Stochastic description of pilus retraction dynamics

MARTIN LINDÉN, Condensed Matter Theory, KTH, Stockholm, Sweden, EMIL JOHANSSON, MATS WALLIN, Condensed Matter Theory, KTH, Stockholm, Sweden, ANN-BETH JONSSON, MTC, KI, Stockholm, Sweden — Motility of certain gram-negative bacteria is mediated by retraction of type IV pili surface filaments, which are essential for infectivity. Type IV pili are helical filaments with 4 nm periodicity and 5 subunits per turn. The retraction is powered by a strong molecular motor protein, PilT, producing very high forces in excess of 100 pN[1]. One possible explanation for the high forces are that several ATP are hydrolyzed to retract each subunit.

We consider a widely used class of discrete hopping models, which has been used to describe well-known motor proteins such as kinesin[2] and myosin[3]. The model describes recent experimental measurements[1] on Neisseria gonorrhoeae well, and makes several interesting predictions for the randomness of the retraction dynamics.