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vortex patch)

vortex ring

Kirchhoff-Routh

Kirchhoff-Routh

On the vanishing viscosity limit of a chemotaxis model

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A vanishing viscosity problem for the Patlak-Keller-Segel model is mentioned in this talk. This is a parabolic-parabolic system in a nD bounded domain with a vanishing viscosity epsilon going to zero. We

show that if the initial value lies in W^{1,p} with p>max{2,n}, then there exists a unique solution (u_epsilon,v_epsilon) with its lifespan independent of epsilon. Furthermore, as, epsilon tends to zero, (u_epsilon,v_epsilon) converges to the solution (u,v) of the limiting system in a suitable sense.

Principal eigenvalues and generalized principal eigenvalues

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ҩ ʿ In the research of operator theory and its applications in partial differential equations and dynamical systems, the principal eigenvalues are always an important topic. In this talk we will introduce some work about the principal eigenvalues and generalized principal eigenvalues of positive operators, differential operators and integral operators.

Propagation of mean curvature flows with unbounded boundary slopes

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ҩ ʿ I will talk about the propagation of some mean curvature flows in a cylinder with certain boundary conditions, which can be used to describe the motion of the level set in Allen-Cahn equations as well as the behavior of a curvature flow just after the singularity. Roughly

speaking, any flow of this kind will converge to a traveling wave solution (also called a translating solution) as the time goes to infinity. The limiting profile, however, depends on the boundary conditions. In particular, if the boundary slopes are unbounded as it moves to infinity, the limiting profile will be a Grim Reaper with unbounded slopes on the boundary. (joint work with Xiaoliu Wang and Lixia Yuan).

Bulk-Surface Coupling: Derivation of Two Models

It is well-known that cell polarization and cell division are caused by protein reaction-diffusion in the cytoplasm and on the cell membrane, which are coupled due to protein cycling between them. To model these cellular phenomena, numerous bulk-surface models have been proposed, which, in the simplest form, consist of one diffusion equation for inactive protein the cytoplasm and another one for active protein on the thickest membrane, with a flux boundary condition coupling the proteins in the bulk and on the surface. A rigorous derivation of such models seems lacking, which motivates this work. We assume

phospholipid molecules in the membrane are optimally aligned and we start with two full models each of which contains reaction-diffusion equations in the bulk and the membrane, respectively, with reasonable transmission conditions linking the two. Then in the limit of \delta tending to zero, we obtain two effective models, with one having the same form as the simplest bulk-surface model mentioned above, the other being a single diffusion equation in the cytoplasm with a dynamical boundary condition. Our models satisfy mass conservation property, which has been a yardstick for the existing bulk-surface models. Our investigation reveals that the optimal alignment of phospholipid molecules and the tangential diffusion in the cell membrane result in the surface diffusion in bulk-surface models, and that a single diffusion equation with a dynamical boundary condition may serve as a simpler alternative model for bulk-surface coupling. This is a joint work with Jingyu Li and Linlin Su.

Existence and instability of two types of blowing-up steady states for the SKT competition model -21(b)-16(ul)19(k)] TJET 0o1o/MCID13.DC BT13 T

This talk is focused on the following simplified SKT two species competition model with cross-diffusion.

$$u_t = \Delta[(d_1+\gamma_1 v)u]+u(a_1-b_1u-c_1v),$$

$$v_t = d_2 \Delta v+v(a_2-b_2u-c_2v)$$

I shall talk about our recent work on the existence and blowing-up

the parabolic-elliptic-fluid counterpart in a 2D or 3D bounded domain with smooth boundary. Under the natural volume-filling assumption, we establish an algebraic convergence rate of the fast signal diffusion limit for general large initial data by developing a series of subtle bootstrap arguments for combinational functionals and using some maximal regularities. In our current setting, in particular, we can remove the restriction to asserting convergence only along some subsequence in Wang-Winkler-Xiang (Cal. Var., 2019). This is a joint work with Dr Min Li.