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Predicting ideal Drug Therapies for Cancer using open Source Machine-Learning Algorithms

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Precision medicine has gained prominence is contemporary medical science; besides, computerized and homogenous assessment of patient data is supported by open source machine learning [1]. The aim of precision medicine includes making correct extrapolations or predicting the ideal pharmacotherapies from the genomic profiles of benign or malignant cancerous polyps among the patients [2]. In an idyllic situation, the predictions mostly depend on any existent robust cause and effect linkages [3]. The researchers propose an open source platform which can be valuable with regards to predicting initialed drug reactions from the gene expression profiles [4]. The platform uses a recursive feature elimination technique and an extremely adaptable support vector machine algorithm (SVM) [5]. They relied on the National Cancer Institute (NCI) to access drug reactiondata in addition to gene expression data from sixty cancer cells [6]. The data was used to build drug specific prototypes which are highly precise in estimating the drug receptiveness of diverse cancer cell [7].

Furthermore, the researchers proved that the predictive precision is maximized in case the learning data does not to pre-filter genes which are regarded as activating factors of cancer commencement or progression in the patient [8]. After applying their model to gene expression sets of data among patients who have been diagnosed with ovarian cancer (OC), they were capable of making correct predictions which can be considered as being similar to the reactions contained in the studies which were reviewed [9]. Importantly, by developing an open source algorithm, the scholars intended to ease its experimentation in diverse cancer settings and cancer categories which can promote modifications and enhancements in the successive future usage [10].

Genome-wide association studies (GWAS), mapping of quantitative trait loci (QTL), and sequencing of human genome processes have immensely assisted in creating greater awareness about the molecular trails linked to human diseases [11]. The usage of open-source writings and substantial dissemination of data have benefitted from such efforts [12]. Lately, drug prediction in cancer treatment has integrated machine learning (ML), each linked with varying levels of achievement, for instance, the pRRophetic and Bioconductor [13]. As indicated, the researchers proposed an open source software platform to predict response of cancer medication whereby during the pilot phase, they explored or accessed dataset which is freely available;then, they were subjected to formatting and later they divided the array files into investigational and learning sets [14-15]. Similarly, the researchers found out that the predictive precision was augmented when a variety of cancer categories were used to construct upon the models [16]. Lastly, the predictive accuracy was considerably lowered after learning data which are built using predetermined biotic models were pre-sorted [17-18]. The researcher proved that the predictive accuracy can be increased by developing Support Vector Machine-based models across diverse categories of cancer [19].

Choosing suitable learning dataset to construct the extrapolative simulations of cancer medication reaction is difficult since scientists or researchers have not fully described the molecular processes which cause cancer progression or onset [20]. Therefore, it is possible that a gene expression arrangement that is linked to a certain cancer disease might be causative factor of cancer development. The researchers made appraisal of two Support Vector Machines-derived frameworks developed to make estimate of the cancer treatment carboplatin which is usually extensively prescribed in the market to determine their relative accuracies [21]. Medication reaction and gene expression profiles were utilized to construct the respective frameworks. There has been a restricted usage of open source algorithms in performing medication prediction due to the lack of online repositories as compared to the resources which are accessible for machine learning applications, for instance, which facilitate depositing of other computational solutions [22]. The researchers are confident that the open source support vector machine algorithm can be valuable towards improving the individualized cancer medicine and drug extrapolation [23]. The algorithm combines a single data standardization approach with an ordinary Support Vector Machine methodology which is then implemented in seven commonly drugs used during chemotherapy as shown below [24-25].

The drug reaction had high levels of prognostic precision when the framework was constructed using data from diverse cancer categories [26]. The study outcome corroborates the current available proof that stipulate

that optimum cancer drug response's molecular signatures are not essentially defined by the tissue that causes cancer disease [27]. Furthermore, the outcomes prove that considerable enhancements can possibly be done in machine learning-based systems to improve their predictive accuracy especially through modulating the format and the kind of learning set of data as utilized in the process of building the model [28].

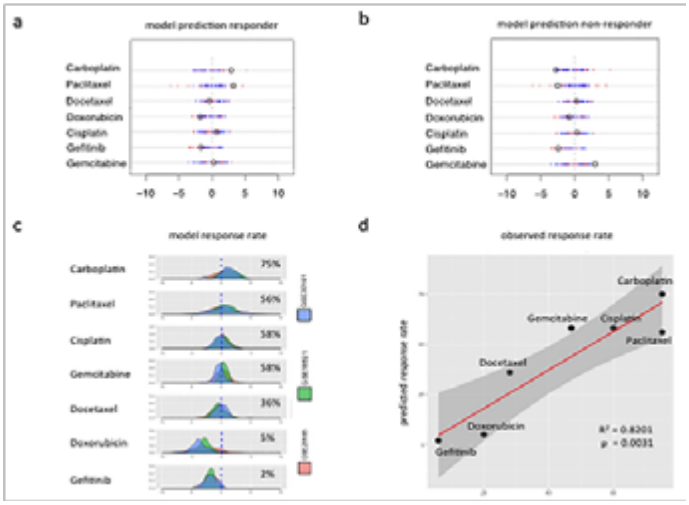

Figure 1: Model prediction and response rate [1].

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