Practical 1 01 August 2022

Discriminate α -helical and β -barrel membrane proteins using amino acid composition

Instructions

- 1. Upload your program files, output files and the report (naming: "roll no.pdf") in a zipped folder (naming: "roll no.zip").
- 2. Do not copy codes, it will be checked for plagiarism.

Steps:

- 1. Go to PDBTM database (http://pdbtm.enzim.hu/)
- 2. Download alpha helical membrane protein sequences (TMH) in FASTA format
- 3. Obtain non-redundant sequences using CD-HIT software (40%) and online (30%)
- 4. Repeat steps 2 and 3 for beta barrel membrane proteins (TMB)
- 5. Compute the overall amino acid composition in TMH and TMB (20 values each)
- 6. For each sequence in TMH
 - (a) Compute the composition
 - (b) Compare with overall composition of TMH and compute the absolute deviation and total for the 20 residues

$$\sigma(TMH) = \sum |comp(x)-comp(TMH)|$$

(c) Compare with overall composition of TMB and compute the absolute deviation and total for the 20 residues

$$\sigma(TMB) = \sum |comp(x)-comp(TMB)|$$

(d) If $\sigma(TMH) < \sigma(TMB)$, the protein is TMH

Otherwise, it is TMB

- (e) Correctly predicted TMH are True Positives (TP)
- (f) Wrongly predicted as TMB are False Negatives (FN)
- 7. Repeat the same with all TMB proteins. In this case,
 - (e) Correctly predicted TMB are True Negatives (TN)
 - (f) Wrongly predicted as TMH are False Positives (FP)
- 8. Compute sensitivity, specificity and accuracy

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Sensitivity = TP/(TP+FN)
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Specificity =
$$TN/(TN+FP)$$

Accuracy = (TP+TN)/(TP+TN+FP+FN)

- 9. Take 50% of TMH and 50% of TMB to compute the composition (step 5). For the remaining set of proteins follow steps 6 to 8 to assess the performance.
- 10. Change the split in question 9 to 30%, 40%, 60% and 70% and repeat the computation. Tabulate the data. (Optional)
- 11. In 6d include a deviation δ (E.g., σ (TMH) + 0.5) estimate the sensitivity, specificity and accuracy. (Optional)

Deadline: 07 August 2022