Cancer relapse is a major complication after treatment of patients and a large number of studies have investigated molecular mechanisms responsible for tumor resistances. In bioinformatics, several cell lines, representative of the panel of human patients, are characterized by high-throughput technologies and exposed to clinically relevant drugs. By integrating biological knowledge with the cellular response of each drug separately, robust preclinical model should offer personalized cancer treatment to patients.

The intratumor heterogeneity fuels the evolution of each subpopulation of cancer cells with distinct biology and drug sensitivity to a single drug.

Here, an algorithm is implemented that aims at delineating cancer subpopulations, relating their respective sensitivities to each drug and ultimately predicting optimal combinations that are complementary in terms of subpopulation targeting. Our ability to understand tumor response offers the possibility to anticipate the escape mechanism that tumors use