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The use of Machine Learning Clustering Techniques to Conduct Analysis of Anticancer Drug Sensitivity

Khan Zhaeer

College of Pharmacy, Ajman University, University Street, Al jerf 1 - Ajman - United Arab Emirates

*Corresponding author: Khan Zhaeer, College of Pharmacy, Ajman University, University Street, Al jerf 1 - Ajman - United Arab Emirates, khanzaheer19@hotmail.com

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Globally, the rates of fatality owing to lung cancer continue to increase each year. Nonetheless, scientists are engaged in studies to develop drugs by evaluating the patients' reactions to chemotherapeutic treatments to choose new targets for enhanced therapies [1]. In this case, the researchers used machine learning techniques to examine the sensitivity of anticancer drug in human lung cancer cells [2].They addressed to the National Cancer Institute to extract the required data for analysis; therefore, the study has used input dataset that included an experimental observation of over 400,000 cases and it clustered them below ninety one diverse cancer cell lines [3]. They used the simple K-means, filtered algorithm to cluster the data from a significant amount of cell lines, and then computed the sensitivity of the drug for all the lung cancer cell line [4]. Furthermore, the study revealed that such anti-drug chemical compounds as Piperlongumine, Phloretin, Parbendazole, and Neopeltolide demonstrated increased sensitivity for all the ninety one cell lines under diverse concentrations [5]. The outcomes of the study show the similarity between the Filtered and Simple K-means clustering methods [6]. Furthermore, analysis of lung cancer cell line data as contained in the available literature revealed that anticancer drugs and lung cancer have a direct relationship [7].

The researchers also conducted experiments which showed that certain compounds exhibit additional sensitivity as compared to others [8]. Therefore, they concluded that their approach offered a methodology on the manner in which the sensitivity of the anticancer drug can be evaluated by utilizing the clustering algorithms which is considered as one of the most effective machine learning methods [9]. The research can be valuable to scientist or scholars who are interested in development of lung cancer pharmacotherapies [10]. Despite being the second cause of death, there is a considerable concern related to prescription of the correct drug for the right cancer patient [11]. Furthermore, it is impractical and ineffective to use many cancer patient assessments to make a prescription of the suitable anti-cancer drugs. Consequently, different organization both non-government and non-profit as well as pharmaceutical firms have invested billions of dollars to develop interventions that can help prevent, diagnose, and treat cancer [12]. Majority of cancer studies seek to evaluate the efficiency of anticancer drugs to help in selection of right combination of drugs on the basis of their cell line and genetic structure to individual patients, for instance, modifying the medicinal products based on the each patient [13]. Therefore, it is significant to identify or understand the causative cell lines with different types of cancer. Nonetheless, there is a challenge related to the method used to converting the genetic measurements into predictive models to help with therapeutic decision making [14].

The researchers sought to perform analysis of lung cancer by utilizing the data mining clustering techniques as well as big data to determine suitable medical applications [15]. The study sought to analyze how filtered clusters and Simple K-means clustering can be used in making prediction of sensitivity of anticancer drug [16]. The researchers argue that it is possible that the profiling the Cancer Cell Line (CCL) sensitivity can greatly assist in development of a therapy that can solely be linked to the individual patient [17]. Scientists have analyzed the different reaction between the cancer cells and small-molecule treatment in CCL [18]. They found out sensitivity profiling studies and effective analysis methodologies can be used to fully control the CCL model and the small-molecule via cancer cells [20]. Additionally, the use of Simple K-means clustering algorithm gave accurate analysis outcomes for the dataset used [21]. The study findings revealed that the k-means clustering can be relied on to determine the sensitive drug for the cell lines [22]. Additionally, the experiment proved that four anticancer drug compounds namely the Piperlongumine, Phloretin, Parbendazole, and Neopeltolide were more sensitive to the entire ninety one cell lines of lung cancer under diverse concentrations as shown below [23].

The drug compounds are usually present in natural sources such as apple leaves and fruits, pepper, sheep intestine, as well as sea sponge respectively [24]. Additionally, it is clear that the findings indicated that the computational difficulty of the Simple K-means algorithm is superior as compared to the Filtered clustering algorithm with the data set of lung cancer [25]. The K-Means algorithm was the most successful in exploring

the dataset; besides, it is well-matched for requirement clustering of medical applications which are mostly related to cancer [26].

Compound Name	Range of micromolar (Mm) Concentration
Parbendazole	31.2378
Phloretin	7.9464 ~ 8.6047
Piperlongumine	28.1711 ~ 29.6638
Neopeltolide	7.4405 ~ 25.5768

Examined final concentration ranges for certain cell lines (Source: Wanigasooriya C, Malka N. Halgamuge, A. Mohamad (2017) The analysis of anticancer drug sensitivity of lung cancer cell lines by using machine learning clustering techniques. International Journal of Advanced Computer Science and Applications (IJACSA) 8: 1-10).

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