ANALYSIS OF THE RELATIONSHIP BETWEEN CANCER CELL LINES AND DRUG SENSITIVITY USING OPEN SOURCE DATA

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KEY WORDS

- ✓ drug sensitivity
- ✓ Z-score
- ✓ integration of multiple data sources
- ✓ data preprocessing
- ✓ machine learning models

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THESIS ABSTRACT

Cancer tissues exhibit a genetically dynamic structure due to the accumulation of mutations, and the emergence of new mutations may alter the efficacy of anticancer drugs. The aim of this study is to analyze the relationship between genetic mutation profiles and drug sensitivity and to develop a machine learning model capable of predicting drug response in cancer cells based on this relationship.
In the first phase of the study, drug–mutation interactions were investigated in small cell lung cancer. Cell line data, mutation burden, tissue information, and IC50 values were integrated into a single dataset. The resulting dataset was used in machine learning analyses to predict drug sensitivity based on mutation burden. In the second phase, a broader approach was adopted by integrating drug sensitivity data from all cancer cell lines, somatic mutation profiles, and gene–drug interaction information obtained from multiple databases.

APPLICATION AREAS OF THE THESIS RESULTS

The developed models provide a predictive decision-support framework that may guide experimental studies. The findings highlight the critical role of genetic mutations in determining drug response and present a robust framework that may contribute to personalized cancer therapy.

ACADEMIC ACTIVITIES

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