

The 16th EASIAM Conference program October 15, 2022, Saturday.

Morning Session: Zoom Meeting ID 949 1695 9490, Security Passcode 728877

09:00am-10:00am

Gilbert Strang, MIT

10:00am-10:10am

Break

10:10am-10:45am

Xiao-Chuan Cai, University of Macau

10:45am-11:20am

Norikazu Saito, The University of Tokyo

Afternoon Session: Zoom Meeting ID 963 3962 1675, Security Passcode 465785

2:00pm-2:35pm

Angelyn Lao, De La Salle University

2:35pm-3:10pm

Shuai Lu, Fudan University

3:10pm-3:20pm

Break

3:20pm-3:55pm

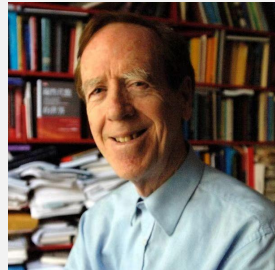
Nuning Nuraini, Institut Teknologi Bandung

3:55pm-4:30pm

Yao Yao, National University of Singapore

Plenary Talk

The Advantages and Disadvantages of $A = CR$

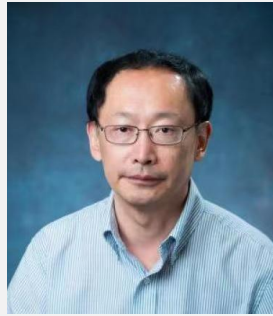


Gilbert Strang

MIT, USA

The factor C contains the first r independent columns of A (rank r). The factor $R = [I \ F] P$ contains the $m - r$ nonzero rows of the reduced row echelon form $\text{rref}(A)$. The good way to see $A = CR$ is $A = [C \ CF] P = [\text{independent cols of } A \text{ in } C \ \text{dependent cols in } CF] (\text{permute columns to get } A)$. This is the row echelon form as a factorization of A instead of an echelon form --- much more useful. The rows of R give a basis for the row space of A . ** So the row rank equals the column rank. ** The nullspace of A (and of R) has a simple basis from $P^T [-F^T \ I]$. The pseudoinverse of $A = CR$ is $A^+ = R^+ C^+ = R^T (C^T A R^T)^{-1} C^T$. Of course CR depends on elimination and is numerically unreliable. But in teaching linear algebra this is normal until you reach $A = QRP^T$ and the SVD. Very large matrices are now factored (approximately) into CUR where the rows of R also come directly from A . The big question in randomized numerical linear algebra is U .

Domain decomposition methods for complex fluid and solid problems in biomechanics



Xiao-Chuan Cai

University of Macau, Macau

We present a highly parallel domain decomposition algorithm for the simulation of fluid and solid mechanical problems in the human body governed by the incompressible Navier-Stokes equations and the hyper-elasticity equations. The systems are discretized with a fully implicit finite element method on unstructured moving meshes in 3D and solved by a Newton-Krylov algorithm preconditioned with an overlapping Schwarz method. Several mathematical, bio-mechanical, and supercomputing issues will be discussed in detail, and some numerical experiments for the simulation of the human heart, and the blood flows in a full-size human body will be presented.

The Keller--Segel system of chemotaxis, finite element method, and finite volume method



Norikazu Saito

The University of Tokyo, Japan

The Keller--Segel system is a mathematical model to describe the aggregation of slime molds resulting from their chemotactic features. If the initial data is non-negative and does not identically vanish, the solution of the system satisfies the conservation of the positivity and the total mass. Moreover, the system processes the total free energy, which is the key property to investigate the crucial number of mass for the global existence of a solution. From the viewpoint of numerical analysis, approximate solutions should preserve these properties and have a convergence property. Actually, many works have been reported to achieve these purposes in the last decade. This talk will summarize the results using the finite element and finite volume methods by our research group.

The Mathematics of Reaction Network and Its Applications to Systems Biology

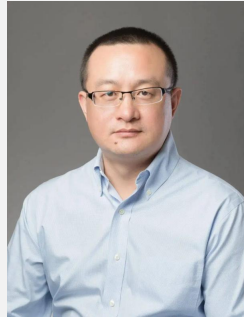


Angelyn Lao

De La Salle University, Philippines

The Mathematics of Reaction Network (MoRN) relates the topological features of a network to the qualitative properties of the corresponding system of ordinary differential equations (ODE). In systems biology, most of the models that are established to reflect the effects of variations in biological processes are ODE-based where parameter uncertainty is predominant. A quantitative tool like MoRN shows potential benefits in studying biological systems without relying on parameter values. In this talk, I will give a brief introduction to MoRN and exhibit how it is applied in Systems Biology.

Data assimilation from a viewpoint of regularization theory



Shuai Lu

Fudan University, China

Inverse problems are ubiquitous in real applications. Understanding of algorithms for their solution has been greatly enhanced by a deep understanding of the linear inverse problem. In the applied communities ensemble-based filtering methods have recently been used to solve inverse problems by introducing an artificial (continuous) dynamical system. This opens up the possibility of using a range of other filtering methods, such as 3DVAR, Kalman(-Bucy) filter and 4DVAR, to solve inverse problems, again by introducing an artificial dynamical system. The aim of this talk is to understand these methods in the context of the regularization theory under the framework of linear inverse problems. It is a series of joint work with J. Cheng, L. Ding, M. Iglesias, K. Lin, P. Niu, A. Stuart, F. Werner.

Mathematical modeling of infectious diseases: lesson learned from COVID-19 pandemic



Nuning Nuraini

Institut Teknologi Bandung
Indonesia

This talk presents a data-driven approach for COVID-19 modeling and forecasting to anticipate its usage by public policy and decision-makers to control the outbreak through Non-Pharmaceutical Interventions (NPI). We developed various model recommendations and expected a few main points to achieve. Studying optimal vaccination schemes, considering existing healthcare conditions and vaccine availability. Predict the effect of COVID-19 on mobility in Java Province around the homecoming model that collaborates with the Ministry of Transportation's R&D Indonesia. Opening school strategies offered to support the task force team for Institut Teknologi Bandung. These results support additional information for stakeholders to benefit education, research, and policymakers. We also provide an extended model to analyze the effect of the COVID-19 pandemic on other diseases, such as Dengue, TB, and DM. The enforcement of health emergencies such as quarantine has a positive impact on reducing the risk of COVID-19 infection. Nevertheless, it also has unwanted adverse regarding health,

social, and economic influences. Here, we generate a mathematical model for the dynamic of COVID-19 transmission that accommodates the quarantine process and includes the compartments of tuberculosis and diabetic people. We highlighted the potential negative impact induced by the implementation of quarantine on the health of people with tuberculosis and diabetes. Finally, numerical simulations of some proposed control strategies measured the efficacy in minimizing the negative impact of quarantine.

Symmetry and uniqueness via a variational approach



Yao Yao

National University of Singapore
Singapore

For some nonlocal PDEs, their steady states can be seen as critical points of some associated energy functional. Therefore, if one can construct perturbations around a function such that the energy decreases to first order along the perturbation, this function cannot be a steady state. In this talk, I will discuss how this simple variational approach has led to some recent progress in the following equations, where the key is to carefully construct a suitable perturbation.

I will start with the aggregation-diffusion equation, which is a nonlocal PDE driven by two competing effects: nonlinear diffusion and long-range attraction. We show that all steady states are radially symmetric up to a translation (joint with Carrillo, Hittmeir and Volzone), and give some criteria on the uniqueness/non-uniqueness of steady states within the radial class (joint with Delgadino and Yan). I will also briefly discuss applications of this variational approach to the 2D Euler equation (joint with Gómez-Serrano, Park and Shi) and a geometry problem (joint with Li and Yan).