Exact Prediction of Various Anticancer Medication Efficacy Using Multi Target Regression and Support Vector Regression Analysis

Germano Almeida*

Department of pharmacology, US

Abstract

Cæ}&^¦ ¦^{æå}• æ •å*}ì,&æ}c *¦[àæ¦ @^æ¦c@ &[}&^¦}, æ}å c@^ å^ç^¦[] {^}c [~ ^ ^&càç^ æ}cå&æ}&^¦ {^åå&æcå[}• å• &¦˘&åæ¦ ~[¦ å{}¦¦[çå}*]æcå^}c [˘c&[{^•. H[¸^ç^¦,]¦^åå&cå}* c@^ ^ &æ&^ [~ åì ^¦^}c æ}cå&æ}&^¦ å¦˘*• å• æ &[{}¦^¢ cæ•\ å˘^ c[c@^ @^c^¦[*^}^åc^ [~ &æ}&^¦ æ}å c@^ {˘¦cå-æ&c[¦åæ¦ }æc˘¦^ [~ å¦˘* ¦^•][}•^. I} c@å• •c˘å^, ¸^]¦[][•^ æ }[ç^¦ æ]]¦[æ&@ c@æc &[{àå}^• {˘¦cå-cæ¦*^c ¦^*¦^••å[} æ}å •˘]][¦c ç^&c[¦ ¦^*¦^••å[} æ}æ¦^•å• c[æ&&˘¦æc^¦^]¦^åå&c c@^ ^ &æ&^ [~çæ¦å[˘• æ}cå&æ}&^¦ {^åå&æcå[}•. V@^ •^¦^&cå[} [~ æ}•^¦^å&c Mæ ç^& ^ &^ Å &æ]c˘¦^ c@^ å}c¦å&æ&c ¦^¦æcå[}•@å] • à^c¸^^} {˘¦cå]¦^ å¦˘*• æ}å c@^å¦ cæ¦*^c•. V[[ç^¦&[{ ^ c@^•^ ¦å{åcæcå[}•, ¸^]¦•^•^}c æ &[{}¦^@^}•åç^ ~¦æ{^¸[¦\ c@æc ˘cå¦å:^• {˘|cå-cæ¦*^c ¦^*¦^••å[} æ}å •˘]][¦c ç^&c[¦ ¦^*¦^••å[} æ}æ¦^•å• ~[¦]¦^åå&cå[} [~ æ}cå&æ}&^¦ {^åå&æcå[} ^ &æ&^. V[~˘¦c@^¦ ^}@æ}&^ c@^]¦^åå&cåç^]^¦-[¦{ æ}&^, ¸^ å}c^*¦æc^ •˘]][¦c ç^&c[¦ ¦^*¦^••å[} æ}æ¦^•å• å}c[[˘¦ -¦æ{^¸[¦\. Ù˘*]][¦c ç^&c[¦ ¦^*¦^••å[} å• æ][¸^¦~˘¦ {æ&@å}^ ¦^æ¦}å}* æ¦*[¦å[@{ c@æc ^ &càç^¦^ @æ}å¦^ @å*@-åå{^}•å[}æ¦ åæcæ æ^c æ}å }[}¦å}^æ¦ ¦^¦æcå[}•@å]•. Ic æ¦¦[¸¸ ˘•c[à˘ì¦å ¦[à˘•c { {å^¦• c@æc &æ} æ&&˘¦æc^¦^]¦^åå&c æ}cå&æ}&^¦ {^åå&æcå[} ^ &æ&^.

Keywords: Exact prediction; Anti-cancer medication e cacy; Multi-target regression; Support vector regression analysis

Introduction

Cancer continues to be a major global health challenge, causing a signi cant burden on individuals, families, and healthcare systems worldwide. e development of e ective anticancer medications plays a critical role in improving patient outcomes and reducing mortality rates. However, predicting the e cacy of di erent anticancer drugs is a complex task due to the heterogeneous nature of cancer and the multifactorial aspects of drug response. Traditionally, the selection of anticancer medications for patients has been based on empirical evidence, clinical trials, and general guidelines. While these approaches provide valuable insights, they are limited in their ability to account for the individual variations in patient response and the diverse molecular mechanisms underlying cancer growth and progression. In recent years, there has been a growing interest in leveraging computational methods and machine learning techniques to enhance the prediction of anticancer medication e cacy. ese approaches aim to utilize the vast amount of available data on molecular targets, pharmacokinetics, and patient characteristics to develop accurate and personalized models for drug response prediction. However, most existing predictive models focus on single drugs and fail to consider the intricate relationships between multiple drugs and their targets. is limitation hinders their ability to capture the synergistic e ects of combination therapies or accurately predict the e cacy of novel, multi-targeted anticancer drugs. To address these challenges, we propose a novel approach that combines multi-target regression and support vector regression analysis for the precise prediction of anticancer medication e cacy. By integrating multiple targets and molecular descriptors into our model, we aim to capture the complex interplay between drugs and their respective targets, thereby improving the accuracy of our predictions [1-5].

Discussion and Conclusion

In this study, we presented a comprehensive framework for the exact prediction of various anticancer medication e cacies using multi-target regression and support vector regression analysis. Our approach aimed to address the challenges associated with predicting drug e cacy in the context of heterogeneous cancers and the intricate relationships between multiple drugs and their targets[6-10].

rough the integration of multi-target regression, we were able to

proteomic data could further enhance the predictive performance of