# Associative Memory with Biologically-Inspired Cell Assemblies

Yuehu Ji[1], David Gamez[1] and Chris Huyck[1]

[1] Middlesex University, The Burroughs, London NW4 4BT, United Kingdom
yj097@live.mdx.ac.uk

**Abstract.** Associative memory is a central cognitive task. However, the actual biological architecture that supports this memory is not currently known, so simulating with biologically plausible neurons and topologies is an ideal mechanism to improve understanding of associative memory. Simulations of spiking networks that perform associative memory tasks lay the groundwork for utilizing biological neurons in cognitive tasks. Specifically, this paper explores simulations of spiking networks that perform associative memory tasks using Hebbian cell assemblies of neurons to represent nodes and synapses to represent associations. The first tasks use binary cell assemblies to perform two well-known cognitive tasks. Then the paper examines different topologies of excitatory neurons for basic assemblies and their performance as short-term memory. Lastly, larger assemblies are associated in 2/3 sets, where two active elements can retrieve the third. Future research is proposed to explore the potential use of these assemblies and associations in cognitive tasks. By investigating biologically and cognitively plausible topologies, learning, and neurons, simulations will lead to an improved understanding of neuro-cognition, and potentially to systems that surpass the brittleness and domain specificity of current AI systems.

**Keywords:** Cell Assemblies, Neurocognitive Model, Stroop Task, Associative Memory, Spiking Network.

## 1 Introduction

Large deep neural networks, such as GPT, can accurately mimic natural language in diverse fields. However, these models depend on statistical patterns in the training data and can only produce shallow models that are detached from reality. They fail to properly comprehend semantic relationships between words and cannot achieve a human-like understanding of the world because the concepts they manipulate have no foundation. They are unable to learn novel ideas or dynamically remember associations between them in the way that humans do. The work presented in this paper seeks to go beyond these limitations by developing a biologically-inspired associative memory system that captures semantic relationships between words, answers questions about their relationships in a psychologically plausible way and learns associations.

When neurons display similar spiking patterns in response to a stimulus, the connections between the neurons may become strengthened through a process first proposed by Hebb [1]. These connections can form a cell assembly (CA), comprising groups of interconnected neurons that facilitate efficient storage and retrieval of related information. Experimental and theoretical evidence support the existence of cell assemblies [2, 3] and theoretical models of neural networks have been developed to simulate the formation and function of CAs [4].

This paper gives an overview of the authors' work constructing biologically-inspired associative memory systems using CAs. The first part describes initial work in which a hard-wired network of cell assemblies was used to model the hierarchical structure of semantic words in a Stroop task and an associative memory task. The next stage (Section 3) investigates good topological structures of CAs particularly those involved in associative memory tasks. These topologies are then used to learn 2-3 cell assembly associations (see Section 4). The final part of this paper describes plans for scaling up this associative memory model for larger associative memory tasks.

## 2 Cell Assembly Models of Semantic Retrieval

It is reasonably simple to implement logic in simulated spiking neurons. Using simple persistent assemblies, the authors developed a model of the Stroop task [5]. In word recognition and colour naming tasks, the subjects are presented with a colour word, such as 'red' or blue' that is written in coloured ink. In the congruent situation, the colour of the ink matches the meaning of the word (for example, 'red' written in red ink). In the incongruent situation the colour of the word is different from the colour of the ink (for example, the word 'red' written in blue ink). The subjects must recognize and repeat the word (WR) or name the colour of the ink (CN). When humans perform these tasks, they have a faster reaction time in WR tasks compared with CN tasks. Subjects also have slower reaction times on CN tasks in the incongruent situation where the word and ink colour disagree, but the difference in reaction time is not significant in incongruent WR tasks. This difference in response times is known as the Stroop effect [6]. The authors' simulation of the Stroop effect was constructed using eight cell assemblies. The simulation was able to re-produce similar timings to human subjects with congruent and incongruent colour word combinations.

Further simulation of a classic semantic net task, [7] has also been completed [8]. Here a small hierarchy has been attributed to people, and psychological experiments have been performed on subjects.

The semantic net examined revolves around animal concepts with for example a canary that is a bird, and a bird that is an animal. Features are associated with these animal classes, so canaries are yellow, birds can fly, and animals eat. Subjects were then queried with a true or false question, for example, "Do canaries fly?" Subjects were observed to take longer to respond to canaries flying than to them being yellow. The explanation of this phenomenon was that features higher in the hierarchy require longer processing time. An overview of the structure of the network is shown in Figure 1.

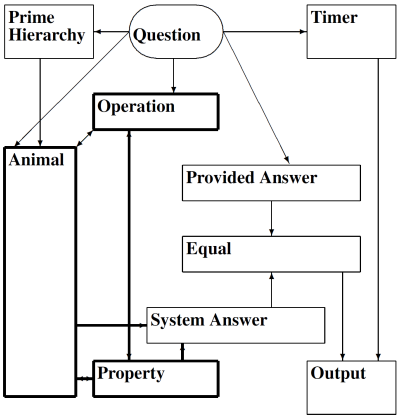


**Fig. 1.** Gross Topology of the Question Answering Associative Memory. Boxes represent sets of neurons. Thick boxes and arrows are the core of the semantic memory. The oval represents the question with spike sources instead of neurons.

The use of spiking neuron models for timing of response is particularly good due to the ability to directly derive performance timings from the collective firing of individual neurons. Additionally, the size and hierarchical structure of the network can directly determine its effectiveness and potentially explain some of the cognitive connections between individual concepts. However, as these models use simple parameters to account for neural activity, they do not guarantee biologically accurate reproduction of neural processes, although they may provide a reasonable approximation. The present associative memory model, for instance, employs only 1130 neurons, whereas the brain uses millions, if not billions, of neurons for similar tasks.

## 3 Finding Good Topologies for Cell Assemblies

The empirical details of cell assembly structure in the brain are challenging to analyze and observe. Even if a CA can be statistically identified, the participating neurons in the cell assembly may vary across different sessions with the same stimulus [9]. Because neurons in the brain fire constantly at a low rate, it can be difficult to differentiate between neurons participating in an active cell assembly from the noise signals. The number of neurons in a CA is not even clear and one neuron may participate in multiple assemblies. Although the biological specifics of cell assemblies remain elusive, various synaptic interaction mechanics have been discovered during their formation. Populations of neurons, whether in computational simulations or neuron reconstruction projects [10], are considered as a combination of statistical connectivity derived from neuron anatomical data and connection rules governed by probabilistic and deterministic principles. Recent research has sought to evaluate the relationship between network topology and the dynamics of biological neuronal networks [11, 12]. Previous evaluation either has not fully captured the working cycle of spiking behav-

iors in neuron groups nor provided in-depth exploration on the performance of individual topologies. Moreover, the analysis and development of proper evaluation methods for neuronal network generation topologies are currently lacking. This section addresses this gap and proposes the development of standard test-sets for topology evaluations.

The topologies are built with pyNN package in python [13]. Networks with different topologies were simulated. All the topologies are coded in a general purpose language to prevent mismatch from the package default connection rules. This study examined several topologies including random networks [14], small world networks [15], and scale free networks [16]. All of the network used probabilistic rules with random generation. Each network is evaluated based on the average performance of 10 samples. Self-connections are prohibited and there are no duplicate connections for all topologies. Networks of 1000 integrate and fire spiking neurons were created with each of these topologies and initialized with different random seeds to explore the range of their behaviors. An illustrative result is shown in Figure 2. Once the CA ignites, neurons fire persistently for over a second.

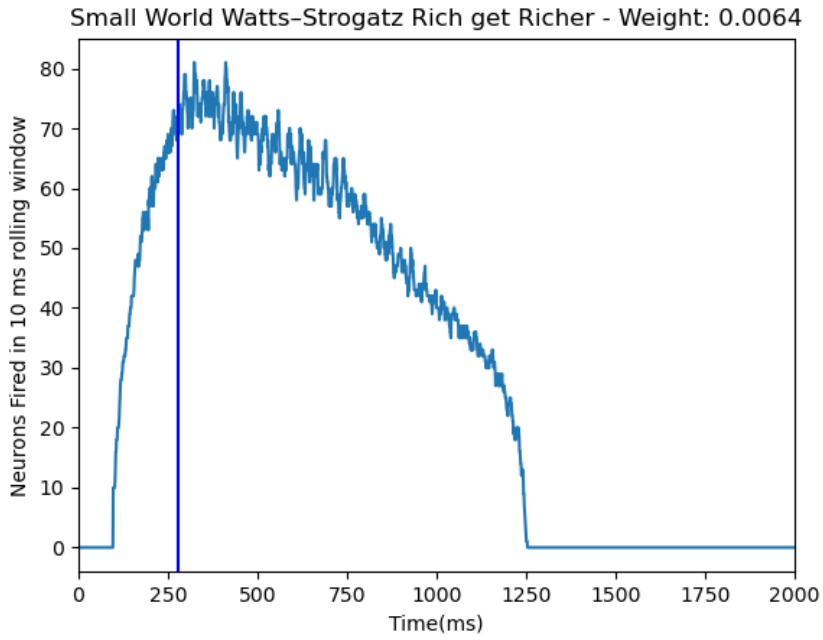


**Fig. 1.** Cell assembly based on small world topology. It was stimulated with external activation from 100 ms. to 280 ms. and exhibited self terminating persistence until 1200 ms.

A CA ignites when its neurons can persistently fire without external input. While the neurons are firing, theory implies, that the item associated with the CA is in short-term memory. Since short-term memories do not persist indefinitely, it is desirable for a CA to self-terminate. Firing patterns were investigated by varying connecting

weights and comparing their tunability, self-terminating persistence, ignitability, and robustness. These experiments revealed that the small world topology with a rich get richer rewiring approach worked best for associative memory among our simulation. This topology exhibited the largest range of synaptic weights for self-terminating persistence for all tested random seeds. Information is sent to other CAs in the forms of population spikes. Longer controlled firing in a CA further enables its participation in more tasks in the following network computation, which maximize its information capacity.

## 4 An Associative Memory Model with Cell Assemblies

More recently, small world CAs, from section 3, were combined into associative memories. The aim is to use the improved control over the behavior of CAs to develop scalable hierarchical networks that can be expanded and dynamically learn new associations.

Five cell assemblies of 1000 neurons are simulated based on small world topologies. There are random synapses between associated cell assemblies. Inhibitory neurons prevent each assembly from continuously firing and global inhibition, stimulated by all assemblies, prevents unassociated assemblies igniting. When two of the associated CAs ignite, they ignite the third, which is a model for retrieval of that memory. Experiments have both hard-wired and plastic intra-assembly synapses.

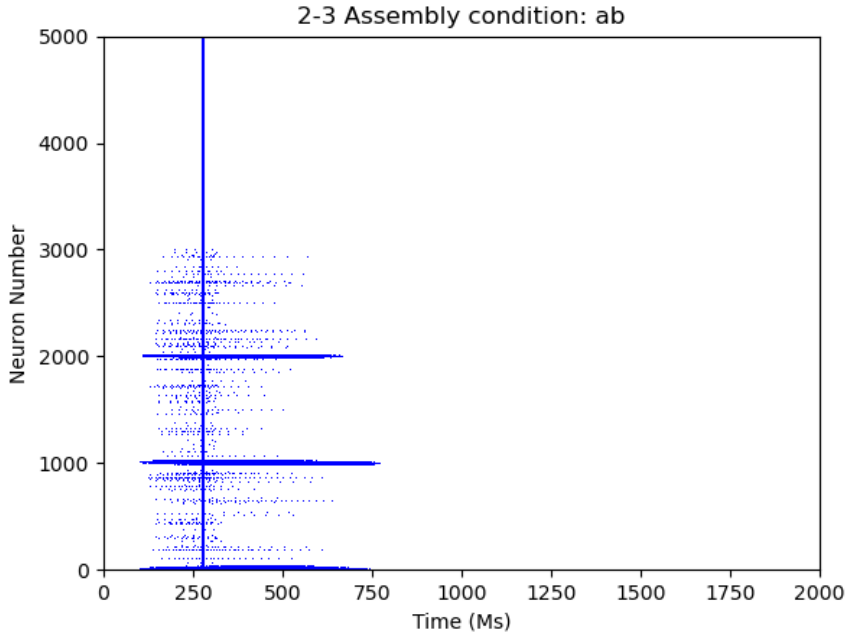


**Fig. 1.** Rastergram of two assemblies (a and b) retrieving a third.

The results, shown in Figure 3, show that a stimulated assembly normally persists for a short amount of time (~500 milliseconds) though inhibitory neurons are not involved in the task. In a network of five assemblies, there are three sets of associations, a-b-c (neurons 0-2999), and c-d-e (neurons 2000-4999). That is there are two sets of overlapping groups, or two 2-3 assemblies. When two assemblies in the same group are stimulated, they persist longer and eventually ignite the third assembly. When two assemblies from different assembly groups are stimulated, they do not ignite any other assemblies. The same results are achieved for both hard-wired and plastic intra-assembly synapses.

## 5 Discussion and Conclusion

This paper has outlined the research that the authors have been doing on the use of cognitive models constructed with biologically-inspired cell assemblies of spiking neurons. In the initial stages of this work, hard-coded cell assemblies modelled the Stroop task and implemented an associative memory semantic network in biologically plausible ways. Further research on cell assembly behavior demonstrated that small world topologies are likely to lead to better behavior for associative memory. This insight was used to develop the networks of 2-3 associated assemblies that was described in Section 4.

The 2-3 assembly system may be extended as an associative memory system, allowing for the incorporation of new memories that do not conflict with previously learned cell assembly groups. This framework may be the basis for internal memory manipulation for other cognitive tasks.

During the above simulations, inhibition played a peripheral role in shaping network dynamics, owing to the efficiency of information transfer via excitatory spikes. Due to the inherently noisy nature of neuron spikes, encoding and decoding of information poses significant challenges without multiple layers of spike controls. While inhibitory neurons are more likely to contribute to network regulation, they may not be involved in information encoding and decoding. Consequently, the system could operate without inhibition, but recalibration would be necessary with the introduction of inhibitory mechanisms.

It would be better for cell assemblies to emerge from a pool of neurons through exposure to external stimuli, rather than being pre-wired. Incorporating Hebbian learning would enhance biological plausibility, but controlling the learning outcomes to prevent catastrophic failures presents a challenge. The compensatory learning approach used in the 2-3 assembly model represents a preliminary step towards on-line modification of synaptic connections, although further evidence is required to establish its effectiveness.

Cell assemblies are internal representations of observations; however, it is still unknown how the brain encodes this information. Some studies suggest that certain forms of synaptic plasticity may result in the strengthening or enhancement of internal information within cell assemblies, while others suggest that activity-dependent synaptic pruning may lead to the selective erasure of certain internal representations.

Ultimately, further research is needed to fully understand the complex dynamics underlying the processing and representation of internal representation within CAs and their role in information processing.

The next stage of this research will be to use small-world cell assemblies to learn new associations between words. Initial exploration will be with small networks like the Quillian network above, then new associations and concepts will be added. The networks will be progressively expanded to networks that are loaded from existing semantic networks, such as WordNet. There are also plans to connect the words in our hierarchical semantic networks to the real world. An image classification library, such as OpenCV could be used to label objects in a live camera stream. These labels could activate the appropriate cell assemblies and then the system could answer questions about the objects that it is perceiving and potentially learn new associations between words based on what it is perceiving.

The work described in this paper has shown that biologically-inspired models of cell assemblies can effectively model human behavior on semantic tasks. The experiments have shown that cell assemblies with small-world topologies have appropriate behavioral characteristics for associative memory models and can learn simple associations between concepts. Future cell assembly-based models will be scaled to model larger semantic networks and grounded in live data from the real world.

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