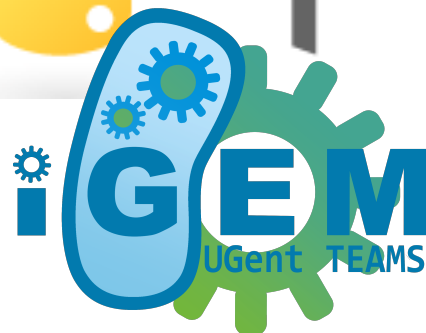


# FROM SEQUENCES TO SIMILARITY

Python series for iGEM Teaching / Bram Jacobs & Shauny Van Hoyer / Advisor: Louis Coussemment

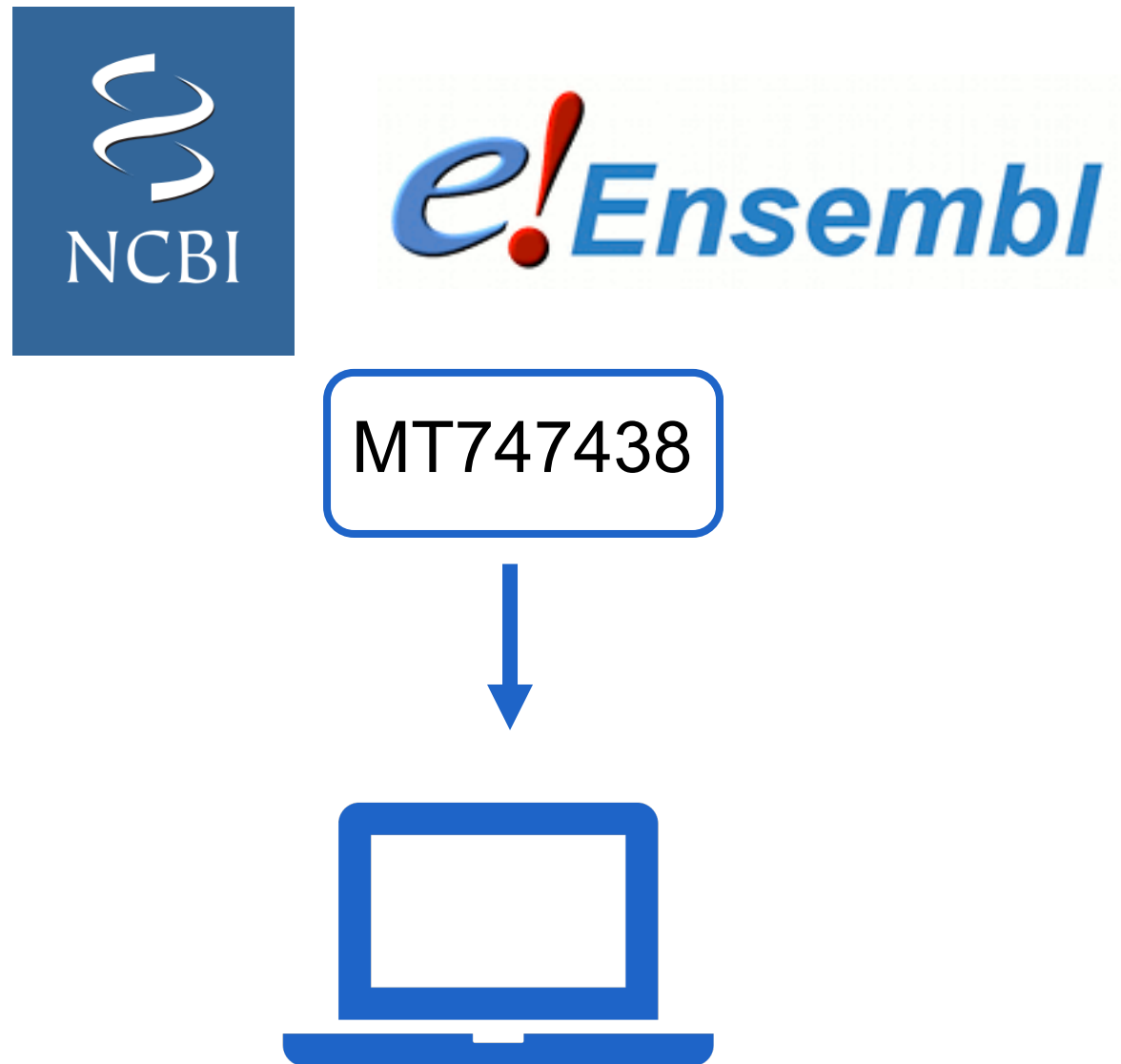
# FROM SEQUENCES TO SIMILARITY

Python 3.8.3  
Biopython 1.77  
Jupyter 6.0.2

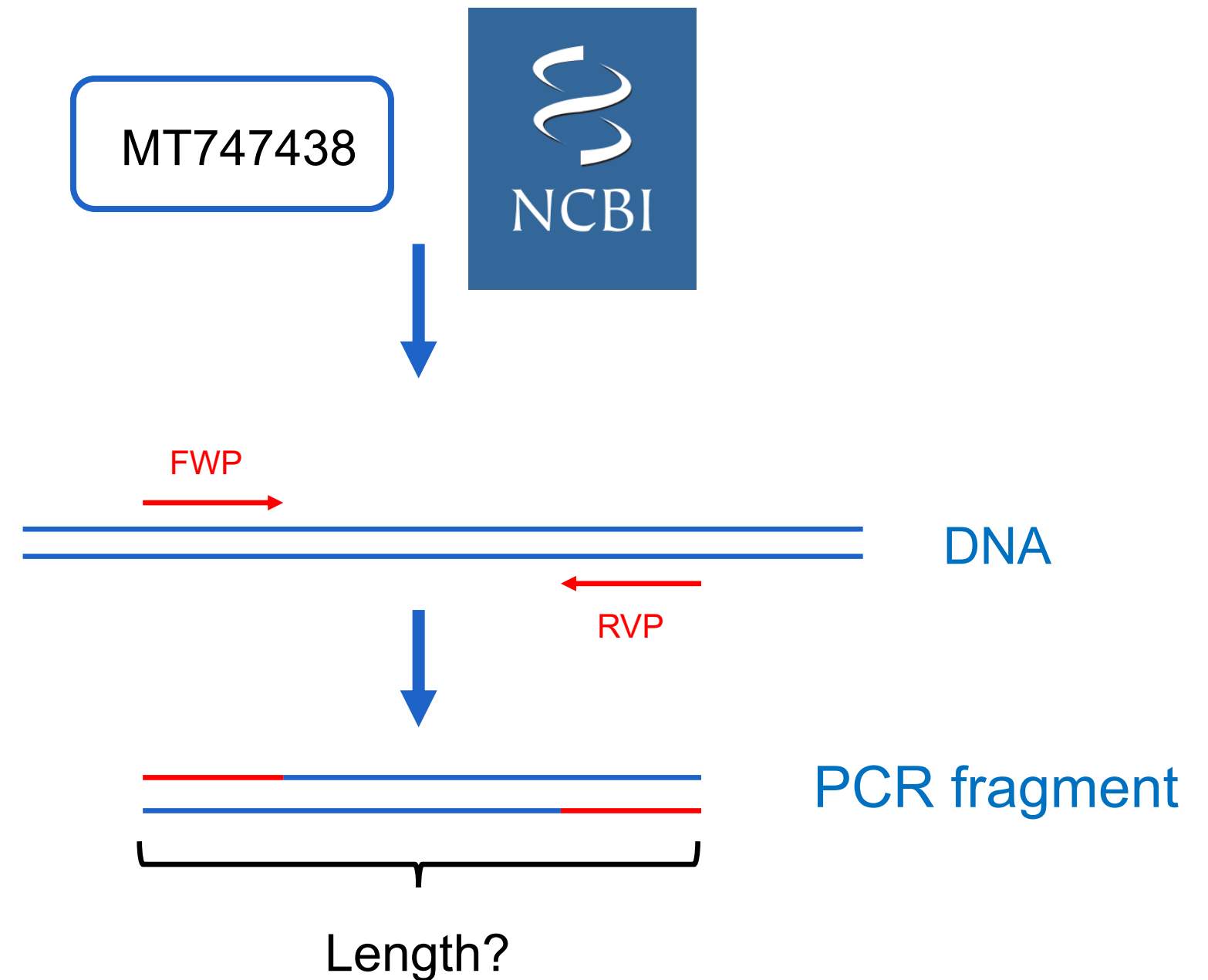


# TUTORIAL SERIES

## (1) Look-up sequences

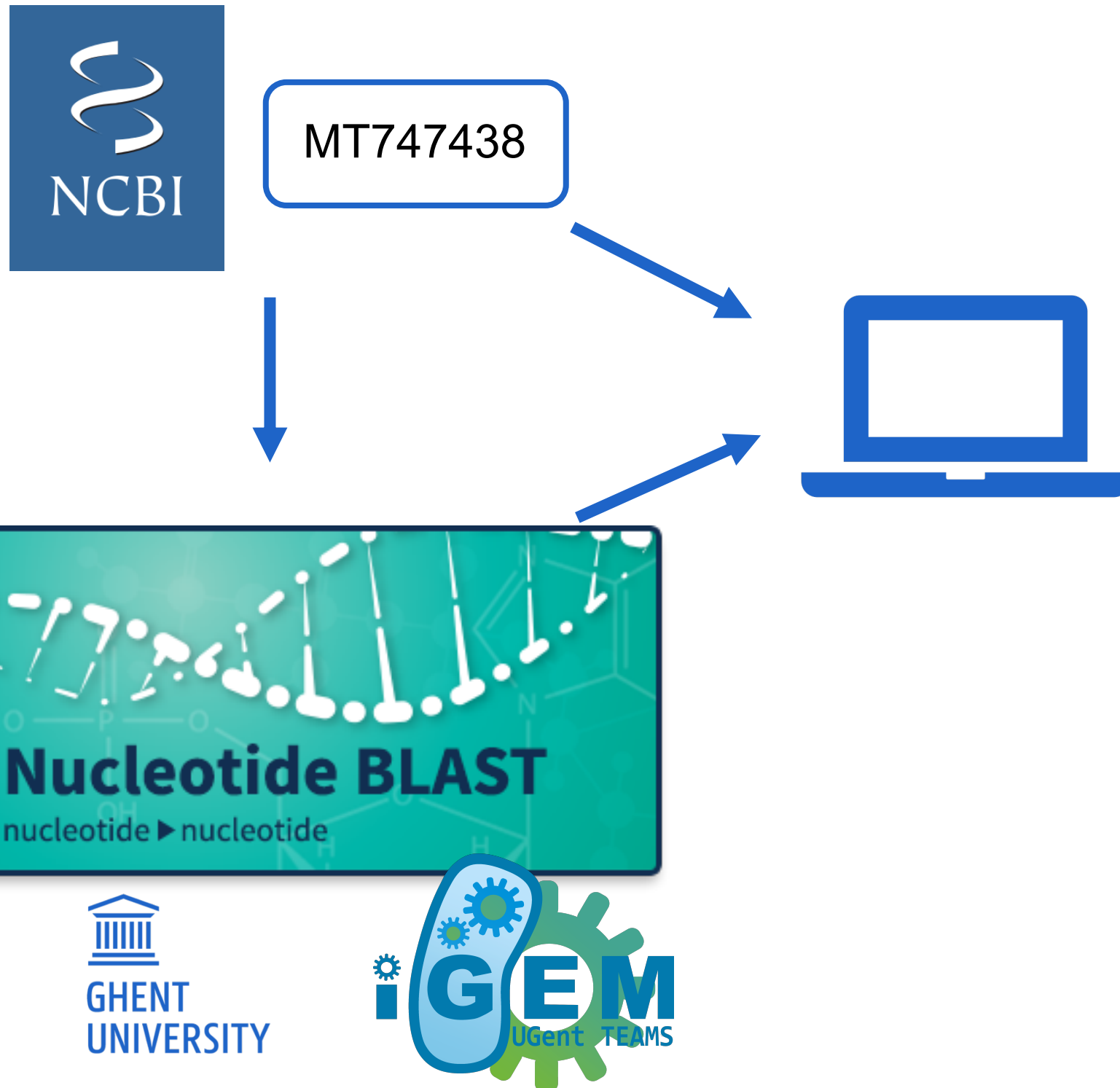


## (2) Length of PCR fragment



# TUTORIAL SERIES

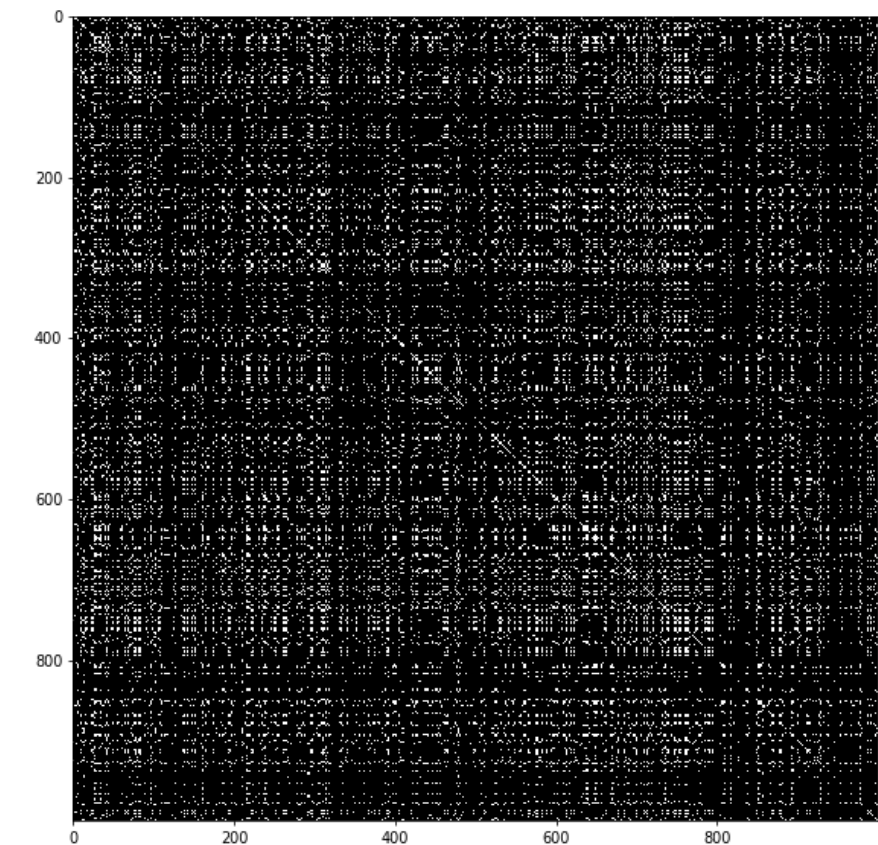
## (3) BLAST



## (4) Dot plots/PSA

Sequence1: MT747438

Sequence2: MT670021



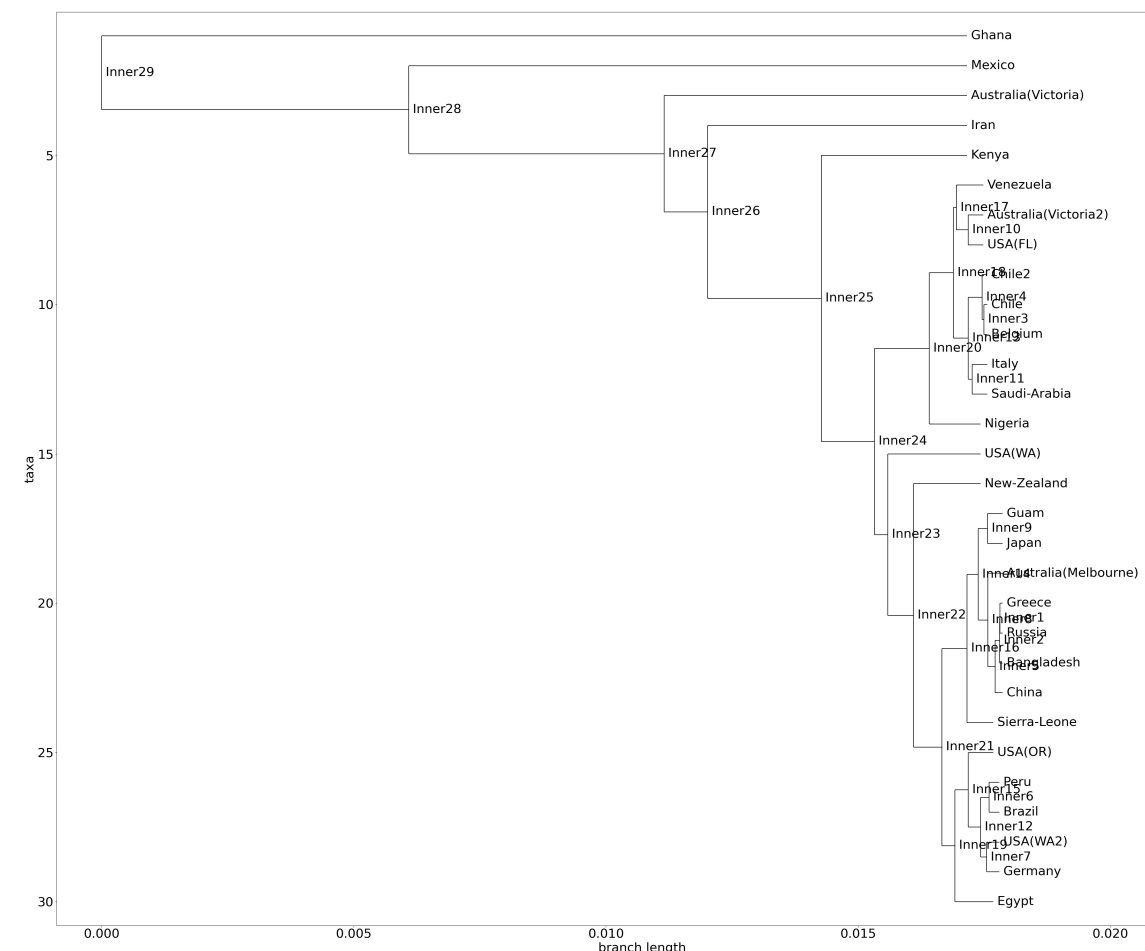
Abbreviations

PSA: pairwise sequence alignment 4

# TUTORIAL SERIES

## (5) Phylogenetic tree

MT670021 MT907518  
MT905416 MT612216  
MT825091 MT890462  
MT706050 ...



# END PRODUCTS

jupyter phylogenetic-tree Last Checkpoint: Last Monday at 20:43 (autosaved)

File Edit View Insert Cell Kernel Widgets Help Trusted Python 3

Phylogenetic Tree Construction

Obtain sequences

In [ ]: # python code

Read sequences

In [1]:

```
from Bio import SeqIO

multi_file = SeqIO.parse("opuntia.fasta", "fasta")

# Check input file
ct = 0
for seq in SeqIO.parse("opuntia.fasta", "fasta"):
    ct += 1
print(len(seq.seq)) # sequence length of last input sequence
print("Number of sequences: ", ct)

input_file = "sequences.txt"

# print first lines of multi-fasta file
"""
ct = 0
for line in multi_file:
    print(line)
    ct += 1
    if ct == 1:
        break
```



Multiple sequence alignment (MSA)



Draw tree

ue, auto=False)

ving code. Replace ... with

# Bram Jacobs

Master student

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 @BramJacobs2  
 BramJacobs2

