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TITLE: Data science in the age of cancer genomics and drug discovery

ABSTRACT: While biomedical research over the last decade has led to significant advances in our knowledge of cancer, pharmacogenomics, development of novel drugs and new drug targets, there still exist challenges in the treatment of many cancers. For example, epithelial ovarian cancer (EOC) is the fifth leading cause of cancer death among women in the United States. The standard treatment for patients with advanced EOC is initial debulking surgery followed by carboplatin-paclitaxel combination chemotherapy. Unfortunately, most patients relapse and die, with the five-year survival around 45%. In addition, those patients that initially respond to taxane-platinum therapy eventually develop platinum-resistant tumors and relapse. Thus, finding novel therapeutics for treating EOC is essential. Often, drug studies have relied on high-dimensional ‘omic data and in vitro drug phenotype data assessed on cancer cell lines (CCL). However, recent publications have highlighted some issues with the use of these standard CCL sets. In this presentation, I will discuss some of the challenges in the use of CCLs and how the wealth of information collected on CCLs and/or cancer patients can be used to determine novel drug and/or drug targets using bioinformatics and statistical methods, including the use of Connectivity Mapping (CMAP).