1. Introduction

1.1. A. *Basic biology of membranes and membrane fusion.* Biological membranes consist of lipids and proteins, with the lipids self-organized into sheets and the proteins embedded into or bound to the sheets. The lipid sheets are arranged as a "bilayer," two lipid monolayers with lipid acyl chains (i.e., hydrophobic tails) directly abutted against each other and sequestered from the aqueous solutions bathing the two sides of the membrane by the polar headgroups of the lipid molecules. The lipid bilayer membrane appeared early in evolution (1), and provides the barrier between interiors and exteriors of all eukaryotic (nucleus-containing) cells and their organelles. The architectural organization of the lipid bilayer is critical to life, and the functioning of proteins embedded in membranes is intrinsically connected to the bilayer structure in which they reside. The lipid bilayer also functions as an insulator for all activity within the body: the generation and propagation of action potentials in neurons and heart cells (2), and the voltage across mitochondrial membranes (which function as cellular "batteries") that drives the production of ATP, the currency of cellular energy (3). Bilayer lipids provide extracellular (4) and intracellular molecules (5) that integrate the functioning of cells within body tissues. These and a host of other cellular functions rely on the integrity of the lipid bilayer structure (6). The bilayer membrane is a complex, dynamic structure. Its lipids are asymmetric in all directions, are in rapid motion, rotating, for example, 10^7 times/sec (7), and both the mass and electron density profiles of each lipid are heterogeneous along its length (1.5 – 2 nm) (8).

Membrane fusion is the central process of many vital cellular functions, such as neurotransmitter release in the brain, insulin release from the pancreas, and trafficking of materials between organelles. Fusion is also the means by which many viruses (e.g., HIV, hepatitis, flu, Ebola) infect cells. On the molecular level, fusion results in the joining of two aqueous compartments and the continuity of two formerly separate membranes. Fusion of membranes is not a spontaneous process—it does not occur through thermal fluctuations: membranes are stable, and when two lipid bilayers with biological compositions are experimentally forced against each other, they do not fuse (9). Proteins provide the specificity of fusion: the ability of one membrane to selectively fuse to another. But it is the lipids that confer the fluidity necessary for membranes to deform into configurations that lead to fusion. During fusion, lipids must temporarily leave the bilayer arrangement for a non-bilayer configuration. Fusion proteins embedded in the membranes supply the energies required for these lipid rearrangements. Most experimental efforts directed toward fusion have focused on proteins, their associations with each other, their conformational changes, and ways they are regulated. Relatively little is understood about the natural behavior of membrane lipids: which motions easily occur and which require the interjection of protein action. To obtain a physically deep understanding of membrane fusion, the movements and reorientations of the lipids must be known.

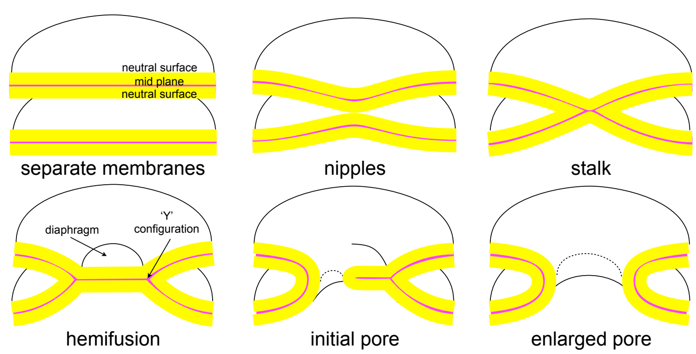

Fig 1

B. *Steps of fusion: hemifusion, pore formation, pore expansion.* Electron microscopy shows that membranes approach each other locally by protruding into "nipples" (10, 11). There is extremely strong experimental evidence that the two initially separate membranes merge to create a configuration known as "hemifusion" (12–17). At hemifusion, contacting proximal lipid monolayers of each bilayer have merged, but the distal monolayers remain distinct (Fig. 1). An hour-glass-shaped "stalk" is the initial hemifusion connection. Stalk geometry has been experimentally deduced by X-ray crystallography (18, 19). In the stalk structure, the distal monolayers have just begun to contact each other. When the stalk expands laterally, the more extensive contact of distal monolayers creates a "hemifusion diaphragm." A hemifusion diaphragm is a pure lipid bilayer devoid of proteins (17). At its circumference, the diaphragm connects to the two original membranes, creating a 'Y' configuration. Formation of an initial pore in the hemifusion diaphragm establishes aqueous continuity, and the transfer of aqueous contents now occurs (Fig. 1). It has been experimentally shown, for several cellular systems, that some states of hemifusion can lead to fusion pore formation whereas other states of hemifusion cannot (12, 13), but the reasons for this are unknown; it remains a fundamental question in the field of membrane fusion. Forces that could cause lipids to rearrange into a fusion pore, such as membrane tension, are known (20), but the lipid rearrangements and the consequences of water movement that must accompany pore formation are unknown. The initial fusion pore must expand to permit the transfer of large molecules, such as proteins (e.g., insulin), from intracellular vesicles to the extracellular space; for virus, pore expansion permits its genetic material to pass into cytosol, initiating infection. The physics of this expansion has been theoretically modeled, but pore geometry was fixed (as a toroid) and consequences of a non-zero aqueous viscosity were ignored (21, 22).

C. *Past theoretical investigations.* Mathematical modeling of membrane fusion has included microscopic all-atom simulations of molecular dynamics (9, 23–25), mesoscopic calculations (26–29), and macroscopic approaches of continuum membrane mechanics (30–34). Each has its range of applicability. All-atom simulations could, in principle, eventually (subject to the accuracy of the force fields and difficulties of multi-scale analysis [ref]) explicitly yield the motion of every atom during steps of fusion. But the time scales of these simulations are presently much too short to compare to experimental results (35–37). Mesoscopic calculations can cover a wide time range, but the coarse grain description of lipids and surrounding water may not capture essential properties of the system (38). Continuum models have the merit that they cover all relevant time ranges and lead to predictions that can be experimentally tested. Continuum theories cannot reveal phenomena caused by molecular interactions that are atypical of the average continuous material, but such lipid interactions are unlikely to drive fusion: lipid interactions are dominated by volume exclusion, van der Waals dispersion forces, and hydrogen bonds, and these interactions are roughly the same for all lipid species. Overlap between the model approaches can be quite fruitful, especially when predictions are experimentally testable and can be compared. Generally, there is overlap between coarse grain and continuum models both spatially and temporally (39).

The continuum mechanical description of membranes predicted that the ability of two membranes to hemifuse should depend on the spontaneous curvature of the contacting leaflets (40, 41): hindered by positive spontaneous curvature and promoted by negative curvature. This was confirmed experimentally (42), and showed that the predictions of continuum mechanics could be successfully "translated" into experimentally controlled variables. Biologists could therefore use theory to investigate phenomena without the need for them to entirely comprehend the complexity of the mathematical equations involved.

But classical continuum formalisms used to date have limitations. They assume that membranes are at equilibrium, and thus time courses of changes during fusion are not calculated. They also assume that elastic energies are conserved. Movements of membrane and aqueous solutions, however, must cause energy dissipation and this can, in fact, be large in membrane processes. For example, we have shown that in osmotic swelling and lytic bursting of vesicles (e.g., as occurs in hemolysis), more than 70% of the elastic energy stored in the vesicle membrane at the time of pore formation converts to heat after the Laplace pressure within the vesicle has collapsed (43). Because cellular environments are viscous, energy is dissipated during virtually every biological process.

Fortunately, several continuum approaches have been developed over the last twenty years or so—phase field (44, 45), level set (46–48) boundary integral (49, 50), immersed boundary (51–53), and direct monolithic (54–56)—that do not assume equilibrium and that account for energy dissipations. These methods have been successful in describing many and complex phenomena of condensed physical matter, but they have not been applied to biological processes. Field theories—systems of differential equations derived from a characterization of an energetic structure— are potentially a powerful way to self-consistently describe steps in membrane fusion.

D. *The phase field approach.* The forces within condensed matter are consequences of their material properties and are described by Navier-Stokes equations, a form of Newton's second law of motion. These forces cause the shape of a diffuse interface (in our case, the membrane) to change, which in turn generates a reactive force that tends to restore the prior shape. In terms of energy (rather than forces), this is the principle of virtual work which is central to the phase field method.

In classical continuum mechanics, the shape of a structure, such as a fusion pore, is assumed to be constant as the system evolves, even though this must run counter to physical reality. In contrast, phase field theory iteratively adjusts geometry over the entire time course, so that the shape of the structure adjusts, yielding energy minima at every time. In practice, this can be quite important: we have found that the energy of the commonly assumed geometry of a fusion pore (a toroid) is much larger than the energy of the minimal surface (see Aim 4).

The phase field method describes energy dissipation through the principle of "maximum dissipation." In essence the principle states that the sum of kinetic and elastic energies is converted to heat as fast as possible, maintaining constant temperature. For incompressible media (such as water and membranes), the phase field method allows the system to evolve so that elastic (and kinetic) energy decreases through the pathway of steepest descent that is consistent with the geometry at each moment.

Also, in the phase field method, an interface is not assumed to be a mathematical surface of zero thickness, but a bulk hydrodynamic material of small thickness, as is the actual case for biological and model bilayer membranes. The changes in energy of a diffuse interface as its shape and topology vary are accounted for by both the Helfrich elastic energy and a continuously varying phase field parameter, $\phi(x, t)$, as given by the Ginzburg-Landau form of energy (57–59). The principle of virtual work gives rise to a set of partial differential equations (PDEs) whose solutions directly yield the forces and velocities of matter at each point in space over time.

E. *Similarities between bilayers, liquid crystals, and interfaces; the use of phase field.* The Ginzburg-Landau formalism has had considerable success improving prior theories for liquid crystals and phase field methods have made it possible to model complicated interfaces between immiscible liquids. These methods can be applied to problems in membrane biology. Lipids within bilayers display positional and directional orders that resemble those of liquid crystals. The classical continuum theories for liquid crystals (60) have been generalized (61, 62) by phase field and other modern energy minimization methods, and this has led to reliable predictions of liquid crystal dynamics (63, 64). By adapting the phase field approach to bilayer membranes, the positional and directional orders of lipids can be calculated as a function of time, yielding the lipid motions that lead to the steps between intermediate states of fusion.

Biological membranes differ from liquid crystals, however, in that membranes are fluid and create an interface with water. The phase field method has been successfully used to calculate the dynamics of shape changes of interfaces, in response to applied forces, between immiscible fluids (65, 66). The phase field method does not pre-assign fixed geometries to interfaces, but rather employs time-dependent PDEs that account for physical properties of the fluids, such as their viscosities (45), to describe the fluids and the interfaces between them. This yields, as a function of time, the geometry of interfaces as an output of the calculations, strategies that can be applied to many biological processes in addition to membrane fusion.

F. *String method.* Phase field finds the minimum energy once a system is within a basin; a different method is needed to calculate the pathway to move from one basin to a higher basin. Biological systems can move energetically uphill since there are many ways to supply energy. For example, prior calculations have shown that, in general, the energy of a stalk is larger than the energy of separate membranes (33, 67, 68). The "string method" (69–71) finds the path that requires the least energy for a system under an external force (e.g., as supplied by fusion proteins) to go from the minimum of one basin to a higher minimum of another basin—the "mountain pass problem." The path of least energy is, by definition, the one whose tangents are everywhere parallel to the gradients of the energy functional. Past efforts by biophysicists have assumed that barriers are surmounted through a favorable confluence of thermal fluctuations, but in almost all biological situations this is not the case, and proteins supply the necessary energy. The string method treats the pathway as a greased string that adjusts until the least energy is found for steady state flow. At steady state, the external force that must be applied to surmount the barrier in a given time is exactly the force that is needed to constrain the system to the given path. Regardless of whether every step of fusion uses the path of least energy, determining this path will yield the features that are energetically optimal and will make explicit predictions as to possible molecular functions of fusion proteins in inducing reconfigurations of lipids.

1.2 Intellectual Merit

1.A major challenge in the large field of mathematical biology has been to generate paradigms in cellular biology that can be experimentally tested. Classical continuum mechanics has been stalled in advancing biological understandings. Our approach calculates geometries, does not assume equilibrium, and accounts for energy dissipation, overcoming the present bottleneck in the accurate depiction of changes in membrane shape and topology during fusion. Computational results, including characteristics of states of hemifusion that can proceed to pore formation and time courses of pore enlargement, can be compared to experimental results.

2. Solutions of PDEs that determine forces and velocities everywhere will require development of novel numerical schemes that can be applied to a large class of minimization problems.

3. The geometries of the stalk and fusion pore that yield minimum energies will be outputs, rather than inputs, of the model, permitting even investigators who continue to use traditional continuum approaches to benefit, as they can start with physically realistic configurations.

4. Topological changes are defining features of the process of membrane fusion. Traditional theoretical approaches cannot describe these changes. Combining the Helfrich Hamiltonian, as generalized by phase field (for the energetic profiles of membranes), and the string method, developed in the last few years, will yield pathways for surmounting energy barriers between topological states. These calculations are a means, not previously available, to obtain descriptions of major aspects of biological membrane fusion. Once other investigators derive the energetic profiles generated by proteins, our adaptation of the string method can be applied to a large class of cell biological processes.

5. The experimental techniques that can monitor lipid orientation–such as nuclear magnetic and electron spin resonance–cannot isolate the small fraction of membrane area that participates in fusion from the bulk of the membranes. The same limitation applies to calorimetric techniques that yield energy changes. The application of phase field theory to yield the dynamics of lipid reorientations in space and time and associated energy changes would reveal the events at the localized site of fusion. This would be a major contribution to the fusion field.

6. Biology poses problems that will require the development of new areas of mathematics. The geometric 'Y' at the boundary of a hemifusion diaphragm is not a true mathematical surface, but rather is a "singular set," so traditional methods applied to interfaces are not directly applicable. The finite element tools we develop (see Aim 3) can lead to new mathematical avenues for singular sets. Also, in using new representations of bilayer structures, we foresee new areas in the calculus of variations, including exploring the existence and regularity of a surface, and determining the director field that minimizes the sum of splay and tilt energies. The study of these nonlinear

and domain-dependent problems will require the development of new mathematical tools that go beyond theories of liquid crystals and harmonic maps (72), and combine them with theories of bending and Willmore energy minimizers (59, 73, 74).

7. Local and non-local interactions together determine the energy of a lipid bilayer. By combining phase field and liquid crystal theory we will be able to account for both types of interactions, and thus the lipid reorienations that lead to changes in membrane topology can be calculated (see Procedures, Aim 2). This new formalism will also benefit other mathematicians interested in describing biological materials which are thin elastic phases.

8. Phase field methods can provide a mathematical description of the heterogeneity of the lipid bilayer portion of a membrane across its thickness. Once we accomplish this for the lipids of the membrane, the method can be extended to account for the proteins embedded in the bilayer by introducing additional phase parameters. This would considerably increase computational complexity, but would provide an initial way to include membrane proteins and biological actions in new physical models.

2. Specific Aims

1. *The string and phase field methods will be combined to calculate the energetically most favored pathway toward membrane hemifusion.*

2. *The phase field method and liquid crystal theory will be used to create a new membrane model that will determine lipid rearrangements during the formation of a pore in a single lipid bilayer.*

3. *Finite element methods will be used to determine the location where a fusion pore is most likely to form within a hemifusion diaphragm.*

4. *Steepest descent and force balance equations will be used to calculate the rate of growth of a fusion pore.*

Aim 1. *Achieving hemifusion. Rationale.* Some pathways are energetically much more expensive than others. We will determine lipid dynamics and energetics for the path of least energy between independent and hemifused membranes. Traditionally, biophysicists have calculated which events are likely to happen when only thermal fluctuations are present. The string method provides a means to discover how external forces effect the transition to hemifusion. Combining the string method, to move between energy basins, with a phase field approach, to reach energy minima within a basin, the minimum energy needed to reach hemifusion will be obtained. These calculations will allow us to generate an animation of the lipid motions that give rise to the stalk and hemifusion diaphragm structures in a way intelligible to non-mathematicians.

Procedures. There exist a few methods for calculating a path of least energy, and each has its advantages. The string method (69) is one such method. It has been used primarily to analyze problems in which a dynamical system jumps from one metastable state to another due to thermal fluctuations (69). As an important consequence of the intrinsic definition of the string, the method avoids the stiffness of differential equations that often arises in other methods (75). It also has good convergence properties, and it can be performed by a splitting procedure. The string method is well suited for calculating how a deterministic system is able to surmount an energy barrier even though the agent driving the system over the energy barrier is unknown. We will calculate the energy barrier separating independent parallel bilayers from the hemifused state.

A hypothetical transition path (although not a minimal one) will be defined by geometrically evolving the initial parallel membranes to the ‘Y’-shape of the hemifusion diaphragm, yielding a one-parameter family of membrane configurations. Since membrane configurations are identified by field variables, the configurations may be linearly averaged to provide an initial path. To find the least-energy path, the two step, improved string method (75) will be used. First, a single implicit steepest descent step yields an intermediate set of images. In the second step, the intermediate images are interpolated on the spatial grid points producing a continuous, piecewise cubic path of configurations connecting the end-states. The path is re-subdivided into equal energy weighted arclength segments yielding the image points on the string in the next iteration. In this procedure, the steady-state path is everywhere normal to the energy contours and hence it is a least-energy path.

The phase space of the least energy path provides the set of membrane geometries. Using a formalism borrowed from the phase field and liquid crystal tradition, we will identify membrane geometries by two field variables: one phase field function identifies the location of the interface and the second field, a director field, identifies the orientation and length of the lipid molecules. The energy landscape as a function of membrane geometry is defined by a Ginzburg-Landau functional, the potential energy, encoding energies associated with the lipid deformations and with steric effects occuring inside the bilayer. Further details of the functionals and the field variables are given in Aim 2.

By graphically plotting the field variables, we will be able to see how the initially parallel bilayer interfaces deform and then apposing monolayers undergo the topological change of merging into the stalk complex. Similarly, we will be able to see how the lipid directors reorient while minimizing the deformation energy. The increase in energy is provided by the evolution of the membrane configuration along the least energy path, allowing us to precisely calculate candidate energy barriers and predict what forces might be involved in these deformations.

In practice, field variables are discretized by axisymmetric finite differences over a two dimensional grid with hundreds of grid points in each coordinate direction. The transformation from separate to hemifused bilayers is resolvable by hundreds of image points along the string, providing sufficient resolution to obtain the sought saddle-point energy landscape. To speed up computation time, the two step splitting method will be performed in parallel by assigning a few of the image points to each processor.

Aim 2. *Lipid rearrangements during pore formation in bilayers. Rationale.* Modeling the pathway for pore formation in a continuous single bilayer involves handling multi-scale forces and changes in topology. Both phenomena arise in many areas of membrane biophysics, but for a number of reasons each is difficult to capture by a comprehensive mathematical theory. The phase field method traditionally uses a label to identify bulk material regions, thereby avoiding the explicit identification of regions with varying topology. However, this method applies only to membrane surfaces that separate two (inside and outside) fluid compartments. When a pore is present in a vesicle, there is one continuous aqueous compartment. In the hemifusion configuration, there are three separated aqueous compartments (two intracellular and one extracellular solution for hemifused cells). Also, the phase field model implicitly assumes that the lipids are parallel to the surface normal and that opposing monolayers deform identically, but this does not apply for the morphologies of a pore or hemifusion. A different approach is needed to accommodate the actual situation. Our formulation combines the elements of liquid crystal and phase field theories in an original way to describe a membrane as a thin, ordered material. In our preliminary work, we allow the directional order of the lipids to change over a diffuse region, which we refer to as an "ordered diffusive interface" (ODI). The ODI model is flexible, and should be able to describe virtually all known membrane configurations. It couples field variables through the energy functional and has precedents in prior membrane modeling studies of bending energy minimizing vesicles (58, 76), vesicles in fluids (44, 77, 78), multicomponent membranes (52, 79), and calculating topological indicators (e.g. Euler number) (80, 81). But ODI describes a much broader range of lipid deformations, including those of stalk creation and pore nucleation in membranes. The idea behind the ODI model is to define a mean field bilayer energy with local and nonlocal interactions.

Procedures. The primary local interactions, similar to those of liquid crystal theory, consist of lipid deformations at the lipid-water interface. To account for these interactions we define

$$W_{\text{local}} = \int_\Omega \Big\{ \underbrace{k_b \left| \operatorname{div} \mathbf{d} - \nabla \mathbf{d} : \frac{\nabla\phi}{|\nabla\phi|} \otimes \frac{\nabla\phi}{|\nabla\phi|} - c_0(x) \right|^2}_{\text{splay}} + \underbrace{k_t \left| \frac{\mathbf{d}|\nabla\phi|}{\mathbf{d}\cdot\nabla\phi} - \frac{\nabla\phi}{|\nabla\phi|} \right|^2}_{\text{tilt}} \Big\} \underbrace{|\nabla\phi|^2 \, dx}_{\text{surface density}} .$$

Here $\mathbf{d} = \mathbf{D}/|\mathbf{D}|$ is the lipid orientation for the lipid director $\mathbf{D}$, and ϕ is the phase field parameter labeling the lipid phase as 1 and the water phase as -1. In prior theories, the bilayer has been described as a level *surface*. In contrast, we label the lipid core of the bilayer and the lipid directors by *bulk* field variables. The first term is the splay energy density where k_b is the bending modulus and c_0 the spontaneous curvature. The second term is the tilt energy with modulus k_t. Tilt measures the degree to which the lipids are aligned with the normal of the water-lipid interface. Splay and tilt are multiplied by a surface energy density because lipid molecules impart a directional order only at the surface of the water-lipid interface, close to the neutral surface. Unlike liquid crystal molecules, lipid molecules can stretch and compress. This will be accounted for by including a term $k_h(|\mathbf{d}|^2 - h_0^2)^2/2h_0$ in the energy, restricting the range of stretch/compression; a surface tension constant σ will account for the lipid-water interface surface energy. The above energy functional is not an exhaustive description of a biological membrane. But it is easily extended to incorporate additional effects such as twist, spatially varying spontaneous curvature, volumetric and surface incompressibility, temperature, and electrostatic dependencies, by modification of the integrands. We will numerically stabilize the energy functional to ensure its coercivity and avoid non-physical singularities.

The nonlocal interactions are what really distinguish membrane bilayers from liquid crystals. These interactions are steric effects stemming from the formation of voids (interstices) and interdigitation of lipid molecules. It is the combination of these two functional relationships which gives the bilayer a thickness:

$$W_{\text{nonlocal}} = \int_\Omega \int_\Omega \{ \underbrace{k_v \exp(-qz(x,y)\cdot\mathbf{d}(y))}_{\text{voids}} + \underbrace{k_d |z(y,x)|^{-p}}_{\text{interdigitation}} \} |\nabla\phi(y)|^2 (\phi(x)+1)^2 \, dy \, dx$$

The calculation of the void penalty is based on the formula for finding the minimum of a function: $\min_\Omega f = \lim_{q\to\infty} q^{-1} \log \int_\Omega e^{-qf} \, dx$ where $z(x,y) = x - y - d(y)$. The formula assigns an exponential weight to a point in the bilayer core if it does not lie on a lipid molecule. Such a point represents a void. The interdigitation term assigns a repulsive potential between the hydrophilic head group of one lipid and the hydrophobic tail group of another. Our definition of the nonlocal interaction yields a bilayer thickness by joining monolayers along their tail groups. Our approach is, to our knowledge, a completely new strategy to model membranes. All the necessary physics is contained in the functional relationship of the total energy—the sum of the local and nonlocal energies—with the field variables, allowing us to determine how the lipids rearrange in pore formation, and to calculate the energies involved. The energy functional is encoded numerically using finite differences; we take advantage of symmetry by assuming an axially symmetric configuration.

Experimentally, increasing surface tension of a membrane (e.g., by osmotic swelling of vesicles) induces pore formation, relieving stresses on the membrane. By treating surface tension σ as an increasing parameter while simultaneously allowing the system to evolve along the path of steepest descent with respect to the ODI energy, we can faithfully imitate, in-silico, the experimental procedure of creating pores. Increasing surface tension will produce one of two effects: either the bilayer remains intact because the initial planar configuration lies in a shallow energy basin, or the lipids spontaneously deviate from parallel order, most likely along the axis of symmetry, leading to a small pore.

If, in experimental reality, a bilayer is locally stable, pore formation would occur as a consequence of thermal fluctuations. That is, the small holes that form in the bilayer would be a result of thermally induced in-plane lipid motions. But thermal fluctuations are not incorporated in continuum models. If the bilayer is locally stable in the simulation, we would employ the string method to find the minimum energy path connecting the planar and punctured state, yielding pore formation as a result of thermal fluctuations. We would also obtain the depth of the basin by a stability analysis on the total energy's second derivatives, and use it to ascertain what reasonable perturbations to the lipid order and lipid-water interface are needed to push the bilayer out of the basin.

Aim 3. *Location of pores in hemifusion diaphragms. Rationale.* Identifying the reasons some states of hemifusion lead to pore formation while others do not could have important consequences in our understanding of the biological factors controlling fusion, and would shed light on processes as diverse at neurotransmitter release and viral infection. One parameter that may control the energy for pore formation is the angles of the 'Y'. We will analyze how pores form in hemifusion diaphragms, and determine the energy barrier against pore formation as a function of the pore's location, either within the interior or along the rim of the diaphragm. Because of their 'Y'-shaped cross sections, hemifused membranes are not mathematical surfaces. Problems of minimization of energy of shapes that are not surfaces are not commonly addressed by mathematicians, and they pose significant analytical challenges. We have developed a novel finite element representation of a membrane. In essence, each monolayer of a bilayer will be represented by a piecewise linear map. The functional for the energy of the hemifusion diaphragm will be calculated and the shape of least energy and lipid orientations for this shape will be read from the minimizers.The next step is a means to define finite elements over a space with nontrivial topology, which we refer to as a "topological finite element" (TFE) method (82). The TFE method will allow us to determine the shapes of the boundary between the unfused portions of the two membranes and their connections to the hemifusion diaphragm, the 'Y,' before and after pore formation.

Procedures. Modeling pore formation in a hemifusion diaphragm cannot be reduced to two dimensions by assuming axial symmetry because the pore may not be situated in the center of the diaphragm. But pore formation can be reduced to two dimensions by approximating the lipid bilayer with finite element surfaces, avoiding the computational difficulties presented by a fully three-dimensional calculation. There remains, however, the problem that a hemifused membrane cannot be parameterized over a single planar domain. We will use two annular domains to represent the unfused portions of the effector and target membranes and a circular domain to represent the diaphragm. To connect the domains, we will use a gluing procedure which not only reduces the problem to two dimensions, but also yields the position of the membrane monolayers and the orientation of the lipid molecules.

Developing mutliple ways to parameterize a bilayer has considerable merit, both biologically and mathematically. Lipid monolayers are essentially incompressible in area and volume, and thus have constitutive relations that are quite different from other fluid interfaces. For this Aim, we will parameterize the mid-plane (the surface where the lipid tail groups meet) and neutral surfaces by piecewise linear (PL) functions. (The neutral surface is the surface for which the deformations of splay and tilt are independent of each other. Experimentally, it lies along the glycerol backbone of lipids, just below head groups (83).) This parameterization implicitly eliminates the formation of voids, which can arise in some monolayer representations, causing energetic quandaries (33, 67, 68).

The coupling between the neutral and mid-plane surface is provided by the incompressibility condition: for a constant area per head group, the infinitesimal ratio of volume to area is equal to the height h_0 of a planar monolayer. A penalty method enforces this constraint. The functional

$$E_{\text{comp}} = p \sum_{\tau} |h_0 - h(\tau)|^2 a(\tau).$$

provides a mean square measure of the monolayer compression. The neutral surface is composed of triangular elements τ with area τ and $h(\tau) = v(\tau)/a(\tau)$ where $v(\tau)$ is the volume of the prism spanned between the neutral and mid-plane surface. For large values of p the monolayer becomes effectively incompressible.

The total energy E_{total} of the membrane consists of the splay $k_b|\text{div}\,\mathbf{d} - c_0|^2$ and tilt $k_t|\mathbf{d}/\mathbf{d}\cdot\mathbf{n} - \mathbf{n}|^2$ energy densities summed over the TFE surface. We do not expect the monolayers to undergo sharp deformations in the shape calculations, and thus we anticipate that a uniform conforming mesh will be sufficient to resolve minimizers. In fact, the minimal energy shapes observed in our preliminary axially symmetric studies were quite smooth. But if sharp gradients do form and require resolution, an equipartition of energy algorithm will be utilized whereby the mesh generator will be passed through with a weight proportional to the energy density possessed by each triangle, and this will be used to further subdivide the mesh. Convergence tests will be performed to ensure that the shapes are stable with respect to the mesh parameter. Our version of bilayer minimization involves first order, elliptic terms, and here finite element convergence theory is well established (84).

The model is complete once boundary conditions are specified. The 'Y'-shaped junction is formed by requiring the values of the neutral and mid-plane surfaces to agree on the boundaries of their respective domains. In a similar fashion, the pore is introduced by inserting a hole in the originally circular diaphragm domain. In practice, the boundary condition is affected by identifying nodes in the mesh adjacency matrix. Thus, we will be able to extend the planar PL functions to a nonplanar domain. Using this model, we will encode arbitrary membrane shapes with and without a pore, a major improvement over prior studies where the membrane shape was assumed (20). Furthermore, necessary physicalities such as incompressibility are built into the model. Because the hemifusion diaphragm is only a few nanometers in diameter, hydrodynamic forces are small and should be less consequential than the thermal fluctuations that occur within the diaphragm. If, however, we were to unexpectedly find otherwise, the TFE representation can be incorporated into a fluid mechanical immersed boundary method.

Physical outcomes (e.g., What type of hemifusion diaphragm leads to pore formation?) are highly sensitive to energy gradients. Thus, it is of the utmost importance to accurately calculate energy dependencies as functions of several physical parameters. The TFE method will allow us to determine these dependencies precisely, because it enables us to determine detailed information about membrane shape: the angles of the 'Y'-junction, the geometry of the unfused membrane, the profile of the pores, the orientation of lipid molecules, and where energy is concentrated. The change in energy $\Delta E = E_{\text{total}}(\text{after pore}) - E_{\text{total}}(\text{prior to pore})$ will allow us to predict the most likely site of pore formation and how the energies depend on factors such as angles of the 'Y', spontaneous curvature, surface tension, and diaphragm diameter.

The one potential difficulty that could arise from a TFE analysis would occur if, mathematically, there is no minimal or metastable pore position, or if the 'Y' shape is not stable. Such a result could reflect experimental reality, or could be a consequence of incorrect physical assumptions placed in the model. If these instabilities arise, pore position would not be obtainable, but the solution of the gradient flow equations would still yield the time courses for a pore to reach its minimal energy.

Aim 4. *Pore growth. Rationale.* The growth of fusion pores is an energetically uphill process. Mathematically, fusion pores would shrink without an external force because the energy of an hourglass-shaped membrane is asymptotically proportional to its radius. Extensive experimental and theoretical investigations have not yet determined the nature of the external forces biology provides for pore growth to occur. In addition, pore growth must be damped by hydrodynamic forces: when fusion pores grow, the displacement of the viscous membranes and the surrounding aqueous medium water must produce dissipations which slow the growth of the fusion pore. However, past theoretical treatments of pore growth have neglected consequences of aqueous viscosity (21, 22). Preliminary to this Aim, we experimentally varied aqueous viscosity to test its relevance and found that increasing aqueous viscosity from the normal 1.1 cP (Fig. 2, thin curve) to ~30 cP (thick curve) significantly slows pore growth. This unambiguously demonstrates that aqueous viscosity must be taken into account for a physically accurate model.

Procedures. In order to model the fusion pore, we will use an axially symmetric version of the bilayer model from Aim 3 to describe the pore and its energy, again parameterizing by piecewise linear functions. The splay and tilt energy density are integrated over the surface (a curve for an axisymmetric surface) and the penalty formulation is included in the total energy to enforce the incompressibility condition. This method has the advantage that we can numerically track an extensive portion of the membrane using relatively few unknowns in the equations of motion.

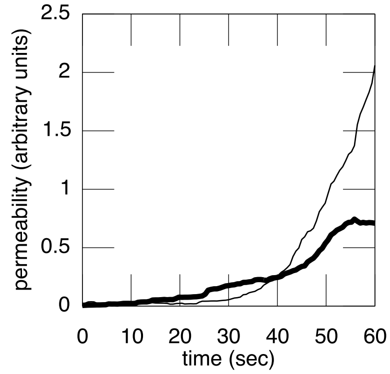

Fig 2

A primary objective is to determine what experimental factors promote pore growth. Changing the value of a parameter may change the minimal energy shape of the membrane. If it does, the minimal energy of the new shape is greater than the minimal energy of the original shape. But there is no way to know, *a priori*, how a change in a parameter's value will affect the energy landscape. Explicit calculations are needed. Because fusion proteins can alter local material properties of lipid mono- and bilayers, we will introduce a material label and use the label to define a spatially varying spontaneous curvature or varying surface tension. (In general, inhomogenities throughout the area of a biological membrane can be modeled by allowing spatially varying parameters.) We will solve the equations of motion by setting the surface velocity fields (for the mid-plane, distal, and proximal surfaces) proportional to the first variation of the modified bilayer energy. Similarly, we will study the effect of applying inhomogeneous Dirichlet and Robin conditions to the director and lipid surface, respectively. This will model changes in contact angles caused by proteins inserting, either partially or fully, into the bilayer.

To study the effect of viscous dissipation on fusion pore dynamics, we will include the velocity field of the external fluid. As is common for fluid-interface problems, the challenge is to couple the flow field with the bilayer as defined on different spatial grids in a way that dissipates the total energy of the system. We will use an idea similar in spirit to the immersed boundary method (53). But rather than define a force on the velocity grid by convolution, as in the immersed boundary method, we will define the force implicitly on a test vector field. Specifically, if E_{Total} is the total energy of the membrane and $\mathbf{v}$ is a finite element velocity field, then we define the force $\mathbf{f}$ by the equation $\int_\Omega \mathbf{v} \cdot \mathbf{f}\, dx = -\frac{d}{d\epsilon} E_{\text{Total}}(M + \epsilon\mathbf{v})\big|_{\epsilon=0}$ where $M + \epsilon\mathbf{v}$ means the following: shift each of the vertex in the bilayer by the value of $\epsilon\mathbf{v}$ at the vertex; the derivative is calculated using numerical differentiation.

Energy dissipation, at length scales comparable to the bilayer, is very sensitive to membrane position and velocity because the membrane occupies a large fraction of the computational domain. We will account for spatially varying friction by defining a dissipation function in terms of the strain tensor $D[\mathbf{u}] = \frac{1}{2}(\nabla\mathbf{u} + \nabla\mathbf{u}^T)$ (85), as

$$\mathscr{D} = \int_\Omega \sum_{i,j=1}^{2} \eta_{ij}(x)(R(x)D[\mathbf{u}]R(x)^T)_{ij}^2\, dx.$$

where $R(x)$ is the rotation matrix for the coordinate frame parallel to the neutral surface and $\eta_{ij}(x)$ is the component-dependent viscosity. In particular, the values $\eta_{ij}(x)$ encode the viscosities of the in-plane, which is large compared to water, and intermembrane viscosity, which can be large or small depending on the degree of interdigitation of the lipid tail groups within the bilayer. In the aqueous region, the viscosity and rotation matrices are set to the viscosity of water and to the identity matrix respectively. A momentum balance equation, obtained from the maximum dissipation principle,

$$\rho(\mathbf{u}_t + \mathbf{u} \cdot \nabla \mathbf{u}) + \nabla p = \frac{1}{2}\frac{\delta \mathscr{D}}{\delta \mathbf{u}} + \mathbf{f}$$

is coupled to the incompressibility condition $\nabla \cdot \mathbf{u} = 0$ to yield the PDEs for the evolution of the system. The dissipative stress calculated from the Euler-Lagrange derivative ($\frac{\delta \mathscr{D}}{\delta \mathbf{u}}$) is symmetric.

As part of our mathematical description of pore expansion to determine how biology could control fusion pore growth, we will obtain realistic energetic values of fusion pores. Lower energies greatly enhance the likelihood that a pore will enlarge, and our preliminary calculations show that energies of pore geometries that have been assumed (21) or calculated (22) in the past are tens of kT higher than for the minimal energy pore shape. Thus, fusion proteins can exert much smaller forces to promote pore expansion than has been realized. We will obtain characteristic asymptotic bilayer shapes for fusion pores; biophysicists may then incorporate these shapes into their own calculations of pore growth. This will be a significant advance over pore geometries assumed in the past (21).

We have proposed three different models of lipid bilayers (ODI for Aims 1 and 2, TFE for Aim 3, and a surface representation for Aim 4), choosing according to the problem posed. The question naturally arises: Is our choice of mathematical representation purely one of convenience, in which the outcomes of more complex calculations would still be the same? The TFE method will be ported to study Aim 4 by replacing the topological configuration of the hemifused membranes by a single, initially axially-symmetric, hour-glass-shaped membrane to confirm that all the representations lead to essentially the same predictions. We will also use the ODI representation, include water and lipid motion through a labeling function to yield viscosity for two phases, and apply appropriate kinematic transport conditions for the phase and director fields. If any differences arise, we will determine why they occur.

3. Past Developments Leading to the Present Proposal. We describe some prior theoretical studies of the PI using classical continuum mechanics to describe aspects of membrane fusion.

A pathway for stalk formation (33). To determine the energy barrier that must be surmounted for hemifusion to occur, we postulated a specific pathway and then calculated the consequences. Hydrophobic surfaces attract at small distances with a characteristic length of ~1 nm (86), and so we considered the appearance of two hydrophobic patches—one within each of the apposing monolayers of two bilayers which we envisioned were biologically created by fusion proteins—directly opposite each other as a function of distance l between the tips of the nipples. The hydrophobic energy (dW_f) favorable for attraction is aided by the work performed by the protein, $-F_p dl$, and opposed by the repulsive energy of hydration (dW_h). We calculated the energy barrier, ΔW, that must be surmounted for the hydrophobic patches to merge into a stalk, where $W = W_h + W_f + F_p l$. We obtained Wh from a standard equation (87) . We estimated the energy provided by a fusion protein as $F_p \sim (W_p - W_n)/L_p$, where L_p is a length that characterizes protein movement during conformational changes and W_p is the energy released by these conformational changes. The process of membrane merger follows from the calculated energy surface which has a saddle-shaped topology; the equipotentials (10 kT apart) of $W(r_f, l)$ are shown in Fig. 3 (circle denotes saddle point; arrows point in direction of decreasing energy). When the membranes are separated by a large distance, hydrophobic patches do not form and the membranes do not attract. If the nipples approach each other through a fluctuation, hydrophobic patches form, promoting greater approach and in turn the radius of the hydrophobic patch (r_f) become larger. In this process of positive

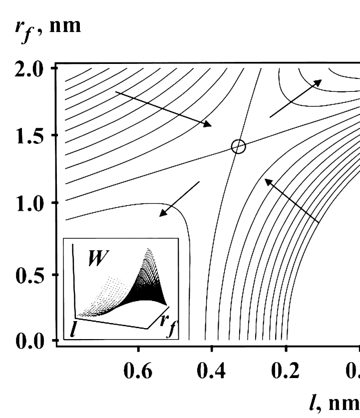

Fig 3

feedback, as l decreases further, patches become larger and at a critical l, the hydrophobic attraction dominates and the tips of the nipples merge. The height of the energy barrier separating the membrane and the stalk for the most favored pathway of our model was between 35 and 40 kT.

We used traditional methods in that study, which necessitated the imposition of a physical assumption on the system—apposed hydrophobic patches to drive hemifusion. That study provides preliminary data for Aim 1. Using the string method, *a priori* assumptions will no longer be needed and the lipid reorientations, including possibly the creation of hydrophobic patches, will be output consequences of the calculations.

Growth of fusion pores (21). We have explored how the physics of membrane bending controls the growth of a fusion pore, including some consequences of energy dissipation caused by lipid movements. We assumed that a pore has a toroidal shape and that the distance between the two original flat membranes outside of the torus, $2H$, remained fixed. In order for the pore to expand, a net influx of lipid from the planar membranes into the wall of the pore must occur because the surface area of the toroid increases. This requires a redistribution of lipid between the planar and toroidal portions of the membranes. Because we assumed a specific geometry, we were able to calculate steady state lipid velocities and thereby obtain the associated dissipated energy, using experimental values of membrane viscosity. We used Lagrange's equations with dissipation (88) to describe motion in the system. We separated dissipation into two terms, one due to shear of lipid movement within a monolayer (i.e., intramonolayer friction) and the other due to intermonolayer friction.

We showed that trans-pore flux and pore growth are independent of each other. This conceptually useful result occurs mathematically because terms associated with pore expansion and lipid flow appear additively in expressions for the energy and the dissipation function, without cross-multiplication terms. Physically it occurs because the trans-pore flux of lipid between the two membranes does not lead to an increase in the surface area of the pore. We also showed that the pore velocity, $\frac{dr}{dt}$ is given by

$$4\pi(4\tilde{\eta})\frac{dr}{dt} = 2\pi\sigma r - 2\pi\gamma(r)$$

where $\gamma(r)$ is the effective line tension of the fusion pore given by the energy W_b required to bend the appropriate portions of the two planar membranes into a curved pore, and σ is the sum of tensions applied to each of the membranes. For bending energy alone (i.e., $\sigma = 0$), the pore will close. The effective line tension is given by

$$\gamma(r) = \frac{\pi}{2}H\sigma + \frac{1}{2\pi}\frac{dW_b}{dr}$$

The equation for fusion pore growth is formally the same as the expression for velocity of a pore within a single bilayer membrane with effective two-dimensional viscosity of $4\tilde{\eta}$ (89). Whereas line tension of a pore within a single bilayer is usually assumed to be independent of pore radius, our explicit calculations showed that the line tension, γ, of a fusion pore is dependent on pore radius, r. The explicit equations we derived for movement in radius space have the form of standard Langevin equations, showing that the growth of a toroidal pore can be thought of as a quasiparticle that both diffuses and migrates in radius space in response to applied forces.

This preliminary study is our conceptual foundation for Aim 4. But we can now calculate pore growth without assuming or fixing pore geometry, and calculate the consequences of aqueous viscosity. We will allow fusion proteins to alter spontaneous membrane curvature at the site of the pore, and by deriving the corresponding Langevin equations determine whether pores can grow without having to impose external forces such as tension.

4. Broader Impacts.

Promotion of learning. Our collaborations have engaged undergraduates from Fordham University. So far, seven students have been mentored and trained–during the course of two summers–through participation in our research program. When students enter the program, they think they do not have the background to contribute to solving the problems we propose. We discovered that they have compartmentalized their classroom experiences and think of the knowledge they have learned only in terms of the courses they learned it in. The biological problems these mathematics students are presented within our program are certainly beyond the textbook exercises they have expertly learned to solve. After we have interactively and iteratively "translated" the biology into physical language and mathematical equations, they begin to realize that they have already learned, through their various course work, many of the tools they now need to think "outside of the box."

During the course of the program, the students learn that they do not have to completely master a subject before they can apply it. We found that their first inclination is to systematically go through an entire book chapter by chapter, as in course work, because they think this is necessary to correctly apply a mathematical technique to their research problem. We teach them a new way to learn: to pull out the understanding they already have in a range of areas, identify what additional information they need and gather it, and integrate all this knowledge into a construct that is their own. By the end of the research collaboration, these students have started thinking independently; they have acquired an understanding of what professional scientists and mathematicians actually do; and they have made a transition from passive participants in their own education to becoming contributing investigators in current, ongoing real-world research questions. Students have been pleased, even amazed, that they have learned and accomplished so much in so little time. The boundaries between courses have been broken, and connections have been made that previously they did not imagine. Our students have told us of the tremendous satisfaction they've derived from this experience, and some have said that it has been the best summer of their lives. Since our approaches have been highly successful, we propose to continue this type of mentoring program as part of the present application.

Training. Our students will be directly involved in answering the scientific questions of the present proposal. As have students in the past, they will learn enough classical differential geometry, differential equations, biology, and physics to make meaningful contributions to our reaseach program. They will become familiar with aspects of the cell biology of membrane fusion, thermodynamics, how to calculate an Euler-Lagrange derivative, and develop an enhanced appreciation of the utility of the physical principle of energy minimization. As direct contributions to the goals of the present proposal, they will write original mathematical software to solve differential equations and process data. Using Octave and Matlab they will solve systems of ODEs and they will program in C to solve larger scale systems of linear and nonlinear finite equations coming from the discretization of PDE. By obtaining and compiling software, the will learn to work in a UNIX-Terminal type environment. They will document their findings in LaTeX, will prepare presentations and posters by using the Beamer class, and use GNUPLot to graphically portray data.

Over the course of the subsequent academic year, they will present their work in undergraduate research symposia. Projects that yield publishable results will be followed by an abstract to the annual Biophysical Society Meeting. The students will be encouraged to be the presenters and will be co-authors of professional journal articles.

Teaching. The physics and biological proficiency at Rush provide the mathematics students with an everyday intellectual richness that they do not experience during their academic year. The summer students meet with the Investigators for in-depth discussion on a daily basis. They make a biweekly presentation of the work in progress and receive feedback from the senior personnel. They attend Journal Clubs and Seminars that are ongoing in the Dept. of Molecular Biophysics and Physiology at Rush, gaining awareness of research areas in biology. So that students enhance their understanding of the scientific area in which they are engaged, they spend time viewing laboratory experiments and process the derived experimental data. We instituted this laboratory aspect this past summer, and it greatly aided the students' ability to understand biophysical/biological research papers and to associate mathematical outputs with experimental results. The graduate students and post-doctoral fellows of Rush (who do the experiments) become more aware of the mathematical possibilities in modeling biological systems.

Opportunities. This past year, 5 students applied for the program. We required each applicatant to review some pertinent biophysical and mathematical material beforehand. Based on the effort they put into understanding the material and on their successes in Mathematics courses at Fordham, three of the students were chosen by Dr. Ryham.

We especially welcome participation by underrepresented minorities. Through active recruiting we have maintained and will continue to maintain equal participation by women: of the seven students in the past two years, three have been women and one of them (an immigrant from Belarus) has begun a Ph.D. program in mathematics. One of the students this past summer, a Mexican-American, now plans to apply for a Ph.D. in mathematics. Our students have also included a Korean and an Albanian immigrant. All three students of this past summer, entering their senior year at Fordham, now plan to apply to programs for advanced degrees.

We will facilitate other biophysicists' theoretical calculations by making our software open access, easily obtainable, and convenient to use. We will do this by writing user interfaces and tutorials that describe our numerical schemes, and create a devoted website that will make our software and tutorials continually available.

Outcomes. We summarize published work directly relevant to the Aims of this proposal that has resulted from the collaboration of the senior investigators with summer students in this section to conform to the 12 page limitation that Program Solicitation NSF 12-561 places on Sections 1, 2, and 3. As stated in Information for this Solicitation, past results may be placed in Broader Impacts.

Aqueous viscosity is the primary source of friction in lipidic pore dynamics (43). Membrane viscosity is at least 100 times greater than water viscosity. It has consequently been assumed that membrane viscosity generally dominates dissipative processes and aqueous viscosity is unimportant. For example, past investigators describing the growth of a pore within a liposome have always made this assumption (90–93). We have shown that this assumption is not valid, and, in fact, causes essential physics to be missed.

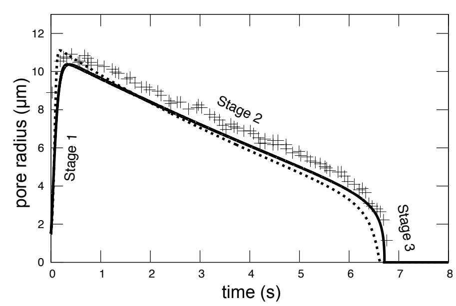

Fig 4

Experimentally, the dynamics of pores within a giant liposome (>20 μm in diameter) under pressure follows a three-phase pattern (Fig. 4, crosses). In the first observed phase after a pore forms, pressure within the liposome induces rapid pore enlargement. The pressure also causes an outflow of the internal aqueous solution. As the force of the ever decreasing pressure becomes balanced by pore edge energy, the pore radius reaches its maximum value. In the second phase, the pore slowly shrinks as the pressure promoting pore enlargement becomes less than the edge energy which promotes contracture. When the pressure has effectively collapsed, the third phase, rapid pore closure, is observed. The long-standing theory in the field (referred to as BGS, based on original authors' initials) accounted for experimental data through fitting parameters, but ignored what turns out to be a dominant limiter of pore expansion—aqueous viscosity.

Irina Berezovik, a summer student, and the PI's formulated a new theory that quantitatively matches data and does so by using experimentally measured aqueous and membrane viscosities, without any free parameters. We accounted for energy dissipation in the aqueous and membrane solutions through the equation $C\eta_s rr' + 2h_0\eta_l r' = \sigma r - \gamma$ where r is pore radius, h_0 is monolayer thickness, $\sigma(r, R)$ is membrane surface tension, γ is line tension, η_s is the viscosity of the aqueous solution, and η_l is lipid membrane viscosity. The first term $C\eta_s rr'$ is critical: it accounts for the lateral stresses generated on the bilayer as water movement shears along the dilating or shrinking pore. C is a coefficient independently obtained by directly calculating the friction for a changing radius of a circular hole in a two-dimensional sheet surrounded by water. We invoked conservation of mass–the rate of volume of the internal solution leaving a liposome of radius, R, $-\frac{d}{dt}\left(\frac{4}{3}\pi R^3\right)$, is equal to the flux through the pore–and conservation of lipid before and after pore formation. This led to the equations necessary to determine the two unknowns, r and R.

BGS ignores aqueous viscosity, so it must use artificially large values of to account for experimental time courses. Our theory, which we named DAV to emphasize the **d**ominance of **a**queous **v**iscosity, yields realistic values of η_l. Fig. 4 shows the experimental record of pore dynamics for a liposome 20 μm in radius surrounded by an aqueous solution with viscosity, η_s = 32 cP, along with the BGS and DAV fits to the experimental data. BGS (Fig. 4, dotted line) has to use η_l = 1,000 Poise to obtain sufficiently slow kinetics in stages I (fast enlargement) and III (rapid closure). This value of η_l is about three orders of magnitude greater than experimental values. An inordinately large membrane friction is necessary because BGS ignores the shearing of water that occurs as the membrane slides against the aqueous solution during changes in pore radius. DAV theory (solid line) accounts for the time course of pore radius using η_l = 1 P, a realistic value for lipid bilayer membranes (94). Although both DAV theory and BGS account for the experimental data quite well, they utilize very different values for the physical parameter.

The importance of accounting for aqueous friction becomes strikingly apparent when it is varied, as we show in Fig. 5 for η_s= 1.13 cP. The curves for both DAV and BGS use their respective values of η_l of Fig. 4. Clearly, DAV (solid line) accurately describes the experimental pore dynamics (crosses), whereas BGS (dotted line) predicts a significantly slower change in pore radius in both the opening and rapid closure stages. For DAV theory, both η_s and η_l are true physical parameters, set by their experimental values, and are independent of each other; DAV theory can be directly compared to experimental data.

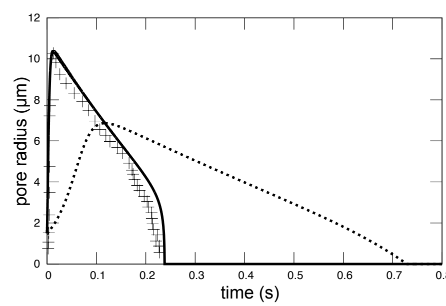

Fig 5

A dynamic model of open vesicles in fluids (95). We solved the same problem as above, but did so through a phase field treatment in order to benchmark the phase field approach for problems in membrane biophysics. At its physical essence, we defined a Hamiltonian as the sum of Helfrich, phase field, and lipid alignment terms, given as by $E = k_b B + \gamma L + k_s \frac{(A-A_0)^2}{2A_0} + \sigma A$ where

$$A = \frac{3}{2\sqrt{2}} \int_\Omega \alpha(\bar{\phi}) \left(\frac{\epsilon}{2}|\nabla\phi|^2 + \frac{1}{4\epsilon}(\phi^2-1)^2\right) dx, \;\; B = \frac{3}{4\sqrt{2}} \int_\Omega \alpha(\bar{\phi})\epsilon \left(\Delta\phi - \frac{1}{\epsilon^2}\phi(\phi^2-1)\right)^2 dx,$$

$$L = \frac{9}{8} \int_\Omega \left(\frac{\epsilon}{2}|\nabla\phi|^2 + \frac{1}{4\epsilon}(\phi^2-1)^2\right)\left(\frac{\epsilon}{2}|\nabla\bar{\phi}|^2 + \frac{1}{4\epsilon}(\phi^2-1)^2\right) dx$$

approximate the membrane area, bending energy, and pore circumference respectively and where $\alpha(p) = \frac{1}{2}(\tanh(\xi p)+1), \bar{\alpha}(p) = \text{sech}^2(\xi p), \xi > 0$ are cut-off functions labeling the position of the pore. We coupled discrete force equations with the Navier-Stokes equations of fluid motion by first expressing kinematic relationships for the field variables in both the aqueous and membrane media. We then calculated forces from variational derivatives. This phase field approach quantitatively yielded the same relationships of pore radius as a function of time as did DAV theory. This supports phase field theory as a reliable formalism to describe phenomena in membrane processes. Because the forces and velocities are obtained over the entire space by field theory, a complete physical description of a phenomenon is acquired.

References

1. T. Cavalier-Smith. The origin of cells: a symbiosis between genes, catalysts, and membranes. *Cold Spring Harb Symp Quant Biol*, 52:805–824, 1987.

2. B. Hille. *Ion Channels of Excitable Membranes*. Sinauer Associates, Sunderland, MA, 2001.

3. J. Prebble. Peter mitchell and the ox phos wars. *Trends Biochem Sci*, 27:209–212, 2002.

4. Y. A. Hannun and L. M. Obeid. Principles of bioactive lipid signalling: lessons from sphingolipids. *Nat Rev Mol Cell Biol*, 9:139–150, 2008.

5. M. J. Berridge. Inositol trisphosphate and calcium signalling mechanisms. *Biochim Biophys Acta*, 1793:933–940, 2009.

6. B. Alberts, D. Bray, J. Lewis, M. Raff, K. Roberts, and J. D. Watson. *Molecular Biology of the Cell*. Garland Publishing,Inc., New York, 1994.

7. C. Bernsdorff, A. Wolf, R. Winter, and E. Gratton. Effect of hydrostatic pressure on water penetration and rotational dynamics in phospholipid-cholesterol bilayers. *Biophys J*, 72:1264–1277, 1997.

8. Y. Liu and J. F. Nagle. Diffuse scattering provides material parameters and electron density profiles of biomembranes. *Phys Rev E Stat Nonlin Soft Matter Phys*, 69, 2004.

9. H. J. Risselada and H. Grubmuller. How snare molecules mediate membrane fusion: recent insights from molecular simulations. *Curr Opin Struct Bio*, 22:187–196, 2012.

10. D. E. Chandler and J. E. Heuser. Arrest of membrane fusion events in mast cells by quick-freezing. *J Cell Biol*, 86:666–674, 1980.

11. R. L. Ornberg and T. S. Reese. Beginning of exocytosis captured by rapid-freezing of limulus amebocytes. *J Cell Biol*, 90:44–54, 1981.

12. L. V. Chernomordik, V. A. Frolov, E. Leikina, P. Bronk, and J. Zimmerberg. The pathway of membrane fusion catalyzed by influenza hemagglutinin: restriction of lipids, hemifusion, and lipidic fusion pore formation. *J Cell Biol*, 140:1369–1382, 1998.

13. C. G. Giraudo, C. Hu, D. You, A. M. Slovic, E. V. Mosharov, D. Sulzer, T. J. Melia, and J. E. Rothman. Snares can promote complete fusion and hemifusion as alternative outcomes. *J Cell Biol*, 170:249–260, 2005.

14. G. W. Kemble, T. Danieli, and J. M. White. Lipid-anchored influenza hemagglutinin promotes hemifusion, not complete fusion. *Cell*, 76:383–391, 1994.

15. X. Lu, F. Zhang, J. A. McNew, and Y. K. Shin. Membrane fusion induced by neuronal snares transits through hemifusion. *J Biol Chem*, 280:30538–30541, 2005.

16. S. Martens, M. M. Kozlov, and H. T. McMahon. How synaptotagmin promotes membrane fusion. *J Biol Chem*, 316:1205–1208, 2007.

17. G. B. Melikyan, J. M. White, and F. S. Cohen. Gpi-anchored influenza hemagglutinin induces hemifusion to both red blood cell and planar bilayer membranes. *J Cell Biol*, 131:679–691, 1995.

18. S. Qian and H. W. Huang. A novel phase of compressed bilayers that models the prestalk transition state of membrane fusion. *Biophys J*, 102:48–55, 2012.

19. L. Yang and H. W. Huang. Observation of a membrane fusion intermediate structure. *Science*, 297:1877–1879, 2002.

20. Y. Kozlovsky, L. V. Chernomordik, and M. M. Kozlov. Lipid intermediates in membrane fusion: formation, structure, and decay of hemifusion diaphragm. *Biophys J*, 83:2634–2651, 2002.

21. Y. A. Chizmadzhev, P. I. Kuzmin, D. A. Kumenko, J. Zimmerberg, and F. S. Cohen. Dynamics of fusion pores connecting membranes of different tensions. *Biophys J*, 78:2241–2256, 2000.

22. M. B Jackson. Minimum membrane bending energies of fusion pores. *J Membr Biol*, 231: 101–115, 2009.

23. P. M. Kasson and V. S. Pande. Control of membrane fusion mechanism by lipid composition: predictions from ensemble molecular dynamics. *PLoS Comput Biol*, 3:e220, 2007.

24. V. Knecht and S. J. Marrink. Molecular dynamics simulations of lipid vesicle fusion in atomic detail. *Biophys J*, 92:4254–4261, 2007.

25. H. H. Tsai, W. X. Lai, H. D. Lin, J. B. Lee, W. F. Juang, and W. H. Tseng. Molecular dynamics simulation of cation-phospholipid clustering in phospholipid bilayers: Possible role in stalk formation during membrane fusion. *Biochim Biophys Acta*, 1818:2742–2755, 2012.

26. K. Katsov, M. Muller, and M. Schick. Field theoretic study of bilayer membrane fusion: Ii. mechanism of a stalk-hole complex. *Biophys J*, 90:915–926, 2006.

27. M. Muller and M. Schick. An alternate path for fusion and its exploration by field-theoretic means. *Curr Top Membr*, 68:295–323, 2011.

28. J. C. Shillcock and R. Lipowsky. The computational route from bilayer membranes to vesicle fusion. *J Phys Condens Matter*, 18:S1191–1219, 2006.

29. A. F. Smeijers, A. J. Markvoort, K. Pieterse, and P. A. Hilbers. A detailed look at vesicle fusion. *J Phys Chem B*, 110:13212–13219, 2006.

30. S. J. Cox and B. Farrell. Estimating the time course of pore expansion during the spike phase of exocytotic release in mast cells of the beige mouse. *Bulletin of Mathematical Biology*, 64 (5):979–1010, 2002.

31. A. Efrat, L. V. Chernomordik, and M. M. Kozlov. Point-like protrusion as a prestalk intermediate in membrane fusion pathway. *Biophys J*, 92:L61–63, 2007.

32. Y. Kozlovsky, A. Efrat, D. P. Siegel, and M. M. Kozlov. Stalk phase formation: effects of dehydration and saddle splay modulus. *Biophys J*, 87:2508–2521, 2004.

33. P. I. Kuzmin, J. Zimmerberg, Y. A. Chizmadzhev, and F. S. Cohen. A quantitative model for membrane fusion based on low-energy intermediates. *Proc Natl Acad Sci USA*, 98:7235–7240, 2001.

34. D. P. Siegel. The gaussian curvature elastic energy of intermediates in membrane fusion. *Biophys J*, 95:5200–5215, 2008.

35. W. L. Ash, M. R. Zlomislic, E. O. Oloo, and D. P. Tieleman. Computer simulations of membrane proteins. *Biochim Biophys Acta.*, 1666(1-2):158–189, 2004.

36. I. Bahar, T. R. Lezon, A. Bakan, and I. H. Shrivastava. Normal mode analysis of biomolecular structures: Functional mechanisms of membrane proteins. *Chem Rev.*, 110(3):1463–1497, 2010.

37. R. O. Dror, R. M. Dirks, J. P. Grossman, H. Xu, and D. E. Shaw. Biomolecular simulation: a computational microscope for molecular biology. *Annu Rev Biophys*, 41:429–452, 2012.

38. M. Stevens, J. Hoh, and T. Woolf. Insights into the molecular mechanism of membrane fusion from simulation: Evidence for the association of splayed tails. *Physical Review Letters*, 91 (18):188102, 2003.

39. R. Delgado-Buscalioni, K. Kremer, and M. Praprotnik. Coupling atomistic and continuum hydrodynamics through a mesoscopic model: application to liquid water. *J Chem Phys*, 131: 244107, 2009.

40. L. V. Chernomordik and M. M. Kozlov. Mechanics of membrane fusion. *Nat Struct Mol Biol*, 15:675–683, 2008.

41. V. S. Markin, M. M. Kozlov, and V. L. Borovjagin. On the theory of membrane fusion. the stalk mechanism. *Gen Physiol Biophys*, 3:361–377, 1984.

42. L. V. Chernomordik and J. Zimmerberg. Bending membranes to the task: structural intermediates in bilayer fusion. *Curr Opin Struct Biol*, 5:541–547, 1995.

43. R. J. Ryham, I. Berezovik, and F. S. Cohen. Aqueous viscosity is the primary source of friction in lipidic pore dynamics. *Biophys J*, 101(12), 2011.

44. Q. Du, C. Liu, R. Ryham, and X. Wang. Energetic variational approaches in modeling vesicle and fluid interactions. *Physica D.*, 238(9-10), 2009.

45. J. Shen and X. Yang. A phase-field model and its numerical approximation for two-phase incompressible flows with different densities and viscositites. *SIAM J. Sci. Comput.*, 32(3): 1159–1179, 2010.

46. S. Osher and R. Fedkiw. *The Level Set Method and Dynamic Implicit Surfaces*. Springer-Verlag, New York, NY, 2002.

47. R. Tsai and S. Osher. Level set methods and their applications in image science. *Commun. Math. Sci.*, 1(4):623–656, 2003.

48. J. Sethian. *Level Sets Methods and Fast Marching Methods*, volume 3 of *Cambridge Monograph on Applied and Computational Mathematics*. Cambridge University Press, Cambridge, U.K., 1986.

49. J. Sohn, Y.-H. Tseng, S. Li, A. Voigt, and J. Lowengrub. Dynamics of multicomponent vesicles in a viscous fluid. *Journal of Computational Physics*, 229(1):119–144, 2010.

50. P. M. Vlahovska, Y.-N. Young, G. Danker, and C. Misbah. Dynamics of a non-spherical microcapsule with incompressible interface in shear flow. *J. Fluid Mechanics*, 678:221–247, 2011.

51. A. Fogelson and R. Guy. Immersed-boundary-typed models of intravascular platelet aggregation. *Computer Methods in Applied Mechanics and Engineering*, 197:2087–2104, 2008.

52. J. S. Lowengrub, J.-J. Xu, and A. Voigt. Surface phase separation and flow in a simple model of multicomponent. *Fluid Dynamics and Materials Processing*, 3(1):1–19, 2007.

53. C. Peskin. The immersed boundary method. *Acta Numerica*, 11:479–517, 2002.

54. G. Guidoboni, R. Glowinski, and M. Pasquali. Operator splitting for the numerical solution of free surface flow at low capillary numbers. *J. Comput. Appl. Math.*, 232(1):72–81, 2009.

55. M. Pasquali and L. E. Scriven. Free surface flows of polymer solutions with models based on conformation tensor. *J. Non-Newtonian Fluid Mech.*, 108:363–409, 2002.

56. J. R. Vélez-Corderoa, D. S'amanoa, P. Yue, J. J. Feng, and R. Zenit. Hydrodynamic interaction between a pair of bubbles ascending in shear-thinning inelastic fluids. *J. Non-Newtonian Fluid Mech*, 166:118–132, 2011.

57. E. de Giorgi. *Some remarks on Γ-convergence and least squares methods*, volume 5 of *Progress in Nonlinear Differential Equations and their Applications*. Birkhäuser, 1991.

58. Q. Du, C. Liu, and X. Wang. A phase field approach in the numerical study of the elastic bending energy for vesicle membranes. *Journal of Computational Physics*, 198:450–468, 2004.

59. M. Röger and R. Schätzle. On a modified conjecture of degiorgi. *Mathematische Zeitschrift*, 254:675–714, 2006.

60. P. G. de Gennes and J. Prost. *The Physics of Liquid Crystals*. Clarendon Press, Oxford, U.K., 1993.

61. F.-H. Lin and C. Liu. Nonparabolic dissipative systems modeling the flow of liquid crystals. *Communications in Pure and Applied Mathematics*, XLVIII:1–37, 1995.

62. Q. Shen, C. Liu, and M. C. Calderer. Axisymmetric configurations of bipolar liquid crystal droplets. *Contin. Mech. Thermodyn.*, 14(4):363–375, 2002.

63. C. Liu and J. Shen. On liquid crystal flows with free-slip boundary conditions. *Discrete and Continuous Dynamic Systems*, 7(2):307–318, 2001.

64. C. Liu and N. Walkington. Approximation of liquid crystal flows. *SIAM J. Numer. Anal.*, 7(3): 725–741, 2000.

65. X. Yang, J. Feng, C. Liu, and J. Shen. Numerical simulations of jet pinching-off and drop formation using an energetic variational phase-field method. *J. Comput. Phys.*, 218:417–428, 2006.

66. X.-P. Wang, T. Qian, and P. Sheng. Moving contact line on chemically patterned surfaces. *Journal of Fluid Mechanics*, 605:59–78, 2008.

67. Y. Kozlovsky and M. M. Kozlov. Stalk model of membrane fusion: Solution of energy crisis. *Biophys J*, 82, 2002.

68. V. S. Markin and J. P. Albanesi. Membrane fusion: stalk model revisited. *Biophys J*, 82: 693–712, 2002.

69. W. E, W. Ren, and E. Vanden-Eijnden. String method for the study of rare events. *PHYSICAL REVIEW B*, 66:052301, 2002.

70. W. E, W. Ren, and E. Vanden-Eijnden. Energy landscape and thermally activated switching of submicron-sized ferromagnetic elements. *J. Appl. Phys.*, 93:2275–2282, 2003.

71. W. E, W. Ren, and E. Vanden-Eijnden. Minimum action method for the study of rare events. *Comm. Pure Appl. Math.*, 57(5):637–656, 2004.

72. R. Hardt, D. Kinderlehrer, and F.-H. Lin. Existence and partial regularity of static liquid crystal configurations. *Commun. Math. Phys.*, 105:547–570, 1986.

73. L. Simon. Existence of surfaces minimizing the willmore functional. *Comm. Anal. Geom.*, 1 (2):281–326, 1993.

74. T. J. Willmore. *Riemannian geometry*. Oxford Science Publications, The Clarendon Press Oxford University Press, New York, 1993.

75. W. E, W. Ren, and E. Vanden-Eijnden. Simplified and improved string method for computing the minimum energy paths in barrier-crossing events. *J Chem Phys*, 2007.

76. Q. Du, C. Liu, and X. Wang. Simulating the deformation of vesicle membranes under elastic bending energy in three dimensions. *J. Computational Phys.*, 212(2):757–777, 2005.

77. Q. Du, M. Li, and C. Liu. Analysis of a phase field navier-stokes vesicle-fluid interaction model. *DCDS B*, 8(3):539–556, 2007.

78. J. Kim and J. S. Lowengrub. Phase field modeling and simulation of three-phase flows. *Interfaces and Free Boundaries*, 7(4):435–466, 2005.

79. X. Wang and Q. Du. Modeling and simulations of multi-component lipid membranes and open membranes via diffuse interface approaches. *J. Math. Biol.*, 56(3):347–371, 2008.

80. Q. Du, C. Liu, and X. Wang. Retrieving topological information for phase field models. *SIAM J. Appl. Math.*, 65(6):1913–1932, 2005.

81. Q. Du, C. Liu, R. Ryham, and X. Wang. Diffuse interface approximations for capturing the euler number: Relaxation and renormalization. *Comm. Math. Sci*, 7:233–242, 2007.

82. S. Gemmrich and N. Nigam. *A boundary integral strategy for the Laplace-Beltrami Dirichlet problem on the sphere S^2*. Frontiers of Applied and Computational Mathematics. World Scientific, 2008.

83. M. M. Kozlov, S. Leikin, and R. P. Rand. Bending, hydration and interstitial energies quantitatively account for the hexagonal-lamellar-hexagonal reentrant phase transition in dioleoylphosphatidylethanolamine. *Biophys J*, 67:1603–1611, 1994.

84. S. Brenner and R. Scott. *The Mathematical Theory of Finite Element Methods*, volume 15 of *Texts in Applies Mathematics*. Springer, New York, 2002.

85. D. Edwards, H. Brenner, and D. T. Wasan. *Interfacial Transport Processes and Rheology*. Butterworth-Heinemann, Boston, 1991.

86. D. E. Chandler. Interfaces and the driving force of hydrophobic assembly. *Nature*, 437:640–647, 2005.

87. S. Leikin, V. A. Parsegian, D. C. Rau, and R. P. Rand. Hydration forces. *Annu Rev Phys Chem*, 44:369–395, 1993.

88. H. Goldstein. *Classical Mechanics*. Addison-Wesley Publishing Company, Reading, MA., 1950.

89. B. V. Deryaguin and A. V. Prokhorov. On the thoeory of the rupture of black films. *J. Colloid Interfac Sci*, 81:108–115, 1981.

90. F. Brochard, P. G. de Gennes, and O. Sandre. Transient pores in stretched vesicles: role of leakout. *Physica A*, 278(1-2):32–51, 2000.

91. T. Portet and R. Dimova. A new method for measuring edge tension and stability of lipid bilayers: Effect of membrane composition. *Biophys J*, 99:3264–3273, 2010.

92. E. Karatekin, O. Sandre, H. Guitouni, N. Borghi, P. H. Puech, and F. Brochard-Wyart. Cascades of transient pores in giant vesicles: Line tension and transport. *Biophys J*, 84, 2003.

93. N. Rodriguez, S. Cribier, and F. Pincet. Transition from long- to short-lived transient pores in giant vesicles in an aqueous medium. *Phys Rev E Stat Nonlin Soft Matter Physi*, 74:061902, 2006.

94. M. A. Bahri, B. J. Heyne, P. Hans, A. E. Seret, A. A. Mouithys-Mickalad, and M. D. Hoebeke. Quantification of lipid bilayer effective microviscosity and fluidity effect induced by propofol. *Biophys Chem*, 114:53–61, 2005.

95. R. J. Ryham, F. S. Cohen, and R. S. Eisenberg. A dynamic model of open vesicles in fluids. *Communications in Mathematical Sciences*, 10(4):1273–1285, 2012.