The text discusses the utilization of drug screening data from extensive bulk gene expression databases for analyzing and determining the optimal clinical application of cancer drugs. With the increasing availability of single-cell RNA sequencing (scRNA-seq) data, there is an opportunity to gain insights into improving therapeutic effectiveness by studying the heterogeneity of drug responses among cancer cell subpopulations. The authors propose a computational approach called scDEAL, a deep transfer learning framework designed for predicting cancer drug responses at the single-cell level. This is achieved by integrating large-scale bulk cell-line data. The key feature of scDEAL is its ability to harmonize drug-related bulk RNA-seq data with scRNA-seq data. It achieves this by transferring a model trained on bulk RNA-seq data to predict drug responses in scRNA-seq. Another notable aspect of scDEAL is its use of integrated gradient feature interpretation to infer the signature genes associated with drug resistance mechanisms. The authors benchmarked scDEAL on six scRNA-seq datasets and demonstrated its model interpretability through three case studies. These case studies focused on drug response label prediction, gene signature identification, and pseudotime analysis. The text concludes by expressing the belief that scDEAL could significantly contribute to the study of cell reprogramming, drug selection, and repurposing, ultimately leading to improvements in therapeutic efficacy.