Abstract

In this paper we study influenza viral membrane deformation related to the refolding of Hemagglutinin (HA) protein. The viral membrane is modeled as a two dimensional incompressible lipid bilayer with bending rigidity. For tensionless membranes, we derive an analytical solution while for membrane under tension we solve the problem numerically. Our solution for tensionless membranes shows that the height of membrane deformation increases monotonically with the bending moment exerted by HA-proteins and attains its maximum when the size of the protein cluster reaches a critical value. Our results also show that the hypothesis of dimple formation proposed in the literature is valid in the two dimensional setting.

Key-Words: bending rigidity, equilibrium membrane shape, HA-protein, influenza virus, lipid bilayer, two-dimensional membrane.