Ising Model based Molecular Associative Memory for Pattern Recall

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패턴 회상을 위한 이징 모델 기반의 분자적 연상 메모리

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Abstract

We combine statistical-mechanical approach for probabilistic image processing with DNA based bio-molecular operations to construct associative memory for pattern recall. The statistical properties of the patterns are learned from the exposed examples, stored in memory and are recalled when presented with partial queries. The results show that our proposed memory model retrieves patterns with high recall accuracy.

1. Introduction

Memory is a critical component for storing information, understanding human intelligence and developing intelligent systems. Associative memory is a function of brain that recalls (retrieves) previously stored data that closely matches the given partial cues. DNA is the information storage material for the biological process of the organisms. Recent works [1, 2] show that molecular systems can exhibit brain-like behaviors. We propose molecular associative memory using Ising model and bio-molecular operations for pattern recall. Ising model is a class of binary-variable graphical models with pairwise interactions. It is a popular model in statistical physics that demonstrates magnetic phenomena and also phase transitions, shared by many complex systems. The two-dimensional Ising model with nearest-neighbor interactions is a typical example of a Markov random field (MRF) [3]. MRF is widely used in image processing to model binary images. It is the set of random variables in which the state of each pixel is dependent only on the configuration of its neighborhood pixels. Our molecular learning algorithm is based on the hypernetwork learning model [4].

2. Molecular Associative Memory Model

We initialize the memory with a set of single strands of DNA molecules, representing location and color of pixels. Initially, pixel color at each location is black. DNA contains four types of bases; Adenine (A), Thymine (T), Guanine (G) and Cytosine (C). Any single-stranded DNA will bind chemically to another single-strand to form a DNA double-stranded helix by the property known as Watson-Crick complementarity: adenine bonds with thymine and vice versa, and cytosine bonds with guanine and vice versa. Our proposed model consists of two phases; learning and recall:

1. Storing molecules in the DNA-based memory – the storage procedure is known as "learning" as it acquires information from examples (MNIST dataset).
2. Retrieving the stored molecules on queries – the retrieving procedure is also known as recall.

Learning:

We model each MNIST training image as a two-dimensional (i=j=28) Ising based binary Markov random field and the information is encoded as a set of DNA single strands; molecules indicating locations are complementary to memory strands. The DNA single strands of memory are hybridized with the single strands of the training images. The conditional probability of a pixel (x_{ij}^m) given its neighborhood ($x_{N_{ij}}^m$) (equivalently, all other pixels in the image), according to the Ising model, is given by [3]

$$p\left(x_{ij}^m \middle| x_{N_{ij}}^m\right) = \frac{e^{\alpha_{ij}^m x_{ij}^m + \sum_{kl \in N_{ij}} \beta_{ij,kl}^m x_{ij}^m x_{kl}^m}}{\sum_{x_{ij} \in \{0,1\}} e^{\alpha_{ij}^m x_{ij}^m + \sum_{kl \in N_{ij}} \beta_{ij,kl}^m x_{ij}^m x_{kl}^m}}$$

$$p\left(x_{ij}^{m}\middle|x_{N_{ij}}^{m}\right)=\frac{e^{\alpha_{ij}^{m}x_{ij}^{m}+\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{ij}^{m}x_{kl}^{m}}}{1+e^{\alpha_{ij}^{m}+\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}$$

$$p\left(x_{ij}^{m}=1\middle|x_{N_{ij}}^{m}\right)=\frac{e^{\alpha_{ij}^{m}+\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}{1+e^{\alpha_{ij}^{m}+\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}$$

$$p\left(x_{ij}^{m}=1\middle|x_{N_{ij}}^{m}\right)=\frac{e^{\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}{1+e^{\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}$$

$$=\frac{1}{1+e^{-\sum_{kl\in N_{ij}}\beta_{ij,kl}^{m}x_{kl}^{m}}}\ ;\ \alpha_{ij}^{m}=0$$

where α is node weight and β is edge weight for m[th] pattern. β is the pair-wise interaction weight. In our model, β represents the hybridization strength. β=1 if the hybridization is complete; otherwise 0. We mutate the portion of the DNA strands, representing the pixel color at the rate of 0.1, on partial hybridization. We use the above computed conditional probabilities to update the weights (w_{ij}) of the foreground pixels of the memory.

$$w_{ij}^{m}=w_{ij}^{m}+\eta*p\left(x_{ij}^{m}=1\middle|x_{N_{ij}}^{m}\right)$$

where $\boldsymbol{\eta}$ is sigmoid decay learning rate.

Recall:

The query patterns (corrupted or noisy), are encoded as a set of DNA single strands (complementary to memory strands), and are hybridized with the learned and stored DNA memory of single strands. The averaged hybridization potentials of each pixel is weighted with the learned weights. The weighted score is computed for each of the stored patterns and the softmax of scores is computed to normalize and retrieve the closest stored memory pattern.

3. Results

The patterns (digits from 0 to 9) are learned and stored in the DNA-based associative memory, when exposed to the MNIST training dataset (50,000 examples; 5000 for each digit). The memory is constructed using Ising model and DNA based bio-molecular operations. We create artificial datasets by corrupting (100 for each digit) the stored patterns at different depths (1 to 10) or adding noise (100 for each digit) to stored patterns at different noise levels (0.1 to 0.5). The recall accuracy for corrupted patterns at various depths and noisy patterns at different noise levels are shown in figure 1 and figure 2 respectively. The recall accuracy of corrupted patterns even at the depth level of 10 is high. The recall accuracy of noisy patterns drops owing to heavy distortion in patterns, when the noise level is above 0.3.

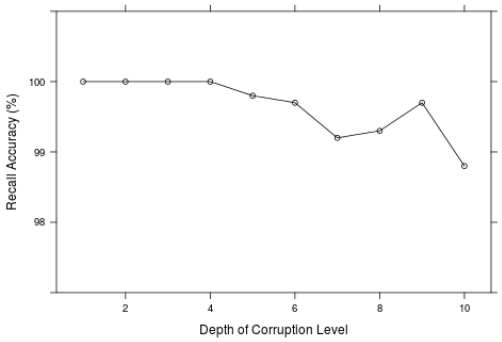

Figure 1 : Recall Accuracy Vs. Corrupted Patterns

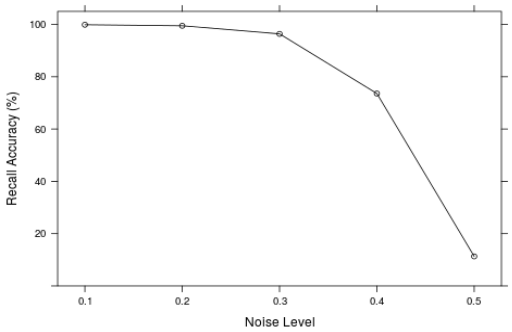

Figure 2 : Recall Accuracy Vs. Noisy Patterns

4. Conclusion

Our proposed model, based on pairwise interaction within local neighborhood system of Ising model and the complementary binding properties (hybridization) of DNA molecules, exhibits brain-like behavior; i.e. recall on incomplete (corrupted or noisy) information. The results demonstrate that the similar patterns are recalled from the molecular memory with high accuracy.

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