Abstract

The study of amino acids was one of the important issues in bioinformatics, and the prediction of the secondary structure of proteins was one of the important steps in the knowledge of the structure and function of the protein. In this research, an algorithm to generate amino acids is suggested using simulation. A software program is built using MATLAB according to the proposed algorithm for the purpose of conducting simulation experiments. Fourteen simulation experiments were performed to generate sequences of different sizes of amino acids of fourteen protein, some of them is private of mitochondria diseases and some other were taken from other types of proteins. Comparisons are performed between the data generated by the proposed algorithm with real data available in international global centers in genetic engineering databases. Percentages of successfulness of similarities and identity between successive cases with those generated by the simulation program were calculated. The practical application of the proposed algorithm indicated that this algorithm gives encouraging results than the similarities proportion between generated data with real data are sometimes exceeds 90%.
References

4. AL-Khayat, B.Y. probability and Random Variables and their Applications using MATLAB. (under preparation ),( in Arabic) .
10. Ussery ,D., Jensen , M., Poulsen, T. and Hallin, P. 2004.: Genome update: alignment of bacterial chromosomes, Microbiology 150:2491-2,

Index Terms

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Keywords

modeling,simulation, bioinformatics, amino acids, prediction, secondary structure of proteins.