

Pair wise sequence alignment of HBB Genes

Install biopython

```
!pip install biopython
```

```
Requirement already satisfied: biopython in /usr/local/lib/python3.12/dist-packages (1.86)  
Requirement already satisfied: numpy in /usr/local/lib/python3.12/dist-packages (from biopython) (2.0.2)
```

Import required libraries

```
from Bio import Entrez, SeqIO  
from Bio.Align import PairwiseAligner
```

Set Entrez Email

```
Entrez.email = "baratamsanjita29@Gmail.com"
```

Fetch HBB Gene Sequences from NCBI

Accession numbers: Human:NM_000518.5 Mouse:NM_008220.2 Chimpanzee:XM_016928727.2

```
def fetch_sequence(accession):  
    handle = Entrez.efetch(  
        db="nucleotide",  
        id=accession,  
        rettype="fasta",  
        retmode="text"  
    )  
    record = SeqIO.read(handle, "fasta")  
    handle.close()  
    return record.seq
```

```
human_seq = fetch_sequence("NM_000518.5")  
Mouse_seq = fetch_sequence("NM_008220.2")  
Chimpanzee_seq = fetch_sequence("XM_016928727.2")  
  
print("Human HBB length:", len(human_seq))  
print("Mouse HBB length:", len(Mouse_seq))  
print("Chimpanzee HBB length:", len(Chimpanzee_seq))
```

```
Human HBB length: 628  
Mouse HBB length: 630  
Chimpanzee HBB length: 3818
```

Initialize Pairwise Aligner

No scores are manually assigned-biopython default settings

Global Alignment

Human vs Mouse

```
aligner.mode = "global"  
global_human_mouse = aligner.align(human_seq, Mouse_seq)  
  
print("Global Alignment Score(Human vs Mouse):")  
print(global_human_mouse[0].score)
```

```
Global Alignment Score(Human vs Mouse):  
484.0
```

Human vs Chimpanzee

```
aligner.mode = "global"  
global_human_chimpanzee = aligner.align(human_seq, Chimpanzee_seq)  
  
print("Global Alignment Score(Human vs Chimpanzee):")  
print(global_human_chimpanzee[0].score)
```

```
Global Alignment Score(Human vs Chimpanzee):  
-2562.0
```

Local Alignment

Human vs Mouse

```
aligner.mode = "local"  
local_human_mouse = aligner.align(human_seq, Mouse_seq)  
  
print("Local Alignment Score(Human vs Mouse):")  
print(local_human_mouse[0].score)
```

```
Local Alignment Score(Human vs Mouse):  
484.0
```

Human vs Chimpanzee

```
aligner.mode = "local"  
local_human_chimpanzee = aligner.align(human_seq, Chimpanzee_seq)  
  
print("Local Alignment Score(Human vs Chimpanzee):")  
print(local_human_chimpanzee[0].score)
```

```
Local Alignment Score(Human vs Chimpanzee):  
273.0
```

Double-click (or enter) to edit

The alignment scores obtained for Human vs Chimpanzee are higher than Human vs Mouse in both global and local alignments.

Based on pairwise sequence alignment of the HBB gene using Biopython, chimpanzee shows greater sequence similarity to humans as compared to mouse. This indicates that chimpanzee is evolutionarily closer to humans than mouse.