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Analysis of protein dynamics in the pericellular matrix JAN SCRIMGEOUR, DYLAN YOUNG, Clarkson Univ — The pericellular matrix (PCM) is a low density, hydrated polymer coating that extends into the extracellular space from the surface of many living cells. The PCM controls access to cell and tissue surfaces, regulating a diverse set of processes from cell adhesion to protein transport and storage. The cell coat consists of a malleable backbone - the large polysaccharide hyaluronan (HA) - with its structure, its material properties, and its bio-functionality tuned by a diverse set of HA binding proteins. These proteins add charge, cross-links and growth factor-like ligands into the brush. Dynamic interactions between the HA and its binding proteins can be observed using single particle tracking in a fluorescence microscope. The resulting single molecule trajectories can contain evidence of site hoping, with the proteins dynamically moving between different states of motion as they bind and unbind from the HA. Here, we present an evaluation of hidden Markov models for the analysis of such multi-mobility trajectories. Simulated trajectories are used to probe the limits of this approach for molecular trajectories of limited length and the results are used to inform the design of particle tracking experiments.

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