



A toolkit for DNA sequence analysis and manipulation

D. Pratas (pratas@ua.pt)

J. R. Almeida (joao.rafael.almeida@ua.pt)

A. J. Pinho (ap@ua.pt)

IEETA/DETI, University of Aveiro, Portugal

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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. Its storage have been made using specific file formats, such as FASTQ and FASTA. Therefore, its analysis and manipulation is crucial [?]. Several frameworks for analysis and manipulation emerged, namely **GALAXY** [?], **GATK** [?], **HTSeq** [?], **MEGA** [?], among others. In the majority, these frameworks require licenses and do not provide a low level access to the information, since they are commonly approached by scripting or interfaces.

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

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

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

1.1 Installation

For **GOOSE** installation, run:

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

1.2 License

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

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

Chapter 2

FASTQ tools

Current available tools for FASTQ format analysis and manipulation include:

1. `goose-fastq2fasta`
2. `goose-fastq2mfasta`
3. `goose-fastqclustreads`
4. `goose-FastqExcludeN`
5. `goose-FastqExtractQualityScores`
6. `goose-FastqInfo`
7. `goose-FastqMaximumReadSize`
8. `goose-FastqMinimumLocalQualityScoreForward`
9. `goose-FastqMinimumLocalQualityScoreReverse`
10. `goose-FastqMinimumQualityScore`
11. `goose-FastqMinimumReadSize`
12. `goose-count`
13. `goose-extractreadbypattern`
14. `goose-fastqpack`
15. `goose-fastqsimulation`
16. `goose-FastqSplit`
17. `goose-FastqTrimm`
18. `goose-fastqunpack`

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

Chapter 3

FASTA tools

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

1. `goose-fasta2seq`: it converts a FASTA or Multi-FASTA file format to a seq.
2. `goose-fastaextract`: it extracts sequences from a FASTA file, which the range is defined by the user in the parameters.
3. `goose-fastaextractbyread`: it extracts sequences from each read in a Multi-FASTA file (splited by `\n`), which the range is defined by the user in the parameters.
4. `goose-fastainfo`: it shows the readed information of a FASTA or Multi-FASTA file format.
5. `goose-mutatefasta`
6. `goose-randfastaextrachars`
7. `goose-geco`
8. `goose-gede`
9. `goose-mutatedna`
10. `goose-randseqextrachars`
11. `goose-reverse`: it reverses the order of a sequence.
12. `goose-reverselm`: it reverses the order of a large sequence. Low memory usage for large files.

3.1 Program `goose-fasta2seq`

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

For help type:

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

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

3.1.1 Input parameters

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

The attribution is given according to:

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

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

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

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

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

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTG
GTGGTTTGAGTGGACCTCCAGGCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCTCCTGCAAA
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

3.1.2 Output

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

An example, for the input, is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAAACAAGATGCCATTGTCCCCGGCCTCCTGCTG
CTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCTGGAGGGTGGCCCCACCGCCGAGACAGCGAGCATATGCA
GGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGTGGTTTGAGTGGACCTCCAGGCCAGTGCCG
```



```

GCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGGCGCACCCCCCAGCAATCCGCGCGCCGGGAC
AGAATGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCTGCAATAAAACCTCACCCATGAATGCTCAGCAAGTT
TAATTACAGACCTGAA

```

3.2 Program goose-fastextract

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

For help type:

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

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

3.2.1 Input parameters

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

The attribution is given according to:

```

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

It extracts sequences from a FASTA file.

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

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

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

```

An example on such an input file is:

```

>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTCCTCCGGGGCCACGGCCCTGGAGGTCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGGAGTGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCACCCCCCAGC
TAAACCTCACCCATGAATGCTCAGCAAGTTTAATTACAGACCTGAA

```

3.2.2 Output

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

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

is:

```
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGG
```

3.3 Program goose-fastaextractbyread

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

For help type:

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

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

3.3.1 Input parameters

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

The attribution is given according to:

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

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

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

Basic options

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

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

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCTGGAGGGT
GGCCCCACCGCGCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCTGACTTTCTCTCGCTTG
GTGGTTTGAGTGGACCTCCAGGCCAGTGCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCTCTGCAAA
```

```
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

3.3.2 Output

The output of the `goose-fastextractbyread` 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
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCC
```

3.4 Program `goose-fastainfo`

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

For help type:

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

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

3.4.1 Input parameters

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

The attribution is given according to:

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

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

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

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

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

An example on such an input file is:

```
>AB000264 |acc=AB000264|descr=Homo sapiens mRNA
ACAAGACGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCCTGGAGGTCCACCGCTGCCCTGCTGCCATTGTCCCC
GGCCCCACCTAAGGAAAAGCAGCCTCCTGACTTTCTCGCTTGGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAA
GTGGTTTGAGTGGACCTCCGGGGCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAGCAGGCCAGTGCC
GCGAATCCGCGCGCCGGGACAGAATCTCCTGCAAAGCCCTGCAGGAACCTTCTTCTGGAAGACCTTCTCCACCCCCCAGC
TAAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
>AB000263 |acc=AB000263|descr=Homo sapiens mRNA
```

```
ACAAGATGCCATTGTCCCCGGCCTCCTGCTGCTGCTGCTCTCCGGGGCCACGGCCACCGCTGCCCTGCCCCCTGGAGGGT
GGCCCCACCGGCCGAGACAGCGAGCATATGCAGGAAGCGGCAGGAATAAGGAAAAGCAGCCTCCTGACTTTCCTCGCTTG
GTGGTTTGAGTGGACCTCCCAGGCCAGTGCCGGGCCCCCTCATAGGAGAGGAAGCTCGGGAGGTGGCCAGGCGGCAGGAAG
GCGCACCCCCCAGCAATCCGCGCGCCGGGACAGAATGCCCTGCAGGAACTTCTTCTGGAAGACCTTCTCCTCCTGCAAA
TAAACCTCACCCATGAATGCTCACGCAAGTTTAATTACAGACCTGAA
```

3.4.2 Output

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

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

Chapter 4

Amino acid sequence tools

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

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

4.1 Program `goose-AminoAcidToGroup`

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

For help type:

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

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

4.1.1 Input parameters

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

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

It converts a amino acid sequence to a group sequence.

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

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

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

```

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

```

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

```

IPFLLKKQFALADKLVLSKLRQLLGGRICKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPNSIG
TLMPKAEVKIGENNEILVRGGMVMKGYKKPEETAQAFTEDGFLKTGDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE

```

4.1.2 Output

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

An example, for the input, is:

```

HSHHHPPUHHHHNPHHHUPHPUHHSSPHPHSSSSHPHNSHHSHHHPHSHUHPHSHSHUNUHUHUSHPNHUHUSUHS
UHHSPhNHPhSNUUNHHHPSSHHHPShHPPSNNUHUHHUNNSHHPUSNHSNNHNNUSUHHHUNPHPNHHPUUUSPHHHSUH
HNUPHSPNPHHNHUUHHHHNHPHHUHHHHSSHNUHNNHHPUHUHPHPNPHNHHPUUNHHPHHN

```

4.2 Program `goose-ProteinToPseudoDNA`

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

For help type:

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

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

4.2.1 Input parameters

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

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

It converts a protein sequence to a pseudo DNA sequence.

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

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

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

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

```
IPFLLKKQFALADKLVLSKLRQLLGGRICKMMPCGGAKLEPAIGLFFHAIGINIKLGYGMTETTATVSCWHDFQFNPNSIG
TLMPKAEVKIGENNEILVRGGMVMKGYKKPEETAQAFTEDGFLKTDAGEFDEQGNLFITDRIKELMKTSNGKYIAPQY
IESKIGKDKFIEQIAIIADAKKYVSALIVPCFDSLEEYAKQLNIKYHDRLELLKNSDILKMFE
```

4.2.2 Output

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

An example, for the input, is:

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


Chapter 5

General purpose tools

1. `goose-comparativemap`: visualisation of comparative maps. It builds a image given specific patterns between two sequences.
2. `goose-BruteForceString`: it generates, line by line, multiple combinations of strings up to a certain size.
3. `goose-char2line`: it transforms each char into a char in each line.
4. `goose-sum`: it adds the second column value to the first column value.
5. `goose-min`: it finds the minimum value between two column values.
6. `goose-minus`: it subtracts the second column value to the first column value.
7. `goose-max`: it finds the mmaximum value between two column values.
8. `goose-extract`: it extracts a subsequence of a sequence by coordinates.
9. `goose-segment`: it segments a sequence given a certain threshold.