

Molecular Associative Memory with Spatial Auto-logistic Model for Pattern Recall

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Abstract

We propose a molecular associative memory model, by combining auto-logistic specifications, which capture statistical dependencies within the local neighborhood systems of the exposed knowledge, with the bio-inspired DNA-based molecular operations, which store and evolve the memory. Our model, characterized by only the local dependencies of the spatial binary data, allows to capture only a few features. Our memory model stores the exposed patterns and recalls the stored patterns through bio-inspired molecular operations. Our molecular memory simulation exemplifies the applications of associative memories in pattern storage and retrieval with high recall accuracy, even with lower order memory traces (pair-wise cliques) and thus exhibits brain-like content-addressing cognitive abilities.

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1 Introduction

Learning and memory are closely related critical concepts for understanding human intelligence and developing intelligent systems. Learning is a biological process of acquiring new knowledge, while memory is a process of encoding, storing and retrieving that acquired knowledge [7]. Associative memory or content-addressable memory (CAM) [8] is a function of brain that recalls (retrieves) previously stored data that closely matches the given partial cues. Associative memory is useful in applications requiring high-speed searches of large databases and search-intensive operations such as information retrieval, pattern matching, image processing, machine vision, etc [12]. In contrast to conventional location-based memory, associative memory requires a higher depth of processing (a huge amount of cognitive effort) to re-access the information. DNA (deoxyribonucleic acid) is found in every cellular organism as storage medium for genetic information, that defines the biological processes of life. The characteristics such as vast storage, massive parallelism and self-assembly are similar between brain [6, 18, 19] and DNA [1, 2, 16]. These properties are useful in realizing the brain-like associative

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memories in molecular systems, which can be vaster than human brain [2, 15]. Recent works [11, 14] show that molecular systems can exhibit brain-like cognitive behaviors.

In this work, we demonstrate the simulation of molecular associative memory for pattern storage and recall. We combine the auto-logistic model [4, 5], a widely used model in image processing, with bio-inspired molecular operations such as hybridization and mutation to demonstrate associative memory for pattern recall. The auto-logistic model, first proposed by Besag in his seminal work [4], is a pairwise interaction Markov random field (MRF) for binary (0-1) spatial data. It defines spatial dependency among random variables within the local neighborhood system. The proposed memory model learns the patterns (digits from 0 to 9) when exposed to MNIST [9] training examples. It defines only the local spatial features, specified by auto-logistic models, of the images, encodes them into DNA sequences and recodes to vector-based representation for computational efficiency and theoretical analysis. We then apply bio-inspired molecular operations (hybridization and mutation) to extract the information from examples and store the patterns with weights in the memory. The stored patterns are retrieved by the hybridization of the memory strands with the query strands. Our model requires only a few features, thus achieving lesser training time and lesser computation during the pattern recall. Our molecular learning algorithm is based on hypernetwork model [20] with the incorporation of auto-logistic specifications.

2 Background on Auto-logistic Model

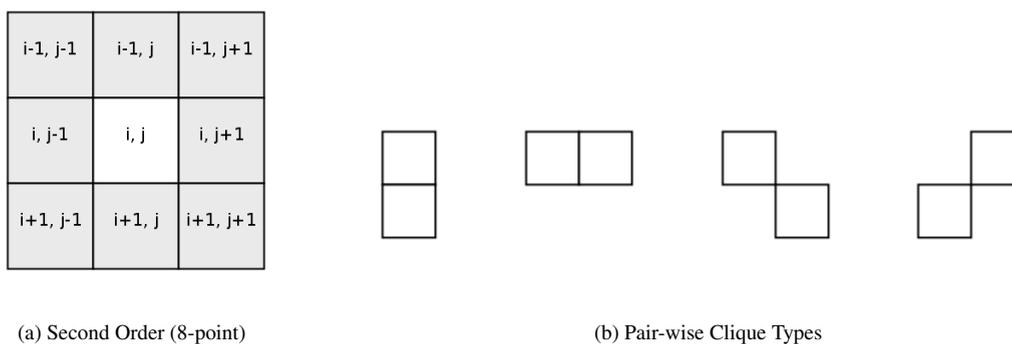


Figure 1: Second-order Neighborhood System with Associated Pair-wise Clique Types

Consider a random field ($X = \{X_{ij}\}$), defined over a discrete finite two-dimensional lattice (L) of points. $\{X_{ij}\}$ represents random variables. A random field is a Markov random field [10] (MRF) if it satisfies the Markov property $p(x_{ij}|x_{kl}, (k, l) \in L, (k, l) \neq (i, j)) = p(x_{ij}|x_{kl}, (k, l) \in \mathcal{N}_{ij}); \forall (i, j) \in L$, where i and k are row indices, j and l are column indices, x_{ij} and x_{kl} are the realizations of the random variables, associated with the specified lattice points and \mathcal{N}_{ij} is the neighborhood of (i, j) .

Two widely used neighborhood systems are first-order and second-order neighborhood systems. A first-order neighborhood system (also called 4-point or von Neumann neighborhood) of any given lattice point (i, j) includes only orthogonal (right, left, up, and down) lattice points. A second-order neighborhood system (also called 8-point or Moore neighborhood) includes orthogonal and diagonal lattice points. In sub figure 1a, the shaded gray lattice points, in the second-order neighborhood system, indicate neighbors of the central lattice point (i, j) . An MRF, characterized by the conditional distributions called the local characteristics of the random field, models the local interactions. Such spatial local dependencies can be defined by the clique potentials. A clique is either a single point or a subset of points

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