The effect of actin filaments organization on membrane patterns and stability

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***Short Abstract* — Actin polymerization is known to be a mechanism for force production in living cells. It is responsible for several dynamical phenomena; in this project we are interested in the formation and destruction of membranal protrusions on the cell membrane, such as: microvilli, stereocilia, filopodia and lamellipodia. These structures are observed to be either stable or highly dynamic and also to interact each other (depending on the cell functionality and its environment). An additional physical ingredient that is taken into account in the modeling of the membranal protrusions is the organization of actin filaments bellow the membrane. The aim of this work is to model these protrusions and understand their behaviors.**

Introduction

Cells come in a great variety of shapes and their shape plays a crucial role in their functionality. The cell's shape is determined by its cytoskeleton, which is composed primarily of actin filaments. Common phenomena in cell morphology are cellular protrusions containing a core of parallel polarized actin filaments [1, 3]. These protrusions have different functions depending on the cell type. They also differ in properties such as length, thickness, lifetime, packing density and more. Their roles include increasing the cell's surface area (microvilli), mechanical sensory (filopodia), tissue invasion (invadopodia, podosomes), cell motility (podosomes, filopodia), extra cellular matrix (ECM) degradation (podosomes) and mechano - electrical signaltransduction (stereocilia). Although the model concept is rather general, the work will be concentrated on the formation, stability and interaction of filopodia protrusions [2], with two main aspects that are taken into account: one is the physical property of the membrane and the other are the biochemical reactions which connect to the organization of actin filaments.

I. Model Details

Our model is a mean-field, continuum model describing the interaction of a lipid membrane with the concentration of two fields of protein complexes: one that nucleates "vertical" (to the membrane) actin filaments, and one that nucleates "horizontal" actin filaments. The membrane dynamics is governed by a Helfrich Hamiltonian. The "horizontal" filaments are taken to increase the membrane surface tension due to the interaction between the cytoskeleton (horizontal) branched filaments and the membrane [4]. While the vertical filaments are taken to form bundles that polymerize and apply a perpendicular force on the membrane. The biochemistry that governs the dynamics of these two concentrations is derived from rate constants of the binding/unbinding process of a Boltzmann factor using a free particle chemical potential in the Landau Ginzburg approximation. The form of the biochemistry part of the dynamical equations is similar to the Fitzhugh-Nagumo model [5].

II. Results

First the general partial differential equations of motion are reduced to coupled algebraic equations and solved for the homogenous state in order to get the fixed points of the dynamical system. The system is chosen to be in the bistable regime where two fixed points are stable and one is unstable for small perturbations. Using linear stability analysis for the general equation we get the dispersion relation and can check the stability of the fixed points. The choice of the system to be stable to small perturbations comes from the belief that biological systems will not develop patterns from small disturbances. Therefore, in order to create a pattern such as filopodia, the biological system "should" apply a high force on the membrane, i.e. above some threshold. Furthermore the filopoda protrusions are observed to be localized structures. Therefore, in order to see if the localization is connected to the interaction between the protein concentrations and the membrane, the system without the coupling to the membrane is chosen to be in the regime of no localized solutions, i.e. any localized perturbation either expands or contracts [6,7]. Then, the coupling to the membrane is added, and we observe localized solutions. The system of equations is solved numerically, and we also calculate the interaction between these localized structures [8].

III. Conclusion

A mean-field model is used to describe the physical behavior of nontrivial actin-driven patterns forming on a membrane. Future comparisons with experiments will allow us to validate this model with respect to observed filopodia.

Acknowledgements: This work was funded by BSF grant no. 2006285.

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