

## 4. NONLINEAR DYNAMICAL SYSTEMS

### 4.1 Uptake by Phytoplankton in a Two-Nutrient Environment

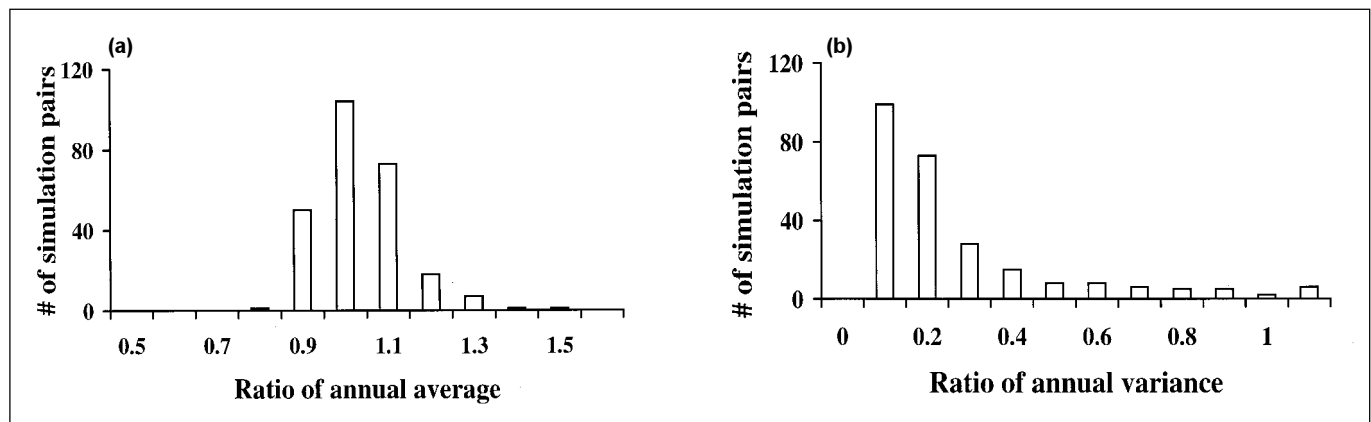
Realistic models for the biogeochemical cycles in the ocean, which are being developed at C-MMACS, has concentrated, as a first task, on capturing the seasonal variation of chlorophyll. A contemporary marine ecosystem model proposed by Fasham, Ducklow and McKelvie (FDM) has been further modified for this purpose. This model describes the interactions of seven components of ecosystem, namely, phytoplankton, zooplankton, bacteria, detritus, nitrate, ammonium and dissolved organic nitrogen in the mixed layer. Since nitrogen is modelled in four different forms, detailed study of new production and regenerated production can be carried out. Also, the influence of microbial loop on regenerating ammonium in the food web is described in this model.

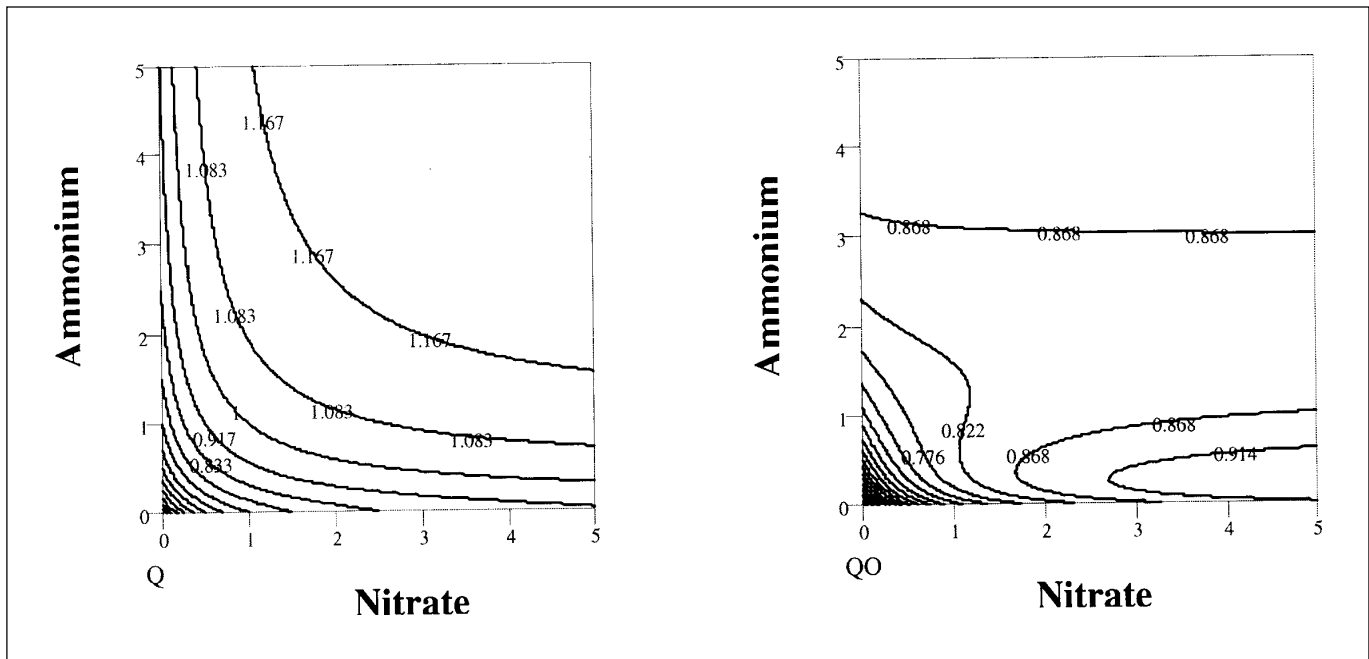
In our earlier studies, a methodology for an objective evaluation of the relative success of an ensemble of simulations in capturing seasonal variability of chlorophyll was described. The ensemble of simulations showed marked difference in the scaled relative errors, for switching-variant in comparison with the nonswitching-variant, for zooplankton grazing. This led to the question whether the former variant supported much larger zooplankton abundance. To verify this, simulation results at each of the eight stations were divided into pairs, one for switching and the other for nonswitching variant. The annual averages of zooplankton as well as their variances were calculated for all pairs at each station. Figure 4.1.1 shows that the ratio of annual averages for these variants

is, on an average, slightly greater than unity and the variance of zooplankton diminishes markedly when switching is present. This result can be interpreted to mean that the zooplankton population does not show marked seasonal variation when switching is present, as the zooplankton is able to switch to whichever food resource is relatively more abundant. Thus, the marked difference in the relative errors is not due to high zooplankton abundance in the present model; it is believed that the difference is due to the variability of the grazing function.

In order to get more realistic simulations, some modifications were introduced in the phytoplankton growth term in the FDM model. These modifications included the incorporation of diurnal variation of solar radiation and seasonal variation of daylength at different locations in Arabian Sea. At present, studies are being carried out, in the various formulations, on the uptake by phytoplankton in a two-nutrient (ammonium and nitrate) environment. In FDM model, the inhibition due to the presence of ammonium on the uptake of nitrate by phytoplankton is modelled as an exponential term. This formulation results in an exponential increase in the inhibitory influence of ammonium on primary production due to nitrate. Further, it can be seen from Fig. 4.1.2 that, when either one or both of the nutrients are increasing in concentration, the total primary production decreases. To overcome these problems, a general law was proposed for the uptake of nutrients by phytoplankton in the presence of two nutrients. According to this law, the inhibitory effect of second nutrient on the first is linear for small concentrations and it saturates for large concentrations. Recent observations (Fig. 4.1.3)

**Fig. 4.1.1.** Effect of switching in grazing model on zooplankton abundance and zooplankton variability. Ratios of switching variant to non-switching variant for, (a) annual average and, (b) annual variance, are shown.





**Fig. 4.1.2.** Contour plots of total primary production in the presence of nitrate and ammonium; Q – total production calculated using the hyperbolic law for ammonium inhibition, QO – total production calculated using the exponential law for ammonium inhibition

on the uptake of nitrate in the presence of ammonium are in good agreement with the proposed law. Two variants of the proposed law have been incorporated in FDM model. Several simulations were carried out at eight stations in the Arabian Sea and the relative scaled errors were calculated using the earlier mentioned methodology (for comparison of simulations with observations), on chlorophyll obtained from satellite data. The proposed law has been found to decrease the relative scaled error, on an average. Fine tuning of parameters in the proposed law is required to get more realistic simulations.

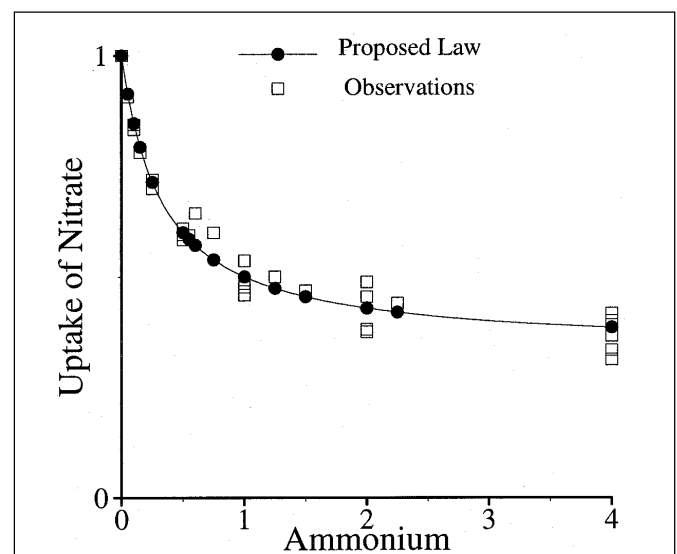
(M. K. Sharada and K. S. Yajnik)

## 4.2 Development of Fisheries Forecast Model

Primary productivity models have been a subject of study at C-MMACS for a few years. These models serve up outputs that can be effectively utilised in models for fish population dynamics, the dynamics of which is at a higher level in the food chain. Fishery Survey of India (FSI), Mumbai, has carried out studies on the population dynamics of six species of fin-fishes occurring along the north-west coast of India. Recently, it has been suggested that both FSI and C-MMACS work jointly for the development of mathematical models which could be used for forecast of fishery production in India.

The aim of fish population dynamics models is to optimize the exploitation of marine resources such as fish. The possibility of optimal exploitation of renewable resources is based on the idea: *rate of increase of fish stock is the difference between the natural growth rate and the harvesting rate of fish.* Models can be constructors describing the processes which link the fishing effort and the fish catch. Processes described in the model can be studied to analyse the historical data and to get an estimate of model parameters. Subsequently, the model can be

**Fig. 4.1.3.** Uptake of nitrate by phytoplankton in the presence of ammonium



used to make predictions of yield for a range of alternative exploitation levels. The expected outputs of the model are optimum fishing levels and maximum sustainable yields.

There are two major categories of models for fish population dynamics. Models in which length or age structure of the population is not considered are known as *holistic* models and they are used in cases where data available are limited. The models in which length or age structure is considered give more reliable predictions and are called *analytical* models; they have more demanding data requirements in terms of quality and quantity.

The primary productivity models can be coupled with fish population models by incorporating the biological processes in the food web with different trophic levels. Since the entire life history of fish and other organisms in the food chain are subject to seasonal or periodic influences, coupling will incorporate the effects of physical forcings in ocean and atmosphere. The multispecies interactions like predator-prey and competition, age composition, migration routes, life cycles of different fish species, size structure of different organisms, concentrations of nutrients, mortality coefficients etc. could be incorporated in these kind of coupled models, depending on the availability of data.

As an immediate activity, simulations will be carried out using the presently available primary productivity model for the area where data on fish is available. It is planned to correlate the output of primary productivity model with the data on growth rates and mortality of each of the six species of fish under study, so that a model of fish population dynamics incorporating the effect of primary productivity can be developed.

(M. K. Sharada and K. S. Yajnik)

### 4.3 Modelling in Epidemiology

The epidemiological simulation model (SIMLEP) is a model for leprosy transmission and control developed by the National Institute of Epidemiology in collaboration with Erasmus University, Rotterdam. It provides a framework for the quantitative description of the dynamics of leprosy transmission- the course of infection and disease and the impact of the interventions in a population over time. It assesses key indicators like prevalence, incidence and case detection. About 70 input steps have to be provided where 40 are parameters.

National Institute of Epidemiology initiated a collaboration

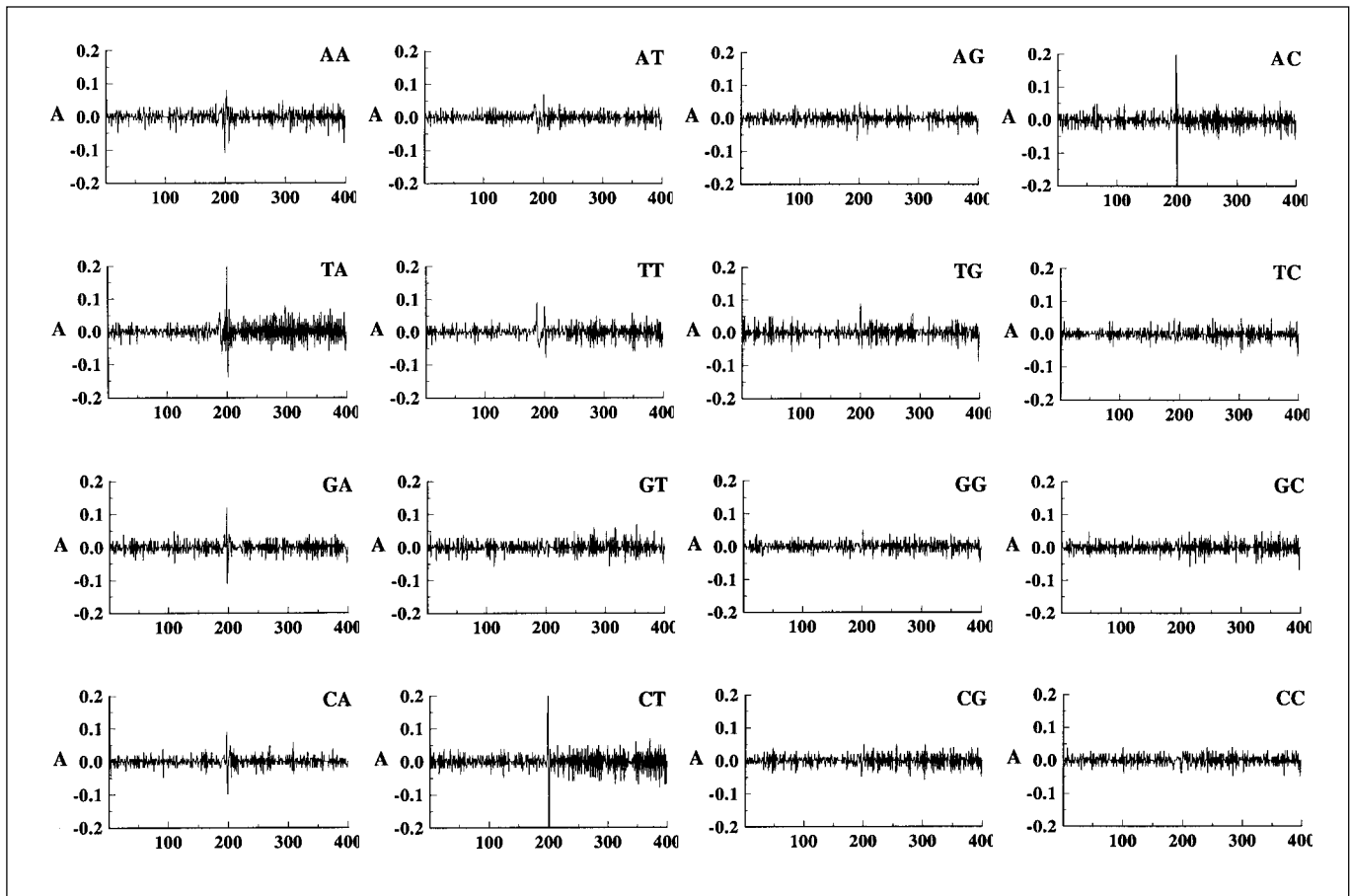
with C-MMACS to understand the structure of SIMLEP model completely. The initial step of assessing the role of key parameters has been carried out. The idea is to make the model run for different endemicity situations in India by examining the sensitivity of various parameters and their inter-relations and then, by making appropriate changes to them. This model can be subsequently used for Indian situations as a managerial tool for the different leprosy programmes.

(N. K. Indira)

## 4.4 Computational Biology

### 4.4.1 Characterization of Interface Between Coding and Non-Coding Regions in Genomic Sequences

Coding and non-coding sequences in DNA have long been characterised on the basis of their differences in base composition and degree of nucleotide variability. However, intrinsic and local measure of the interface between the coding and non-coding regions has not been described. Here, we describe a position-dependent di-nucleotide gradient function (DGF) to identify the characteristics of a typical interface between non-coding and coding regions in genomes. This function is observed to exhibit a sharp gradient, uniquely, at such interfaces. The DGF signal is found to be both statistically robust and phylogenetically conserved. The absence of a simple correlation between the di-nucleotide counts (or frequencies) and this distribution function shows that the gradient is a characteristic of the interface and cannot be deduced from the overall composition of the sequence alone. Furthermore, a randomly generated sequence of the same overall di-nucleotide composition as a given genome, does not show the appearance of sharp gradients, implying that the gradient signal is a characteristic property of genomic sequences in general and of the coding and non-coding interface, in particular. In the set of representative organisms studied in this work, the gradients corresponding to AC, TA and CT appear to be most prominent and conserved. Genome-specific signals are also present in some DGFs such as those of AA and AT. Hence we propose the existence of a position-dependent property of some di-nucleotides that shows a marked change at the start of protein-coding regions, which is presumably interpreted by the read-out machinery of the cell. We have also examined and compared statistical measures like standard deviation of coding and non-coding regions with the DGF gradient signal.



**Fig. 4.4.1.1.** Amplitude of DGF (marked A on Y-axis) shown as a function of nucleotide position (200 pre-interface to 200 post-interface) for the 16 possible nucleotide pairs (indicated in the panels). The sharp peak of DGF at the interface of coding and non-coding regions can be easily seen in the panels of AC, TA, CT etc.

Figure 4.4.1.1 shows a typical plot of DGF as a function of nucleotide position, from 200 nucleotides before ATG, upto 200 nucleotides after ATG; the genome is of *E. Coli*.

(P. Goswami and Sowmya Raghavan)

#### 4.4.2 Exploration of Implicit Structure in Genetic Sequences Using Neural Networks

Neural networks have emerged as efficient and versatile tools for simulating complex processes. They are particularly useful for investigating processes where a precise description of the cause and effect scenario is not available. They are therefore ideally suited for exploring data like genetic sequences. The present study is based on the basic hypothesis that genetic sequences are characterized by certain implicit and generic structures. This implies that a genetic sequence can be looked upon as a (non-linear) function in the distribution of the

nucleotides. We use and explore this hypothesis through neural networks; the neural network thus acts like a map generator. The network is first trained on a part of a genetic sequence (the training set). The trained network is then used to predict a subsequent portion of the sequence. Better than random success in the prediction then indicates an inherent predictability, and hence an inherent characteristic structure in the sequence. In our study, using genetic sequences from a number of eukaryotes and prokaryote genomes, it was found that the neural network (with a three-layer-architecture) was capable of constructing the sequences upto a 100-nucleotide long segment with an average success rate of about 80%. One of the significant findings was that the network needed very little modification, and none in the basic architecture, for different genomes, implying order in terms of the configuration and the parameters. The trained network allows us to extract distinctive features of coding and non-coding sequences.

(P. Goswami)

## 4.5 Earthquake Studies

Successful prediction of earthquakes is one of the big challenges that science is yet to master; it has even been debated whether they can be predicted at all. Mathematical models of earthquakes are able to reproduce some of the well-identified statistical features like the Gutenberg-Richter law (power-law relationship between energy and frequency of earthquakes) but further clarifications have not been possible. Sparse data sets available do not allow for easy refinement and extraction of reliable statistical details. Notably, most of the models are able to reproduce the power laws without taking into account the inhomogeneities of the lithosphere. This leaves the role of the inhomogeneities, which is a readily observed feature of the lithosphere, poorly understood.

In an attempt to study the role of lithospheric inhomogeneities, we are investigating various properties of two fractal surfaces sliding past one another. We have started with the convolution of two such surfaces which, in the literature, has been suggested to be a power law in the distribution of contact areas. We are numerically investigating this. First results show that, for deterministic fractals like cantor sets, the distribution is indeed a power law with an exponent close to (negative) unity.

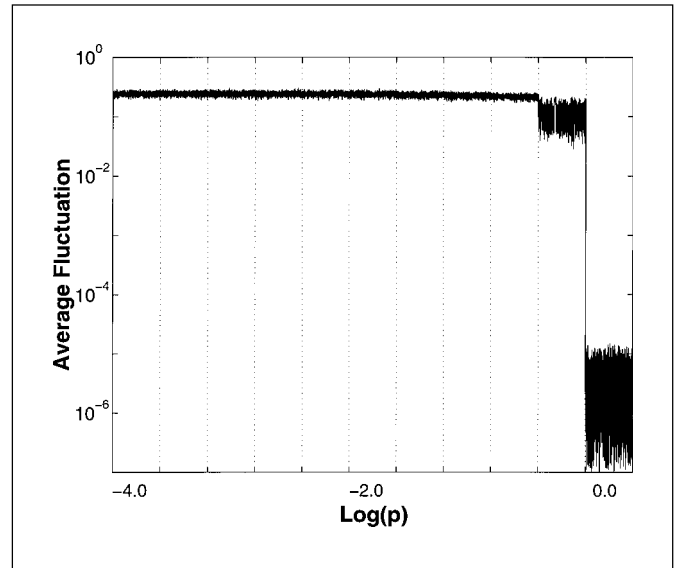
(T. R. Krishna Mohan)

## 4.6 Dynamics on Small-World Networks

Connection topology used usually in coupled networks of dynamical systems is either regular or completely random. But, in realistic systems, it lies in between these two extremes. Recently, such a network has been introduced in literature known as *Small-World* network, which has attracted a lot of attention in the scientific community. Such networks have been demonstrated to occur in various real systems ranging from collaboration graph of film stars, power grid of western United States, neural network of *Caenorhabditis elegans*, world wide web, conformation space of polymer chains etc. Applications of small-world networks to some dynamical systems are reported below.

### **Chaotic Synchronization with Small-World Topology**

We have studied the chaotic synchronization properties of coupled map lattices with logistic map for the site dynamics. When the coupling is regular, it shows several interesting spatio-temporal dynamical phenomena and, when it is random, the system synchronizes (Fig. 4.6.1).



**Fig. 4.6.1.** Time evolution of average fluctuation from the mean for different values of the randomness parameter  $p$ ; between each pair of grid lines, the time evolution is given for selected values of  $p$ , which are indicated on the x-axis. Synchronization does not occur in the *small-world* regime which is in between the regular and random configurations; it occurs only when  $p=1$ , corresponding to a random network.

We have investigated how the small-world connectivity affect the synchronization properties. We have shown that there is no synchronization in the small-world regime contrary to expectation. The number of random connections is the important parameter determining the synchronization. We use both directed and undirected graphs for the network topology.

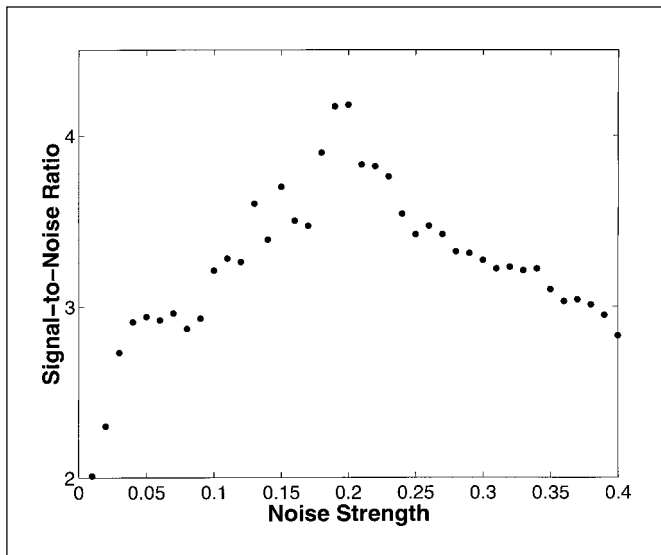
### **Evolution with Small-World Topology**

There exist many spatially and temporally scale invariant phenomena in nature, modelled using the concept of self organized criticality (SOC). Biological evolution is one such phenomenon. A simple model by Bak and Sneppen describes essential properties of evolution. We have studied the properties of the Bak-Sneppen model with small-world connectivity. This model shows SOC and weak sensitivity to initial conditions (SIC) in the regular case and no SOC or SIC in the random neighbour case. Preliminary investigations show that, in the intermediate range there is SOC, but no SIC. This has relevance in biological as well as other systems where there is SOC.

(M. P. Joy)

## 4.7 Noise in Nonlinear Dynamical Systems

In modelling realistic systems, one has to consider the

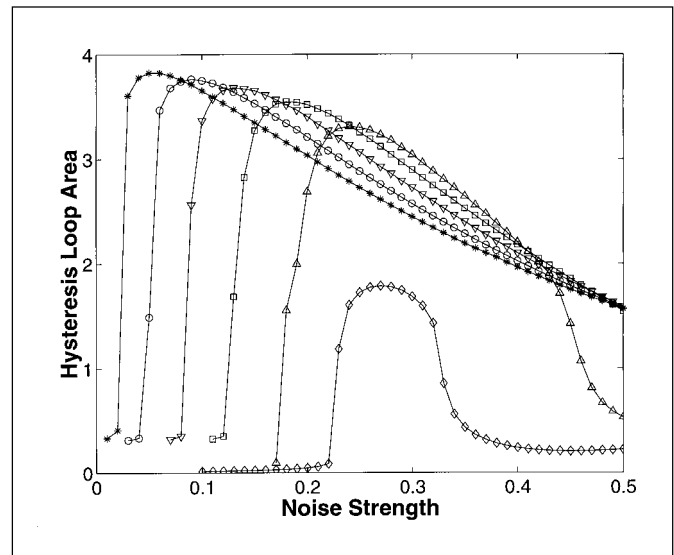


**Fig. 4.7.2.** Plot of Signal-to-Noise Ratio versus noise strength, showing autonomous stochastic resonance (ASR).

effects of noise because it is present in all natural systems and it cannot be eliminated completely; almost all natural systems are nonlinear too. Hence it is important to study the effects of noise in nonlinear dynamical systems. Presence of noise can produce various interesting effects on the dynamics. Noise induced coherence of nonlinear dynamical systems, known as stochastic resonance (SR), is one among them. SR is a phenomenon in which weak signals get amplified by noise. In this case, noise is useful in detecting weak signals, instead of being a nuisance. In the following, we report on two problems related to noise in nonlinear dynamical systems.

#### ***Autonomous Stochastic Resonance with Quasi-monochromatic Noise***

SR has been widely studied in neuron models because of its relevance in understanding sensory functions. Even in the absence of an applied external signal, certain nonlinear systems, in the presence of noise, show SR like behaviour. This is known as autonomous stochastic resonance (ASR). We have studied ASR in FitzHugh-Nagumo neuron model, with quasi-monochromatic noise



**Fig. 4.7.3.** Plot of hysteresis loop area as a function of noise strength for different values of signal amplitude,  $\alpha = 0.1$  ( $\diamond$ ),  $0.15$  ( $\Delta$ ),  $0.2$  ( $\nabla$ ),  $0.25$  ( $\square$ ),  $0.3$  ( $\circ$ ), and  $0.35$  ( $\star$ ).

(QMN); intrinsic slow time scale of QMN acts as the signal component in this case. To characterize the coherence, we calculate the signal-to-noise ratio (SNR). A clear non-monotonicity of SNR with noise strength, which is the signature of SR, is observed (Fig. 4.7.2). This has got relevance in biology, especially in neuroscience.

#### ***Gaussian Decoupling and Stochastic Resonance***

Simulation of Langevin equations to study any statistical quantity of a noisy system is computationally a time consuming task because of the large number of realizations needed for calculating averages. We used gaussian decoupling scheme to obtain the deterministic equations for the first two moments for the noise-driven, overdamped particle in a double well potential, under the influence of an external periodic signal. These equations have been, in turn, used to study the hysteresis behaviour of the system. Hysteresis loop area shows an optimum value with noise intensity (Fig. 4.7.3), which is used as a signature of SR. This method enables us to study SR in an easier fashion.

(M. P. Joy)