1. Preliminary Results

Our model problem is the steady state conservation law \( f(u)_x = h(u, x) \). Our goal is to try to solve this steady state differential equation directly without using time marching methods. We successfully designed the algorithms for one dimensional equations and some special two dimensional equations. And the results are very good: we are able to capture the shock at it’s right location, while shock-capturing is the most important thing in solving a conservation law; we can find our solution in one iteration for both one and two dimensional cases: one iteration in one-dimensional case means two sweepings (one from left to right, and the other one from right to left), one iteration in two-dimensional case means 4 sweepings (from bottom to top and from left to right; from bottom to top and from right to left; from top to bottom and from left to right; from top to bottom and from right to left). Our one-dimensional algorithm can be applied to all general one-dimensional conservation laws, therefore we have no trouble in dealing with one-dimensional problems. But our two-dimensional algorithm can only be applied to some specific linear and nonlinear two-dimensional conservation laws. We are working on the general algorithm that can be fitted to all general two-dimensional problems. I discussed this issue with my collaborators Hong-Kai Zhao and Yongtao Zhang when I went to San Diego for the annual SIAM conference meeting. We came up with some new ideas over the discussion, then I tried those ideas, so far they are still not working. We will keep working on this.

In the mean time, I started a new project related to biology. In the last decade, the zebrafish, Danio rerio, has received rapidly increasing attention as a model for vertebrate development due to two significant advantages: a short life cycle of approximately 12 weeks, which makes genetic analysis much easier; and transparency of the embryo, so that the fate of individual cells during development can be observed. The mathematical models for the development of zebrafish are often reaction-diffusion partial differential equations: \( \partial_t u = D \Delta u + F(u) \). Therefore efficient and accurate numerical methods for this type of differential equations are required. The stiffness (both small and large eigenvalues exist in the system) requires us to use very refined time steps, which means expensive computational cost. We take advantage of its linear diffusion term, and use Integrating Factor method to discretize the time derivative. This way, there is no error in time direction at all, and therefore eliminate the small time step requirement. But this will end up with huge exponential matrix, which requires huge computation cost. We solved this issue by using Krylov Subspace Approximations. I also choose discontinuous Galerkin finite element method to discretize the spatial direction. Since this method can easily handle complex computational domain. And we will need to handle two or three dimensional complex domain due to complex embryo shapes.

Up to now, I have wrote up second and third order algorithms and codes for our model problem on a rectangle two-dimensional domain, and have obtained very good results.
(desired accuracy and desired efficiency). What I need to do next is to use my already developed codes to compute a real mathematical model from biology field with complex domain.

I have confidence that both of my projects will end up with manuscripts, and I plan to submit them to a very well-known journal in computational mathematics—Journal of Computational Physics.

2. Description of grant-supported activity

In the summer, I participated two conferences. The first one was in June, the annual SIAM (Society for Industrial and Applied Mathematics) meeting in San Diego, CA. During the meeting, I met and discussed my progress and difficulties with my collaborators Hong-Kai Zhao and Yongtao Zhang.

The second conference was SIAM Conference on Life Sciences in Montreal Quebec, Canada in August, 2008. I got a chance to listen to many talks involves mathematical modeling in biology. This conference was very helpful when I started doing my second project.