

Installing Biopython

```
pip install biopython
pip install --upgrade biopython
# import the library
import Bio
```

Creating Sequences

```
from Bio.Seq import Seq
my_seq = Seq("AA TGC ACG TTG ")
```

To create a sequence we use the `Seq` function from `Bio` library

Filling Sequences

```
# filling sequences
fragments = [Seq("G TAT "), Seq("TA CT")]
filler = Seq("A"*3)
print( filler.join( fragments))
#output :
>>> GTATAA ATACT
```

Slicing Sequences

```
# defining sequences
my_seq = Seq("AA GTC CAG TGT ")
my_seq_2 = Seq("AA AA")
# slicing sequences
print( my_seq [1:6])
print( my_seq [0::2])
# output :
>>> AGTCC
>>> AGCATT
```

Slicing Sequences is the same as that of a python list (we use `[]`)

Appending Sequences

```
my_seq = Seq("AAGTCCAGTGT")
my_seq_2 = Seq("AA AA")
#appending sequences
print( my_seq + my_seq_2)
# output
```



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Appending Sequences (cont)

```
> >>> AAGTCCAGTGTA AAA
```

Appending sequences is the same as appending strings in python

Sequence Counting

```
from Bio.Seq import Seq
# creating a sequence
seq_example = Seq("AG TAC ACT GGT ")
seq_length = len(seq_example)
occ = seq_example.count(" C")
print("The length of the sequence is", len(seq_example))
print("The number of occurrences for nucleotide C is ", occ)
#output :
The length of the sequence is 11
The number of occurrences for nucleotide C is 2
```

This provides how to get the length of a sequence and the number of occurrences of a specific nucleotide

Finding Sub-sequence Index

```
my_seq = Seq("AAGTCCAGTGT")
index = my_seq.find(" GTC ")
print(f"GTC index is {index}")
# output :
GTC index is 2
```

This returns the start index of the selected sub-sequence

Reading Sequence Files

```
from Bio import SeqIO
records = SeqIO.parse("sequence_file.fasta", "fasta")
for record in records:
    print(record.seq)
```

We can also access other attributes from the records :

- record.seq : returns one sequence from list of records
- record.id : returns the identifier of the sequence
- record.description : returns the sequence description

Writing Sequences into a file

```
from Bio import SeqIO
# Define your sequence as a string
sequence = " ATC GAT CGA TCG ATC GAT C"
```



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Writing Sequences into a file (cont)

```
> # Defining file name and format
filename = "my_sequence.fasta"
format = "fasta"
# defining the sequence
seq = SeqIO.SeqRecord(SeqIO.Seq(sequence1),
                      id="my_id", description="My sequence description")
# Open the file for writing in text mode
with open(filename, "w") as file:
    # Create a SeqRecord object
    record = SeqIO.SeqRecord(seq)
    # Write the record to the file using the specified format
    SeqIO.write(record, file, format)
```

Converting Files

```
# syntax
SeqIO.convert(inp_file, inp_format, out_file, out_format, alphabet=None)
#example
SeqIO.convert("sequence.gbk", "genbank", "sequence_converted.fasta", "fasta")
```

inp_file : path to input file

inp_format : input file format/extension

out_file : path to output file

out_format : output file format/extension

alphabet : specify the correct alphabet (DNA, RNA or Protein) to avoid conversion confusion

Sequence Molecular Weight

```
from Bio.SeqUtils import molecular_weight
from Bio.Seq import Seq
seq_example = Seq("TG TAC CCT GGT ")
mw = molecular_weight(seq_example)
print(mw)
#output :
>>> 3403.1577
```

Molecular weight is a way to guess how heavy a tiny building block of life (like a protein or piece of DNA) is compared to a single carbon atom where the bigger the building blocks, the higher the molecular weight

GC-Content

```
from Bio.SeqUtils import gc_fraction
from Bio.Seq import Seq
```



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GC-Content (cont)

```
> # creating a sequence
seq_example = Seq("AGATTCAGTGGT")
gc_content = gc_fraction(seq_example)
print(gc_content)
# output :
>>> 0.41
```

G-C content refers to the percentage of **guanine (G)** and **cytosine (C)** molecules out of all the building blocks (called nucleotides) in a strand of DNA or RNA.

Reverse Complement

```
from Bio.Seq import Seq
#creating a sequence
seq_example = Seq("AG TAC ACT GGT ")
print( " Sequence is :", seq_example)
# getting the reverse compliment
rev_comp = seq_example.reverse_complement()
print( " Reverse complement:", rev_comp)
#output :
>>> Sequence is : AGTACA CTGGT
>>> The reverse complement : ACCAGT GTACT
```

Reverse complement of a DNA sequence is like a mirror image on the opposite strand.

- **Reverse:** Flips the order of the DNA letters (A, C, G, T) from left to right to right to left.
- **Complement:** Swaps each letter according to its pair: A pairs with T, and C pairs with G.

Transcription & Translation

```
seq_example = Seq("ATGAAGTTTTAG")
transc = seq_example.transcribe()
print( " Transcription:", transc)
transl = seq_example.translate()
print( " Translation: ", transl)
#output :
>>> Transcription: AUGAAG UUUUAG
>>> Translation: MKF*
```

Transcription and translation are the two main steps that turn the instructions in our genes (DNA) into the building blocks of life (proteins).

- **Transcription** : is going from DNA to RNA (creating a copy)
- **Translation** : is going from RNA to Protein

Accessing NCBI Database using esearch()

```
from Bio import Entrez
```



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Accessing NCBI Database using esearch() (cont)

```
> handle = Entrez.esearch(db="nucleotide", term="BRCA1 gene", retmax=20)
record = Entrez.read(handle)
```

- db : The name of the Entrez database to search ("nucleotide", "protein"....)
- term : The search term (e.g., gene name, protein ID)
- retmode (str, optional): The format (return mode) to return results in (default: "xml").
- retmax (int, optional): Maximum number of IDs to return (default: 10).
- sort (str, optional): Sorting criteria for results (default: "relevance")

Accessing NCBI Database using efetch()

```
from Bio import Entrez
id_list = ["NM_007294.3", "NM_000546.5"]
handle = Entrez.efetch(db="nucleotide", id=id_list, rettype="gb")
records = Entrez.read(handle)
```

- db : The name of the Entrez database to search ("nucleotide", "protein"....)
- id (list or str): A single ID or a list of IDs to retrieve
- rettype (str, optional): The type of information to return (default: "gb" for GenBank format)
- retmode (str, optional): The format to return results in (default: "xml").



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