to pseudo FASTQ file format.
For help type:

```
./gto_fastq_from_seq -h
```

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

Input parameters

The `gto_fastq_from_seq` program needs two streams for the computation, namely the input and output standard. The input stream is a sequence group file.
The attribution is given according to:

```
Usage: ./gto_fastq_from_seq [options] [[--] args]
   or: ./gto_fastq_from_seq [options]

It converts a genomic sequence to pseudo FASTQ file format.

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

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

Optional options
    -n, --name=<str>       The read's header
    -l, --lineSize=<int>   The maximum of chars for line

Example: ./gto_fastq_from_seq -l <lineSize> -n <name> < input.seq > output.fastq
```

An example on such an input file is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

Output

The output of the `gto_fastq_from_seq` program is a pseudo FASTQ file.

An example, using the size line as 80 and the read's header as "SeqToFastq", for the input, is:

```
@SeqToFastq1
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq2
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq3
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq4
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq5
```

```
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq6
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq7
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq8
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq9
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
+
FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF
@SeqToFastq10
TAATTACAGACCTGAA
+
FFFFFFFFFFFFFFFF
```

3.11 Program gto_fastq_mutate

The `gto_fastq_mutate` creates a synthetic mutation of a FASTQ file given specific rates of mutations, deletions and additions. All these paramenters are defined by the user, and their are optional.
For help type:

```
./gto_fastq_mutate -h
```

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

Input parameters

The `gto_fastq_mutate` 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 FASTQ File.
The attribution is given according to:

```
Usage: ./gto_fastq_mutate [options] [[--] args]
   or: ./gto_fastq_mutate [options]

Creates a synthetic mutation of a FASTQ file given specific rates of mutations,
deletions and additions

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

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

Optional
    -s, --seed=<int>               Starting point to the random generator
    -m, --mutation-rate=<dbl>      Defines the mutation 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: ./gto_fastq_mutate -s <seed> -m <mutation rate> -d <deletion rate> -i
<insertion rate> -a < input.fastq > output.fastq
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_mutate` program is a FASTQ file whith the synthetic mutation of input file. Using the seed value as 1 and the mutation rate as 0.5, an example for this input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGACTTTGAGGTGTGGCGATAGACTGAAAACACTTCAGGGTAAAATCACTCGCAAAAGTGCTATGGTTATGG
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGAGCCTTTACCGTAGGGGTGTAAGATTTTATACAAAAAGTCCAGGTCAAGAGGAATCGGACAACCGA
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

3.12 Program gto_fastq_split

The `gto_fastq_split` splits Paired End files according to the direction of the strand ('/1' or '/2'). It writes by default singleton reads as forward stands.
For help type:

```
./gto_fastq_split -h
```

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

Input parameters

The `gto_fastq_split` program needs a stream for the computation, namely the input standard. The input stream is a FASTQ file.
The attribution is given according to:

```
Usage: ./gto_fastq_split [options] [[--] args]
   or: ./gto_fastq_split [options]

It writes by default singleton reads as forward stands.

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

Basic options
    -f, --forward=<str>    Output forward file
    -r, --reverse=<str>    Output reverse file
    < input.fastq          Input FASTQ file format (stdin)
    > output               Output read information (stdout)

Example: ./gto_fastq_split -t <output_forward.fastq> -r <output_reverse.fastq> < input.fastq > output

Output example :
Total reads      : value
Singleton reads  : value
Forward reads    : value
Reverse reads    : value
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_split` program is a set of information related to the file read.
An example, for the input, is:

```
Total reads     : 2
Singleton reads : 0
Forward reads   : 65536
Reverse reads   : 1
```

Also, this program generates two FASTQ files, with the reverse and forward reads.
An example of the forward reads, for the input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
```

3.13 Program gto_fastq_pack

The `gto_fastq_pack` packages each FASTQ read in a single line. It can show the read score first or the dna sequence, depending on the execution mode.
For help type:

```
./gto_fastq_pack -h
```

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

Input parameters

The `gto_fastq_pack` 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: ./gto_fastq_pack [options] [[--] args]
   or: ./gto_fastq_pack [options]

It packages each FASTQ read in a single line.

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

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

Optional
    -s, --scores           When active, the application show the scores first

Example: ./gto_fastq_pack -s < input.fastq > output.fastq
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_pack` program is a packaged FASTQ file.
An example, for the input, is:

```
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72+ 0
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72+ 1
```

Another example for the same input, but using the scores first (flag "s"), is:

```
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72+ 0
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72+ 1
```

3.14 Program gto_fastq_unpack

The `gto_fastq_unpack` unpacks the FASTQ reads packaged using the `gto_fastq_pack` tool.
For help type:

```
./gto_fastq_unpack -h
```

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

Input parameters

The `gto_fastq_unpack` 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: ./gto_fastq_unpack [options] [[--] args]
   or: ./gto_fastq_unpack [options]

It unpacks the FASTQ reads packaged using the gto_fastq_pack tool.

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

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

Optional
    -s, --scores           When active, the application show the scores first
```

```
Example: ./gto_fastq_unpack -s < input.fastq > output.fastq
```

An example on such an input file is:

```
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72+ 0
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72+ 1
```

Output

The output of the `gto_fastq_unpack` program is a packaged FASTQ file.
An example, for the input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

3.15 Program gto_fastq_quality_score_info

The `gto_fastq_quality_score_info` analyses the quality-scores of a FASTQ file.
For help type:

```
./gto_fastq_quality_score_info -h
```

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

Input parameters

The `gto_fastq_quality_score_info` 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: ./gto_fastq_quality_score_info [options] [[--] args]
   or: ./gto_fastq_quality_score_info [options]

It analyses the quality-scores of a FASTQ file.

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

Basic options
```

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

Optional
    -m, --max=<int>        The lenght of the maximum window

Example: ./gto_fastq_quality_score_info -m <max> < 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:

```
@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=72 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+111
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=72 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+222
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_quality_score_info` program is a set of information related to the file read. Using the max window value as 30, an example for this input, is:

```
Total reads     : 2
Max read length : 72
Min read length : 72
Min QS value    : 41
Max QS value    : 73
QS range        : 33
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73
```

3.16 Program gto_fastq_quality_score_max

The `gto_fastq_quality_score_max` analyses the maximal quality-scores of a FASTQ file.
For help type:

```
./gto_fastq_quality_score_max -h
```

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

Input parameters

The `gto_fastq_quality_score_max` 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: ./gto_fastq_quality_score_max [options] [[--] args]
   or: ./gto_fastq_quality_score_max [options]

It analyses the maximal quality-scores of a FASTQ file.

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

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

Optional
    -m, --max=<int>        The maximum window length (default 40)

Example: ./gto_fastq_quality_score_max -m <max> < input.fastq > output
```

An example on such an input file is:

```
@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=72 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIII9IG9ICIIIIIIIIIIIABAAABCIIIIFFGIIAACBBIIIII6IBIIIIIII>IIIIII/
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=72 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIABAAABCIIIIFFGIIAACBBIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_quality_score_max` program is a set of information related to the file read, considering the maximal quality scores.
Using the max window value as 30, an example for this input, is:

```
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
73 73 73 73 73 73 73 73 73 73 73 73 66 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73
```

3.17 Program gto_fastq_quality_score_min

The `gto_fastq_quality_score_min` analyses the minimal quality-scores of a FASTQ file.
For help type:

```
./gto_fastq_quality_score_min -h
```

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

Input parameters

The `gto_fastq_quality_score_min` 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: ./gto_fastq_quality_score_min [options] [[--] args]
   or: ./gto_fastq_quality_score_min [options]

It analyses the minimal quality-scores of a FASTQ file.

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

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

Optional
    -m, --max=<int>        The maximum window length (default 40)

Example: ./gto_fastq_quality_score_min -m <max> < input.fastq > output
```

An example on such an input file is:

```
@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=72 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGGTTNTCAAATAGA
+
IIIIIIIIIIII9IG9ICIIIIIIIIIIIABAAABCIIIIFFGIIAACBBIIIII6IBIIIIIII>IIIIII/
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=72 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCGNCGTTTTATCAN
+
IIIIIIIABAAABCIIIIFFGIIAACBBIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_quality_score_min` program is a set of information related to the file read, considering the minimum quality scores.
Using the max window value as 30, an example for this input, is:

```
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
73 73 73 73 73 73 73 65 66 65 65 65 57 67 71 57 73 67 70 70 71 73 73 65 65 67 66 66 73 65
```

3.18 Program gto_fastq_cut

The `gto_fastq_cut` cuts read sequences in a FASTQ file. It requires that the initial and end positions for the cut.
For help type:

```
./gto_fastq_cut -h
```

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

Input parameters

The `gto_fastq_cut` program needs 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: ./gto_fastq_cut [options] [[--] args]
   or: ./gto_fastq_cut [options]

It cuts read sequences in a FASTQ file.

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

Basic options
    -i, --initial=<int>   Starting position to the cut
    -e, --end=<int>       Ending position to the cut
    < input.fastq         Input FASTQ file format (stdin)
    > output.fastq        Output FASTQ file format (stdout)

Example: ./gto_fastq_cut -i <initial> -e <end> < input.fastq > output.fastq
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_cut` program is a FASTQ file cut.
Using the initial value as 10 and the end value as 30, an example for this input, is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
CGCTGCCGATGGCGTCAAATC
+
IIIIIIIIIIIIIIIIIII9
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
ACGACGTTTGTATTTTAAGAA
+
IIIIIIIIIIIIIIIIIIII
```

3.19 Program gto_fastq_minimum_local_quality_score_forward

The `gto_fastq_minimum_local_quality_score_forward` filters the reads considering the quality score average of a defined window size of bases.
For help type:

```
./gto_fastq_minimum_local_quality_score_forward -h
```

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

Input parameters

The `gto_fastq_minimum_local_quality_score_forward` program needs 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: ./gto_fastq_minimum_local_quality_score_forward [options] [[--] args]
   or: ./gto_fastq_minimum_local_quality_score_forward [options]

It filters the reads considering the quality score average of a defined window size
of bases.

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

Basic options
    -k, --windowsize=<int>    The window size of bases (default 5)
    -w, --minavg=<int>        The minimum average of quality score (default 25)
    -m, --minqs=<int>         The minimum value of the quality score (default 33)
    < input.fastq             Input FASTQ file format (stdin)
    > output.fastq            Output FASTQ file format (stdout)

Example: ./gto_fastq_minimum_local_quality_score_forward -k <windowsize> -w <minavg>
-m <minqs> < input.fastq > output.fastq

Console output example:
Minimum QS       : value
<FASTQ output>
Total reads      : value
Trimmed reads    : value
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_minimum_local_quality_score_forward` program is a FASTQ file with the reads filtered following a quality score average of a defined window of bases. The execution report only appears in the console.
An example using the default values, for the input, is:

```
Minimum QS     : 33
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTT
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIGII>IIII
Total reads    : 2
Trimmed reads  : 1
```

3.20 Program gto_fastq_minimum_local_quality_score_reverse

The `gto_fastq_minimum_local_quality_score_reverse` filters the reverse reads, considering the quality score average of a defined window size of bases.
For help type:

```
./gto_fastq_minimum_local_quality_score_reverse -h
```

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

Input parameters

The `gto_fastq_minimum_local_quality_score_reverse` program needs 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: ./gto_fastq_minimum_local_quality_score_reverse [options] [[--] args]
   or: ./gto_fastq_minimum_local_quality_score_reverse [options]

It filters the reverse reads, considering the quality score average of a defined
window size of bases.

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

Basic options
    -k, --windowsize=<int>    The window size of bases (default 5)
    -w, --minavg=<int>        The minimum average of quality score (default 25)
    -m, --minqs=<int>         The minimum value of the quality score (default 33)
    < input.fastq             Input FASTQ file format (stdin)
    > output.fastq            Output FASTQ file format (stdout)

Example: ./gto_fastq_minimum_local_quality_score_reverse -k <windowsize> -w <minavg>
-m <minqs> < input.fastq > output.fastq

Console output example:
Minimum QS       : value
<FASTQ output>
Total reads      : value
Trimmed reads    : value
```

An example on such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCGTCGTTTTATCAT
+SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=72
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGII>IIIII-I)8I
```

Output

The output of the `gto_fastq_minimum_local_quality_score_reverse` program is a FASTQ file with the reads filtered following a quality score average of a defined window of bases. The execution report only appears in the console.
An example using the default values, for the input, is:

```
Minimum QS: 33
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=72
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGGTTTTCAAATAGA
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIIIIIII>IIIIII/
Total reads    : 2
Trimmed reads  : 1
```

Chapter 4

FASTA tools

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

1. `gto_fasta_to_seq`: it converts a FASTA or Multi-FASTA file format to a seq.
2. `gto_fasta_from_seq`: it converts a genomic sequence to pseudo FASTA file format.
3. `gto_fasta_extract`: it extracts sequences from a FASTA file, which the range is defined by the user in the parameters.
4. `gto_fasta_extract_by_read`: 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.
5. `gto_fasta_info`: it shows the readed information of a FASTA or Multi-FASTA file format.
6. `gto_fasta_mutate`: it reates a synthetic mutation of a fasta file given specific rates of editions, deletions and additions.
7. `gto_fasta_rand_extra_chars`: it substitues in the DNA sequence the outside ACGT chars by random ACGT symbols.
8. `gto_fasta_extract_read_by_pattern`: it extracts reads from a Multi-FASTA file format given a pattern in the header.
9. `gto_fasta_find_n_pos`: it reports the "N" regions in a sequence or FASTA (seq) file.
10. `gto_fasta_split_reads`: it splits a Multi-FASTA file to multiple FASTA files.
11. `gto_fasta_rename_human_headers`: it changes the headers of FASTA or Multi-FASTA file to simple chrX by order, where X is the number.

4.1 Program gto_fasta_to_seq

The `gto_fasta_to_seq` converts a FASTA or Multi-FASTA file format to a sequence.
For help type:

```
./gto_fasta_to_seq -h
```

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

Input parameters

The `gto_fasta_to_seq` 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: ./gto_fasta_to_seq [options] [[--] args]
   or: ./gto_fasta_to_seq [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: ./gto_fasta_to_seq < input.fasta > output.seq
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_to_seq` program is a group sequence.
An example, for the input, is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
```

```
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

4.2 Program gto_fasta_from_seq

The `gto_fasta_from_seq` converts a genomic sequence to pseudo FASTA file format.
For help type:

```
./gto_fasta_from_seq -h
```

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

Input parameters

The `gto_fasta_from_seq` program needs two streams for the computation, namely the input and output standard. The input stream is a sequence group file.
The attribution is given according to:

```
Usage: ./gto_fasta_from_seq [options] [[--] args]
   or: ./gto_fasta_from_seq [options]

It converts a genomic sequence to pseudo FASTA file format.

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

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

Optional options
    -n, --name=<str>       The read's header
    -l, --lineSize=<int>   The maximum of chars for line

Example: ./gto_fasta_from_seq -l <lineSize> -n <name> < input.seq > output.fasta
```

An example on such an input file is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_from_seq` program is a pseudo FASTA file.
An example, using the size line as 80 and the read's header as "SeqToFasta", for the input, is:

```
>SeqToFasta
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

4.3 Program gto_fasta_extract

The `gto_fasta_extract` extracts sequences from a FASTA file, which the range is defined by the user in the parameters.
For help type:

```
./gto_fasta_extract -h
```

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

Input parameters

The `gto_fasta_extract` program needs two paramenters, 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: ./gto_fasta_extract [options] [[--] args]
   or: ./gto_fasta_extract [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: ./gto_fasta_extract -i <init> -e <end> < input.fasta > output.seq
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_extract` 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
```

4.4 Program gto_fasta_extract_by_read

The `gto_fasta_extract_by_read` extracts sequences from a FASTA or Multi-FASTA file, which the range is defined by the user in the parameters.
For help type:

```
./gto_fasta_extract_by_read -h
```

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

Input parameters

The `gto_fasta_extract_by_read` program needs two paramenters, 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: ./gto_fasta_extract_by_read [options] [[--] args]
   or: ./gto_fasta_extract_by_read [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: ./gto_fasta_extract_by_read -i <init> -e <end> < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_extract_by_read` program is FASTA or Multi-FASTA file wiht 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
```

4.5 Program gto_fasta_info

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

```
./gto_fasta_info -h
```

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

Input parameters

The `gto_fasta_info` 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: ./gto_fasta_info [options] [[--] args]
   or: ./gto_fasta_info [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: ./gto_fasta_info < 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
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_info` program is a set of information related to the file read.
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
```

4.6 Program gto_fasta_mutate

The `gto_fasta_mutate` 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:

```
./gto_fasta_mutate -h
```

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

Input parameters

The `gto_fasta_mutate` 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: ./gto_fasta_mutate [options] [[--] args]
   or: ./gto_fasta_mutate [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: ./gto_fasta_mutate -s <seed> -e <edit rate> -d <deletion rate> -i
<insertion rate> -a < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_mutate` program is a FASTA or Multi-FASTA file whith 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
NCTTNCANGTNANCGCTAGCAGGCTACNGTTTNTCCTCNCCTANNCCAANCNGGCGTNNNTACACTGGCACGTGCAGGCA
TNGGTCGGCNGGNNCCTCCGGNAACGGCACCGGAGACGAAGCTCGGNGGNTATACAGGTGTCANGAAACATCCCCGCGNC
GNGTGNCCNNGAANCCANAGAGTATCTCACTCACAACCCTGCGTGCACNTCTAGAGNANGACCTTACNCACCNTCCCNTT
NNGTACCACACCAATGAACGCTGCAGAAAGTCTGTTTNNAGGNGNGCA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ATTTGAAGGCAANCGGNCCAGNAATNCGGNGGGTGCNGCTCNTGTNGGCTACGGNCATCGCGGCCCTGCTNTANTAAGCN
TGAACCACCGNTCGNNGCACTTAGCAATNGCGNAANCCGTCGGCACGGCGGAGACNAANCCGCTANTNNTTTCCCGCTNA
ATGGNTGTACAAGACCNACTANACCANCCTCCGTCACCACACTGGAGCGCANGATGGNNCGCTGNCTAGNAGNCNNTGAG
GCGCTCCNTCCTANAAANCCGTGGNCGAGCNCCCTATGGNAGNGTGGGGGTTTTACCGGAAGACCNTCGNGCCCTATGGG
AGCAATCANAANCTAGAAAGCTTACNGATGGTGANGAANTAGACTANG
```

4.7 Program gto_fasta_rand_extra_chars

The `gto_fasta_rand_extra_chars` substitues 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:

```
./gto_fasta_rand_extra_chars -h
```

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

Input parameters

The `gto_fasta_rand_extra_chars` 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: ./gto_fasta_rand_extra_chars [options] [[--] args]
   or: ./gto_fasta_rand_extra_chars [options]

It substitues 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: ./gto_fasta_rand_extra_chars < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ANAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGNCCCTGGAGGGTCCNCCGCTGCCCTGCTGCCATTGNCNCC
NGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCNGGAAGCGGCAGGAA
GNGGTTTGAGTGGACCTCCNGGCCCCTCATAGGAGAGGAAGCNNGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGNC
GCGAATCCGNGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCNNN
TAAANNNTCACCCATGAATGCTCACGCAANTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
GCGAATCCGNGCGCCGGGACAGAATCTCCTTCTCCACCCCCCCNNNTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACC
NGCCCCACCTAAGGAAAAGCAGCCTCCAGGAACTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCNGGAAGCGG
ANAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGNCCCTGGCNCCAGGGTCCNCCGCTGCCCTGCTGCCATTGN
GAGGAAGCNNGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGNCGNGGTTTGAGTGGACCTCCNGGCCCCTCATAGGA
TCACGCAANTTTAATTACAGACCTGAATAAANNNTCACCCATGAATGC
```

Output

The output of the `gto_fasta_rand_extra_chars` program is a FASTA or Multi-FASTA file.
An example, for the input, is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ATAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCCCCGCTGCCCTGCTGCCATTGTCCCC
TGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCGGGAAGCGGCAGGAA
GAGGTTTGAGTGGACCTCCCGGCCCCTCATAGGAGAGGAAGCCGGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGTC
GCGAATCCGGGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCTTG
TAAAAGATCACCCATGAATGCTCACGCAAATTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
GCGAATCCGTGCGCCGGGACAGAATCTCCTTCTCCACCCCCCCATCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACC
GGCCCCACCTAAGGAAAAGCAGCCTCCAGGAACTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCGGGAAGCGG
AGAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGTCCCTGGCTCCAGGGTCCTCCGCTGCCCTGCTGCCATTGC
GAGGAAGCGGGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGGCGCGGTTTGAGTGGACCTCCTGGCCCCTCATAGGA
TCACGCAACTTTAATTACAGACCTGAATAAAATGTCACCCATGAATGC
```

4.8 Program gto_fasta_extract_read_by_pattern

The `gto_fasta_extract_read_by_pattern` extracts reads from a Multi-FASTA file format given a pattern in the header. Also, this pattern is case insensitive.
For help type:

```
./gto_fasta_extract_read_by_pattern -h
```

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

Input parameters

The `gto_fasta_extract_read_by_pattern` program needs two streams for the computation, namely the input and output standard. The input stream is a Multi-FASTA file.
The attribution is given according to:

```
Usage: ./gto_fasta_extract_read_by_pattern [options] [[--] args]
   or: ./gto_fasta_extract_read_by_pattern [options]

It extracts reads from a Multi-FASTA file format given a pattern in the header (ID).

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

Basic options
    -p, --pattern=<str>    Pattern to search in the file header
    < input.fasta             Input Multi-FASTA file format (stdin)
    > output.fasta            Output Multi-FASTA file format (stdout)

Example: ./gto_fasta_extract_read_by_pattern -p <pattern> < input.fasta > output.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_extract_read_by_pattern` program is a Multi-FASTA file.
An example, using the pattern "264", for the provided input, is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

4.9 Program gto_fasta_find_n_pos

The `gto_fasta_find_n_pos` reports the "N" regions in a sequence or FASTA (seq) file.
For help type:

```
./gto_fasta_find_n_pos -h
```

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

Input parameters

The `gto_fasta_find_n_pos` program needs two streams for the computation, namely the input and output standard. The input stream is a FASTA file or a sequence.
The attribution is given according to:

```
Usage: ./gto_fasta_find_n_pos [options] [[--] args]
   or: ./gto_fasta_find_n_pos [options]

It reports the 'N' regions in a sequence or FASTA (seq) file.

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

Basic options
    < input.fasta          Input FASTQ file format or a sequence (stdin)
    > output               Output report of 'N' positions (stdout)

Example: ./gto_fasta_find_n_pos < input.fasta > output

The output obeys the following structure:
Begin   End Positions
<value> <value> <value>
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
NCNNNACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GNCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTNGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACNTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAN
```

Output

The output of the `gto_fasta_find_n_pos` program is a structured report of "N" appearances in the sequence or FASTA file. The first column is the first position of the "N" appearance, the second is the position of the last "N" in the interval found, and the last column is the count of "N" in this interval.
An example, for the input, is:

```
1   1   1
3   5   3
82  82  1
163 163 1
289 289 1
```

4.10 Program gto_fasta_split_reads

The `gto_fasta_split_reads` splits a Multi-FASTA file to multiple FASTA files.
For help type:

```
./gto_fasta_split_reads -h
```

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

Input parameters

The `gto_fasta_split_reads` program needs one stream for the computation, namely the input standard. This input stream is a Multi-FASTA file.
The attribution is given according to:

```
Usage: ./gto_fasta_split_reads [options] [[--] args]
   or: ./gto_fasta_split_reads [options]

It splits a Multi-FASTA file to multiple FASTA files.

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

Basic options
    < input.fasta          Input Multi-FASTA file format (stdin)

Optional options
    -l, --location=<str>  Location to store the files

Example: ./gto_fasta_split_reads < input.fasta
```

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_split_reads` program is a report summary of the execution, and the files created in the defined location.
An example, for the input, is:

```
1 : Splitting to file:./out1.fasta
2 : Splitting to file:./out2.fasta
```

4.11 Program gto_fasta_rename_human_headers

The `gto_fasta_rename_human_headers` changes the headers of FASTA or Multi-FASTA file to simple chrX by order, where X is the number.
For help type:

```
./gto_fasta_rename_human_headers -h
```

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

Input parameters

The `gto_fasta_rename_human_headers` 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: ./gto_fasta_rename_human_headers [options] [[--] args]
   or: ./gto_fasta_rename_human_headers [options]

It changes the headers of FASTA or Multi-FASTA file to simple chr$1 by order.

    -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: ./gto_fasta_rename_human_headers < input.fasta > output.fasta
```

An example on such an input file is:

```
> AB000264 | acc = AB000264 | descr = Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
> AB000263 | acc = AB000263 | descr = Homo sapiens mRNA
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Output

The output of the `gto_fasta_rename_human_headers` program is a FASTA or Multi-FASTA file.
An example, for the input, is:

```
>chr1
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>chr2
ACAAGATGCCATTGTCCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

Chapter 5

Genomic sequence tools

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

1. `gto_genomic_gen_random_dna`: it generates a synthetic DNA.
2. `gto_genomic_rand_seq_extra_chars`: it substitues in the DNA sequence the outside ACGT chars by random ACGT symbols.

5.1 Program gto_genomic_gen_random_dna

The `gto_genomic_gen_random_dna` generates a synthetic DNA.
For help type:

```
./gto_genomic_gen_random_dna -h
```

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

Input parameters

The `gto_genomic_gen_random_dna` program needs one stream for the computation, namely the output standard.
The attribution is given according to:

```
Usage: ./gto_genomic_gen_random_dna [options] [[--] args]
   or: ./gto_genomic_gen_random_dna [options]

It generates a synthetic DNA.

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

Basic options
    > output.seq              Output synthetic DNA sequence (stdout)

Optional
    -s, --seed=<int>          Starting point to the random generator (Default 0)
```

```
    -n, --nSymbols=<int>       Number of symbols generated (Default 100)
    -f, --frequency=<str>      The frequency of each base. It should be represented
                               in the following format: <fa,fc,fg,ft>.

Example: ./gto_genomic_gen_random_dna > output.seq
```

Output

The output of the `gto_genomic_gen_random_dna` program is a sequence group file whith the synthetic DNA.
Using the seed value as 1 and the number of symbols as 400, an example of an execution, is:

```
TCTTTACTCGCGCGTTGGAGAAATACAATAGTGCGGCTCTGTCTCCTTATGAAGTCAACAATTTCGCTGGGACTTGCGGC
TCTTTACTCGCGCGTTGGAGAAATACAATAGTGCGGCTCTGTCTCCTTATGAAGTCAACAATTTCGCTGGGACTTGCGGC
GACTTCATCGTGGTCTCTGTCATTATGCGCTCCAACGCATAACTTTGCGCCAGAAGATAGATAGAATGGTGTAAGAAACT
GTAATATATATAATGAACTTCGGCGAGTCTGTGGAGTTTTTGTTGCATTAGAGAGCCAAGAGGTCGGACGTCCTCACGTA
GCCCGAGACGGGCAGGGCGATGGCGACTGAACGGGCTCCATATCACTTTGAGCTTTTATGCTTTCGACTCCTCCAGGAGC
TGAACAACCTTGTTCCCGGCAAAGCCCACTGCGTCATGGAGCTCACGGTCTACATTCATGACTGACTAACCGTAAACTGC
```

5.2 Program gto_genomic_rand_seq_extra_chars

The `gto_genomic_rand_seq_extra_chars` substitues in the DNA sequence the outside ACGT chars by random ACGT symbols. It works in sequence file formats.
For help type:

```
./gto_genomic_rand_seq_extra_chars -h
```

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

Input parameters

The `gto_genomic_rand_seq_extra_chars` 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: ./gto_genomic_rand_seq_extra_chars [options] [[--] args]
   or: ./gto_genomic_rand_seq_extra_chars [options]

It substitues in the DNA sequence the outside ACGT chars by random ACGT symbols.
It works in sequence file formats


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

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

```
Example: ./gto_genomic_rand_seq_extra_chars < input.seq > output.seq
```

An example on such an input file is:

```
ANAAGACGNNNTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
NNCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCNNNNNGGAGAGGAAGCTCGGGAGNGTNNNGGCCAGGCGGCAGNNNNCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TANNNNCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGNNNAAGCAGCCTCCTGACTTTCCTCGCTTGNNNNTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
NNATTACNNNCCTGNN
```

Output

The output of the `gto_genomic_rand_seq_extra_chars` program is a sequence file.
An example, for the input, is:

```
ATAAGACGGCTTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
CTCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCGACCGGGAGAGGAAGCTCGGGAGTGTGTTGGCCAGGCGGCAGGAGACCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAATATCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGCGGAAGCAGCCTCCTGACTTTCCTCGCTTGGTTTTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
CGATTACGGCCCTGTC
```

Chapter 6

General purpose tools

1. `gto_char_to_line`: it splits a sequence into lines, creating an output sequence which has a char for each line.
2. `gto_reverse`: it reverses the order of a sequence.
3. `gto_new_line_on_new_x`: it splits different rows with a new empty row.
4. `gto_upper_bound`: it sets an upper bound in a file with a value per line.
5. `gto_lower_bound`: it sets an lower bound in a file with a value per line.

6.1 Program gto_char_to_line

The `gto_char_to_line` splits a sequence into lines, creating an output sequence which has a char for each line.
For help type:

```
./gto_char_to_line -h
```

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

Input parameters

The `gto_char_to_line` 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: ./gto_char_to_line [options] [[--] args]
   or: ./gto_char_to_line [options]

It splits a sequence into lines, creating an output sequence which has a char for each line.

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

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

Example: ./gto_char_to_line < input.seq > output.seq
```

An example on such an input file is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

Output

The output of the `gto_char_to_line` program is a group sequence splited by \n foreach character.
An example, for the input, is:

```
A
C
A
A
G
A
C
G
G
C
C
T
C
C
T
G
C
T
G
C
T
...
```

6.2 Program gto_reverse

The `gto_reverse` reverses the order of a sequence file.
For help type:

```
./gto_reverse -h
```

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

Input parameters

The `gto_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: ./gto_reverse [options] [[--] args]
   or: ./gto_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: ./gto_reverse < input.seq > output.seq
```

An example on such an input file is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCACCCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCCAGGCCAGTGCCG
GGCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAATAAAACCTCACCCATGAATGCTCACGCAAGTT
TAATTACAGACCTGAA
```

Output

The output of the `gto_reverse` program is a group sequence.
An example, for the input, is:

```
AAGTCCAGACATTAATTTGAACGCACTCGTAAGTACCCACTCCAAAATAAACGTCCTCCTCTTCCAGAAGGTCTTCTTCA
AGGACGTCCCGTAAGACAGGGCCGCGCGCCTAACGACCCCCCCACGCGGAAGGACGGCGGACCGGTGGAGGGCTCGAAGG
AGAGGATACTCCCCGGGCCGTGACCGGACCCTCCAGGTGAGTTTGGTGGTTCGCTCCTTTCAGTCCTCCGACGAAAAGGA
ATAAGGACGGCGAAGGACGTATACGAGCGACAGAGCCGGCCACCCCGGTGGGAGGTCCCCGTCCCGTCGCCACCGGCACC
GGGGCCTCTCGTCGTCGTCGTCCTCCGGCCCCCTGTTACCGTAGAACAAAGTCCAGACATTAATTTGAACGCACTCGTAA
GTACCCACTCCAAAATCGACCCCCCCCACCTCTTCCAGAAGGTCTTCTTCAAGGACGTCCCGAAACGTCCTCTAAGACAGG
GCCGCGCGCCTAAGCGCCGTGACCGGACGAAGGACGGCGGACCGGTGGAGGGCTCGAAGGAGAGGATACTCCCCGGGCCT
CCAGGTGAGTTTGGTGAAGGACGGCGAAGGACGTATACGAGCGACAGAGCCGGGTTCGCTCCTTTCAGTCCTCCGACGAA
AAGGAATCCACCCCGGCCCCTGTTACCGTCGTCCCGTCGCCACCTGGGAGGTCCCGGCACCGGGGCCTCTCGTCGTCGTC
```

```
GTCCTCCGGCAGAACA
```

6.3 Program gto_new_line_on_new_x

The `gto_new_line_on_new_x` splits different rows with a new empty row.
For help type:

```
./gto_new_line_on_new_x -h
```

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

Input parameters

The `gto_new_line_on_new_x` program needs two streams for the computation, namely the input and output standard. The input stream is a matrix file format with 3 columns.
The attribution is given according to:

```
Usage: ./gto_new_line_on_new_x [options] [[--] args]
   or: ./gto_new_line_on_new_x [options]

It splits different rows with a new empty row.

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

Basic options
    < input        Input file with 3 column matrix format (stdin)
    > output       Output file with 3 column matrix format (stdout)

Example: ./gto_new_line_on_new_x < input > output
```

An example on such an input file is:

```
1   2   2
1   2   2
4   4   1
10  12  2
15  15  1
45  47  3
45  47  3
45  47  3
45  47  3
55  55  1
```

Output

The output of the `gto_new_line_on_new_x` program is a 3 column matrix, with an empty line between different rows.
An example, for the input, is:

```
1.000000    2.000000    2.000000
1.000000    2.000000    2.000000

4.000000    4.000000    1.000000

10.000000   12.000000   2.000000

15.000000   15.000000   1.000000

45.000000   47.000000   3.000000
45.000000   47.000000   3.000000
45.000000   47.000000   3.000000
45.000000   47.000000   3.000000

55.000000   55.000000   1.000000
```

6.4 Program gto_upper_bound

The `gto_upper_bound` sets an upper bound in a file with a value per line.
For help type:

```
./gto_upper_bound -h
```

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

Input parameters

The `gto_upper_bound` program needs two streams for the computation, namely the input and output standard. The input stream is a numeric file.
The attribution is given according to:

```
Usage: ./gto_upper_bound [options] [[--] args]
   or: ./gto_upper_bound [options]

It sets an upper bound in a file with a value per line.

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

Basic options
    -u, --upperbound=<int>    The upper bound value
    < input                   Input numeric file (stdin)
    > output                  Output numeric file (stdout)

Example: ./gto_upper_bound -u <upperbound> < input > output
```

An example on such an input file is:

```
0.123
3.432
2.341
1.323
7.538
4.122
0.242
0.654
5.633
```

Output

The output of the `gto_upper_bound` program is a set of numbers truncated at the a defined upper bound. An example, for the input, is:

```
Using upper bound: 4
0.123000
3.432000
2.341000
1.323000
4.000000
4.000000
0.242000
0.654000
4.000000
```

6.5 Program gto_lower_bound

The `gto_lower_bound` sets an lower bound in a file with a value per line.
For help type:

```
./gto_lower_bound -h
```

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

Input parameters

The `gto_lower_bound` program needs two streams for the computation, namely the input and output standard. The input stream is a numeric file.
The attribution is given according to:

```
Usage: ./gto_lower_bound [options] [[--] args]
   or: ./gto_lower_bound [options]

It sets an lower bound in a file with a value per line.

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

```
Basic options
    -u, --lowerbound=<int>     The lower bound value
    < input                    Input numeric file (stdin)
    > output                   Output numeric file (stdout)

Example: ./gto_lower_bound -u <lowerbound> < input > output
```

An example on such an input file is:

```
0.123
3.432
2.341
1.323
7.538
4.122
0.242
0.654
5.633
```

Output

The output of the `gto_lower_bound` program is a set of numbers truncated at the a defined lower bound. An example, for the input, is:

```
Using lower bound: 2
2.000000
3.432000
2.341000
2.000000
7.538000
4.122000
2.000000
2.000000
5.633000
```