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Learning and perturbing the evolutionary mechanisms driving therapeutic resistance in cancer

In this talk I will describe efforts to directly measure evolution of bacterial pathogens under antibiotic stress and lung cancer cells under targeted therapy. The measurements I will describe are designed specifically to parameterize two different mathematical models, and represent novel assays. The first, which we term an evolutionary 'game assay' allows us to parameterize a payoff matrix from time lapse data of cells under therapy. The second, a high throughput evolution and collateral sensitivity experiment, allows us to create collateral sensitivity likelihood maps, which we hope can be translated into tools to aid clinical decision making.