

# Analysis of Dynamics and Object Recognition Performance in Coupled Map Networks

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**Abstract:** Coupled logistic map lattices can perform object recognition by mapping class members to a point in a space defined by densities (partition cell occupancies) measured at a readout time  $t$  for the entire lattice. Each unit represents average spiking dynamics in mixed excitatory-inhibitory neuronal populations. Non-stationary parameters improve peak recognition rate and recognition time, suggesting one role for interaction of multiple time scales in neural oscillations. A hypothesis that recognition functions by modulating the approach to an invariant measure was rejected by examining the response to noise. Moderate correlation ( $r=.3$ ) between a configuration entropy measure and recognition rate is found.

**Keywords:** density coding, population codes, nonlinear dynamics, object recognition

This report presents new results in ongoing study of oscillations in coupled map lattices (CML) used for the recognition of three dimensional objects [1, 2, 3]. Such networks are interpreted as in the tradition of oscillatory neuronal ensemble models [4], where each units stands for the collective behavior of a mixed pool of excitatory and inhibitory neurons, and the entire network as a homogeneous spatial ensemble of locally connected column-like units. Previously it was shown that such systems could be trained via a genetic algorithm to map various viewpoints of paperclip objects to approximately the same distribution of at some readout time. Recognition rates of 85% were obtained with complete training on a set of 20 objects using a recognizer CML trained to recognize each object, and choosing as the match object the recognizer producing the nearest matching distribution to the characteristic distribution for the object. Important features

of the network and population coding method include rapid processing (only a few iterations) , ease of learning, translation invariance, and generalization between outlines and filled objects.

The short range or local mean field coupled logistic map was used. In the locally coupled system, each unit is connected to nearest neighbors. The computation is divided into two steps; first a diffusive coupling step is applied:

$$S_d(x,y) = (1 - c)S_t(x,y) + \frac{c}{4}[S_t(x,y+1) + S_t(x,y-1) + S_t(x+1,y) + S_t(x-1,y)] \quad (1)$$

where  $S_d$  is a temporary array holding the state of the diffusion computation,  $t$  is the current time step,  $x,y$  are the spatial indices of the pixel array  $S$  at the center of the diffusion neighborhood,  $S$  is the continuous state variable at each pixel of the array restricted to the range  $[-1.0$  to  $1.0]$ , and  $c$  is the coupling constant restricted to the range  $[0.0$  to  $1.0]$ . The factor  $1-c$  is a squashing function, preventing the sum of the surround from exceeding the stable range of the map.

The second computational unit applied in each time step is the logistic map:

$$S_{t+1}(x,y) = 1 - bS_d(x,y)^2 \quad (2)$$

where  $S$ ,  $t$ ,  $x$ , and  $y$  are as above and where  $b$  is the bifurcation parameter, restricted to the interval  $[0.0 < b < 2.0]$ . Initial and intermediate states  $S$  are restricted to the interval  $[-1.0 < S < 1.0]$ .

The basic iterations described above are applied at every lattice site, and are imbedded in an "outer loop" computation with the parameters  $b$  and  $c$  changing as a step function at time  $t_1$  and  $t_2$ . This is interpreted in biological terms as a periodic modulation of the local and short range synchronization dynamics in a cortical column and its

neighborhood, induced by bursting behavior from long range excitatory connections from memory areas which control the computation. Compared with constant parameters, these modulations have been demonstrated to provide small gains in both recognition rate and average recognition time. Each recognition parameter epoch consists of a triplet  $\{b, c, t\}$ , where  $t$  is number of iterations in the epoch. Two such epochs are applied in turn, and after the last iteration the occupancy statistics (density) of all units are read out. During evolutionary search for the parameter sets, each epoch is constrained to 7 iterations. The total iterations required to create the representation space across all classifiers ranges from 6 to 14 iterations, with a mean of 12.7 across 50 learning trials.

Two follow-up studies are presented here. A key feature of the network is intrinsic non-stationarity (i.e. the two dynamical parameter epochs) uniformly applied to each cell in a nearest neighbor connected lattice. This non-stationarity was motivated by a hypothesis on the operational principle of such networks, and consideration of a possible functional role for interactions between slow (i.e. delta-alpha) and fast (gamma) oscillations in biological systems. The original hypothesis was that the coverage of state space would be uniformly expanding in the first parameter epoch and contracting in the second, and that in biological systems the slow oscillations repeatedly controlled computations in a “sample and iterate” scheme by varying the parameters. This conception proved to be an oversimplification, as revealed by fluctuating state space coverage in the time series of the network evolution, and by observing that stationary bifurcation and coupling parameters performed almost as well as non-stationary. Early results indicated that a small advantage in both average and peak recognition rates, as well as the number of iterations (i.e. recognition time) were obtained with non-

stationarity. The following table summarizes a more extensive series of 50 learning trials with each condition; these advantages were confirmed.

**Comparison of CML Recognition: Stationary and Two Parameter Epochs**

Scenario	Average Rec. rate	Maximum Rec. rate	Average Time (iterations)	Time variance	Learning Trials
Stationary	75.2	82.9	13.4	1.39	50
Two epochs	78.8	87.9	12.7	2.7	51

A second series of computational studies was undertaken based on the resulting large set of network parameters, with a goal of improved understanding of underlying network operating principles. While the network is understood from a computer science standpoint as a generalization of the dynamical recognizer framework [5], a better *physical* understanding might give insight into the variations in performance, and might lead to performance improvements within the genetic algorithm learning framework or suggest more direct adaptive learning methods.

#### **Distance from Noise Response**

During recognition, a particular network characterized by a parameter 6-tuple  $\{b1,c1,s1,b2,c2,s2\}$  must achieve two goals – to map diverse views of an object to a point in the space whose axes are defined by state space intervals, and to map other objects to different points in space. Differential rates in the approach to equilibrium of the target object and other stimuli might serve the latter.

It is known the state occupancy statistics of a large set of uncoupled maps at fully developed chaos may reach a stationary distribution in only a few iterations ; with

coupling or other nonlinearity conditions, the systems may not reach a stationary distribution so rapidly, but rather reach a state of statistical periodicity, in which a cycle of low period is observed in the population statistics. The ensemble evolution will depend on the stimulus.

The first set of measurements was formulated to test a hypothesis that networks ability to obtain a unique distribution for a particular object is predicated on an anomalous time course in an approach to statistical equilibrium.

I examined the Euclidean distance between the characteristic distribution for each object and the distribution created by that object's recognizer parameters applied to a noise initial configuration (a 300x300 matrix of states uniformly distributed in range  $-1 < s < 1$ ). This distance was computed and averaged separately for correct and error object presentations in a given learning trial, and the ratio between distances of matching and non-matching trials was evaluated against the error rate. No significant correlations were found ( $r < .1$ ).

This negative result suggests that the *density coding* hypothesis of by Milton and Mackey [6] may not be applicable to highly structured initial conditions, where the a line extraction subsystem is presumed to present initial conditions along object boundaries constrained to small regions of state space (i.e. highly active or at background).

However, their calling attention to the density evolution phenomena and the rapid approach to equilibrium is welcome and closely related to the present work. Instead, the deeper underlying mechanism for separation of classes may be similar to the Markov relaxation and information bottleneck framework recently described [7]. In Markov relaxation, clustering of stimulus configurations into classes is supported by the

differential rates of mutual information loss, with stimuli in the same class reaching temporary plateaus in loss at a characteristic time. The present process proceeds orders of magnitude more rapidly, presumably due to the rapid state mixing of chaotic systems.

### Sum of Configuration Entropies

A well known measure of dynamical systems is the information dimension, closely related to Shannon entropy and the capacity dimension of a dynamical system [8]. Normally, this measure is *defined* for infinite times, and practically *measured* for a long time series for a one dimensional system. Given the transient nature of the processing in the present system, a different but related measure is required.

The measure employed here is the sum of the Shannon information for each configuration (lattice state at iteration  $i$ , computed over partition cells in the usual manner for information dimension:  $H_s$ , the Shannon entropy of the current signature (occupancy distribution at the readout time of a recognizer) with  $k$  bins is

$$H_s = \sum_{i=1}^k S_i \log_2 S_i \quad (3)$$

and the measure I designate as sum of configuration entropies is

$$H_c = \sum_{i=1}^t H_s \quad (4)$$

where  $t$  is the total number of iterates, in this case over two parameter epochs.

It is conjectured that the reason for the slight performance edge of the two epoch dynamics is attributable to a higher entropy obtainable by increasing the reachable states, increasing the chance of finding dynamical trajectories leading to the common subspace

from different views, and of diverting undesired configurations and partial trajectories (of distractor memories) away from the subspace corresponding to the best match.

In figure 1 below, this measure is plotted against recognition rate for a set of 16 two epoch trials, exhibiting a low-moderate positive correlation ( $r=0.28$ ); individual data points are shown along with a least squares linear fit. In figure 2, the ratio of this measure for correct identification trials to error trials is plotted. In this case, the correlation is negative, again with a low-moderate correlation ( $r=0.33$ ). This inverted relationship - with matching views having slightly lower entropy than error views - suggests that one error mechanism occurs when misidentified views spread out in state space during recognition dynamics; successful recognition is enhanced by limited entropy for distractor objects. It should be plausible to test whether this proposition holds in biological subsystems involved in coding object representations.

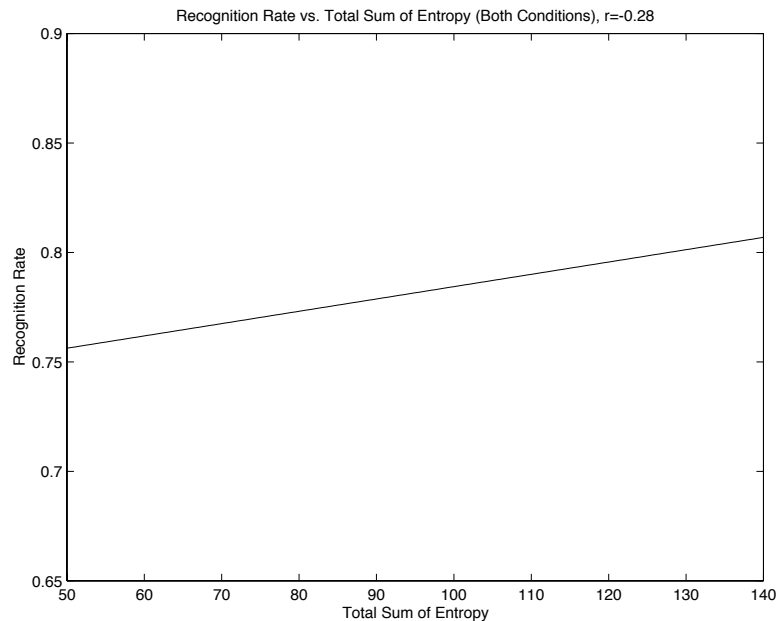


Fig 1: Total sum of point wise entropy over all iterations vs. recognition rate for 16 trials of the CML recognition system applied to 20 paperclip objects.

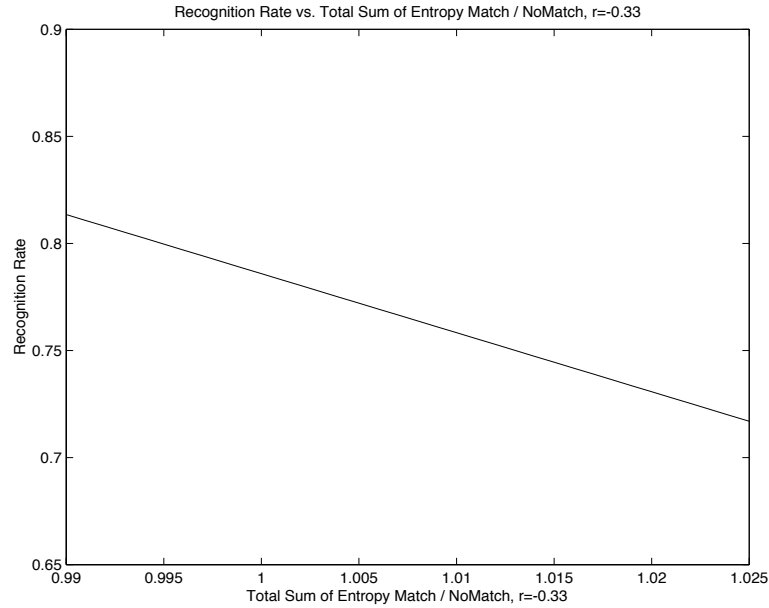


Fig 2: Ratio of Match to Non-matching sum of point wise entropy over all iterations vs. recognition rate for 16 trials of the CML recognition system applied to 20 paperclip objects.

### Conclusions

The lack of correlation between performance of matching and non matching distributions and a suggests that the recent proposal of density coding, while close in spirit, does not reflect the underlying dynamics of this system. After examining the recognition dynamics, the nature of the processing in the homogeneous CML seems best conceived of as a parallel, distributed stochastic switching network in the state space of the recurrent spatio-temporal dynamics. The evidence of the point wise entropy measures in particular (figures 1 and 2) suggests that specific pathways through slightly lower entropy configurations are visited in successful matches, while the overall high point wise entropy is correlated with higher performance.

Other questions of interest to computational neuroscience include what sorts of readout mechanisms would be suitable to read such a code, and what constraints on the



resolution would apply. Single neurons with dendritic which are sensitive to a particular distribution of inter-spike intervals received in a short time window are one plausible mechanism. One would like to know something about the discrimination between different spike intervals (corresponding to the state space interval or bin width in the distribution), and the discrimination for a particular subspace in the space of arrival time distributions.

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