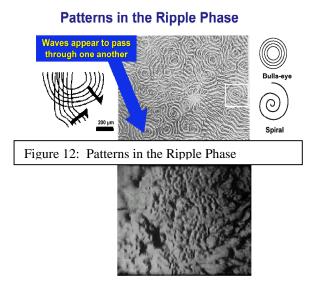
FROM THE COMPARTMENT TO THE FLUID

The mathematical modeling presented in the previous two sections was mainly based on compartment models, models that lead to differential equations with unknown rate parameters. Another approach, taken by two other workshop presenters, is to investigate the fluid dynamics of the underlying biological system and use those principles to enhance our biological understanding.

George Oster of the University of California at Berkeley started his talk by showing a computer-generated movie representative of myxobacteria movement and then presenting a mathematical model that describes the collective behavior, the "ripple phase".



The ripple phase has two patterns: bulls-eye and spiral (see Figure 12). Ripple waves have the ability to appear to pass through one another, and they can occur without any matter actually moving (see Sager and Kaiser, 1993).

Knowing that myxobacteria move with a combination of two motility mechanisms, labeled A and S and controlled by different physiology, Oster sought to combine mathematical models of these mechanisms plus a model of a communication system into a

dynamic model that could produce the ripple phase. The resulting model succeeded in emulating important characteristics of the motion of myxobacteria, such as how the bacteria in crests move *with* the wave while bacteria in troughs move *against* the wave. The model also captures the ability of ripple waves to move through one another and to operate without actual transfer of mass. In addition, when waves collide certain myxobacterial cells continue moving forward and other ones reverse, in accordance with experimental observations.

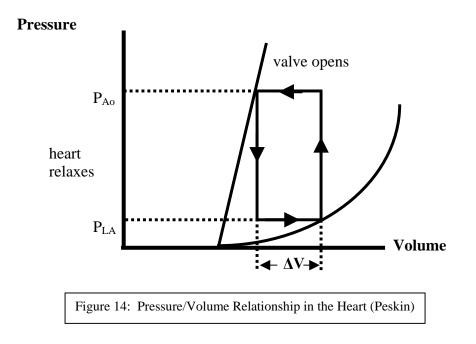
The model also suggests that the ripple phase may be a mechanism for optimal fruiting body products but that it is not necessary for fruiting body formats, and that the rippling phase is not robust—it exists only under certain conditions. This last prediction might lead to an experimental method that can be used to probe the intercellular communication system.

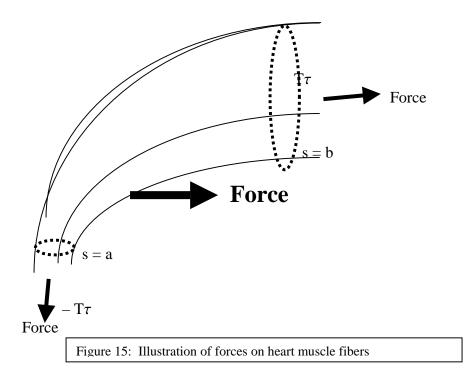
In another application of fluid dynamics, Charles Peskin of New York University described a mathematical model for the heart that considers the muscle tissue to be a time-dependent elastic material, which can be modeled using fluid dynamics. The

geometry of his model builds on work in the 1950s by Carolyn Thomas, which described the fiber architecture of the heart as a system of spiraling muscle fibers (see Figure 13).

< insert Figure 13 here >

By considering the heart as a composite material of fiber and fluid, Peskin developed equations of a viscous incompressible fluid to describe the force applied by the fibers to the fluid. Figure 14 illustrates the relationship between pressure and volume, and how it changes as the valves open and close, while Figure 15 shows the force vectors, illustrating the forces on the muscle fiber of the heart.





Using the following definitions,



Peskin derived the following differential equations:

1. The *fluid equation*, in Cartesian coordinates, which describes the force of the fibers on the fluid

$$F(x,t) = \int \frac{\partial}{\partial s} (T\tau) \delta[x - X(q,r,s,t)] dq dr ds$$

2. The *fiber equations*, which describe the stress on the fibers

$$T = \sigma \left(\frac{\left| \frac{\partial X}{\partial s} \right|}{\left| \frac{\partial s}{\partial s} \right|} - 1; q, r, s, t \right)$$
$$\tau = \frac{\frac{\partial X}{\partial s}}{\left| \frac{\partial X}{\partial s} \right|}$$

3. The *interaction equation*, which ties them together

$$\frac{\partial X}{\partial t}(q, r, s, t) = \underbrace{u[X(q, r, s, t), t]}_{= \int \underbrace{u(x, t)}_{= -} \delta[x - X(q, r, s, t)] dx}_{= -}$$

Note that the equations are expressed using the Dirac delta function, an alternative to computing a Jacobean. Use of the delta functions results in an algorithm that is numerically more stable than one that relies on a Jacobean.

Peskin also described a numerical method for solving the equations, using a second-order immersed boundary method derived by M-C Lai, which is based on an extension of the Runge-Kutta method. This method can also be used in traditional fluid mechanics problems.

The model output (Figures 16-17) compares admirably with MRI scans. Perhaps most impressive, the model captures the swirling movement of blood within the ventricles, a phenomenon of physiological importance that had not emerged in simpler models. This swirling explains why less force is required to exit the chamber than would otherwise be predicted, and it also eliminates leakage in valves from back pressure. However, some improvements are still needed in the model, including refinements of the representation of the up-down valve motion, getting a larger valve opening, and decreasing the movement of the base of the heart.

Peskin figures go here.

It is interesting to note that the Peskin work reflects two of the major themes common to other workshop talks. First, the evolution of his heart model over the years has been guided by a clear understanding of what physiological features must be captured and what mathematical methods might be suitable to do so, rather than by, say, simply increasing model resolution. For instance, his previous model, although doing an adequate job of reproducing some heart actions, displayed an irregular pattern of blood flow and leakage in the valves that was significantly different from that in a functioning heart. His current version has become more complex in a way that can capture this important phenomenology. Second, the Peskin model is an illustration of how a mathematical representation can suggest insights (subject to experimental validation) that would not be apparent from current experimental data. The Peskin heart model is an approximate surrogate for a beating heart, a surrogate that can be manipulated and inspected in ways that a living heart cannot.