Tracking Cellular Senescence: A Single-Cell Analysis Approach

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ABSTRACT

The evolution of single cells during time is a heterogeneous and complex process, influenced by interactions between surrounding cells and between cells and their environment. The standard method for analyzing cell dynamics involves time-lapse microscope videos. During the period of observation, various processes occur: cells may die, duplicate and form agglomerations. In our analysis we are particularly focused in the phenomenon of senescence (permanent cell cycle arrest) [1].

We conducted an experiment with living HEK 293T cells. The culture medium - DMEM (Dulbecco's Modified Eagle Medium), FBS (Fetal Bovine Serum) and penicillin-strepromycin - on the well plates was additioned with different levels of doxorubicin to induce senescence. The images were captured using the Incucyte S3 microscope every 20 minutes for 72 hours.

To develop a single-cell analysis approach for studying senescence, the primary challenge is to accurately extract cell trajectories [2, 3]. We utilized the dataset in order to generate a gold-standard ground truth benchmark. This was done by manually tracking the positions of individual cells over time using a custom-built application. Additionally, we will show how an empirically grounded agent based model [4] able to faithfully reproduce the cells' behavior under different conditions, can be used in conjunction with the ground truth data to enhance the prediction capabilities of an automatic tracking algorithm.

We will use the extracted trajectories to characterize the morphological evolution and the dynamical behavior of senescent cells. Eventually we will assess if and how contagion effects among normal and senescent cells exist.

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