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MATHEMATICAL BIOLOGY NEWSLETTER

Program and abstracts for the 1986 Annual Meeting of the Society for Mathematical Biology, to be held at Boston University on June 6 and 7.

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Editor's Note

The 1986 annual meeting is being hosted by Stephen Grossberg and Gail Carpenter of the Center for Adaptive Systems at Boston University.

John Jacquez and Torcom Chorbajian contributed to the production of this issue of the newsletter. We hope that using the newsletter as an instrument for publishing meeting abstracts will establish a beneficial tradition.

Michael Conrad

Program and Abstracts
for the 1986 Annual Meeting
of the Society for Mathematical Biology

PROGRAM

Friday, June 6

8:30 am - 12:20 pm — Symposium: Pattern Recognition by Natural and Artificial Neural Systems. School of Education, Room 130, 605 Commonwealth Ave.

David Waltz: Pattern Recognition Reasoning on the Connection Machine

Gail Carpenter: Stable, Self-Organizing Category Learning and Pattern Recognition by Neural Networks

Harold Szu: Unsupervised Pattern Identification by Fast Simulated Annealing Cauchy Machines

Jacob Schwartz: Conjectures Concerning Neural Structures for Associative Memory

12:30 - 2:00 — Luncheon meeting, Board of Directors, SMB. Faculty Dining Room, 5th Floor, George Sherman Union, 775 Commonwealth Ave.

2:00 - 6:00 — Symposium: Pattern Recognition by Natural and Artificial Neural Systems. School of Education, Room 130

David Mumford: Integrating Edge and Region Information

Stephen Grossberg: A Neural Network Architecture for Three-D Form and Color Perception

Demetri Psaltis: Optical Implementations of Neural Networks

Robert Hecht-Nielsen: Artificial Neural System Principles and Processors

Saturday, June 7

9:00 am - 11:20	Contributed Papers, George Sherman Union, Room 320, 775 Commonwealth Ave.
11:30 - 12:30	Business Meeting, SMB, George Sherman Union, Room 320
12:30 - 2:00	Luncheon Meeting, Board of Directors

Parking: Parking Garage at 700 Commonwealth Avenue, Hinsdale Street entrance, $4.00/day.

"Latin Hypercube Sampling and the Parameter Sensitivity Analysis of a Monte Carlo Epidemic Model", Susan K. Seaholm, Shu-Chen Wu, and Eugene Ackerman, Division of Health Computer Sciences, Department of Laboratory Medicine and Pathology, University of Minnesota, Minneapolis, MN.

Monte Carlo models of viral epidemics often involve many probabilistic, interacting input parameters. This allows a variety of assumptions about population mixing and effects of the viral agent to be simulated, including random variation. The VESPERS package for infectious disease simulation is an example, available at the Facility for Simulation of Stochastic Population Models. However, due to the variety of model input and outcome variables, the testing of hypotheses and the analysis of outcome sensitivity to the variation in the parameter values can be difficult. Fixed-point stratified sampling, considering many factors (parameters) at several levels of each, leads to large numbers of simulations. Alternative methods of sampling from the parameter space may reduce the number of input sets required, while providing adequate estimates of model parameter sensitivity.

Latin Hypercube Sampling has been used to reduce the number of simulations of VESPERS, while allowing finer sampling within each interval. Supporting software generates samples within selected parameter intervals, and performs the resulting simulations automatically. Response surfaces constructed from the outcomes at the sampled parameter sets are used to identify important model features, and areas of high outcome sensitivity to the changes in input variable values. Comparisons of these surfaces generated from the Latin Hypercube and the fixed-point stratified samples indicate that, for outcomes related monotonically to the input parameters, the Latin Hypercube method produces an adequate response surface while vastly reducing the time required for simulation. This work is supported in part by NIH grant RR 1632.

DYNAMICAL MECHANISMS OF PATTERN RECOGNITION IN BIOLOGICAL CELLS

Michael Conrad* and Kevin G. Kirby, Department of Computer Science, Wayne State University, Detroit, MI 48202

Biological cells must respond appropriately to patterns of mediator and transmitters impinging on their external membrane. Experimental evidence suggests that second messenger mechanisms play an important role in this process. We have constructed computational models of neurons in which reaction-diffusion processes involving cyclic nucleotides are used to recognize spatiotemporal patterns of presynaptic input. The pattern of presynaptic input is converted to a cyclic nucleotide concentration pattern which is then read out by kinases on the membrane. This system is well suited to generalization and to evolutionary learning. The model suggests that organism level pattern processing is largely mediated by biochemical and enzymatic processes inside neurons. Recent experimental evidence suggests that cytoskeletal dynamics may also play a role.

*Presenting author

A COMPUTATIONAL MODEL OF CELLULAR PATTERN PROCESSING FOR MOTOR CONTROL

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The dynamic mechanisms by which a neuron responds to external patterns are highly constrained by cell geometry and rates of biochemical reactions. It is through these constraints that the neuron can recognize and generalize specific classes of spatiotemporal input patterns. We have constructed a continuous-time model of a neuron which realistically represents several aspects of internal biochemical signalling. These neurons are linked together to form a system capable of rudimentary motor control. For a particular two-dimensional navigation task we can characterize the motor responses the system can generate. In this system the positioning of enzymes on the cell membrane is the primary determinant of the response; variations in the diffusion dynamics of second messenger substances provide for generalization. These elements give the cell substantially more power as a pattern recognizer than the discrete devices which are often used to model neurons. Furthermore, the system is amenable to control by an evolutionary learning algorithm, and we have verified through computer simulation that tasks such as target-seeking can be learned rapidly.

*Presenting author

PHOTOCHEMICAL MANIPULATION OF PATTERNS IN ACTIVE MEDIA OF REACTION-DIFFUSION TYPE

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As well known, chemical systems or cell populations may form various patterns as plane or spherical fronts, leading centers, spiral waves etc. which can be modelled by reaction-diffusion equations (RDE). By application of light the reaction rates (the coefficients in the RDE) may be changed as given functions of space and time. It is shown here, that in this way patterns may be manipulated, this might be useful for medical applications and for the developement of new information processing methods. As a first example in this paper the influence of Laser light on the critical radius of nucleation in bistable systems is demonstrated. The model is of the type (1)

$$\rightarrow X,\quad X \rightarrow 2X\ ,\quad E_0 + X \rightarrow E_1 \rightarrow E_0 + P\ ,\ X \underset{b}{\overset{a}{\rightleftarrows}} Y \xrightarrow{g} P$$

$$\dot{X} = D\Delta X + bY - aX + (k_1 + k_2X/N)(N - X) - k_3E_tX/(1 + (k_3X/k_4))$$

$$\dot{Y} = aX - bY - gY$$

The light strength and the concentration of a photosensitizer strongly influence the coefficients a, b and g . In this way the critical radius can be manipulated to increase what may lead to the spontaneous disappearance of certain spherical patterns. The second example concerns with the influence of ligth-induced stochastically distributed modulations of the medium on plane front propagation (2-3). The model reads

$$\dot{X} = D\Delta X + W(X;\ k_0(r,t),\ \dots,\ k_1(r,t))$$

where W is an s-shaped reaction function with 3 zeroes and the reaction constants $k_i(r,t)$ represent stochastical fields. As a third example a light-sensitive Ruthenium-catalized modification of the Belousov-Zhabotinsky reaction is studied (4-6). The following model of the reaction is used

$$\dot{X} = D_1\Delta X + X(1 - X) + (L - X)Y\ , \qquad X = [HBrO_2]$$

$$\dot{Y} = D_2\Delta Y + F - Y(bX + M) \qquad Y = [Br^-]$$

The input of Br^- given by the constant F strongly depends on the light amplitude which is due to the fact that light changes the redox properties of the catalyst Ru(II). The theoretical analysis of the RDE and experimental examples (4-5) show that even complicated patterns as e.g. letters can be manipulated. Possible applications to dynamical information storage and processing are discussed.

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PATTERN RECOGNITION AND LEARNING IN A HIERARCHICAL NEURAL MODEL

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An anatomically-based hierarchical neural model has been developed, where each level of the hierarchy has a distinct role in pattern recognition. The hierarchy results from distinguishing node types based on axon shape and neurotransmitter effect. The shape of the connection patterns formed by nodes in the model are designated short-range, long-range-directional, and long-range-diffuse, corresponding to the classification of neurons as interneurons, relay cells, and monoamine transmitters (Shepherd 1974). In accordance with physiological data on neurotransmitters, a node may have excitatory, inhibitory, or long-lasting (Bloom 1979) effects on its targets. Of the nine combinations of these characteristics, five cell types have been found in the brain.

It has been shown that a neural network including these five node types, (i.e. excitatory and inhibitory short-range, excitatory and inhibitory long-range-directional, and long-lasting long-range-diffuse) contains groups of nodes that work together as individual functional units (Eilbert 1986). These multinode functional units consist of sets of widely scattered columns, where column are defined as the volume filled by the connections of a long-range-directional node. These multinode columns are modelled as single units that contain complete short-range systems of nodes. The sets of columns contacted by the long-range diffuse nodes form the highest level in a three-level hierarchy. The validity of similar hierarchical organization in vertebrate brains is supported by physiological and behavioral evidence.

The level mediated by short-range connections carries out the first stage in the pattern recognition process, i.e. local feature extraction. Regularization techniques proposed for solving ill-posed problems of low vision could be implemented at this level. In more complex, global recognition problems, constraints on the system come predominantly from previous experience, rather than from the structure of objects in the world. The role of the column level of the model is to store experiences in the form of stable states that link sets of low level features into recognizable objects (Hopfield 1982). Finally, the role of the long-range-diffuse level is to select the overall mode of operation for the entire system. In particular, this highest level determines whether the incoming signal is processed in either the recognition or learning mode.

A simulation of the model demonstrates how the column level of the system can learn a complex image and can be trained to discriminate similar images. The structure of the cloumn level is closely related to the 'hierarchical' model presented by Fukushima (1984) and to the self-organizing model that Kohonen (1982) discusses. However, in this model, each column in the second level is a multi-output well as a multi-input device. In this way, each column closely resembles the Associative Search Elements proposed by Barto and Sutton (1981). This three level hierarchy allows the synthesis of a number of different modelling approaches, and results in a sophisticated pattern recognition system.

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Molecular Pattern Recognition in the Immune System

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I will discuss the general problem of pattern recognition faced by the immune system. In particular, I will show that small changes in the molecular structure of an antigen can lead to large changes in the immune response. I will indicate what this implies about the immune detection system and discuss how random, self-reproducing, sloppy detectors in the presence of a selection algorithm can provide an adaptive means of recognizing patterns.

Numerical Solution of Large Sparse Structured Problems.

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Computational techniques that have been found efficient in terms of cost, storage and run times are discussed. It is shown that the model connectivity information can be utilized to classify both the variables and equations into two subsets: basic and non-basic, and then this classification is utilized to optimize the solution process. The development of highly accurate discretized techniques that do not increase the connectivity of the system is outlined. The non-linear algebraic equations resulting for the discretization are solved by a variety of algorithms based on Newton and Secant type methods especially tailored to the solution of this type of equations. Applications to models of renal concentrating mechanism are described. (Research supported by NIH Grants: AM 17593 and AM31550)