Practical 6
28 Feb 2022

Questions

1. Using AL2CO server (http://prodata.swmed.edu/al2co/al2co.php), obtain the positional conservation scores from multiple sequence alignment (MSA) of given set of protein sequences (set1 and set2) using the methods given below:

      (i) Unweighted frequency and entropy based measure

      (ii) Unweighted frequency and variance based measure

      (iii) Unweighted frequency and sum of pairs measure

      (iv) Weighted frequency and variance based measure

      (v) Normalize the scores obtained with (i)

Sequences:

Set 1
P69905, P01946, P01942, P01966, P01958, P01959, P01965, P06635, P60529, P80043 and P01980

Set 2
TPIS_HUMAN, TPIS_YEAST, TPIS_GRAVE, TPIS_TRYCR, TPIS_MAIZE, TPIS_MOUSE, TPIS_DROME, TPIS_RABIT, TPIS_CAEEL

2. Tabulate the topmost 10 residues with highest and lowest conservation scores obtained with method (i).

3. Write a program to compute the conservation score from MSA using unweighted frequency, and entropy, variance and sum of pairs based measures.

4. Using the program written in Q3 (unweighted frequency and entropy based measure), compare the MSA from Clustal Omega, MAFFT, and MUSCLE. Identify the residues with (i) similar and (ii) different conservation scores among the three alignment methods.

5. Check the scores manually at positions 9, 11, 20, 22 and 30.

6. Obtain the conservation score of 1BTM, A-chain using Consurf server (https://consurf.tau.ac.il/)

Deadline: 6th March 2022