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BestBiBin: BiBinAlter, BiBinSim, BiBinCons

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Two way clustering has recently is a powerful tool that allows to circumvent some limitations of classical clustering approach. This type of clustering is referred as Biclustering, block clustering, co-clustering, two-way clustering or two-mode clustering. A wide range of different articles were published dealing with different algorithms and methods of simultaneous clustering. Comparisons of several biclustering algorithms can be found. In this paper, we present a new algorithm called BestBiBin, for biclustering of DNA microarray data. It is a novel alternative to extract biclusters from sparse, binary datasets. The main features of this algorithm include the evaluation function called CroBin. Applied on synthetic datasets, our algorithm shows better performances compared to other biclustering algorithms. Biclusters with different numbers of rows and columns can be detected, varying from many rows to few columns and few rows to many columns. It allows the user to guide the search towards biclusters of specific dimensions. For our versions of our algorithms, we also detail the structure of our package proposed and implemented in R language. The source and binary codes, the datasets used in the experiments and the results can be found by mail contact.

Biography

Haifa Ben Saber is a PhD student of the BioInformatics Group (BIG) of The Laboratory of Technologies of Information and Communication, and Electrical Engineering (LaTICE), National High School of Engineers of Tunis (ENSIT), University of Tunis, Tunisia, and is also an Assistant Professor at the Time Université, Tunisia.

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