

Abstract

Cancer genomes often harbour hundreds of genetic variants. These variants can be drivers or passengers of tumorigenesis and can create new vulnerabilities for therapeutic interventions. Approaches to systematically map genetic vulnerabilities have provided fundamental insights into the genetic architecture of cells. Genetic maps, based on gene-gene or gene-small molecule interactions can be used to functionally annotate uncharacterized genes, to delineate cellular pathways and to identify resistance mechanisms in cancer. Recent studies, however, also highlighted the context-dependency of synthetic lethal interactions in tumor cells, requiring novel approaches to map landscapes of static and cell-state dependent genetic interactions. In the seminar, experimental and computational approaches to integrate large-scale genetic vulnerability data towards the next iteration of genetic interaction maps of cancer cells will be discussed. We are particularly interested in increasing resolution of these maps and to understand how genetic networks differ between individual cancer types. We further explore how machine learning methods can be applied to predict gene function based on the similarity of genetic interaction profiles. We envision that these approaches will help to predict new drug targets and understand mechanisms of drug resistance.