Bayesian Sequential Analysis of T-Cell Migration Data

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We consider $CD8^+$ cytotoxic T lymphocytes, one of the main cytotoxic killer cells present in the human body to eliminate target cells that are pathogen-infected or tumorigenic. During their search, T-cells pass through various complex biological microenvironments, of which the extracellular matrix (ECM) is one of the core elements. Collagen matrices of different densities were used to simulate the ECM of different tissues and to examine the migration behavior of the T-Cells. We use the single cell tracking data obtained in [1] as an input for an analysis method developed by Metzner et al. [2]. In this method, an autoregressive process of order 1 (AR-1) with time varying parameters is imposed as the governing model of motion and the distribution of the parameters is inferred via a Bayesian sequential updating scheme per cell and per time step. It is found that some cells undergo an abrupt parameter switch, which can be attributed to a fast and slow motion of the cell. Especially for the lowest density collagen matrix, this leads to two distinct parameter regimes in the time and ensemble averaged distribution. When the slow moving cells migrate through the collagen matrix, they interact with it thus causing deformation by forming channels in the matrix. Other cells can enter these channels and hence it is presumed that the fast motility mode arises through cells moving inside the channels.

[1] Z. Sadjadi et al., Biophysical Journal 119, 2141–2152 (2020)
[2] C. Metzner et al., Nature Communications Volume 6, 7516 (2015)