

# A Free Boundary Problem Modeling Tumor Growth

by

**Avner Friedman**

Mathematical Biosciences Institute  
Ohio State University

**Abstract:** I shall present a model of tumor growth which involves proliferating cells, quiescent cells, dead cells, and nutrient supplies in a velocity field. The model is described as an elliptic-parabolic-hyperbolic free boundary system. Partial results on existence, asymptotic behavior and stability of solutions will be stated, and open problems will be described.

# Threshold Periodic Bio-dynamics with Bernoulli Diffusion of A Couple of Paired Conjugate Endocrines - Hormone Change Free from Diffusion Location

by

**Kuang-Ho Chen**

Institute of Epistatistics  
National Taiwan University

**Abstract:** Mother nature allows beings to enrich life. Beings enjoy knowing nature inside from observed phenotypic phenomenon through inference and knowledge. Qualitative investigation identifies partial differential equations that make the knowing process manageable, and differential equations that afford means to interpret the process outcome.

Differentiating occurrence or not in probability taking the consideration of location and/or time-course, as well as variation factors, has demonstrated the power in knowing the nature. Bernoulli distribution has been demonstrated to identify the DNA locus for a SNP genetic marker, physiologically localized effective bones causing malocclusion in class III - even for bone-growth determination and bone-morphological identification. Moreover, the identification has clarified endocrine involvement in terms of the number of involved hormones. The 1st order wave equation statistically determined from the observed data characterizes the Bernoulli distribution. The characteristics of the PDE describe the relations for the explanatory variables linked with the Bernoulli distribution as a logistic analysis. The relations afford locus- or bone-information. Invisible properties of endocrine system have to make use of the threshold periodic dynamics for phenotypic phenomenon.

The modeling begins from the qualitatively investigating mother nature, establishes then the relationship in the expression of PDE together with related ODEs, determines next the equations systems statistically based on phenotype data, and makes conclusion finally through interpreting the relation outcomes resulted from the characteristics for the PDE. The modeling interdisciplinarily integrates PDE, ODE, statistical hypothesis-testing into bioinformatics.

# Mathematical Models of Competition with an Inhibitor

by

**Sze-Bi Hsu**

Department of Mathematics  
National Tsing Hua University

**Abstract:** In this talk we will survey mathematical models of two organisms competing for a nutrient in a chemostat in the presence of an inhibitor. The inhibitor is detrimental to one of the organisms. For the other organism, however, it can take up the inhibitor with no deleterious effect. The inhibitor is either occurring externally or generated internally by one of the competitors at some cost to its own growth. The inhibition effect is either causing the decrease of the growth rate of a competitor or the increase of its death rate. We shall discuss the extinction cases (two species or only one species), the existence of two species and bistable case. We also discuss the case when the two species are plasmid-bearing and plasmid-free organisms.

The mathematical models take the forms of systems of nonlinear ordinary differential equations. We will determine the asymptotic behavior of the solutions of the ODE by the methods of dynamical systems, such as monotone flows, asymptotic autonomous systems, uniform Lyapunov functions, and perturbations on a globally stable steady state.

# Algorithmic Methods in Bioinformatics

by

**Kuan-Tsae Huang**  
Taskco Corporation

**Abstract:** Recent explosion in the amount of available biological (particularly molecular biological) data creates the advances, which have caused the amount of information available in international DNA databases to increase exponentially over the last few years. Organization, retrieval, and interpretation of this vast amount of data has become a key computational challenge. Current drug discovery methods are capital-intensive and risky. Gene data provides early insight in to causes of diseases and potential complications. There are many commercial incentives to leverage the available biological data for drug development and other discoveries. For example, Pattern discovery in unaligned DNA sequences is a challenging problem in both computer science and molecular biology. Several different methods and techniques have been proposed so far, but in most of the cases signals in DNA sequences are very complicated and avoid detection. Exact exhaustive methods can solve the problem only for short signals with a limited number of mutations. Bioinformatics is a discipline using mathematical, statistical and computing methods that aim to solve biological problems using DNA and amino acid sequences and related information. This talk will focus on of algorithm methods for Bioinformatics and microarray databases for drug discovery.

# Self-organized patterns in biological systems

by

**Masayasu Mimura**

Department of Mathematical and Life Sciences  
Hiroshima University

**Abstract:** It is well known that diverse regular and irregular spatio-temporal patterns have been observed in biological and chemical systems. Among them, most of self-organized patterns are described by reaction-diffusion (RD) system models. Numerics have revealed that RD systems generate a variety of unexpected complex patterns, even if the systems look so simple. The occurrence of such self-organized patterns in RD systems was originally stated by Alan Turing who introduced the idea of "diffusion-induced instability" understanding of cell-differentiation and morphogenesis in developmental biology. Since then, his idea has been found not only in biology but also in physics, chemistry, ecology and in other scientific fields. In my lecture, I would like to discuss with patterns of self-organized growth and aggregation in RD systems.

# Universal bounds for global solutions of superlinear parabolic problems

by

**Philippe Souplet**

Laboratoire de Mathématiques Appliquées  
Université de Versailles

**Abstract:** We are concerned with various parabolic problems which admit both blowing-up and global bounded solutions. In many cases, it has been known for some time that all global solutions are bounded and that the bounds are uniform with respect to initial data. We present recent results which show that the bounds are actually universal, that is, independent of initial data, giving rise to instantaneous attractors for all global solutions. Some methods and applications will be discussed.

# Detecting Inclusion or Cavity in An Inhomogeneous Transversely Isotropic Medium

by

**Jenn-Nan Wang**

Department of Mathematics  
National Taiwan University

**Abstract:** In this talk, I would like to discuss the inverse problem of identifying an inclusion or a cavity embedded in an elastic body with transversely isotropic medium. The method consists of two ingredients—oscillating-decaying solutions and Runge approximation property. This is a recent joint work with Gen Nakamura.