

Bioinformatics Report

Module 5

4624650

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Exercise 1:

In this exercise will be computed the distances of the sequences of mitochondrial DNA from the mammoth, African elephant and the Asian elephant. The identifiers of these sequences are in GenBank: NC_007596, NC_000934, NC_005129 respectively.

Before computing the distance between these sequences, you should first remove the control region (D-loop) and then to the global alignment thereof. Following these steps are described:

A) Only the following nucleotides should be KEPT in the sequences:

Mammoth: 1 to 15421

African elephant: 1 to 15417

Asian elephant: 1 to 15419

B) Perform the global alignment of the remaining sequences using the Clustal OMEGA.

C) To analyze the distances of DNA sequences from the Percent Identity Matrix created by the Clustal OMEGA

Answer:

In order to complete this exercise, I created a python [Script](#) to remove the D-loop region. After running the global alignment at [Clustal Omega](#) , the percent identity matrix was the following:

Percent Identity Matrix - created by Clustal2.1

1:	NC_000934.1	100.00	95.09	94.96
2:	NC_007596.2	95.09	100.00	95.59
3:	NC_005129.2	94.96	95.59	100.00

Analyzing the matrix it is possible to observe that the Mammoth, African Elephant and the Asian Elephant have a not so distant common ancestor.

Exercise 2:

Do the local alignment of the 12S ribosomal RNA gene-tooth tiger saber () against the base of nucleotide collections.

- Enter the name of the 5 organisms whose sequences are more similar to the tiger tooth desabre gene. Provide E.Value and the Total Score for each. Do you think that these organisms have some relationship?

Answer:

Follows the results of the local alignment of the gene-tooth tiger saber obtained by using the [Blastn Tool](#) :

	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/> Smilodon populator isolate ZMA20.041 12S ribosomal RNA gene, partial sequence; mi	728	728	100%	0.0	100%	DQ097171.1
<input type="checkbox"/> Catopuma badia mitochondrion, partial genome	604	604	100%	4e-169	94%	KR135746.1
<input type="checkbox"/> Catopuma badia isolate PBA mitochondrion, complete genome	604	604	100%	4e-169	94%	KP202256.1
<input type="checkbox"/> Catopuma temminckii mitochondrion, partial genome	599	599	100%	2e-167	94%	KR135745.1
<input type="checkbox"/> Catopuma temminckii isolate PTE mitochondrion, complete genome	599	599	100%	2e-167	94%	KP202267.1
<input type="checkbox"/> Catopuma temminckii mitochondrion, partial genome	599	599	100%	2e-167	94%	KR132594.1
<input type="checkbox"/> Catopuma temminckii mitochondrion, complete genome	599	599	100%	2e-167	94%	KP271500.1
<input type="checkbox"/> Prionailurus viverrinus mitochondrion, partial genome	582	582	100%	2e-162	93%	KR135742.1
<input type="checkbox"/> Pardofelis marmorata isolate PMA mitochondrion, complete genome	582	582	100%	2e-162	93%	KP202263.1
<input type="checkbox"/> Prionailurus bengalensis isolate PBE_45 mitochondrion, complete genome	582	582	100%	2e-162	93%	KP202258.1
<input type="checkbox"/> Prionailurus bengalensis isolate PBE_44 mitochondrion, complete genome	582	582	100%	2e-162	93%	KP202257.1
<input type="checkbox"/> Puma concolor mitochondrion, partial genome	582	582	100%	2e-162	93%	KR132588.1
<input type="checkbox"/> Prionailurus bengalensis mitochondrion, partial genome	582	582	100%	2e-162	93%	KR132587.1
<input type="checkbox"/> Puma concolor mitochondrion, complete genome	582	582	100%	2e-162	93%	JN999997.1
<input type="checkbox"/> Lynx rufus mitochondrion, complete genome	582	582	100%	2e-162	93%	GQ979707.3
<input type="checkbox"/> Prionailurus rubiginosus mitochondrion, partial genome	577	577	100%	8e-161	93%	KR135744.1
<input type="checkbox"/> Felis chaus isolate G 12S ribosomal RNA gene, partial sequence; mitochondrial	577	577	100%	8e-161	93%	KU963205.1
<input type="checkbox"/> Felis chaus isolate A 12S ribosomal RNA gene, partial sequence; mitochondrial	577	577	100%	8e-161	93%	KU963204.1
<input type="checkbox"/> Felis chaus isolate R 12S ribosomal RNA gene, partial sequence; mitochondrial	577	577	100%	8e-161	93%	KU963202.1
<input type="checkbox"/> Felis chaus isolate B1 12S ribosomal RNA gene, partial sequence; mitochondrial	577	577	100%	8e-161	93%	KU963201.1
<input type="checkbox"/> Leopardus geoffroyi isolate OGE mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202292.1
<input type="checkbox"/> Lynx rufus isolate LRU mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202285.1
<input type="checkbox"/> Puma yagouaroundi isolate HJA mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202279.1
<input type="checkbox"/> Felis chaus isolate FCH mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202274.1
<input type="checkbox"/> Prionailurus rubiginosus isolate PRU mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202266.1
<input type="checkbox"/> Puma concolor isolate PCO mitochondrion, complete genome	577	577	100%	8e-161	93%	KP202261.1
<input type="checkbox"/> Prionailurus rubiginosus mitochondrion, partial genome	577	577	100%	8e-161	93%	KR132593.1
<input type="checkbox"/> Lynx rufus mitochondrion, partial genome	577	577	100%	8e-161	93%	KR132584.1
<input type="checkbox"/> Felis concolor 12S rRNA gene, mitochondrial gene encoding mitochondrial rRNA	577	577	100%	8e-161	93%	U33495.1

Among all the similar organism I chose 5 that their names are more familiar to me. It is possible to affirm that all those organism belong to the same group, they are feline. The 5 I choose they have the same max score and E values, which means they are ancestors of the tiger saber and that they all migrated to the same region and kept their mitochondrial genes more similar among that group. If you observe other organisms in this table, I is possible to notice that are other ancestors groups with higher similarity to the tiger saber. Which could mean those organisms migrated far less than the others and also they could be much older feline races.

Exercise 3:

The mitochondrial DNA sequences of the blue whale, hippo and cow are respectively NC_001601, NC_000889 and. The blue whale is genetically closer to the cow or hippo?

Percent Identity Matrix - created by Clustal2.1

1: NC_006853.1	100.00	79.70	80.44
2: NC_001601.1	79.70	100.00	80.70
3: NC_000889.1	80.44	80.70	100.00

Answer:

According to [Clustal Omega](#) global alignment percent percent identity matrix the whale is closer to the hippo. They had a better alignment between them.