Artificial Development of Connections in SHRUTI Networks Using a Multi-Objective Genetic Algorithm

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ABSTRACT

SHRUTI is a model of how first-order logic can be represented and reasoned upon using a network of spiking neurons in an attempt to model the brain's ability to perform reasoning. This paper extends the biological plausibility of the SHRUTI model by presenting a genotype representation of connections in a SHRUTI network using indirect encoding and showing that networks represented in this way can be generated by an evolutionary process.

Categories and Subject Descriptors

I.2 [**Artificial Intelligence**]: Miscellaneous

Keywords

Neural-Symbolic Integration; SHRUTI; Artificial Development; Indirect Encoding

1. INTRODUCTION

Neural-symbolic integration concerns the representation of symbolic information in neural networks [3]. One motivation of this field is to produce models of symbolic representation in the brain's biological neural network. SHRUTI is a neural-symbolic network which models reasoning in the brain in a way that is claimed to be *biologically plausible* [6], owing to its use of spiking neurons [5] and Hebbian learning [4]. Predicates are represented by clusters of nodes and role instantiations are performed by firing these nodes in synchrony with nodes representing the role-fillers. These role bindings then propagate along connections between clusters that represent relations between predicates.

The developers of SHRUTI discuss the idea that the prerequisite structure required to enable it to learn logical relations can be realised in a way which is itself biologically plausible known as *indirect encoding* [7]. Rather than explicitly defining the topology of the phenotype (*direct encoding*), indirect encoding provides a set of developmental rules for the gradual development of the phenotype. This

paper presents the first indirect encoding of SHRUTI networks and shows that developmental genomes for creating connections between SHRUTI's neurons can be produced through evolution using *artificial development* [1], a form of evolutionary computing which uses indirect encoding.

2. EVOLVING SHRUTI NETWORKS

2.1 The SHRUTI Genome

A genome for developing connections in a SHRUTI network has recently been produced by the authors [8]. The genome takes the form of a decision tree in which each path from the root node to a leaf node respresents a different rule. A network is presented with a temporal sequence of predicate instances supporting a set of causal relations. At each time t, all predicate instances occurring at t are observed and any existing connection weights are updated according to SHRUTI's learning algorithm. The rules in the genome are then assessed and the actions of any satisfied rules are executed. Owing to the use of indirect encoding, the same genome is able to develop networks of different sizes depending on the size of the represented logic program, even though the size of the genome is fixed, showing that the size of the genotype is independent of the size of the phenotype and that the genome is therefore scalable.

2.2 Fitness Function

The goal was to minimise two objectives. As the network develops, error will change during development as more relations are learned. Therefore the area beneath the error-time graph (referred to as *e-area*) was chosen as the first objective in order to encourage the algorithm to converge not only towards networks of minimum error but towards networks that can achieve minimum error as early as possible. Error is based on the number of training questions a network answers incorrectly. A question takes the form of a predicate instance, for example $P(a, b)$, which a developed network must evaluate as true, false, or unknown.

The second objective was to minimise the number of weight updates performed on the network. Minimising this reduces the workload of the learning algorithm and constrains the number of connections in the network, because as the number of connections in a network increases, so does the number of the weights the algorithm has to update.
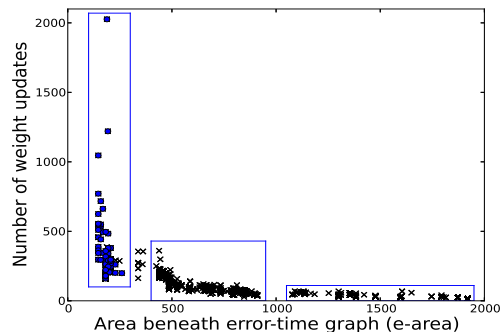
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Figure 1: Points obtained from 50 trials on training data. Points marked with a dot represent genomes that answered all training questions correctly.

Figure 2: Points obtained by running all genomes developed in all 50 trials on a set of test questions.

2.3 Evolutionary Algorithm

A multi-objective algorithm NSGA-II [2] was chosen to minimise both objectives, with a population size of 100 over 500 generations, repeated over 50 trials. Binary tournament selection with replacement was used to select genomes for recombination. Crossover and mutation were performed at rates of 90% and 10% respectively.

3. RESULTS

3.1 Performance on Training Questions

Fig. 1 shows samples obtained from 50 trials. Points marked with a dot indicate genomes which developed networks capable of answering all training questions correctly and therefore yielded an error of zero. In most trials a zero-error network was found at some point before the 100th generation, suggesting that such networks are easily found. However the number of updates required to train the network to this level of accuracy is high compared to networks found in later generations, suggesting that even though finding genomes for constructing zero-error networks may be a trivial task for the algorithm, maximising the speed at which such networks learn is not.

In general, three very distinct groups of networks emerged (indicated by the three boxes in Fig. 1), though there were a few exceptions. The first group contains the zero-error networks discussed above, which correctly learns all relations based on training observations. Genomes in the second group develop networks which always produce the same answer for any given predicate, for example always answering 'true' for predicate P and always answering 'false' for predicate Q. In the third group, most genomes develop a very small number of connections if any at all, and the resulting networks always answer 'unknown' for every question.

3.2 Performance on Test Questions

The evolved genomes were tested by asking the developed networks a set of test questions distinct from and larger than the set of training questions. Fig. 2 shows how the networks performed on the test set. The general shapes of the Pareto fronts remain roughly the same for both sets and every genome capable of developing networks which answered all training questions correctly could also answer
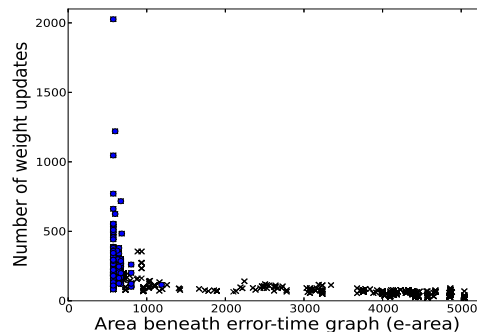
every test question correctly, suggesting that the evolved genomes adapt well to unseen test questions.

4. CONCLUSIONS

Three groups of genomes for developing connections in SHRUTI networks emerged, each with its own distinct strategy for answering questions. One of these groups was successful in producing networks that learned to answer all training and test questions correctly. These findings support the claim of the SHRUTI developers that the prerequisite structure required to enable the learning of relations in SHRUTI can be realised through a model of biological development, adding another dimension of biological plausibility to the model. However, to support the idea of a developmental SHRUTI model even further, we plan to also produce the neurons themselves rather than just the connections between them, and other representational structures such as episodic facts and type hierarchies.

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