

[illegible]

Complete pairwise sequencing code:

WARNING, PLEASE READ: You can use the code below to conduct a sequence alignment between each sequence in the SEED file; however, this will take up a lot of memory, a lot of computer processing power, and it may even crash your computer. Running the code on VS studio may give you a bunch of random numbers in the terminal. You can simply exit VS studio, and you should still have some, if not all pairwise sequences, analyzed on the output .txt file.

```
1  from Bio import AlignIO, pairwise2
2
3  sto_file = r"C:\Users\Tania\Downloads\PF01650.alignment.seed\PF01650.alignment.seed" #Insert your .seed filepath here
4  output_file = r"C:\Users\Tania\Documents\Bio notepad reads\pepc13_read.txt" #insert your .txt filepath here
5
6  alignment = AlignIO.read(sto_file, "stockholm")
7
8  with open(output_file, "w") as outfile:
9      for i in range(len(alignment)):
10         for j in range(i + 1, len(alignment)):
11             seq1 = str(alignment[i].seq)
12             seq2 = str(alignment[j].seq)
13
14             alignments = pairwise2.align.globalxx(seq1, seq2)
15
16             for aligned_pair in alignments:
17                 outfile.write(f"Pairwise alignment between sequences {i+1} and {j+1}:\n")
18                 outfile.write(pairwise2.format_alignment(*aligned_pair))
19                 outfile.write("\n")
20
```