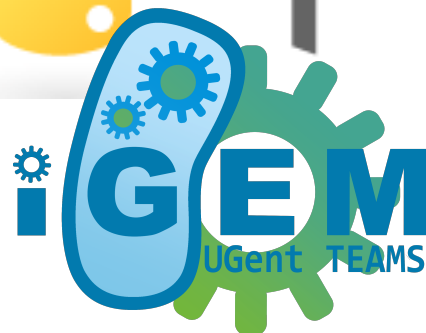


FROM SEQUENCES TO SIMILARITY

Python series for excellence in teaching/Bram Jacobs & Shauny Van Hoyer/Advisor: Louis Coussemment

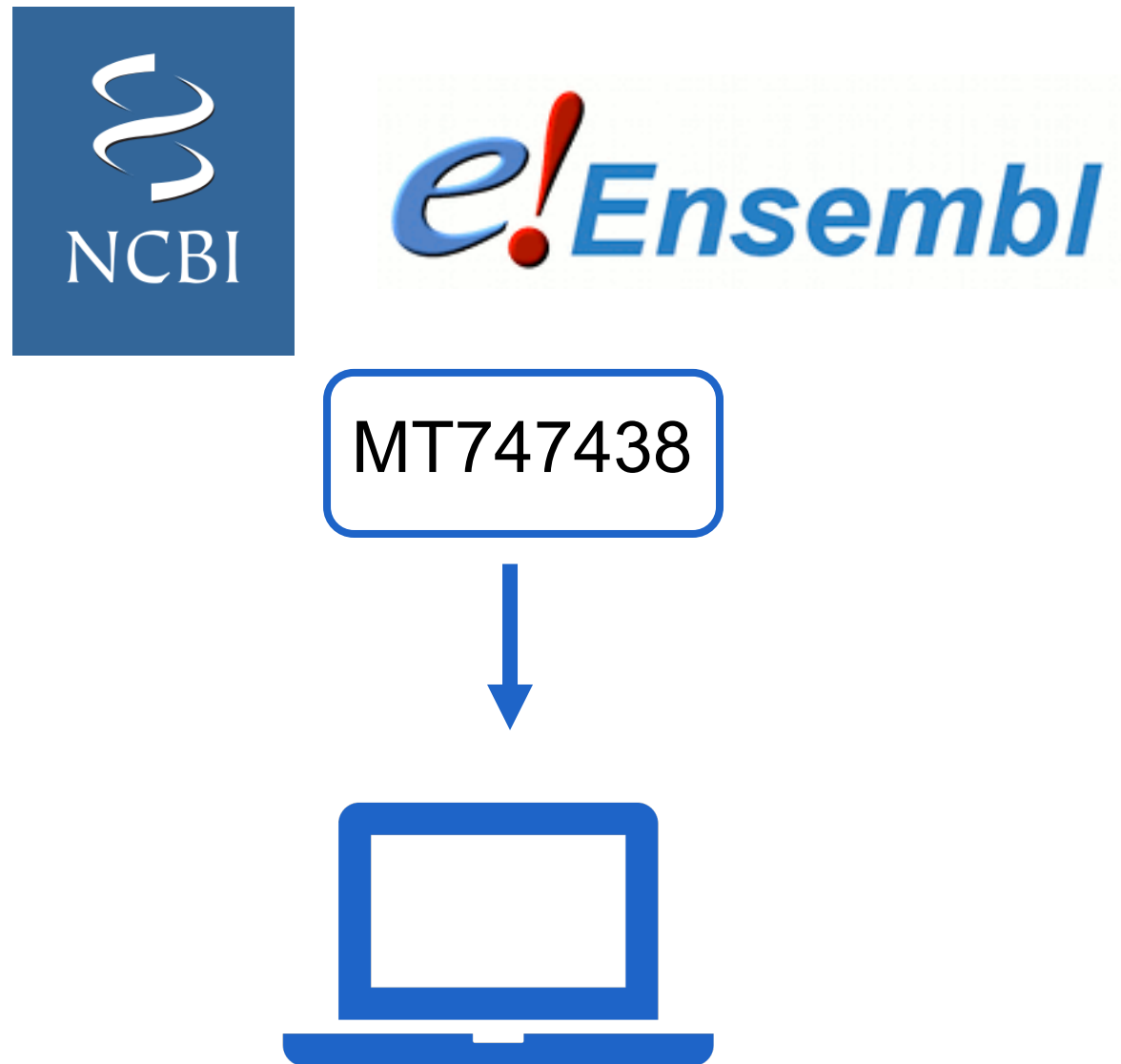
FROM SEQUENCES TO SIMILARITY

Python 3.8.3
Biopython 1.77
Jupyter 6.0.2

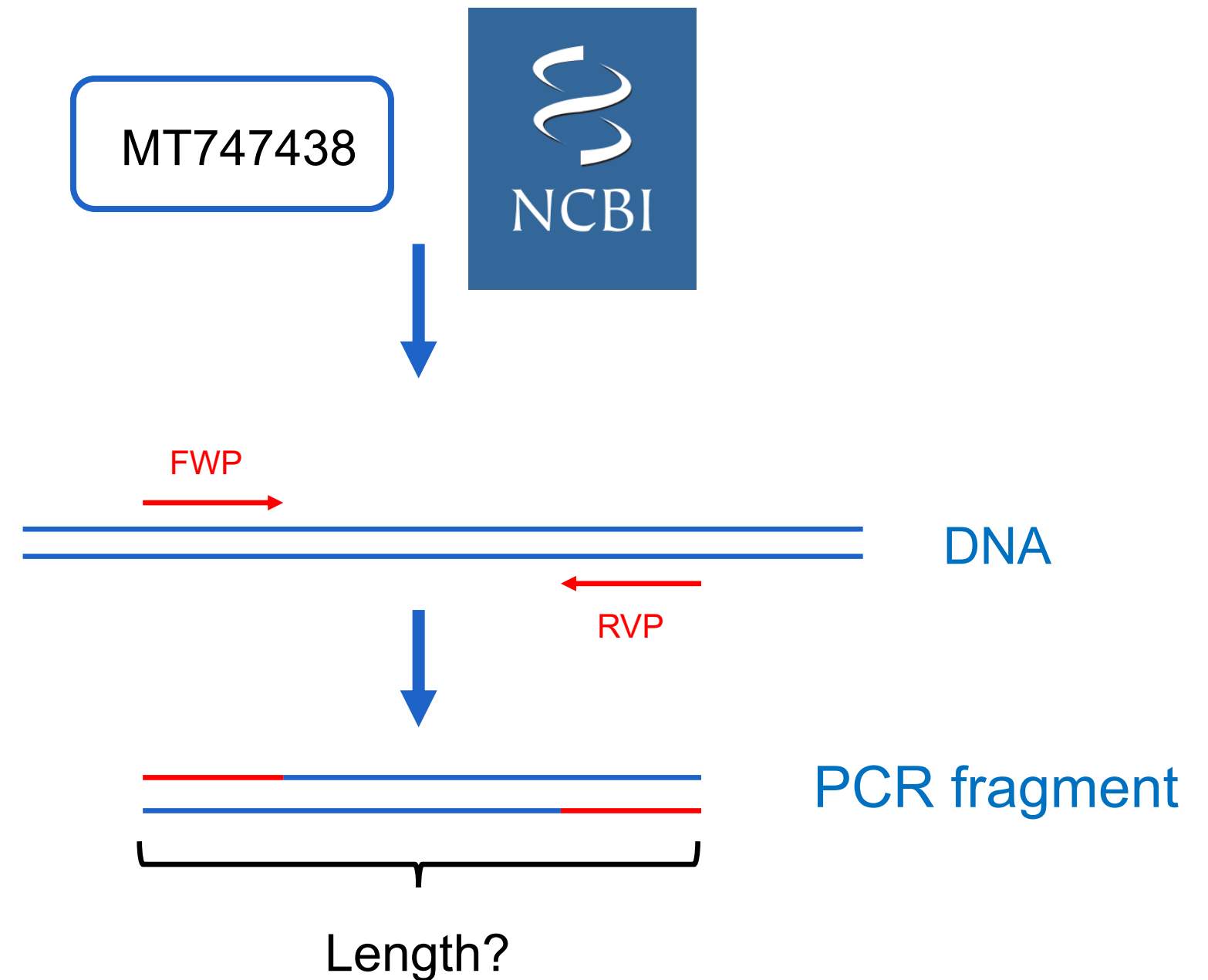


TUTORIAL SERIES

(1) Look-up sequences

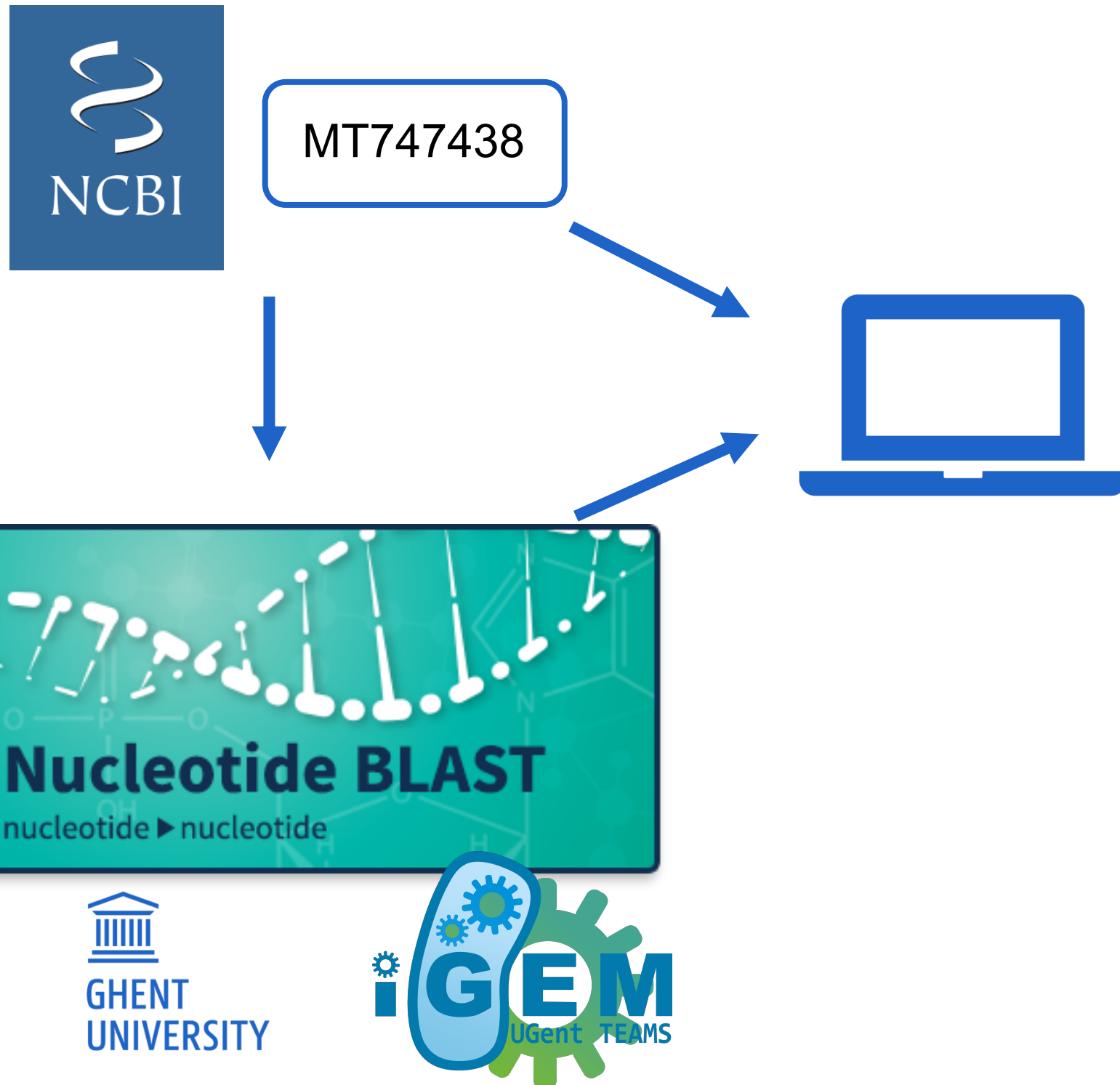


(2) Length of PCR fragment



TUTORIAL SERIES

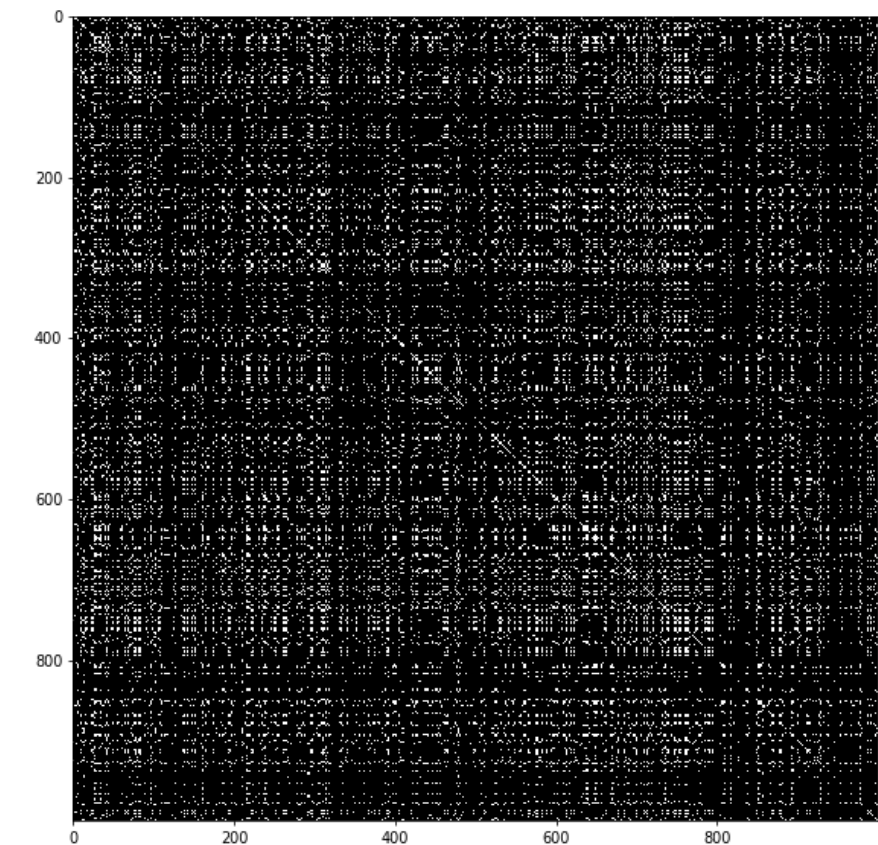
(3) BLAST



(4) Dot plots/PSA

Sequence1: MT747438

Sequence2: MT670021



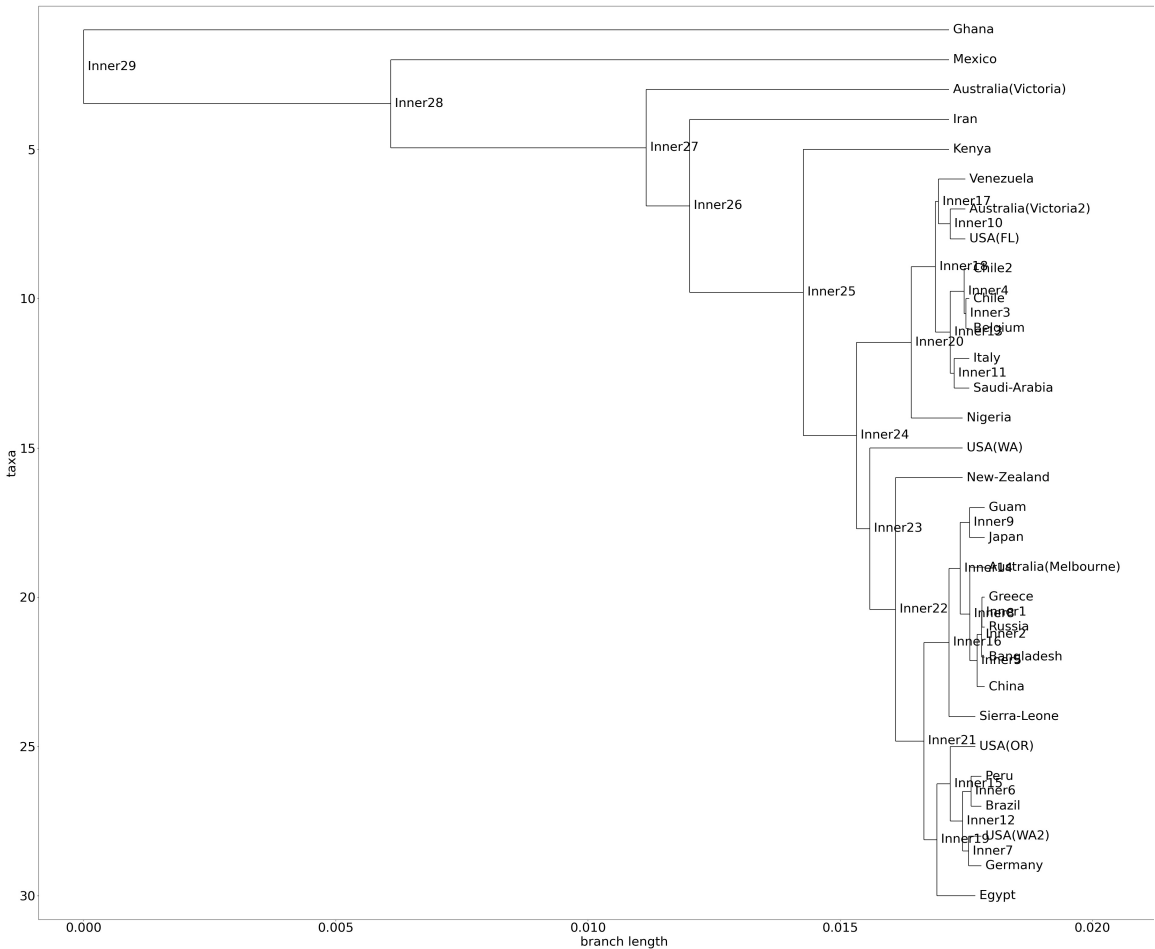
Abbreviations

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)

Logout

File

Edit

View

Insert

Cell

Kernel

Widgets

Help

Trusted

Python 3

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▶ Run

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Markdown

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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

E b.jacobs@ugent.be

 @BramJacobs2

 BramJacobs2



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