

The usage of the CPO package

1. Unzip the CPOpackage.zip into a directory.
2. Open the R and set the work directory to the directory.
3. Source the package.
4. Call the CPO function with the protein sequence.

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1 > source("CPO.R") # Load the CPO package.
2 >
   pro="MVSTGVQPLDDCIQKFHDLKMKQTFRYIIYKIDGDNIVTDSVGN
   REETFENFIKVIPQNNARYAVFDYYFKTNEVPSREIQKLIFIFYCPDTA
   PLKEKMLYASSKDD" # The protein sequence.
3 > ret=CPO(pro)      # Call the CPO function.
4 > ret$codon.list    # Return the Optimized codon
   sequence.
5 [1] "AUG-GUU-UCC-ACU-GGU-GUU-CAA-CCG-UUG-GAU-GAU-
   UGC-AUU-CAA-AAG-UUU-CAU-GAU-CUC-AAA-AUG-AAA-CAG-
   ACG-UUU-CGC-UAU-AUC-AUC-UAC-AAG-AUU-GAU-GGU-GAC-
   AAU-AUU-GUC-ACU-GAC-UCU-GUU-GGA-AAU-CGA-GAG-GAA-
   ACG-UUU-GAG-AAU-UUC-AUC-AAA-GUC-AUU-CCU-CAA-AAU-
   AAU-GCU-CGU-UAU-GCU-GUG-UUU-GAC-UAC-UAC-UUC-AAG-
   ACC-AAU-GAA-GUU-CCU-UCA-AGG-GAA-AUU-CAG-AAA-CUG-
   AUA-UUC-AUU-UUC-UAC-UGU-CCU-GAC-ACU-GCU-CCU-CUC-
   AAA-GAA-AAG-AUG-CUC-UAU-GCU-UCU-UCC-AAA-GAU-GAU"
6 > ret$value.list    # The weight for each codon
   pairs.
7 [1] "(0)-(2)-(2)-(2)-(2)-(1)-(0)-(2)-(0)-(2)-(0)-
   (1)-(2)-(0)-(2)-(0)-(0)-(1)-(2)-(0)-(0)-(2)-(0)-
   (2)-(0)-(0)-(0)-(2)-(1)-(2)-(1)-(2)-(0)-(1)-(2)-
   (0)-(2)-(2)-(0)-(2)-(0)-(2)-(0)-(0)-(0)-(2)-(0)-
   (2)-(2)-(2)-(0)-(2)-(2)-(0)-(2)-(2)-(2)-(0)-(0)-
   (2)-(2)-(0)-(2)-(0)-(2)-(2)-(2)-(2)-(0)-(2)-(0)-
   (2)-(2)-(0)-(2)-(2)-(2)-(0)-(0)-(0)-(2)-(2)-(2)-
   (1)-(2)-(0)-(2)-(1)-(0)-(0)-(0)-(2)-(2)-(0)-(2)-
   (2)-(2)-(0)-(0)-(1)-(2)-(1)-(2)-(2)-(2)-(2)"
8 > ret$total        # The sum of the weight.
9 [1] 122
10 > ret$value.tab    # The distribution of weight.
11 value
12  0  1  2
13 40 10 56

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