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Customized Drug Recommendation for Lung Carcinoma using Deep Learning of Drug-Drug Interaction and Drug-Gene Interaction Methods †

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Abstract: Patients taking more than one drug have various side effects, add toxicity, and has adverse effects on the treatment of cancer patients. To overcome these adverse drug effects, the DDI patterns are studied and analyzed. The DDI patterns are accessible as Restful API function calls in some standard datasets like Drug Bank. The Drugs related to cancer treatment are first identified, and their interactions with other drugs are retrieved from the Drug-Drug Interaction Checker of Drug Bank. XML parser is used to parse the content retrieved from the search, and the result is in the form of a description of the drug's inter-activeness, severity level, and procedure to deal with the interaction. Using Natural language processing techniques, the underlying objects, concepts, and their relationships are extracted from description and also from the procedure. The extracted information is then represented in a standard format using UMLS standardized naming system. This is represented in the form of a feature vector that has one or more drug names with their ids as input attributes and the resultant interactions as a relationship between these interacting drugs.
DGI patterns are also analyzed using various datasets like RNA Sequencers, Gene expressions, Pathway datasets, and PharmGKB datasets. First, the effective biomarkers for lung cancer patients are identified using a genomic approach. This will give a gene expression as output diverse cancer gene mutations are implicated as markers of sensitivity or resistance to a broad range of anticancer drugs, indicating that genomic biomarkers could inform the therapeutic selectivity of many cancer drugs.

Keywords: Drug-Drug Interaction, Drug-Gene Interaction, Deep Learning techniques

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Conflicts of Interest

The authors declare no conflict of interest.