SQUAB: Simultaneous quantification and biomarker detection for in-vitro drug combination screens

High-throughput drug sensitivity screens enable rapid in-vitro testing of compounds on cancer cell lines, in order to determine the efficacy of a certain treatment. Coupled with various "omics" characterisations of the cancer cell lines, these experiments provide the ingredients necessary to discover predictive biomarkers of treatment effect. However, in-vitro cell viability measurements are frequently corrupted by measurement error due technical error sources and natural biological variability, making the precise quantification of treatment efficacy difficult. Furthermore, the process of biomarker discovery is usually completely disentangled from the noisy reality of the raw viability measurements, utilising crude summary measures of treatment efficacy, estimated with no uncertainty quantification. In SQUAB, we propose a model that jointly estimates dose-response for drug combinations, while at the same time providing biomarker discovery for synergistic interaction effects. This is achieved through a multi-output Gaussian process formulation that allows the estimation of non-linear dose-response relationships, while at the same time incorporating high-dimensional "omics" measurements for biomarker discovery. The selection of potential biomarkers is achieved using a horseshoe prior within the multi-output GP kernel construction.