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Research Article **Published Date:- 2021-01-30**

Classification of diseases using a hybrid fuzzy mutual information technique with binary bat algorithm

Genetic datasets have a large number of features that may significantly affect the disease classification process, especially datasets related to cancer diseases. Evolutionary algorithms (EA) are used to find the fastest and best way to perform these calculations, such as the bat algorithm (BA) by reducing the dimensions of the search area after changing it from continuous to discrete. In this paper, a method of gene selection was proposed two sequent stages: in the first stage, the fuzzy mutual information (FMI) method is used to choose the most important genes selected through a fuzzy model that was built based on the dataset size. In the second stage, the BBA is used to reduce and determine a fixed number of genes affecting the process of classification, which came from the first stage. The proposed algorithm, FMI_BBA, describes efficiency, by obtaining a higher classification accuracy and a few numbers of selected genes compared to other algorithms.

Research Article **Published Date:- 2020-07-03**

In silico comparative analysis of HIV protease inhibitors effect on 2019-nCoV coronavirus 3CLpro

The novel coronavirus 2019-nCoV has become a bane to mankind and spread worldwide and infected many people. Thus, there is an urgent need of a cure for the severe pneumonia disease caused by this virus. In this study, In silico comparative analysis has been done for HIV protease inhibitors on coronavirus 3CLpro protein which has shown the major interactions and common amino acid residues involved in interactions. The amino acid interaction analysis has revealed two amino acids ARG4, LYS5 to be the major amino acids targets among selected ligands. The binding energy analysis has also revealed Cobicistat as one of these best suited ligand for 3CLpro.

Research Article **Published Date:- 2020-02-11**

Improving cancer diseases classification using a hybrid filter and wrapper feature subset selection

In the classification of cancer data sets, we note that they contain a number of additional features that influence the classification accuracy. There are many evolutionary algorithms that are used to define the feature and reduce dimensional patterns such as the gray wolf algorithm (GWO) after converting it from a continuous space to a discrete space. In this paper, a method of feature selection was proposed through two consecutive stages in the first stage, the fuzzy mutual information (FMI) technique is used to determine the most important feature selection of diseases dataset through a fuzzy model that was built based on the data size. In the second stage, the binary gray wolf optimization (BGWO) algorithm is used to determine a specific number of features affecting the process of classification, which came from the first stage. The proposed algorithm, FMI_BGWO, describes efficiency and effectiveness by obtaining a higher classification accuracy and a small number of selected genes compared to other competitor algorithms.
