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Stochastic description of pilus retraction dynamics MARTIN

LINDÉN, Condensed Matter Theory, KTH, Stockholm, Sweden, EMIL JOHANSSON, MATS WALLIN, Condensed Matter Theory, KTH, Stockholm, Sweden, ANNBETH 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.

1. Maier et al, PNAS 101:10961 (2004)
2. M. E. Fisher and A. B. Kolomeisky, PNAS 98:7748 (2001)
3. A. B. Kolomeisky and M. E. Fisher, Biophys. J. 84:1650 (2003)

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