Molecular associative memory

An associative memory framework with exponential storage capacity for DNA computing

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1. Introduction

Associative memory problem : Find the closest stored vector (in Hamming distance) to a given query vector.

Neural implementation

- Using neural networks, connection weights are adjusted in order to perform association.
- Recall procedure is iterative and relies on simple neural operations.
- Design criteria: maximizing the number of stored patterns C while having some noise tolerance.

Molecular implementation

- Synthesize C DNA strands as stored vectors.
- Recall procedure is usually done in one shot via chemical reactions and relies on highly parallelism of DNA computing.
- Design criteria: finding proper DNA sequences to minimize probability of error during the recall phase.

2. The problem

Current molecular associative memories are either

- **low in storage capacity**, if implemented using molecular realizations of neural networks [3].

Or

- **very complex to implement**, if all the stored sequences have to be synthesized [7], [1].

3. The proposed solution

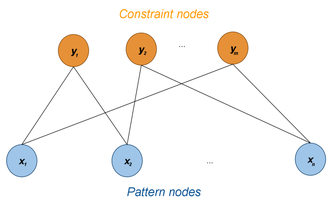
We introduce an associative memory framework with exponential storage capacity based on transcriptional networks of *DNA switches* proposed by [3].

Advantages over current methods

- Exponential storage capacities with current neural network-based approaches can not be achieved.
- For other methods, although having exponential storage capacities is possible, it is very complex as it requires synthesizing an extraordinarily large number of DNA strands.

4. Model and method

- We utilize a bipartite network of *DNA switches* with n pattern nodes and m constraint nodes.
- The connectivity of the network is determined by the adjacency matrix H.



- The state of each pattern node j, denoted by x_j, can either be 1 (activation) or -1 (suppression).
- The state of each constraint node i (denoted by y_i) can be 1 (activation), -1 (suppression) or 0 (non-transcribed).
- Each constraint node y_i has a decision threshold b_i.
- Given the vector of decision thresholds b and pattern nodes states x, we fix H such that $Hx = b$.

Hence, instead of *memorizing* all possible random sequences of length n, we store only those that satisfy m constraints.

5. The association process

The proposed framework finds the closest stored pattern to the probe $\hat{x}$ via forward and backward iterations.

Forward iteration

- Constraint nodes decide their state based on simple *neural* operations:

$$y_i = \begin{cases} 1, & h_i < b_i \\ 0, & h_i = b_i \\ -1, & \text{otherwise} \end{cases}.$$

where $h_i = \sum_{j=1}^{n} H_{ij} x_j$,

Backward iteration

- Each pattern node j computes the quantity

$$g_j = \frac{\sum_{i=1}^{m} H_{ij} y_i}{d_p}.$$

The sign of g_j is an indication of the sign of the noise that affects x_j, and $|g_j|$ indicates the confidence level in the decision.

- The state of pattern DNA node j is updated using either of the following two strategies:
  1. *Winner-take-all* strategy: only the node with the maximum $|g_j|$ is updated.
  2. *Bit-flipping* strategy: all pattern nodes are updated based on the sign of g_j.

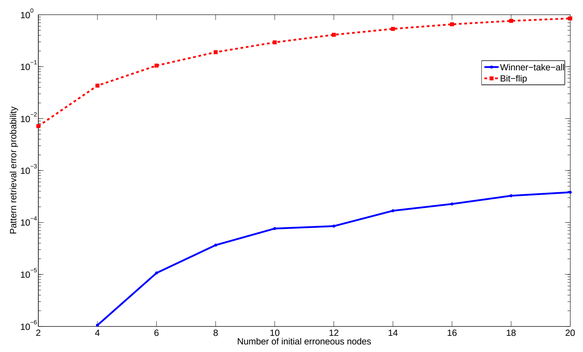
6. Results

Theoretical results

- The proposed framework is guaranteed to correct two erroneous nodes [4].
- For proper choice of row degrees in the constraint matrix, it also admits an exponential storage capacity in terms of n.

Numerical results

- The following graph illustrates the pattern retrieval error probability against the number of initial erroneous nodes.



7. Some remarks

Full details about the approach can be found in [4].

The proposed method have other possible applications as well:

- Designing artificial transcriptional networks to govern the activity of cells, for instance in combating certain diseases.
- Iterative error correction in DNA computing instead of pre-designed *error-avoiding* DNA sequences.

8. Previous works

Neural Associative Memory

- Extensive studies in past decades [2], [5].
- Storage capacity has been shown to be at best equal to n, the number of neurons, *when required to memorize purely random patterns*.
- Recently, some works have been done to improve the storage capacity by memorizing *structured patterns* (see [4] and references therein).

Molecular Associative Memory

- In contrast to neural associative memory, most approaches are already concerned with memorizing *structured patterns* to minimize recall probability of error.
- These approaches synthesize all the stored patterns and store them in a vessel [7], [1].
- Coding theory can help in designing DNA strands that admit low probability of error in the recall process [6].
- Some approaches that implement neural networks using DNA strands can be used as a means of implementing associative memory as well [3].
- However, the *storage capacity* of molecular associative memory is not well-studied yet.

References

[1] J. Chen, R. Deaton, Y. Z. Wang, *A DNA-based memory with in vitro learning and associative recall*, Lect. Notes in Comp. Sci., Volume 2943, 2004, pp. 145-156.

[2] J. J. Hopfield, *Neural networks and physical systems with emergent collective computational abilities*, Proc. Natl. Acad. Sci., Vol. 79, 1982, pp. 2554-2558.

[3] J. Kim, J. J. Hopfield, E. Winfree, *Neural network computation by in vitro transcriptional circuits*, Adv. Neur. Inf. Proc. Sys. (NIPS), Vol. 17, 2004, pp. 681-688.

[4] K. R. Kumar, A. H. Salavati, A. Shokrollahi, *Exponential pattern retrieval capacity with non-binary associative memory*, submitted to Information Theory Workshop 2011.

[5] R. McEliece, E. Posner, E. Rodemich, S. Venkatesh, *The capacity of the Hopfield associative memory*, IEEE Trans. Inf. Theory, Jul. 1987.

[6] O. Milenkovic, N. Kashyap, "On the Design of Codes for DNA Computing" Lect. Notes in Comp. Sci., Vol. 3969, 2006, pp. 100-119.

[7] J. H. Reif, T. H. LaBean, *Computationally inspired biotechnologies: improved DNA synthesis and associative search using error-correcting codes and vector-quantization*, Lect. Notes in Comp. Sci., Vol. 2054, 2001, pp. 145-172.

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