Q-omics: smart software for assisting oncology and cancer research

The heterogeneity of cancers limits the reproducibility of drug response and target-biomarker relationships in patient samples. A large amount of multiomics data such as mutations, gene/protein expression, immune scores (tumor-infiltrating cells), drug response, and RNAi (shRNAs and CRISPRs) screening data, enables pan-cancer surveys for finding common oncogenic drivers and tumor-agnostic therapeutics. Q-omics, comprehensive tool for multiomics data mining, provides consensus analyses of associated data pairs in diverse cancer lineages and subtypes, improving the reproducibility of prognostic power of biomarkers and anticancer efficacy of targets (or drugs). All of RNA/protein expression, drug response, patient survival, CRIRSPR/shRNA screening data were integrated from TCGA, GDSC, CCLE datasets, etc. Improvements in data access and user interfaces make it easy for general scientists to carry out their data mining practices without computational expertise. In our analysis, genes in cell proliferation, migration, DNA repairs and apoptosis, were prioritized as most consensus, pan-cancer prognostic biomarkers in patient survival. In the association between CRISPR (targets) knockout and RNA (biomarkers) expression data in ~1,000 cell lines, the lineage consensus of the association increased the reproducibility of the target-biomarker relationships in the validation experiment. Q-omics (http://qomics.io) improves the utility of cancer omics big data for both computational and experimental researchers at all levels of cancer research.