Evolution and heterogeneity

Brief Synopsis:

Each patient's cancer has a unique population of tumor subclones and evolutionary trajectory during treatment. DNA and single cell RNA sequencing has revealed a significant degree of heterogeneity and subclone diversity, which combine with effects of the microenvironment to provide a substrate for evolution over time under the selective pressure of treatment. We use unique sets of patient biospecimens and dynamic models that account for tumor cell evolution, phenotype, and interactions during progression to a drug resistant state. We will show how tumor cells evolve during treatment with endocrine and CDK4/6 therapy, and how resistant populations shift states from estrogen dependence to growth factor signaling during therapy. Our single cell data will also provide an understanding of how cancer cells can communicate and provide survival benefits to each other during treatment.