Mansoura University
Faculty of Computers and Information
Department of Bioinformatics

PROJECT PROPOSAL

English Title

BCAWT

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PROJECT ABSTRACT:

The redundancy in the genetic code means that apart from methionine and tryptophan, an amino acid is encoded by at least two codons. Different codons for the same amino acid are termed synonymous codons. Synonymous codon usage is strongly influenced by evolutionary forces namely, selection and mutation and may vary strongly within or among organisms The preference of specific codons over others contributes to this variation and this phenomenon is called codon usage bias (CUB).

PROJECT OBJECTIVES:

BCAW tool was developed to analyze such phenomena (Codon Usage Bias) by the aforementioned measurements. Various tools are available to analyze and measure CUB, but they lack some important measurements and plots for CUB analysis. What BCAW tool does is an automated workflow to study the CUB of an organism's genes by all the measurements and plots mentioned above. Further, using the correlation method to determine the optimal codons

described by (Hersh- berg & Petrov, 2009) is implemented for the first time in the BCAW tool. The tool also includes statistical analysis such as correspondence analysis, correlation analysis, and t-test.

WHO ARE THE PROJECT COMPETITIVE? AND HOW WILL YOUR PROJECT BE DIFFERENT?

Many measurements have been developed to analyze and study CUB; effective number of codons (ENc) (Wright, 1990), codon adaptation index (CAI), relative synonymous codon usage (RSCU) (Sharp & Li, 1987) and, translational selection index (P2-index) (Liyuan Wang & Sun, 2018). Also, statistical analysis has been used to investigate the effect of different factors as selection and mutation on shaping CUB such as; Correspondence analysis, Parity Rule 2-plot Analysis and, Neutrality Plot (Hui Song & Nan, 2017).

TOOLS, HARDWARE AND SOFTWARE RESOURCES:

Tools:

- Biopython.
- Pandas.
- CAI
- Scipy
- Matplotlib.
- Numpy
- Prince

Software:

- Pycharm App.

Hardware:

- Processor – i3.

- Hard Disk – 5GB.
- Memory – 1GB RAM.
- Internet Connection.

REFERENCES:

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- Lee, B. D. (2018). Python implementation of codon adaptation index. Journal of Open Source Software, 3(30). doi:10.21105/joss.00905

- Liyuan Wang, Y. Y., Huixian Xing, & Sun, X. (2018). Genome-wide analysis of codon usage bias in four sequenced cotton species. PLoS ONE, 13(3), 1–17. doi:10.1371/journal.pone. 0194372

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- Wright, F. (1990). The “effective number of codons” used in a gene. Gene, 87(1), 23–29. doi:10.1016/0378-1119(90)90491-9