

## SOME NOTES ON COMPETITION AMONG CELL ASSEMBLIES

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We discuss a family of competitive dynamics useful for pattern recognition purposes. Derived from a physical model of mode competition, they generalize former concepts to include populations of cells working as grandmother cell assemblies. Also the notion of unfair competition is introduced.

### 1. Introduction

The grandmother cell approach to pattern recognition has had considerable success. Originally being a concept of neurophysiology (for recent developments<sup>1</sup>), modellers of neural networks have used this concept for performing tasks in artificial neural networks more and more frequently in the last decades.<sup>2–5</sup> Within the grandmother cell approach, each pattern—even a very complicated one—is assigned to a cell in the network responsible for that pattern (the grandmother cell recognizes the grandmother). If and when similar patterns are presented to the network corresponding cells are strongly excited and able to dominate the network's reaction to this particular input. This method has merits in a world where correlations between patterns are not too high. In other words, the pattern space should be sparsely populated.

At least two procedures exist to remove correlations, one being static, the other being dynamic. The static procedure consists of storing variants of the original patterns, called adjoint patterns. By storing adjoint patterns which are computed by correcting for correlations, the pattern space is basically rectified. The dynamic procedure, on the other hand, consists of competition between different grandmother cells for a certain input pattern. Inhibitory connections may link grandmother cells with each other or with a certain reservoir mediating competition. After some time has

elapsed, the cell best fitted to an input pattern has succeeded in suppressing the activity of other cells. In a sense, correlations have been removed by a dynamical process in time. The same network architecture can be used not only for pattern recognition but also for pattern classification. Its strength is the efficiency with which patterns or pattern classes can be coded: One cell per pattern or class.

There is, however, a serious drawback to this efficiency. It concerns the local concentration of knowledge. In natural as well as artificial systems, damage may occur resulting in the removal of certain parts of localized knowledge. In order to avoid trouble caused by such damage, a distributed representation of knowledge should be introduced. This will be the subject of our contribution. We shall extend a specific neural network for pattern recognition based on grandmother cells to a distributed model. In the course of this extension, we will retain the mathematical beauty of the original model as much as possible. Since adaptation and learning are outside the scope of this paper, these issues will be addressed in a separate contribution.

The rest of this paper is organized in the following order: In Sec. 2, we shall briefly introduce the mode competition network in its original form and then derive some of its variants. Especially, the quadratic variant will be introduced. Section 3 deals with the first extension to a population model of grandmother cells. The abstract notion of a grandmother cell will give way to the notion of a grandmother cell popula-



tion or grandmother cell assembly performing the same function. In Sec. 3, the competition between populations is still fair. In Sec. 4, a more general model will be introduced, allowing for what we call unfair competition between grandmother cell populations. Finally, Sec. 5 summarizes our results.

## 2. The Competitive Dynamics

The original model was conceived from the study of pattern formation in natural systems. There, complicated patterns could be described by the competition and co-operation of certain modes.<sup>6</sup> In fact, the competitive dynamics studied to describe light modes in laser materials closely resembles the pattern recognition dynamics given by Haken in 1987.<sup>4,7</sup>

Activities of grandmother cells  $x_i$ ,  $i = 1, \dots, M$ , each with its own codebook vector or pattern stored in connections  $A_{ik}$ ,  $k = 1, \dots, N$ , obey the dynamics

$$\dot{x}_i = x_i(1 + x_i^2 - 2X^{(2)}), \quad (1)$$

where  $X^{(2)}$  is the sum of quadratic activities

$$X^{(2)} \equiv \sum_{l=1}^M x_l^2. \quad (2)$$

(1) can be rewritten as in (3) to make the actual mechanism more evident.

$$\dot{x}_i = x_i \left( 1 - \sum_{l \neq i} x_l^2 - \sum_l x_l^2 \right). \quad (3)$$

This dynamics first causes  $x_i$  to grow, as long as  $\|x_i\| \ll 1 \forall i$ . Then the discrimination term (second in the parenthesis of Eq. (3)) gains influence and causes more and more differentiation of growth rates between different cells (the largest activity grows fastest). Finally, the global sum in (3) assures a saturation at  $\|x_i\| = 1$  for one cell,  $x_i = 0$  for all others. This network implements the winner-take-all function<sup>3</sup> in a dynamical way and is therefore well suited for learning tasks where the transient state of the system can be used.<sup>8</sup>

One particular aspect of Eq. (1) is that it can be derived from a scalar potential

$$V(x_i) = -\frac{X^{(2)}}{2} + \frac{X^{(2)^2}}{2} - \frac{1}{4} \sum_i x_i^4. \quad (4)$$

Restricting activities to positive values  $x_i \geq 0$  we consider a more general dynamics

$$\dot{x}_i = x_i^m(1 + x_i^n - 2X^{(n)}) \equiv F_i \quad m, n \in \mathbb{N}, \quad (5)$$

where we define

$$X^{(n)} \equiv \sum_k x_k^n. \quad (6)$$

In order to achieve a consistent naming, any dynamics will be called according to the sum of powers  $p = m + n$ . The original model of Eq. (1) we therefore call the cubic dynamics.

For the general case, a scalar potential exists only if

$$\text{rot } \mathbf{F} = 0 = \frac{\partial F_i}{\partial x_j} - \frac{\partial F_j}{\partial x_i}. \quad (7)$$

It can be shown that to this end

$$x_i^m x_j^{n-1} = x_j^m x_i^{n-1} \quad (8)$$

should hold. This is fulfilled if and only if

$$m = n - 1. \quad (9)$$

Thus, for special cases (8), dynamics (5) can be derived from a potential function

$$V(\mathbf{x}) = -\frac{1}{n} X^{(n)} + \frac{1}{n} (X^{(n)})^2 - \frac{1}{2n} X^{(2n)}. \quad (10)$$

Two cases should be mentioned here,

$$\boxed{n=1} : \quad \dot{x}_i = 1 + x_i - 2X^{(1)} \quad (11a)$$

$$\boxed{n=3} : \quad \dot{x}_i = x_i^2(1 + x_i^3 - 2X^{(3)}). \quad (11b)$$

The equilibrium values of Eq. (11a) (linear dynamics) do not allow for

$$x_l^{\text{equi}} = 0 \quad (12a)$$

and may therefore appear to be useless. It turns out, however, that the linear dynamics is in fact very useful for application purposes.<sup>9</sup>

The dynamics of Eq. (11b) behaves similarly to the cubic model of Eq. (1) in that

$$x_l^{\text{equi}} = \begin{cases} 1 & \text{for an element } l' \\ 0 & \text{for all other elements } l \neq l' \end{cases}. \quad (12b)$$



Another interesting special case of dynamics (5) is the quadratic competitive dynamics  $m = 1, n = 1$

$$\dot{x}_i = x_i(1 + x_i - 2X^{(1)}), \quad (13)$$

which does not possess a scalar potential.

In Simulation 1, we compare the dynamics of Eqs. (1), (11b) and (13) with respect to their decision speed. We will refer to these dynamics as the cubic, quintic and quadratic competitive dynamics respectively.

### Simulation 1

We study the decision speed of the quadratic, cubic and quintic dynamics under the same initial conditions. We say that the network has decided on a certain winner if, for one cell  $l, l \in 1, \dots, N$ ,

$$x_l = 1 - \epsilon, \quad \epsilon = 0.01$$

holds. In other words, we count the iterations until saturation has set in up to an uncertainty  $\epsilon$ . Dynamics (1), (11b) and (13) are discretized with the same time resolution  $\Delta t$  in order to get comparable data. 100 random initial conditions are run for network dimensions of  $N = 10, 20, 40, 70, 100$  cells respectively.

Results can be read off from Fig. 1. We can see that the cubic dynamics is the fastest of the three dynamics. The reason is that the power  $n = 2$  appearing in the parenthesis of Eq. 1 tends to increase differential growth rates between modes, as compared to  $n = 1$ . This effect, however, is off-set by  $m = 2$  in the quintic dynamics which results in a general deceleration of all growth rates. From this, we conclude that the cubic dynamics is rather special in that it is the fastest self-saturating competitive dynamics of Eq. (5) possessing a potential function.

### 3. The Population Model

We now extend the competitive model for  $m = 1$

$$\dot{x}_i = x_i(1 + x_i^n - 2X^{(n)}), \quad (14)$$

by considering  $x_i$  as a collective variable of an assembly of  $J_i$  cells with activities  $x_{ij}$ ,

$$x_i \equiv \sum_{j=1}^{j=J_i} x_{ij}. \quad (15)$$

In order to be consistent with the dynamics of Eq. (14) on the global level, we choose the following equation

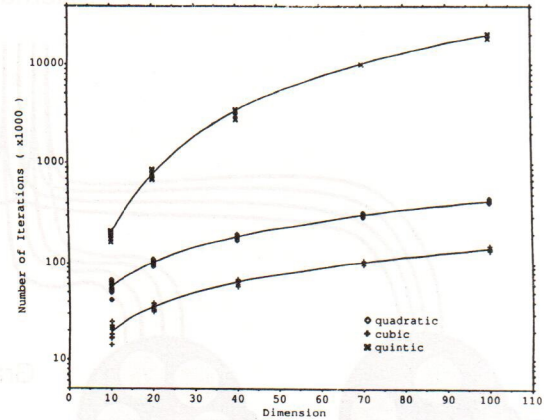


Fig. 1. Decision speed for competitive dynamics of equation (1), cubic, (11b), quintic and (13), quadratic, respectively. The number of iterations until saturation  $x_l = 1 - \epsilon$  with  $\epsilon = 0.01$  is shown in a logarithmic scale. The cubic dynamics is fastest.

for the time development of activities  $x_{ij}$ ,

$$\dot{x}_{ij} = x_{ij}(1 + x_{ij}^n - 2X^{(n)}), \quad (16)$$

where by definition (6),

$$X^{(n)} \equiv \sum_{i=1}^M x_i^n = \sum_{i=1}^M \left( \sum_{j=1}^{J_i} x_{ij} \right)^n. \quad (17)$$

By construction, the arrangement of the  $N$  cells  $i, j$ ,

$$N = \sum_{i=1}^M J_i$$

may be considered as consisting of  $M$  assemblies of  $J_i$  cells co-operating to form "fat" grandmother cells governed by collective variables  $x_i$ .

Figure 2 gives an overview of the system. External input is connected to assemblies acting like grandmother cells on the global level. Their activity is summed by an inhibitory interneuron which feeds back its activity to every assembly. Figure 3 gives a more detailed picture of one of the assemblies.

Turning to Eq. (16), the feedback to a cell  $i, j$  uses three different sources of signals:

- activity of  $x_{ij}$ , excitatory,
- integrating activity of the population  $x_i^n$ , modulated by  $x_{ij}$ , excitatory,
- global field  $X^{(n)}$ , modulated by  $x_{ij}$ , inhibitory.

In other words, the cells in a population excite each other via an intermediate neuron which sums up their



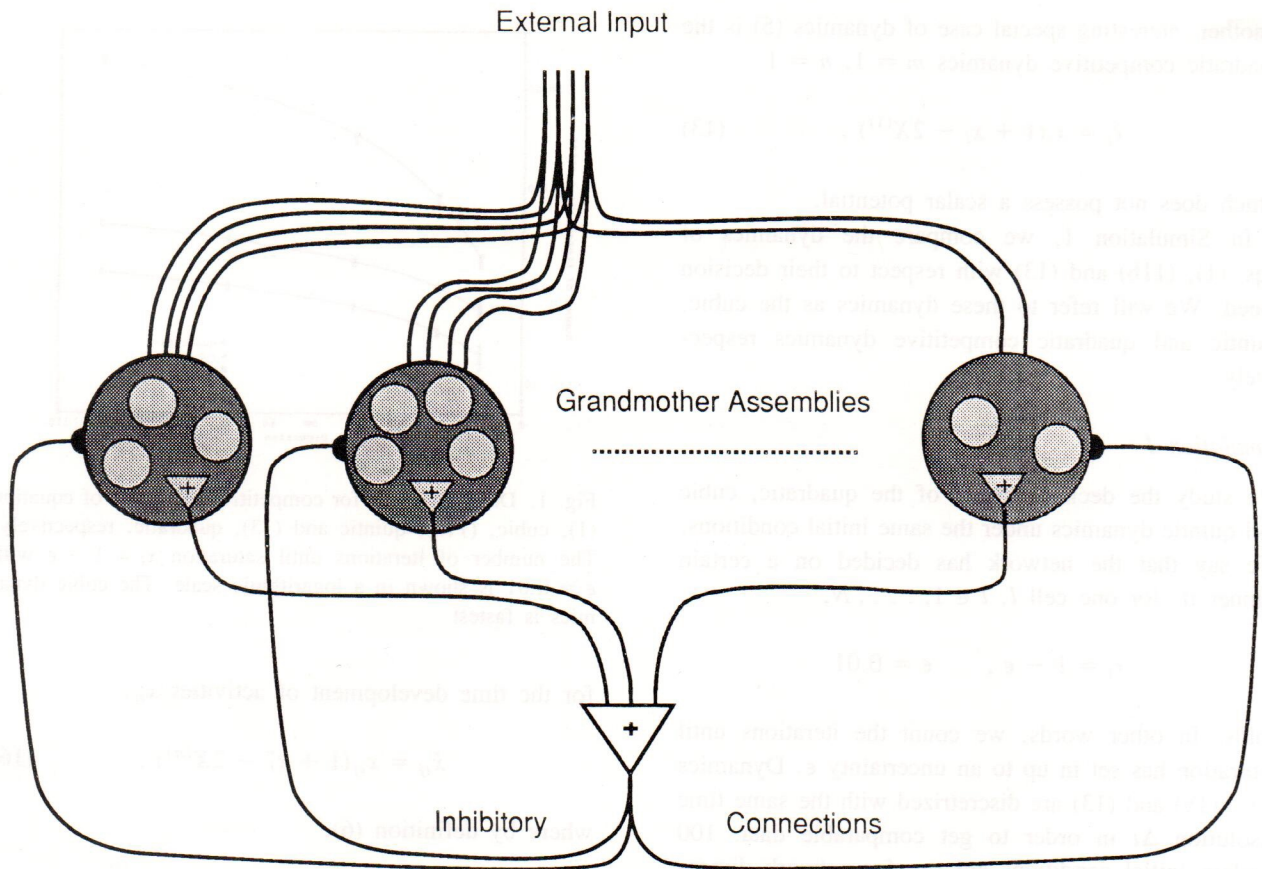


Fig. 2. Overview of the competitive network. Grandmother cell assemblies compete for the patterns from the external input. The interneuron which sums the activity of all assemblies is inhibitorily connected back to all assemblies.

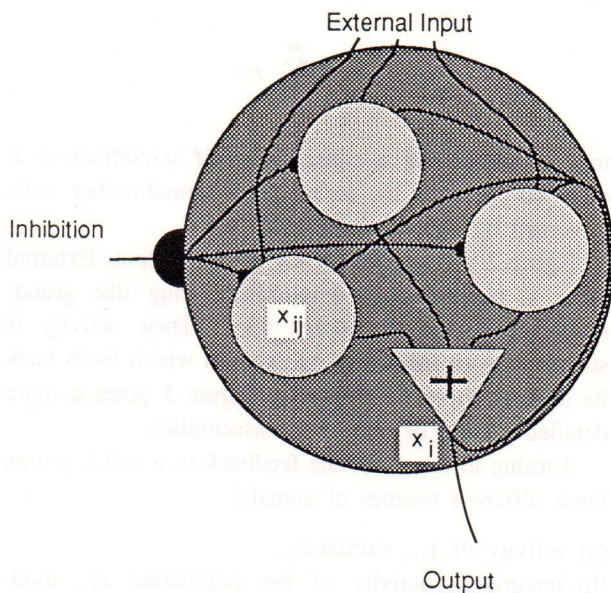


Fig. 3. A single grandmother cell assembly. Each cell connects to an excitatory interneuron which feeds back via multiplicative connections to all cells of the population.

activities (Fig. 3). Connections at cell  $x_{ij}$  should be multiplicative for Eq. (16) to be fulfilled. Additionally, the total activity  $x_i^n$  of the assembly interneuron provides a signal to yet another intermediate neuron which feeds back the sum of all populations as an inhibitory signal.

A further step towards a more general model is to relax the summing condition (15). Summing up is substituted by "weighting" through individual connections to the assembly interneuron

$$x_i = \sum_j \alpha_{ij} x_{ij} \tag{18}$$

with

$$\alpha_{ij} \geq 0 .$$

This is more realistic, since a natural system usually has at least some small deviations from the standard value. It turns out that the replacement of (15) by (18) has no effect on the dynamics at the population level



but results in minor changes for the saturation activities of individual cells.

The stable states for the population are therefore still  $x_i^0 = 1$ ,  $x_i^0 = 0$  but these do not uniquely determine the activities of individual cells;

$$x_i^0 = 1: \sum_j \alpha_{ij} x_{ij}^0 = 1$$

$$x_i^0 = 0: x_{ij}^0 = 0.$$

Instead,  $x_{ij}^0$  is determined by its initial values  $x_{ij}(0)$ , since relations are conserved between different  $x_{ij}$  in the same assembly. To observe this, suppose a pair of cells  $j, j'$  belongs to assembly  $i$  with

$$\dot{x}_{ij} = x_{ij}(1 + x_i^n - 2X^{(n)}) \quad (19)$$

$$\dot{x}_{ij'} = x_{ij'}(1 + x_i^n - 2X^{(n)}).$$

Since parentheses in Eq. (19) are identical

$$\frac{x_{ij}(t)}{x_{ij'}(t)} = \text{const.} \quad (20)$$

More generally, let activity of cell  $r$  be the reference quantity for winning assembly  $i$ ,

$$x_{ij} = k_j x_{ir} \quad j \in J_i, j \neq r. \quad (21)$$

From

$$\left( \sum_{j \in J_i, j \neq r} \alpha_{ij} k_j + \alpha_{ir} \right) x_{ir}^0 = 1, \quad (22)$$

it then follows that

$$x_{ir}^0 = 1 / \left( \sum_{j \in J_i, j \neq r} \alpha_{ij} k_j + \alpha_{ir} \right) \quad (23)$$

and

$$x_{ij}^0 = k_j x_{ir}^0 \quad j \in J_i, j \neq r. \quad (24)$$

All other assemblies lose the competition and end up with zero activity.

In Simulation 2 we demonstrate the usefulness of having populations of grandmother assemblies instead of single grandmother cells. The populations bring in a new degree of freedom which can be used to realize certain invariances. Since every cell in a population will contribute to the winning or losing process this

population is undergoing (Eq. (16)), it is not too important which cell actually fired the most in response to a stimulation. The overall result of having won the competition against the other populations is more important. On the other hand, even after competition has settled to a stable state, information about the cell which contributed most is still present since the relations between activities have been conserved during competition, as we have seen from Eq. (20).

### Simulation 2

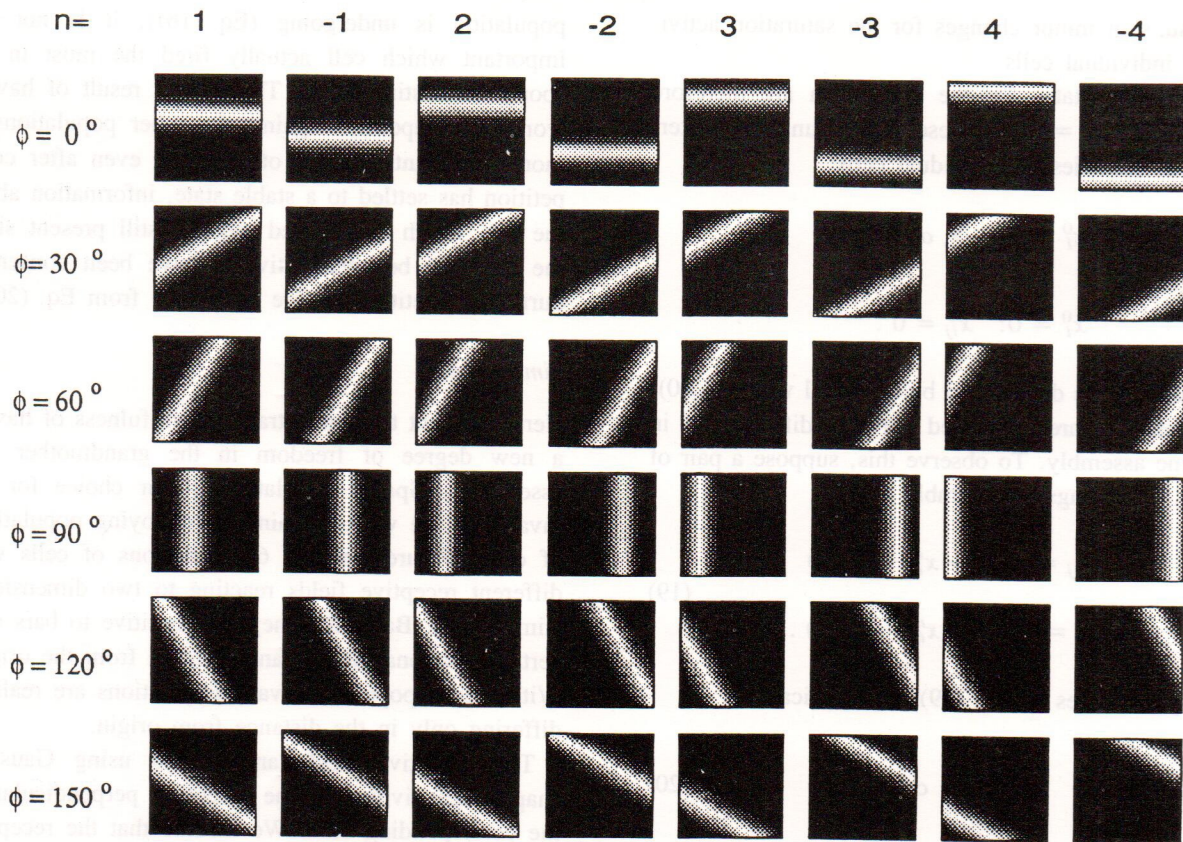
Here we want to demonstrate the usefulness of having a new degree of freedom in the grandmother cell assemblies. Spatial translation is our choice for the invariance we want to gain by employing populations of cells. Figure 4 shows 6 populations of cells with different receptive fields reacting to two dimensional stimulations. Basically, they are sensitive to bars of a certain rotational degree and distance from the origin. Within each population, various positions are realized differing only in the distance from origin.

The receptive fields are formed using Gaussian shaped sensitivities in the direction perpendicular to the corresponding bars. We assume that the receptive fields within a population can be formed using a competitive learning process as described in Ref. 8. For this simulation, we assume regular translations in symmetrical directions from the origin. We have chosen the quadratic dynamics ( $n = 1$ ). For the sake of simplicity,  $\alpha_{ij}$  has been set to 1 for all cells in each population. All assemblies possess the same number of cells but this is not strictly necessary. What we observe is an approximate translational invariance at the population interneuron level even in the absence of strong inhibition between perpendicular cell populations.

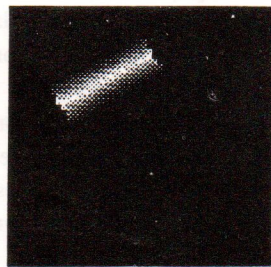
Figure 5 shows the development of the winning assembly with time. The cell with the largest overlap at the beginning is also largest in activity at the end of the relaxation process whereas its neighbors in the population grew proportionally. Thus, in principle, the cell (and therefore the translation) can be recovered from analyzing the detailed activity pattern (Fig. 6).

Note that according to Eq. (16), the activity of the population interneuron plays a decisive role in the relaxation process. Therefore, it is possible that a large number of smaller activities summed up in a certain population outperforms a population with a single cell showing very high activity with its partners being nearly silent. This problem can be addressed appropriately only in the context of the actual application of assemblies. In the present example, an additional





(a)



(b)

Fig. 4. (a) Six populations of cells respective to bars of different orientation  $\phi$ . Members of each population are distinguishable by their varying displacement  $d = nd_0$  from the center. Receptive fields are Gaussian in the direction of the displacement,

$$I(x, y) = \exp \left[ -\frac{(- (x - \frac{1}{2}) \sin \phi + (y - \frac{1}{2}) \cos \phi - d)^2}{8s} \right].$$

White represents strong excitation, black represents weak excitation. (b) Stimulus used for Figs. 5 and 6.

inhibition between assemblies depending on the size of angle difference between them would help considerably.

The phase diagram in Fig. 7 shows the region in the  $s, d$  plane for which the system gives the correct answer. The smaller the width of the stimulating bar, the broader the region where translational invariance occurs.

#### 4. Unfair Competition

In Sec. 3 we have maintained the requirement that every population contributes its fair and equal share to the globally inhibiting activity  $X$ . By inspection of

Fig. 2 however, we can see that the connections to the inhibitory interneuron as well as feed-back connections from the interneuron may be subjected to variations. And whereas individual excitatory connection strengths to the interneuron should only generate an altered global signal, differences in inhibitory feed-back connections will have the effect of forcing a different outcome for the competition. Since everything can be seen on the assembly level, we disregard for the moment the discrete contributions from individual member cells of each assembly. Here we consider only the quadratic dynamics,  $n = 1$ . A similar analysis can be done for the general case.

Let us first substantiate the statement concerning



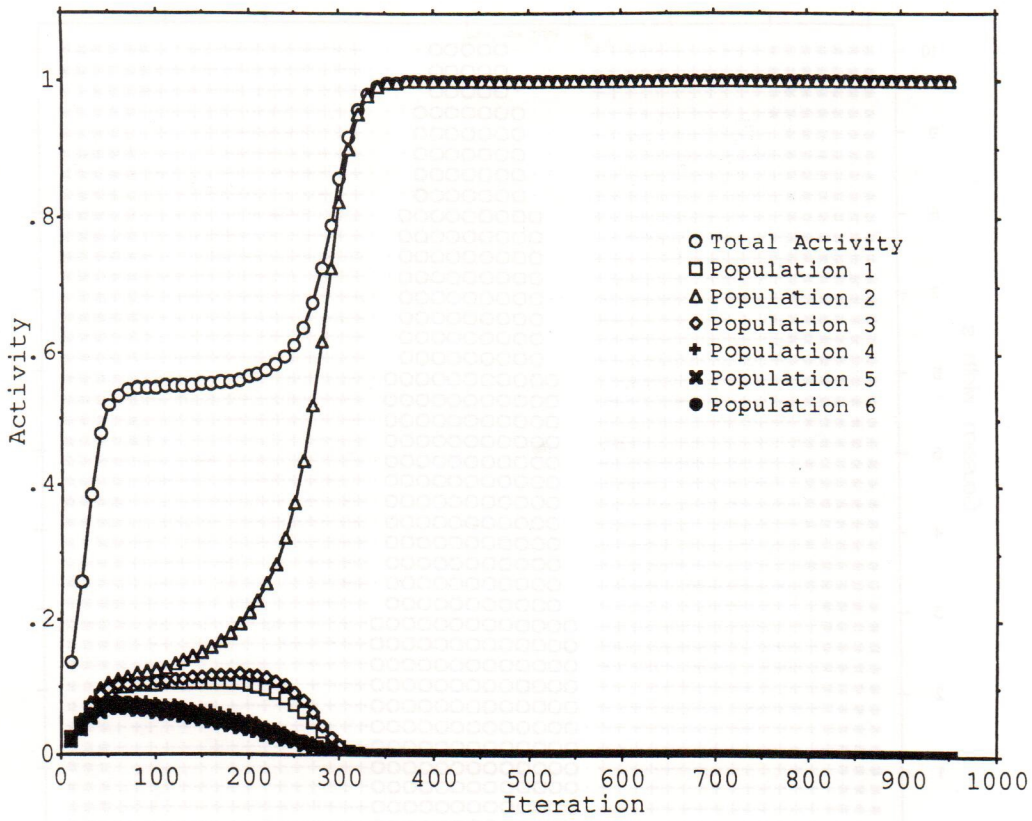


Fig. 5. Time development of the population interneurons. Interneurons summing up the activity of a population serve as an indicator of which bar direction was present in the input pattern.

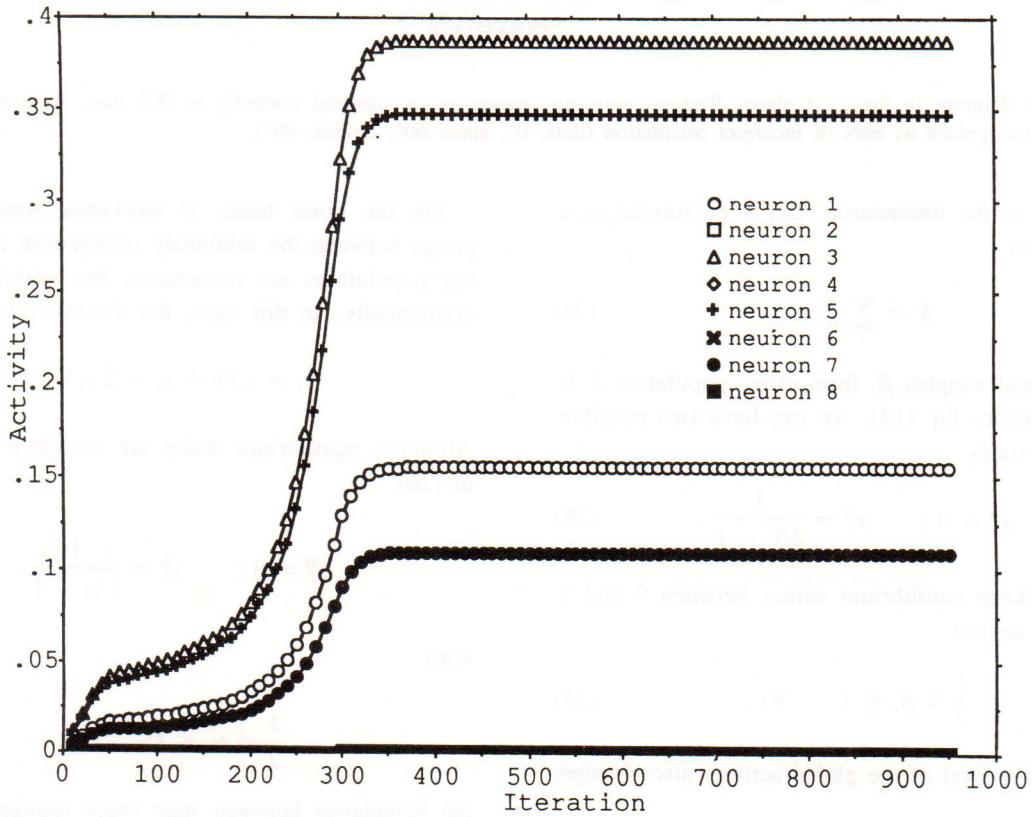


Fig. 6. Time development of cells in the winning population. Since relations between excitation levels are conserved, one can read off that cell 3 was excited mostly by that input pattern.



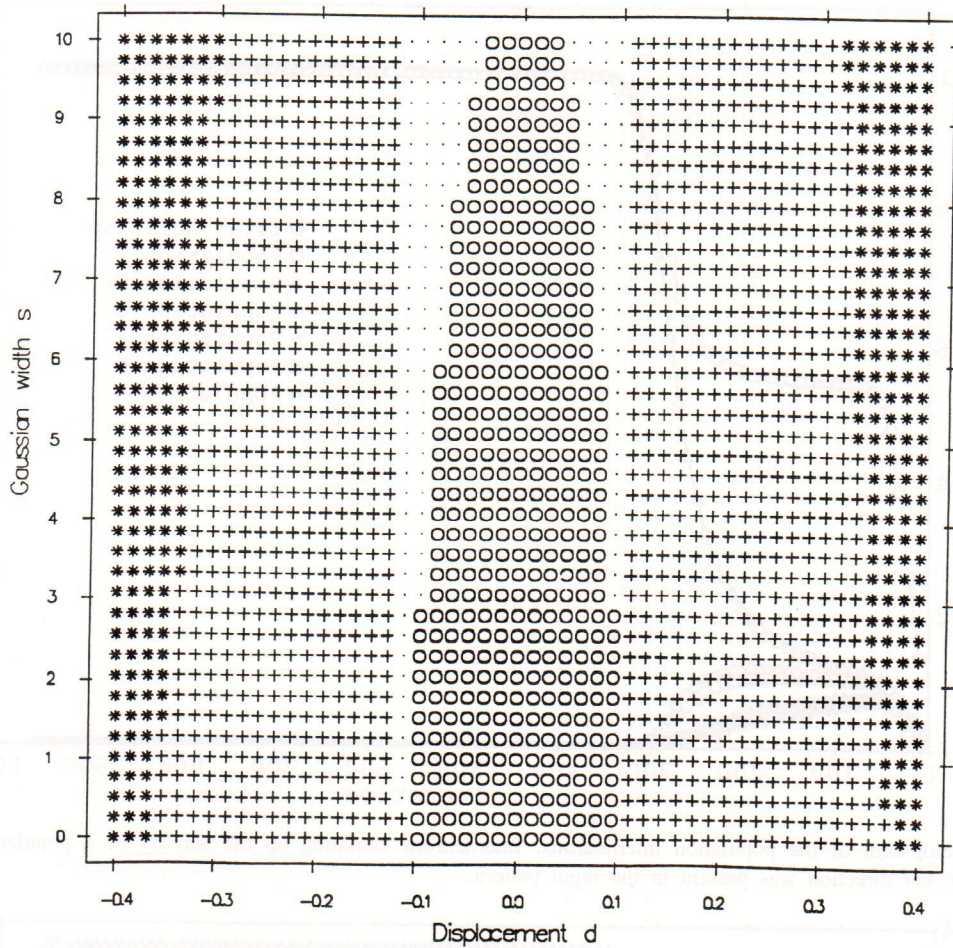


Fig. 7. Phase diagram in the  $s, d$  plane. Regions carrying crosses are recognized correctly as  $30^\circ$  bars. Regions with other symbols are recognized as bars of incorrect orientation (dots:  $0^\circ$ , stars:  $60^\circ$ , circles:  $90^\circ$ ).

connections to the interneuron. Let  $X$  be formed as a weighted sum

$$X = \sum_i \beta_i x_i, \quad (25)$$

with individual weights  $\beta_i$  from every population  $i$ . If we then consider Eq. (13), we can have two possible equilibrium states

$$x_i^0 = 0; \quad x_i^0 = \frac{1}{2\beta_i - 1}. \quad (26)$$

In order to keep equilibrium values between 0 and 1 we have to restrict

$$\frac{1}{2} < \beta_i \leq 1 \quad \forall i. \quad (27)$$

The saturation level of the global activity also changes to

$$X^0 = \beta_i x_i^0 = \frac{\beta_i}{2\beta_i - 1}. \quad (28)$$

On the other hand, if individual feed-back couplings between the inhibitory interneuron and competing populations are introduced, the situation changes dramatically. In this case, the dynamics reads

$$\dot{x}_i = x_i(1 + x_i - 2\gamma_i X). \quad (29)$$

Although equilibrium states are similarly changed as in (26)

$$x_i^0 = 0; \quad x_i^0 = \frac{1}{2\gamma_i - 1}, \quad (30)$$

with

$$\frac{1}{2} < \gamma_i \leq 1 \quad \forall i, \quad (31)$$

the boundaries between state space regions where one population or another wins the competition are changed.



In order to observe this, we introduce a threshold activity  $x_i^t$  for every population

$$x_i^t = X \left( \frac{1}{N} + \frac{1}{N-1} \sum_j \Delta_{ij} \right) \quad (32)$$

with

$$\Delta_{ij} \equiv \gamma_i - \gamma_j. \quad (33)$$

Every population whose activity is below this threshold value, will *lose* the competition. From the remaining populations  $l_1, \dots, l_m$  the population with the largest equilibrium value will win the competition. Thus if we assume an ordering of indices in the form

$$x_{l_1}^0 > x_{l_2}^0 > \dots > x_{l_m}^0, \quad (34)$$

population  $l_1$  will win. In the event that no population exceeds its own threshold, the population which is nearest to its own threshold will win. In the simulation below, we shall demonstrate this behaviour for the case of two competing populations in detail.

For the moment, we note that in the general case  $\beta_i, \gamma_i \neq 1$ ,  $\beta_i$  also influences the boundaries between competing populations by contributing to  $x_i^0$ ,

$$x_l^0 = 0; \quad x_l^0 = \frac{1}{2\gamma_l\beta_l - 1} \quad (35)$$

and to  $x_i^t$  via  $X$  as stated in Eqs. (28, 32).

By changing the connection strengths  $\beta_i$  and  $\gamma_i$  the system wins another degree of freedom. Under the conditions of unfair competition, even a higher activity value may lose since it may belong to a population with a stronger coupling to the global inhibitory interneuron. Vice versa, lower activity values may win the competition despite participation of momentarily stronger competitors. This boundary shift may be considered as a prejudice of the system toward one decision. If it is only temporary it may also be interpreted as a shift in attention as was pointed out by Haken and Ditzinger<sup>10,11</sup> in the context of another variation to the original model.

### Simulation 3

Here we wish to demonstrate the behaviour of competing cells in the case of unfair competition,  $\beta_i, \gamma_i \neq 1$  for only 2 competing cells. The boundary between decision regions can easily be computed for the 2-dimensional case. It takes the form of a function

$x_2 = f(x_1)$  where the boundary is determined by

$$x_1^t - x_1 = x_2^t - x_2. \quad (36)$$

Substituting Eq. (32) into Eq. (36) and solving for  $x_2$ , we get

$$x_2 = \frac{1 - 2\beta_1\Delta}{1 + 2\beta_2\Delta} x_1 \quad (37)$$

with

$$\Delta = \gamma_1 - \gamma_2.$$

Figure 8 shows a phase diagram for the special choice of

$$\gamma_1 = \frac{1}{\beta_1} = 0.8 \quad \gamma_2 = \frac{1}{\beta_2} = 1.0$$

in order to keep equilibrium values at  $x_i^0 = 1$ . The boundary line given by Eq. (37) is also depicted in Fig. 8.

Figure 9 shows the angle  $\delta$  between the boundary line and the horizontal line for various values of  $\beta_1, \gamma_1$ .  $\delta = 45^\circ$  is the special case of fair competition between both cells.

## 5. Summary

Our most general model can now be formulated as follows:

$$\dot{x}_{ij} = x_{ij}^m (1 + x_i^n - 2\gamma_i X^{(n)}) \quad (38)$$

with

$$x_i \equiv \sum_{j=1}^{J_i} \alpha_{ij} x_{ij} \quad (39)$$

and

$$X^{(n)} \equiv \sum_k \beta_k x_k^n, \quad (40)$$

where the weights  $\alpha_{ij}, \beta_i, \gamma_i$  obey the relations

$$\alpha_{ij}, \beta_i, \gamma_i > 0; \quad \beta_i \gamma_i > \frac{1}{2}. \quad (41)$$

Interpreting  $x_{ij}$  as the activity of a neuron, it is observed that now every weight in Fig. 2 has become adaptable. Though we have not mentioned the extra



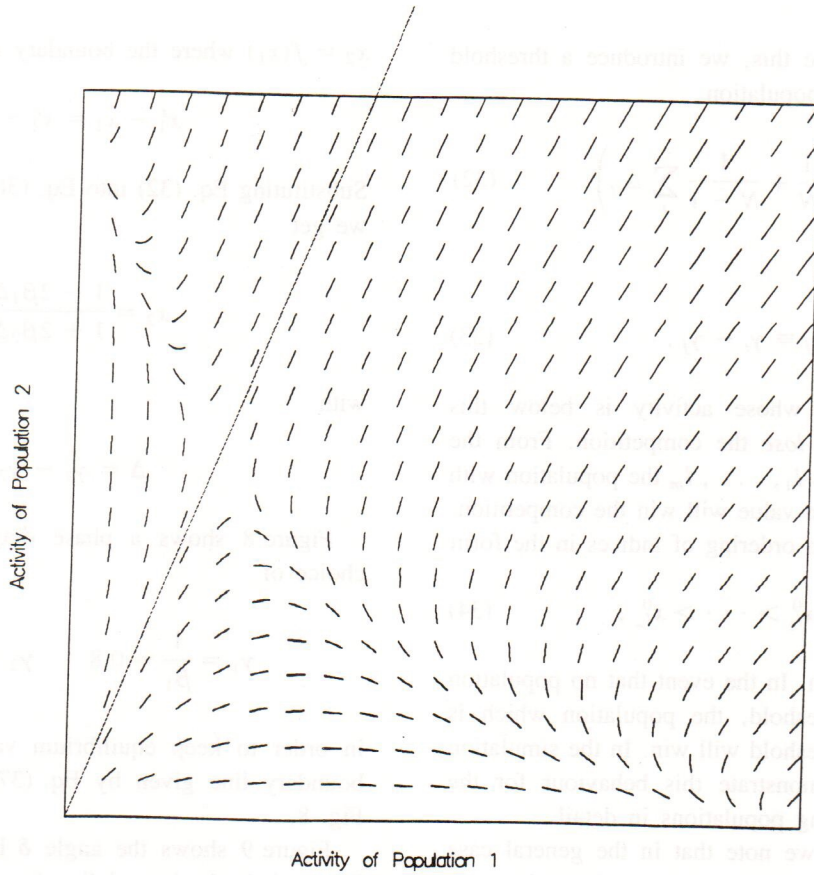


Fig. 8. Unfair competition between two cells, phase diagram.  $\gamma_1 = 1/\beta_1 = 0.8$ ,  $\gamma_2 = \beta_2 = 1.0$

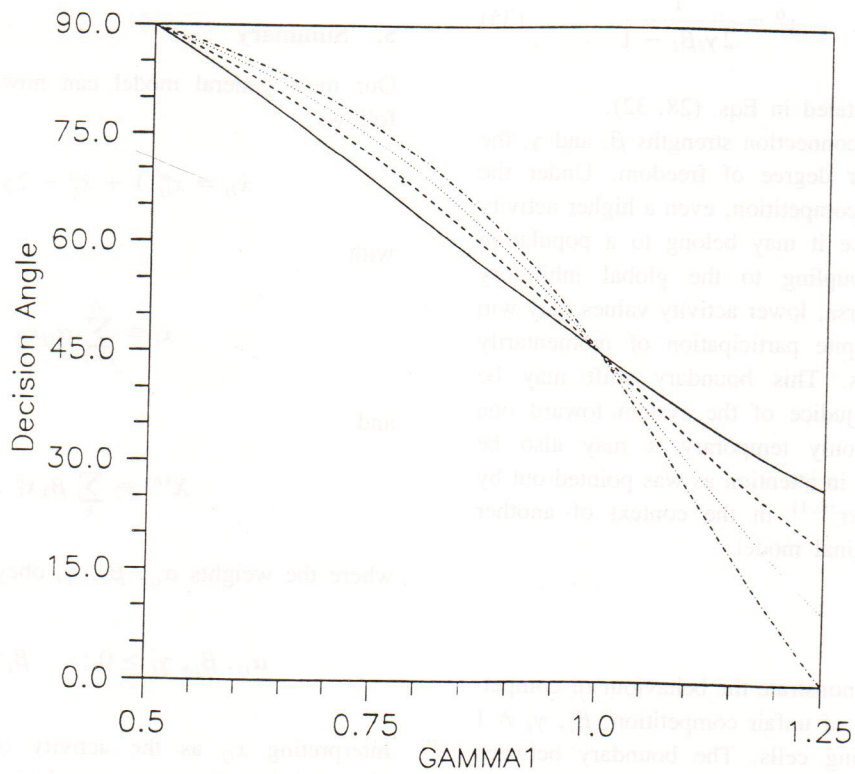


Fig. 9. Unfair competition between two cells, decision boundary angle as a function of  $\gamma_1 \cdot \beta_2 = \gamma_2 = 1.0$ . Solid line:  $\beta_1 = 0.5$ ; dashed line:  $\beta_1 = 1.0$ ; dotted line:  $\beta_1 = 1.5$ ; dashed/dotted line:  $\beta_1 = 2.0$



weights  $A_{ijk}$  connecting external input  $q_k$  to the cells  $ij$ , we may assume now that every connection can be subjected to a learning process.

Adjusting  $A_{ijk}$  fine-tunes the access to outside information for cell  $j$  in assembly  $i$ . Adjusting  $\alpha_{ij}$  will change the internal importance a given assembly assigns to a certain cell. Adjusting  $\beta_i$  and  $\gamma_i$  will finally determine the decision boundaries between assemblies as well as the equilibrium values for all cells involved.

In summary, we have indicated the benefits of these extensions to the original competitive dynamics model. They are:

- (a) The ability to select from a variety of competitive network types,
- (b) distribution of knowledge about pattern classes over a population of cells,
- (c) obtaining an additional degree of freedom for the assemblies, useful for introducing invariances and
- (d) choosing from a continuous spectrum of competition boundaries.

A great variety of learning processes is imaginable to take advantage of the newly won freedom of the system to self-organize. Just to give two examples:

- (1) Different cells in the same population could become susceptible to different aspects of the same pattern. Cells in the same population would learn to excite each other to gain an edge over competing populations much as learning in the olfactory system is supposed to work (generalization-over-equivalent input, see Ref. 12).
- (2) Adaptive weights to and from the inhibitory interneuron could be used to stabilize competitive learning schemes such as the unsupervised learning rule proposed by Banzhaf and Haken<sup>8,13</sup> which is based on the specialization state of a grandmother cell (resp. assembly). In this scheme, an assembly which has not yet specialized enough to certain input would only weakly be inhibited by other assemblies enabling it to learn more about the environment by a Hebbian learning rule.

Studying these and other adaptation processes certainly has to be a subject of further investigations.

The interpretation of variables in this paper is but one of the possible ways of looking at the system of equations presented here. An alternative approach would be to interpret  $x_{ij}$  or  $x_i$  as the concentration levels of certain chemical substances or biological cells e.g. lymphocytes of the immune system. The mechanisms of competition and co-operation at work here

may give enough freedom in the behaviour of such a system to allow for useful applications.

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