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GTO 2: The genomics-proteomics toolkit



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Preface

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¹<https://rmarkdown.rstudio.com>

²<https://bookdown.org>



1

Introduction

Recent advances in DNA sequencing, specifically in next-generation sequencing (NGS), revolutionised the field of genomics, making possible the generation of large amounts of sequencing data very rapidly and at substantially low cost(Mardis, 2017). This new technology also brought with it several challenges, namely in what concerns the analysis, storage, and transmission of the generated sequences(Brouwer et al., 2016, Liu et al. (2012)). As a consequence, several specialised tools were developed throughout the years in order to deal with these challenges.

Firstly, the storage of the raw data generated by NGS experiments is possible by using several file formats, the FASTQ and FASTA are the most commonly used(Zhang, 2016). FASTQ is an extension of the FASTA format, that besides the nucleotide sequence, also stores associated per base quality score and it is considered the standard format for sequencing data storage and exchange(Cock et al., 2009).

Regarding the analysis and manipulation of these sequencing data files many software applications emerged, including **fqtools**(Droop, 2016), **FASTX-Toolkit**(Gordon et al., 2010), **GALAXY**(Afgan et al., 2018), **GATK**(DePristo et al., 2011), **MEGA**(Kumar et al., 2016), **SeqKit**(Shen et al., 2016), among others. **Fqtools** is a suite of tools to view, manipulate and summarise FASTQ data. This software also identifies invalid FASTQ files(Droop, 2016). **GALAXY**, in its turn, is an open, web-based scientific platform for analysing genomic data(Goecks et al., 2010). This platform integrates several specialised sets of tools, e.g. for manipulating FASTQ files(Blankenberg et al., 2010). **FASTX-Toolkit** is a collection of command-line tools to process FASTA and FASTQ files. This toolkit is available in two forms: as a command-line, or integrated into the web-based platform **GALAXY**(Gordon et al., 2010). **SeqKit** is another toolkit used to process FASTA and FASTQ files and is available for all major operating systems(Shen et al., 2016). The Genome Analysis Toolkit (**GATK**) was designed as a structured programming framework

to simplify the development of analysis tools. However, nowadays, it is a suite of tools focused on variant discovering and genotyping (Van der Auwera et al., 2013). More towards the evolutionary perspectives, Molecular Evolutionary Genetics Analysis (**MEGA**) software provides tools to analyse DNA and protein sequences statistically (Tamura et al., 2011). Several of these frameworks lack on variety, namely the ability to perform multiple tasks using only one toolkit.

Compression is another important aspect when dealing with high-throughput sequencing data, as it reduces storage space and accelerates data transmission. A survey on DNA compressors and amino acid sequence compression can be found in (Hosseini et al., 2016). Currently, the DNA sequence compressors HiRGC (Liu et al., 2017), iDoComp (Ochoa et al., 2014), GeCo (Pratas et al., 2016), and GDC (Deorowicz et al., 2015) are considered to have the best performance (Hernaez et al., 2019). Of these four approaches, GeCo is the only one that can be used for reference-free and reference-based compression. Furthermore, GeCo can be used as an analysis tool to determine absolute measures for many distance computations and local measures (Pratas et al., 2016).

Amino acid sequences are known to be very hard to compress (Nalbantoglu et al., 2010), however, Hosseini et al. (Hosseini et al., 2019) recently developed AC, a state-of-the-art for lossless amino acid sequence compression. In (Pratas et al., 2018) the authors compared the performance of AC, in terms of bit-rate, to several general-purpose lossless compressors and several protein compressors, using different proteomes. They concluded that in average AC provides the best bit-rates.

Another relevant subject is genomic data simulation. Read simulations tools are fundamental for the development, testing and evaluation of methods and computational tools (Huang et al., 2011, price2017simulome). Despite the availability of a large number of real sequence reads, read simulation data is necessary due to the inability to know the ground truth of real data (Baruzzo et al., 2017). Escalona et al. (Escalona et al., 2016), recently, reviewed 23 NGS simulation tools. XS (Pratas et al., 2014), a FASTQ read simulation tool, stands out in relation to the other 22 simulation tools because it is the only one that does not need a reference sequence. Furthermore, XS is the only open-source tool for simulation of FASTQ reads produced by the four most

used sequencing machines, Roche-454, Illumina, ABI SOLiD and Ion Torrent.

Although a large number of tools are available for analysing, compressing, and simulation, these tools are specialised in only a specific task. Besides, in many cases the output of one tool cannot be used directly as input for another tool, e.g. the output of a simulation tool cannot always be used directly as input for an analysis tool. Thus, unique software that includes several specialised tools is necessary.

In this document, we describe **GTO2**, a complete toolkit for genomics and proteomics, namely for FASTQ, FASTA and SEQ formats, with many complementary tools. The toolkit is for Unix-based systems, built for ultra-fast computations. **GTO2** supports pipes for easy integration with the sub-programs belonging to **GTO2** as well as external tools. **GTO2** works as **LEGOs**, since it allows the construction of multiple pipelines with many combinations.

GTO2 includes tools for information display, randomisation, edition, conversion, extraction, search, calculation, compression, simulation and visualisation. **GTO2** is prepared to deal with very large datasets, typically in the scale of Gigabytes or Terabytes (but not limited). The complete toolkit is an optimised command-line version, using the prefix `gto2_` followed by the suffix with the respective name of the program. **GTO2** is implemented in **C** language and it is available, under the MIT license, at <https://github.com/cobilab/gto2>

1.1 Installation

To install **GTO2** through the GitHub repository:

```
git clone https://github.com/cobilab/gto2.git
cd gto2/src/
make
```

Or by installing them directly using the Cobilab channel from Conda:

```
conda install -c cobilab gto2 -y
```

1.2 Testing

The examples provided in this document are available in the repository. Therefore, each example can be easily reproduced, which it will also test and validate each tool. To replicate those tests, it can be done in two different ways:

- Running one test for a specific tool:
 - `cd gto2/tester/gto2_{tool}`
 - `sh runExample.sh`
- Running the batch of tests for all the tools:
 - `cd gto2/tester/`
 - `sh runAllTests.sh`

Some of these tests require internet connection to download external files and it will create new files.

1.3 Execution control

The quality control in Unix/Linux pipelines using GTO's tools is made in three ways:

- Input verification: where the tools verify the format of the input file;
- Stderr logs: Some execution errors are directly sent for the stderr channel.
- Scripting validation: In complex pipelines, the verification of all the tools in the pipeline were executed properly, it is used the PIPESTATUS variable, e.g.:

```
gto2_fa_rand_extra_chars < input.fa | \  
gto2_fa_to_seq > output.seq  
echo "${PIPESTATUS[0]} ${PIPESTATUS[1]}"  
0 0
```

2

FASTA Tools

2.1 gto2_fa_to_fq

to do



3

FASTQ Tools

The toolkit has a set of tools dedicated to manipulating FASTQ files. Some of these tools allow the data conversion to/from different formats, i. e., there are tools designed to convert a FASTQ file into a sequence or a FASTA/Multi-FASTA format, or converting DNA in some of those formats to FASTQ.

There are also tools for data manipulation in this format, which are designed to exclude ‘N’, remove low quality scored reads, following different metrics and randomize DNA sequences. Succeeding the manipulation, it is also possible to perform analyses over these files, simulations and mutations. The current available tools for FASTQ format analysis and manipulation include:

- **gto2_fq_to_fa**: to convert a FASTQ file format to a pseudo FASTA file.
- **gto2_fq_to_mfa**: to convert a FASTQ file format to a pseudo Multi-FASTA file.
- **gto2_fq_exclude_n**: to discard the FASTQ reads with the minimum number of “N” symbols.
- **gto2_fq_extract_quality_scores**: to extract all the quality-scores from FASTQ reads.
- **gto2_fq_info**: to analyse the basic information of FASTQ file format.
- **gto2_fq_maximum_read_size**: to filter the FASTQ reads with the length higher than the value defined.
- **gto2_fq_minimum_quality_score**: to discard reads with average quality-score below of the defined.
- **gto2_fq_minimum_read_size**: to filter the FASTQ reads with the length smaller than the value defined.
- **gto2_fq_rand_extra_chars**: to substitute in the FASTQ files, the DNA sequence the outside ACGT chars by random ACGT symbols.

- **gto2_fq_from_seq**: to convert a genomic sequence to pseudo FASTQ file format.
- **gto2_fq_mutate**: to create a synthetic mutation of a FASTQ file given specific rates of mutations, deletions and additions.
- **gto2_fq_split**: to split Paired End files according to the direction of the strand ('/1' or '/2').
- **gto2_fq_pack**: to package each FASTQ read in a single line.
- **gto2_fq_unpack**: to unpack the FASTQ reads packaged using the **gto2_fq_pack** tool.
- **gto2_fq_quality_score_info**: to analyse the quality-scores of a FASTQ file.
- **gto2_fq_quality_score_min**: to analyse the minimal quality-scores of a FASTQ file.
- **gto2_fq_quality_score_max**: to analyse the maximal quality-scores of a FASTQ file.
- **gto2_fq_cut**: to cut read sequences in a FASTQ file.
- **gto2_fq_minimum_local_quality_score_forward**: to filter the reads considering the quality score average of a defined window size of bases.
- **gto2_fq_minimum_local_quality_score_reverse**: to filter the reverse reads, considering the average window size score defined by the bases.
- **gto2_fq_xs**: a skilled FASTQ read simulation tool, flexible, portable and tunable in terms of sequence complexity.
- **gto2_fq_complement**: to replace the ACGT bases with their complements in a FASTQ file format.
- **gto2_fq_reverse**: to reverse the ACGT bases order for each read in a FASTQ file format.
- **gto2_fq_variation_map**: to identify the variation that occurs in the sequences relative to the reads or a set of reads.
- **gto2_fq_variation_filter**: to filter and segments the regions of singularity from the output of **gto2_fq_variation_map**.
- **gto2_fq_variation_visual**: to depict the regions of singularity using the output from **gto2_fq_variation_filter** into an SVG image.
- **gto2_fq_metagenomics**: to measure the similarity between any FASTQ file, independently from the size, against any multi-FASTA database.

3.1 Program `gto2_fq_to_fa`

The `gto2_fq_to_fa` converts a FASTQ file format to a pseudo FASTA file. However, this tool does not align the sequence, instead, it extracts the sequence and adds a pseudo-header.

For help type:

```
./gto2_fq_to_fa -h
```

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

Input parameters

The `gto2_fq_to_fa` 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: ./gto2_fq_to_fa [options] [--] args]
       or: ./gto2_fq_to_fa [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: ./gto2_fq_to_fa < input.fastq > output.fasta
```

An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGG
```

```

+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the **gto2_fq_to_fa** program is a FASTA file. Using the input above, an output example of this is the following:

```

> Computed with Fastq2Fasta
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCCTTAACAACCTTAAGGG
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG

```

3.2 Program gto2_fq_to_mfa

The **gto2_fq_to_mfa** converts a FASTQ file format to a pseudo Multi-FASTA file. However, this tool does not align the sequence, instead, it extracts the sequence and adds a pseudo header.

For help type:

```
./gto2_fq_to_mfa -h
```

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

Input parameters

The **gto2_fq_to_mfa** 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: ./gto2_fq_to_mfa [options] [-- args]
or: ./gto2_fq_to_mfa [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: `./gto2fq_to_mfa < input.fastq > output.mfasta`

An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTCAGGGATACGACGTTTGTATTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the `gto2_fq_to_mfa` program is a Multi-FASTA file. Using the input above, an output example of this is the following:

```
>SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAAATCCCACCAAGTTACCCTTAACAACTTAAGGG
>SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGGATACGACGTTTGTATTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
```

3.3 Program `gto2_fq_exclude_n`

The `gto2_fq_exclude_n` discards the FASTQ reads with the minimum number of "N" symbols, and it will erase the second header (after +), if presented.

For help type:

```
./gto2_fq_exclude_n -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_exclude_n [options] [--] args
      or: ./gto2_fq_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: ./gto2_fq_exclude_n -m <max> < input.fastq >
output.fastq
```

```

Console output example :
<FASTQ non-filtered reads>
Total reads      : value
Filtered reads   : value

```

An example of such an input file is:

```

@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the `gto2_fq_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 input above with the max value as 5, an output example for this is the following:

```

@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
Total reads      : 2
Filtered reads   : 1

```

3.4 Program `gto2_fq_extract_quality_scores`

The `gto2_fq_extract_quality_scores` extracts all the quality-scores from FASTQ reads.

For help type:

```
./gto2_fq_extract_quality_scores -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_extract_quality_scores [options] [--]args]
      or: ./gto2_fq_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: ./gto2_fq_extract_quality_scores < input.fastq >
output.fastq
```

Console output example:

<FASTQ quality scores>

```
Total reads      : value
```

Total Quality-Scores : value

An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60  
GGGTGATGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACA ACTTAAGGG  
+  
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII  
@SRR001666.2 071112 SLXA-EAS1 s_7:5:1:801:338 length=60
```



```
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the `gto2_fq_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. Using the input above, an output example of this is the following:

```
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
Total reads          : 2
Total Quality-Scores : 144
```

3.5 Program `gto2_fq_info`

The `gto2_fq_info` analyses the basic information of FASTQ file format.

For help type:

```
./gto2_fq_info -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_info [options] [--] args]
       or: ./gto2_fq_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: `./gto2_fq_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 of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the `gto2_fq_info` program is a set of information related to the file read. Using the input above, an output example of this is the following:

```
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 `gto2_fq_maximum_read_size`

The `gto2_fq_maximum_read_size` filters the FASTQ reads with the length higher than the value defined.

For help type:

```
./gto2_fq_maximum_read_size -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_maximum_read_size [options] [--] args]
or: ./gto2_fq_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: ./gto2_fq_maximum_read_size -s <size> < input.fastq
> output.fastq
```

```
Console output example :
<FASTQ non-filtered reads>
Total reads      : value
Filtered reads   : value
```

An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=59
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCGTTAACAACCTTAAGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIIIDII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the **gto2_fq_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 input above with the size values as 59, an output example for this is the following:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=59
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCGTTAACAACCTTAAGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIIIDII
Total reads      : 2
Filtered reads   : 1
```

3.7 Program `gto2_fq_minimum_quality_score`

The `gto2_fq_minimum_quality_score` discards reads with average quality-score below of the defined.

For help type:

```
./gto2_fq_minimum_quality_score -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_minimum_quality_score [options] [--] args]
or: ./gto2_fq_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: ./gto2_fq_minimum_quality_score -m <min> <
input.fastq > output.fastq
```

Console output example:

```
<FASTQ non-filtered reads>
```

An example of such an input file is:

Output

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

3.8 Program gto2_fq_minimum_read_size

For help type:

```
./gto2_fq_minimum_read_size -h
```

Input parameters

The attribution is given according to:

If present, it will erase the second header (after +).

Basic options

```

Console output example:
<FASTQ non-filtered reads>
Total reads      : value
Filtered reads   : value

```

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=50  
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAAC  
+  
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIII  
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60  
GTTCAGGGATAACGACGTTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACCGG
```

```

+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the **gto2_fq_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 input above with the size values as 55, an output example of this is the following:

```

@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
Total reads      : 2
Filtered reads   : 1

```

3.9 Program gto2_fq_rand_extra_chars

The **gto2_fq_rand_extra_chars** substitutes the outside ACGT chars by random ACGT symbols in the DNA sequence of FASTQ files.

For help type:

```
./gto2_fq_rand_extra_chars -h
```

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

Input parameters

The **gto2_fq_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:

3.10 Program `gto2_fq_from_seq`

The `gto2_fq_from_seq` converts a genomic sequence to pseudo FASTQ file format.

For help type:

```
./gto2_fq_from_seq -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_from_seq [options] [--] args]
or: ./gto2_fq_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: ./gto2_fq_from_seq -l <lineSize> -n <name> <
input.seq > output.fastq
```

An example of such an input file is:

ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCT
GCCCTGCTGCCATTGTCCCCGGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCTCGC
TTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAAGTGGTTTGAGTGGAACCTCCG
GGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAAGTCTTCTGGAAG

Output

The output of the `gto2_fq_from_seq` program is a pseudo FASTQ file. An example, using the size line as 60 and the read's header as "SeqToFastq", for the input, is:

[illegible]

3.11 Program `gto2_fq_mutate`

The `gto2_fq_mutate` creates a synthetic mutation of a FASTQ file given specific rates of mutations, deletions and additions. All these parameters are defined by the user, and their are optional.

For help type:

```
./gto2_fq_mutate -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_mutate [options] [--] args
       or: ./gto2_fq_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              Starting point to the random generator
-m             Defines the mutation rate (default 0.0)
```


3.12 Program gto2_fq_split

The **gto2_fq_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:

```
./gto2_fq_split -h
```

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

Input parameters

The **gto2_fq_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: ./gto2_fq_split [options] [--] args
      or: ./gto2_fq_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: ./gto2_fq_split -f <output_forward.fastq>
-r <output_reverse.fastq> < input.fastq > output
```

Output example :

```
Total reads      : value
Singleton reads   : value
```


3.13 Program gto2_fq_pack

The **gto2_fq_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:

```
./gto2_fq_pack -h
```

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

Input parameters

The **gto2_fq_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: ./gto2_fq_pack [options] [--] args]
or: ./gto2_fq_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.fastqpack Output packaged FASTQ file format
                    (stdout)
```

Optional

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

```
Example: ./gto2_fq_pack -s < input.fastq > output.fastqpack
```


An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
NTTCAGGGATACGACGNTTGTATTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the `gto2_fq_pack` program is a packaged FASTQ file. Using the input above, an output example of this is the following:

```
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGG
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60+ 0
NTTCAGGGATACGACGNTTGTATTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60+ 1
```

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

```
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACTTAAGGG
SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60+ 0
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
NTTCAGGGATACGACGNTTGTATTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60+ 1
```

3.14 Program `gto2_fq_unpack`

The `gto2_fq_unpack` unpacks the FASTQ reads packaged using the `gto2_fq_pack` tool.

For help type:

```
./gto2_fq_unpack -h
```

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

Input parameters

The `gto2_fq_unpack` program needs two streams for the computation, namely the input and output standard. The input stream is a packaged FASTQ file.

The attribution is given according to:

Usage: ./gto2_fq_unpack [options] [--] args]
or: ./gto2_fq_unpack [options]

It unpacks the FASTQ reads packaged using the `gto2fq_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

| | |
|---------------------------|----------------------------------------------------|
| <code>-s, --scores</code> | When active, the application show the scores first |
|---------------------------|----------------------------------------------------|

Example: `./gto2_fq_unpack -s < input.fastqpack > out.fastq`

An example of such an input file is:

GNNATGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACCTTAAGGG
 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
 SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60+ 0
 NTTCAGGGATACGACGNTTGTATTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
 SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60+ 1

Output

The output of the **gto2_fq_unpack** program is a FASTQ file. Using the input above, an output example of this is the following:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCGTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

3.15 Program `gto2_fq_quality_score_info`

The **gto2_fq_quality_score_info** analyses the quality-scores of a FASTQ file.

For help type:

```
./gto2_fq_quality_score_info -h
```

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

Input parameters

The **gto2_fq_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: ./gto2_fq_quality_score_info [options] [--] args]
       or: ./gto2_fq_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: ./gto2_fq_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 of such an input file is:

```

@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=60 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=60 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the **gto2_fq_quality_score_info** program is a set of information related to the file read. Using the input above with the max window value as 30, an output example of this is the following:

```

Total reads      : 2
Max read length : 60

```

```

Min read length : 60
Min QS value    : 54
Max QS value    : 73
QS range        : 20
 1  ...  24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40
---+ ... +---+---+---+---+---+---+---+---+---+---+---+---+---+---+
73  ...  73 73 73 73 73 73 73 65 73 62 65 69 70 73 73 73 73
                                     *   * * * *
                                     *   * * * *
                                     *   * * * *
                                     *   * * *
                                     *   * *
                                     *   * *
                                     *   * *
                                     *   * *
                                     *   * *
                                     *
                                     *
                                     *

```

3.16 Program `gto2_fq_quality_score_min`

The `gto2_fq_quality_score_min` analyses the minimal quality-scores of a FASTQ file.

For help type:

```
./gto2_fq_quality_score_min -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_quality_score_min [options] [--] args]
or: ./gto2_fq_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: ./gto2_fq_quality_score_min -m <max> < input.fastq
> output
```

An example of such an input file is:

```
@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=60 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACCTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=60 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the **gto2_fq_quality_score_min** program is a set of information related to the file read, considering the minimum quality scores. Using the input above with the max window value as 20, an output example of this is the following:

```
 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
--+-+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+--+
73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73
```

3.17 Program `gto2_fq_quality_score_max`

The `gto2_fq_quality_score_max` analyses the maximal quality-scores of a FASTQ file.

For help type:

```
./gto2_fq_quality_score_max -h
```

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

Input parameters

The `gto2_fq_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: ./gto2_fq_quality_score_max [options] [--] args]
or: ./gto2_fq_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: ./gto2_fq_quality_score_max -m <max> < input.fastq > output
```

An example of such an input file is:

```
@111 071112_SLXA-EAS1_s_7:5:1:817:345 length=60 1
GNNTGATGGCCGCTGCCGATGGCGNANAATCCCACCAANATACCCTTAACAACCTTAAGGG
```

```

+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@222 071112_SLXA-EAS1_s_7:5:1:801:338 length=60 2
NTTCAGGGATACGACGNTTGTATTTTAAGAATCTGNAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the **gto2_fq_quality_score_max** program is a set of information related to the file read, considering the maximal quality scores. Using the input above with the max window value as 20, an output example of this is the following:

```

 1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 20
---+---+---+---+---+---+---+---+---+---+---+---+---+---+---+
73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73 73

```

3.18 Program gto2_fq_cut

The **gto2_fq_cut** cuts read sequences in a FASTQ file. It requires that the initial and end positions for the cut.

For help type:

```
./gto2_fq_cut -h
```

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

Input parameters

The **gto2_fq_cut** 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: ./gto2_fq_cut [options] [--] args]
       or: ./gto2_fq_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: ./gto2_fq_cut -i <initial> -e <end> < input.fastq
> output.fastq
```

An example of such an input file is:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCGTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTACAGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the **gto2_fq_cut** program is a FASTQ file cut. Using the initial value as 10 and the end value as 30, an example of this input, is the following:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
CGCTGCCGATGGCGTCAAATC
+
IIIIIIIIIIIIIIIIIIII9
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
ACGACGTTTGTATTTTAAGAA
```

```

+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

```

3.19 Program `gto2_fq_minimum_local_quality_score_forward`

The `gto2_fq_minimum_local_quality_score_forward` filters the reads considering the quality score average of a defined window size of bases.

For help type:

```
./gto2_fq_minimum_local_quality_score_forward -h
```

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

Input parameters

The `gto2_fq_minimum_local_quality_score_forward` 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: ./gto2_fq_minimum_local_quality_score_forward [options] [--] args]
or: ./gto2_fq_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                  The window size of bases (default 5)
-w                  The minimum average of quality score
                    (default 25)
-m                  The minimum value of the quality score
```

```

                                (default 33)
    < input.fastq               Input FASTQ file format (stdin)
    > output.fastq              Output FASTQ file format (stdout)

```

```

Example: ./gto2_fq_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 of such an input file is:

```

@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIII-I)8IIIIIIIIIIIIIIIIII

```

Output

The output of the **gto2_fq_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. Using the input above with the default values, an output example of this is the following:

```

Minimum QS      : 33
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTTCAGGGATACGACGTTTGTATTTTAAGAATCTGAA

```

```
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBII
Total reads      : 2
Trimmed reads    : 1
```

3.20 Program gto2_fq_minimum_local_quality_score_reverse

The `gto2fq_minimum_local_quality_score_reverse` filters the reverse reads, considering the quality score average of a defined window size of bases.

For help type:

```
./gto2_fq_minimum_local_quality_score_reverse -h
```

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

Input parameters

The `gto2_fq_minimum_local_quality_score_reverse` 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: ./gto2_fq_minimum_local_quality_score_reverse [options] [--] args]
or: ./gto2_fq_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 The window size of bases (default 5)

+

For help type:

```
./gto2_fq_xs -h
```

ters.

Input parameters

The `gto2fq_xs` program needs a FASTQ file to compute.

An example of such an input file is:

+

```

IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
G TTCAGGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI

```

Output

The output of the **gto2_fq_xs** program is a FASTQ file. Using the input above using the common usage with 5 reads (-n 5), an output example of this is the following:

3.22 Program *gto2_fq_complement*

The **gto2_fq_complement** replaces the ACGT bases with their complements in a FASTQ file format.

For help type:

```
./gto2_fq_complement -h
```

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

Input parameters

The **gto2_fq_complement** 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: ./gto2_fq_complement [options] [--] args]
       or: ./gto2_fq_complement [options]

```



```
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338
GTTCAAGGATACGACGTTTGTATTTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

Output

The output of the **gto2_fq_reverse** program is the FASTQ file complement with the flag “(Reversed)” added in the header. Using the input above, an output example of this is the following:

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 (Reversed)
GGGAATTCAACAATTCCCATTGAACCACCCTAACTGCGGTAGCCGTCGCCGTAGTGGG
+
IIIDIIIIIIIIIIIIIIIIIIIIIC19GI9IIIIIIIIIIIIIIIIIIIIIIIIIIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 (Reversed)
GCGCATAATAGTAGCTGAAGACGAAGTCTAAGAATTTTATGTTTGCAGCATAGGGAAGT
+
IGIIIIIIIIIIIIIIIIIIIIIBI6IIIIIIIIIIIIIIIIIIIIIIIIIIIIII
```

3.24 Program gto2_fq_variation_map

The **gto2_fq_variation_map** identifies the variation that occurs in the sequences relative to the reads or a set of reads.

For help type:

```
./gto2_fq_variation_map -h
```

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

Input parameters

The **gto2_fq_variation_map** program needs FASTQ, FASTA or SEQ files to be used as reference and target files.

The attribution is given according to:

```
Usage: ./gto2_fq_variation_map <OPTIONS>... [FILE]:<...>
[FILE]:<...>
```

The *gto2_fq_variation_map* is a tool to map relative singularity regions. The (probabilistic) Bloom filter is automatically set.

```
-v                verbose mode,
-a                about CHESTER,
-s <value>        bloom size,
-i                use inversions,
-p                show positions/words,
-k <value>        k-mer size (up to 30),

[rFile1]:<rFile2>:<...> reference file(s),
[tFile1]:<tFile2>:<...> target file(s).
```

The reference files may be FASTA, FASTQ or DNA SEQ, while the target files may be FASTA OR DNA SEQ. Report bugs to <{pratas,raquelsilva,ap,pjf}@ua.pt>.

An example of a reference file (Multi-FASTA format) is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCT
CCCTGCTGCCATTGTCCCCGGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCT
TGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAAGTGGTTTGAGTGGACCTCCGG
GCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCCG
CGAATCCGCGCGCCGGACAGAATCTCCTGCAAAGCCCTGCAGGAAGTTCTTCTGGAAGA
CCTTCTCCACCCCCCAGCTAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAG
ACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCG
CTGCCCTGCCCCTGGAGGGTGGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGG
CAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGTGGTTTGAGTGGACCTCCC
AGGCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAAGTTCTTCTGGA
AGACCTTCTCCTCCTGCAAATAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACA
GACCTGAA
```

```
@SRR001666.1 071112_SLXA-EAS1_s_7:5:1:817:345 length=60
GGGTGATGGCCGCTGCCGATGGCGTCAAATCCCACCAAGTTACCCTTAACAACCTTAAGGG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII9IG9ICIIIIIIIIIIIIIIIIIIIDIII
@SRR001666.2 071112_SLXA-EAS1_s_7:5:1:801:338 length=60
GTTCAGGGATACGACGTTTGTATTTAAGAATCTGAAGCAGAAGTCGATGATAATACGCG
+
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII6IBIIIIIIIIIIIIIIIIIIIIIGI
```

The output of the `gto2_fq_variation_map` program is a text file identifying the relative regions. Using the inputs above, an output example of this is the following:

```
111111111111111111111111111100000000000000000000000000000000000000  
111111111111111111111111111100000000000000000000000000000000000000  
000000000000
```

to do

to do

3.27 Program *gto2_fq_metagenomics*

to do



4

Amino Acid Tools

4.1 gto2_aa

to do



5

Genomic Tools

5.1 gto2_dna

to do



6

General Purpose Tools

6.1 gto2_

to do



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