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Stochastic Regulation of Actin Bundles Growth Dynamics¹

PAVEL ZHURAVLEV, YUEHENG LAN, GAREGIN PAPOIAN, Department of Chemistry, The University of North Carolina at Chapel Hill, Chapel Hill, NC, 27599-3290 — Actin polymerization in living cells exemplifies biological dynamical processes where mechanics is intrinsically coupled to chemistry. Modeling the dynamics of biochemical reaction networks may by itself be challenging, because ordinary chemical kinetics is often inapplicable when a small copy number of individual proteins are involved. Instead, to treat large fluctuations, the reaction dynamics should be computed with stochastic methods. We have developed an extensible mechano-chemical model describing the dynamics of actin bundle growth and retraction, where all reaction and diffusion processes are treated stochastically. We have applied our computational algorithm to study the dynamics of filopodia, where polymerization rate at the tip is coupled to the membrane force and fluctuations. Our approach allows to investigate how a particular regulatory protein, participating in the relevant signaling network, influences the distribution of filaments in the bundle, growth and retraction rates and other dynamical characteristics. Among these proteins, the most interesting are capping proteins (that block polymerization), formins (that promote polymerization), fascinins (that connect the filaments in the bundle together) and myosins (molecular motors that have been observed in filopodia and may participate in active transport to the tip).

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