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Fate of a naive T cell: a stochastic journey

L. Higuera Romero; M. López García; M. Castro Ponce; N. Abourashchi; G. Lythe; C. Molina París

Abstract-

The homeostasis of T cell populations depends on migration, division and death of individual cells (1). T cells migrate between spatial compartments (spleen, lymph nodes, lung, liver, etc.), where they may divide or differentiate, and eventually die (2). The kinetics of recirculation influences the speed at which local infections are detected and controlled (3). New experimental techniques have been developed to measure the lifespan of cells, and their migration dynamics; for example, fluorescence-activated cell sorting (4), in vitro time-lapse microscopy (5), or in vivo stable isotope labeling (e.g., deuterium) (6). When combined with mathematical and computational models, they allow estimation of rates of migration, division, differentiation and death (6, 7). In this work, we develop a stochastic model of a single cell migrating between spatial compartments, dividing and eventually dying. We calculate the number of division events during a T cell's journey, its lifespan, the probability of dying in each compartment and the number of progeny cells. A fast-migration approximation allows us to compute these quantities when migration rates are larger than division and death rates. Making use of published rates: (i) we analyse how perturbations in a given spatial compartment impact the dynamics of a T cell, (ii) we study the accuracy of the fast-migration approximation, and (iii) we quantify the role played by direct migration (not via the blood) between some compartments.

Index Terms- T cell, stochastic model, continuous-time Markov chain, single cell, cellular fate, migration, division, apoptosis

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