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Point Process based Detection of Drug Induced Cell Morphology Changes

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The development of drugs targeting the cancer stem cell population in solid tumors is hampered by the lack of a valid cell model and the complex genetic heterogeneity across tumors. Both factors make it hard to assess new targets for the drugs or to predict drug responses in individual patients. We tackle this problem by combining mathematical and experimental approaches to develop a biobank of highly characterised cancer stem cell cultures as a model for cancer heterogeneity.

In our study, we use image-based high-throughput cell screening to define the spectrum of therapeutically relevant regulatory differences between patients. That means we expose cultured cells to different treatments and drug doses followed by fluorescence as well as bright-field microscopy. The effect of the treatment is assed by extracting morphological features from the image data.

Low dimensional features, such as cell intensity, indicate if cell proliferation is affected by the presence of a drug. In this work, we suggest a point process statistics based method to reliably detect the dose at which cell morphology becomes significantly effected by the treatment. Knowing this dose provides the foundation to study higher dimensional features, like subtle changes in cell morphology and cell-cell interaction, to understand the mechanism how the drug perturbs the life cycle of the cell. Quantifying and characterising such changes will eventually contribute to the goal to accurately treat disease subgroups.