Molecular Self-Organisation in a Developmental Model for the Evolution of Large-Scale Artificial Neural Networks

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Abstract

We argue that molecular self-organisation during embryonic development allows evolution to perform highly nonlinear combinatorial optimisation. A structured approach to architectural optimisation of large-scale Artificial Neural Networks using this principle is presented. We also present simulation results demonstrating the evolution of an edge detecting retina using the proposed methodology.

Introduction

One of the attractions of Artificial Neural Networks (ANNs) has been the possibility of designing intelligent systems capable of optimising their functionality according to application requirements.

Adapting the architecture of an ANN (number of neurons, connectivity pattern, and neuron function) to a given application can be viewed as a combinatorial optimisation problem. For sophisticated applications, the problem tends to be high-dimensional and highly nonlinear. Direct applications of current combinatorial optimisation methods to such problems tend to be unacceptably inefficient.

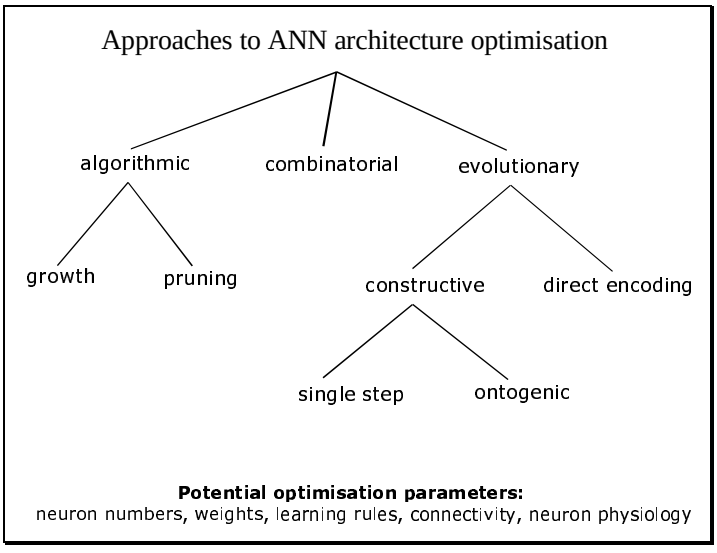

Figure 1, approaches to ANN architecture optimisation

Figure 1 presents an overview of current approaches to ANN architecture optimisation. Much research in self-adapting ANNs has focused on the design of unsupervised learning algorithms, and the use of algorithmic (generative) techniques to 'grow' or 'prune' neurons and their connections. Unsupervised learning, and generative algorithms both make strong assumptions about the ANN architecture and the characteristics of the target application domain. To alleviate these restrictions, a number of researchers have exploited evolutionary methods to design adaptive generative algorithms (see [Rust98a] for a review). The generative algorithm is encoded in a genome. Its execution (the mapping from genotype to phenotype) mimics embryonic development. Current implementations of this approach limit the architectural search space through apriori assumptions and algorithmic restrictions. However, restricting the range of genotype to phenotype mappings can hinder rather than help the optimisation process: nonoptimal mappings result in more nonlinear search spaces which are more difficult to search. We argue that it is possible to evolve unconstrained optimal mappings through the use of two strategies:

1) Cellular (neuron) characteristics should be defined in terms of interacting molecular processes. These molecular interactions result in nonlinear genotype-phenotype mappings. Their evolutionary optimisation reduces the degree of nonlinearity in the genotype search space and simplifies the optimisation process.

2) Evolution should be staged, mimicking the process of speciation. Specifically, evolution should start with the simplest set of generative rules, search for the best achievable phenotype, then incorporate new (more sophisticated) rules (mimicking the emergence of a new species), and search again; repeating this procedure until satisfactory phenotypes emerge.

The paper presents simulation results demonstrating molecular, staged evolution of a simple edge detecting retina.

Methodology

Our strategy is based on a molecular model of the evolution of embryonic development with the following characteristics:

1) Neurons are modelled as cells. Each distinct cell type is defined by the interactions of a specific subset of genes within the genome.

2) The genome, and the evolutionary operators mutation and cross-over, are defined at the molecular level (i.e. a much

finer level of detail than cell characteristics such as receptive field size).

3) The translation from genetic encoding to neural network (genotype to phenotype mapping) is performed using sequences of operations defined by individual genes. These operations mimic gene regulation (the sequential activation and interaction of genes) and embryonic development in biological systems.

4) Although cells of the same type (ensembles of neurons) share the same genetic description, individual neurons within an ensemble may differ from each other if differences in cell-cell or cell- environment interactions lead to different developmental histories.

5) Hierarchic network structures can be defined with nested loops of gene interactions. Thus, similar cells in different parts of a network may utilise common segments of the genome to define the parts they have in common.

6) A gene (more accurately a gene product) has two aspects: the definition of what it will interact with, and the definition of the nature of its interactions (affinity and function respectively). In the simulations presented here, the space of all possible protein functions was predefined by mimicking known biological functions. We carried out numerous developmental simulations to ensure that the set of functions included in our repertoire was sufficient to generate a wide variety of neuron morphologies [Rust98a,b]. Similarly, each affinity value (interaction rate) is discretised to a finite range of possible values. Molecular evolution thus becomes a combinatorial optimisation task. A developmental program is evolved by constructing sequences of gene interactions where each gene is selected from among a large, but finite ensemble of predefined genes.

7) The genome is defined as a (variable) number of distinct chromosomes each comprising a set of genes which may, in principle, interact with each other. During cross-over only alike chromosomes can exchange parts.

8) The neural system is evolved gradually and in stages reminiscent of the emergence of new species. Speciation is achieved by allowing the size of the genome to vary through addition of new genes to the genome by the user when a genome of a certain size is deemed close to its peak fitness.

9) Evolution starts by using only the simplest of developmental programs. In this case, neuron connectivity is specified using only intrinsic growth rules. When this type of genome is deemed to have been adequately optimised, additional genes describing potentially more powerful developmental processes are added to the genome and a new cycle of evolutionary optimisation starts. Some examples of the developmental processes modelled are given in figure 2.

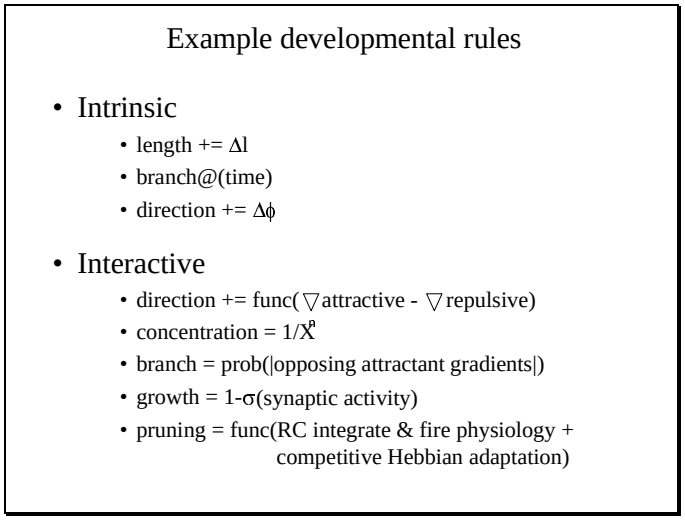

Figure 2, example developmental processes modelled

10) No information other than the performance of the evolved networks is used to guide the evolutionary process.

Example self-organising molecular evolution

We present the modelling of a simple edge-detecting retina as a testbed application. Starting from a random genome, we evolve a retina with on-centre/off-surround bipolar cells performing edge detection. The choice of a retina as our testbed application has a number of advatages, summarised in figure 3. In particular, the simple, layered structure of the retina allows us to simplify embryonic development to the formation of connections between growing axons and dendrites.

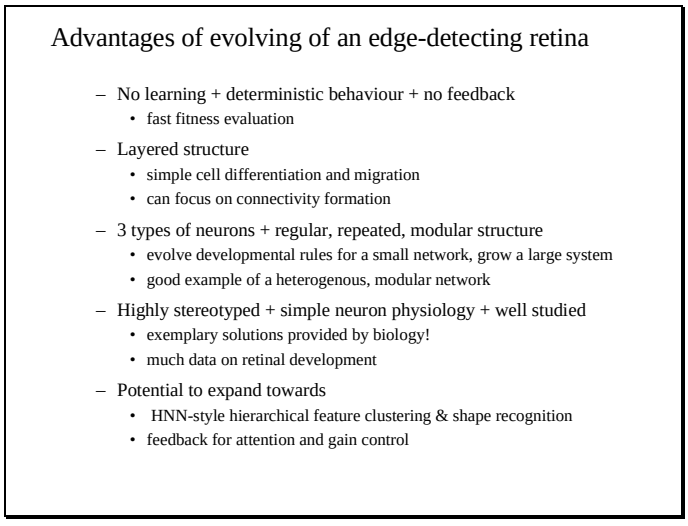

Figure 3, the selected testbed application allows investigations to focus on the most pertinent issues.

Experimental details

The edge-detecting retina comprises 3 types of cells: cones, horizontal cells, and bipolar cells. Cones are photodetectors which transmit the input signal to specialized synapses named triad junctions. Horizontal cells average the signal value they

receive through their connections to triad junctions. Bipolar cells are inhibited by input from horizontal cells (surround activity) and excited by cones (centre activity). Figure 4 shows a single triad junction and its connections. Figure 5 shows plan views of the target network structure and illustrates the desired network functionality. Note that the ANN structures we evolve are 3 dimensional in order to allow neurites to pass across each other without colliding. This is necessary because our long term objective is to evolve a Neocognitron-like image recognition system [Sabisch97, 98]. The retina reported here may be viewed as the first stage of such a network. Figure 6 shows the 3 dimensional structure of an example evolved network. Figure 7 shows a plan view of the same network so that it can be related to figure 6.

Evolution was performed using the GENESIS Genetic Algorithm package [Grefenstette90]. In all cases, the population size was 50, and the cross-over rate was 0.6. In the first 2 stages of evolution a fixed mutation rate of 0.001 was used, in the final stage the mutation was initially set to 0.01 and was reduced gradually to 0.001. Selection was rank based using elitist criteria. Five visually salient images (edges at various orientations) were used to evaluate the fitness of all evolved networks.

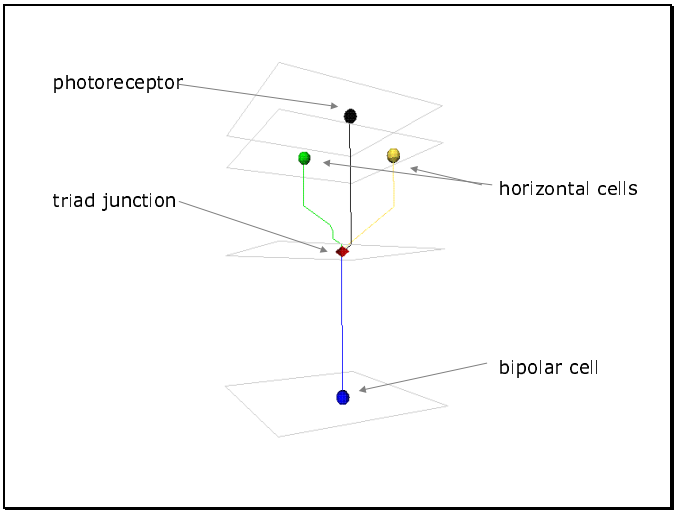

Figure 4, a single triad junction and its connections

To reduce computational load, we took advantage of the modular, repeated structure of our retinas to evolve networks responding to 8x8 retinal cones (i.e. 64 cones, 36 horizontal cells, 25 bipolar cells). The developmental parameters thus evolved were then used to grow larger retinas (1024 cones, 900 horizontal cells, and 481 bipolar cells).

Results

As can be seen from figure 8(a), intrinsic developmental processes alone are sufficient to evolve perfect functionality for a network of deterministically placed neurons. This is similar to results achieved by other researchers in the field (see [Rust98a] for a review). However, when the starting positions of the neurons are perturbed (neuron positions varied in any of three directions by 10% with a 25% probability), intrinsic rules result in very poor evolved perfomance (figure 8(b)).

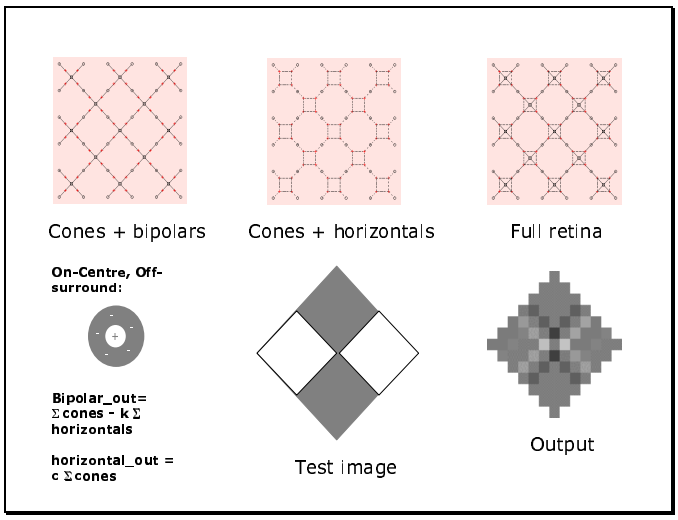

Figure 5, the target retinal structure and function. Note that cones and horizontal cells occupy the same grid point in plan view, but are spatially distinct in 3D.

In the next stage of evolution, interactive parameters were added to the genome permitting neurites to self organise by interacting with each other and producing extra branches determined by local needs. The new population was seeded using the best parameters from the intrinsic growth stage. See figure 8(c) for resultant edge detection functionality. Note that performance from intrinsic only growth has been improved, but is still not optimal .

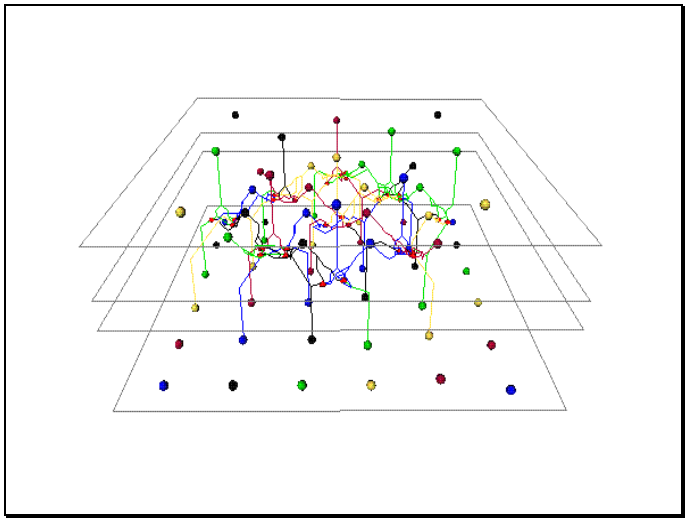

Figure 6, 3D view of an evolved retina

In the final stage of evolution, parameters for self-organising pruning mechanisms (see [Rust97] for details) were added to the genome. The new population was seeded using the best parameters from the previous two stages. Multiple retinas were again grown and evaluated. The final set of evolved parameters were used to grow a 32x32 retina where the

positions of the neurons were perturbed as before. Figure 8(d) shows the resultant edge detection behaviour. Note that all 4 edges in the image are now fully detected. Figure 9 shows the results of another run of our staged evolution algorithm. Note the the evovled network behaviours are different, but exhibit the same progressive improvement in functionality as more self-organising developmental interactions are added.

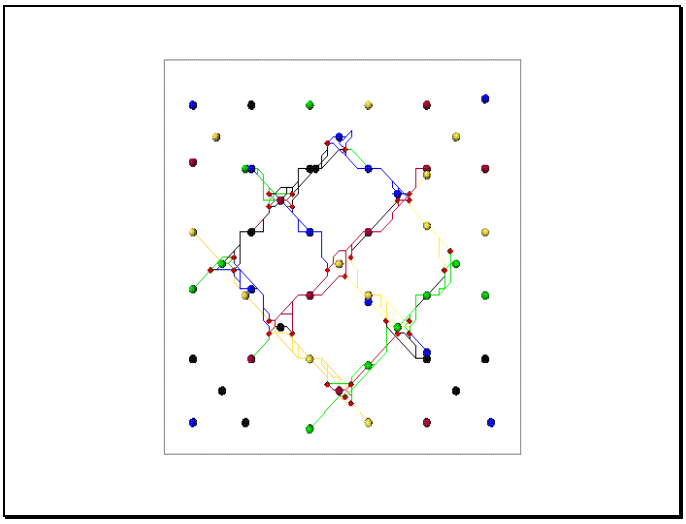

Figure 7, plan view of the 3D retina structure

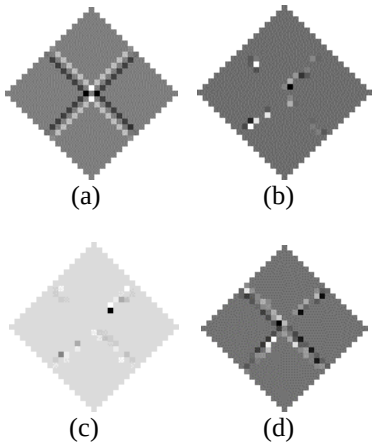

Figure 8, evolved functionality for a 32x32 retina. The input image and desired output are shown in figure 5. (a)-(e) show outputs of retinas grown using the parameters from the best evolved individuals. (a) Intrinsic growth rules, symmetric retina. (b) Intrinsic growth rules, perturbed retina. (c) Intrinsic and interactive rules, perturbed retina. (d) Intrinsic, interactive and pruning rules, perturbed retina.

Conclusions

A methodology to evolve complex ANN structures using molecular self-organisation during embryonic development was presented. Our simulations of the evolution of an edge-detecting retina demonstrate the benefits of molecular self-organisation and staged speciation in providing increased developmental robustness and functional fitness.

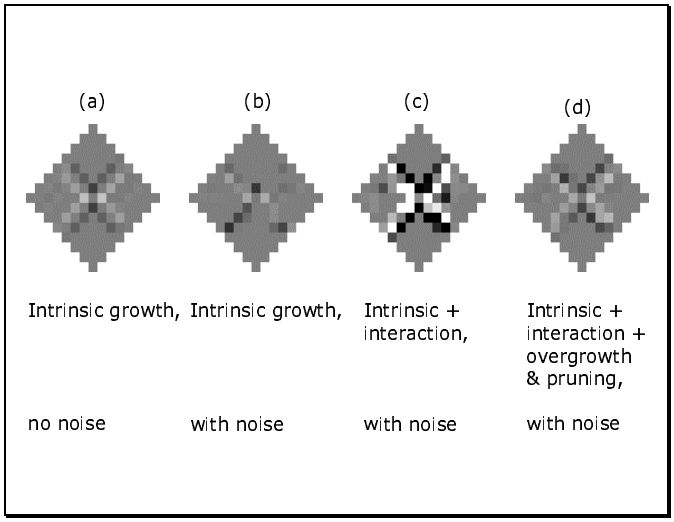

Figure 9, another example of the benefits of staged evolution (in this case of an edge detecting retina)

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