Biological Modeling of Neural Networks

Hopfield Model

Storage of Sequences of patterns in asymetric hopfield networks with delayed synapses

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1 Exercise 1 : Standard Hopfield Network

1.1 Exercise 1.1 : Implementation

We created a class hopfieldNetwork which has the following attributes :

- N : number of neurons
- pattern : array of $P \times N$ states, where P is the number of patterns
- weight : array of $N \times N$ that represents the matrix of interaction between neurons
- x : state of the network at each time step, e.g., $x = \{1, -1, -1, \ldots\}$

and the following functions :

__init__ creates an instance of the class hofieldNetwork with the number of neurons N

makePattern creates a numpy array of N×P of ones, then randomly flips a given ratio of neurons in each pattern using the function numpy.random.choice.

makeWeight calculates the interaction weights using simple for loops according to the formula : $w_{ij} = \frac{1}{N} \sum_{m=1}^{P} \xi_i^\mu \xi_j^\mu$

dynamic updates the state of neuron i according to the formula : $S_i = \text{sign}(\sum_{j=1}^{N} w_{ij} S_j)$ using the weight matrix and the current state of the network

After creating an instance of the class hopfieldNework and creating the desired number of patterns, we run the simulation using the run function which does the following steps :

1. initialize the network by copying one of the patterns ξ^μ then flipping the state of randomly chosen neurons
2. Select a random neuron and update its state using the dynamic function, and do this for all the neurons of the network
3. repeat until convergence

For the convergence criterion, we store the value of the network x at each step, and after each iteration we compare the old value of x to the new one by a simple subtraction. If the difference is negligible, we stop. In addition, we set a time limit tmax = 100 steps, so that we exit even if the model doesn't converge.
The runAndPlot function performs the same steps as run, but plot at the same time the network and illustrates the convergence in a overlap w.r.t. time curve.
At each time step, we store the value of the overlap and the normalized pixel distance which will be useful later.

1.2 Exercise 1.2 : Pattern retrieval

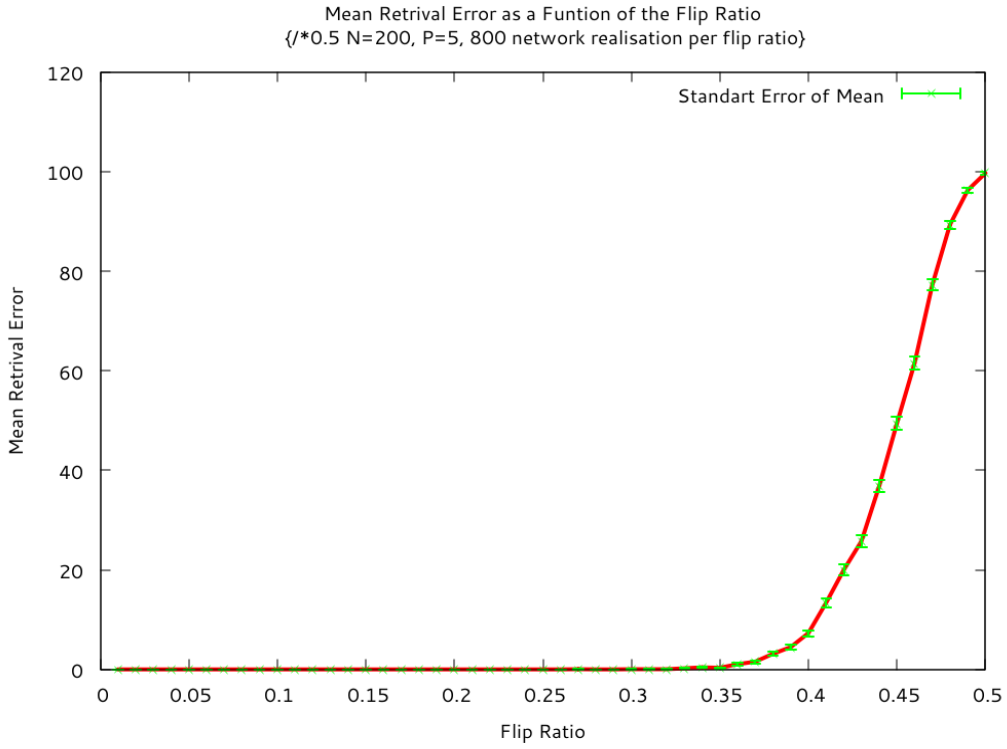
At this step we add two functions :

overlap calculates the overlap between the pattern ξ^μ and the current state of the network according to the formula : $m^\mu = \frac{1}{N}\sum_{i=1}^{N} \xi_i^\mu S_i(t)$

pixeldistance calculates the percentage of neurons in the network that differ from the pattern ξ^μ using the formula : $(1 - m^\mu) \times 100$, where m^μ is the overlap returned by the aforementioned function.

To get the retrieval error as a function of the ratio c of the flipped bits at the initialization of the network, we define the function patternRetrieval. We fix N=200 and P = 5. We take 50 values of c in the interval [0.01, 0.51]. For each value of c, we get run the simulation 50 times, and get the pixel distance at the end of each simulation. We show the average of the retrieval error in figure 1.2. The error bar represents the standard error of the mean, and is given by SciPy function stats.sem.
As we could expect it, the error is negligible ($< 1\%$) if we flip a reasonable ratio of the neurons at the initialization step. According to the figure, this threshold value is $c = 0.35$. As the number of flipped neurons increases, the error grows exponentially. For $c = 0.5$, meaning that we start with a network where half of the neurons are different from the retrieved pattern, the error reaches 100%.
(What happens when m=-1???)
We conclude that the Hopfield model works well only if the initial state of the Network is close to the target pattern.

Figure 1: Mean retrieval error as a function of the flip ration $c \in [0.01, 0.51]$.



1.3 Exercise 1.3 : Capacity estimation

The number of patterns that can be stored and retrieved correctly by a neurons network depends on the number of neurons. In Hofield model, the storage capacity of a network is defined by :

$$C_{stor} = \frac{P^{max}}{N} \tag{1}$$

where P^{max} is the maximum number of patterns that the network can retrieve correctly.
To study this capacity, we define the function maxLoad. To obtain the capacity of the Hopfield Network, we create a network of N neurons and a growing number of patterns $P \leq 51$. We fix $c = 0.1$. For each P we try to retrieve a random pattern 10 times and we get the mean error. When the mean error reaches 2% we stop and save the number of patterns created P_{max}. To speed up the simulation, we start from P=???. Finally, we calculate the average value of P_{max} for a given N, and we calculate the maximal load $\alpha_{max} = P_{max}/N$. We will do this for several values of N. The results are shown in table 1.3. The error on the value of α_{max} is calculated by ...

N	100	250	500
P_{max}	≈ 14	≈ 38	≈ 77
α_{max}	0.1480 ± 0.007423	0.1532 ± 0.003322	0.1546 ± 0.001550
α_{th}	–	–	–

Table 1: Capacity storage of a network of N neurons

As we could expect, we observe that the capacity of the network increases with the number of neurons. Moreover, we see that the maximal load that we obtain corresponds extremely well to the theoretical value.
Note that we only retrieve one pattern at a time. If we want to retrieve a sequence of patterns, the literature says that C_{stor} should not exceed 0.138[1], otherwise, the error will propagate at each pattern of the sequence. From our table, we see that this threshold is exceeded for N=250 and N=500. Therefore, we should to modify the model if we want to retrieve a sequence of patterns.

2 Exercise 2

2.1 Exercise 2.1 : Implementation

A lot of the function used for exercice 1 are reused for the 2. Here we want to implement a particular type of Hopfield Network that have a compoment added : the assymetrical weight. We used Oriented-Object Inheritance to derive our class hopfieldNetworkAsymmetric from the hopfieldNetwork. Our attributes are the same than in the first part, with the addition of :

- Assymweight : array of $N \times N$ that represents the projections of the weight from a pattern on the one of the next.
- SPrev : array of $N \times t_{max}$ that contain the evaluation of S for all $t \in [0, now]$. It is used to calculate the $Sbar$ that will stabilize our transitions.

We add the following methods :

makeAssymetricWeight calculates the projections of weights on each other using the other weight according to the formula : $w_{ij}^L = \frac{\lambda}{N} \sum_{\mu=1}^{P} \xi_i^{\mu+1} \xi_j^{\mu}$

dynamic updates the state of neuron i according to the formula : $S_i = \text{sign}(\sum_{j=1}^{N} w_{ij} S_j)$ using the weight matrix and the current state of the network, TODO : Syncrone and Sbar

2.2 Exercise 2.2 : λ range estimation

We used the heaviside filter function. We had a bit of freedom to define *sequencial behaviour*. We decreased lambda to get the minimum value for which all pattern are visited. We found :

$$\lambda_{min} \approx 0.9$$

For values below this one, the network get stuck in a particular pattern. Due to the random generation of some variables, the value of λ_{min} is approximative.

For the calculus of λ_{max}, we saw that for high lambda the network jump over some frame, not getting an overlap of one. Therefore we defined the sequencial behaviour as all state are visited with a overlap of 1, one after each other. We found :

Figure 2: Illustration of the sequencial behaviour

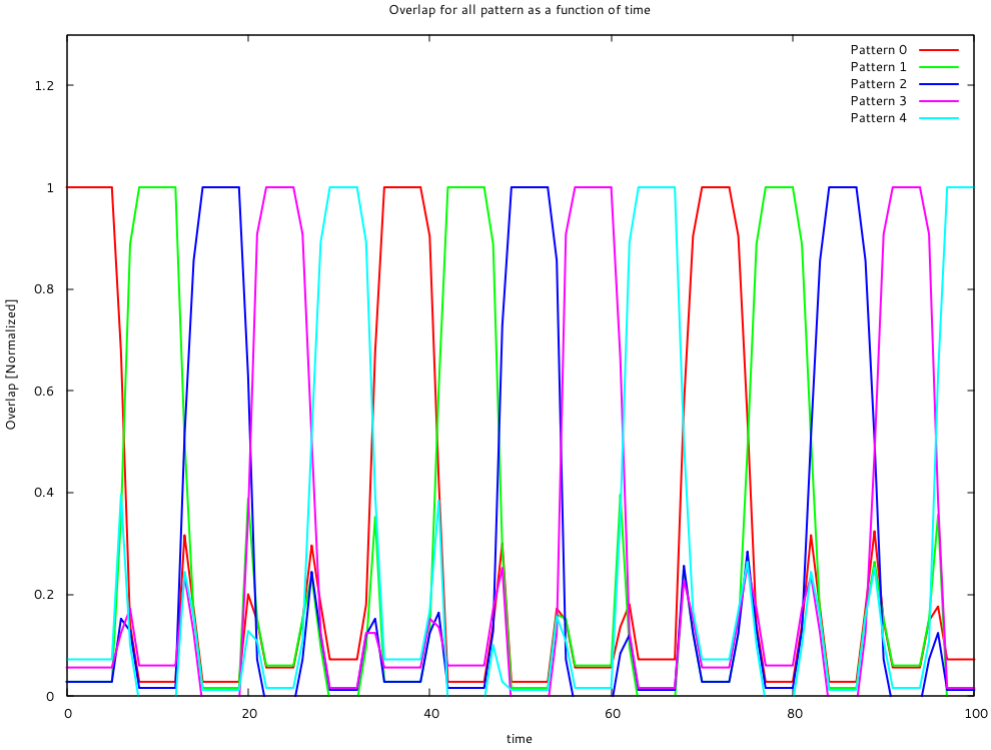
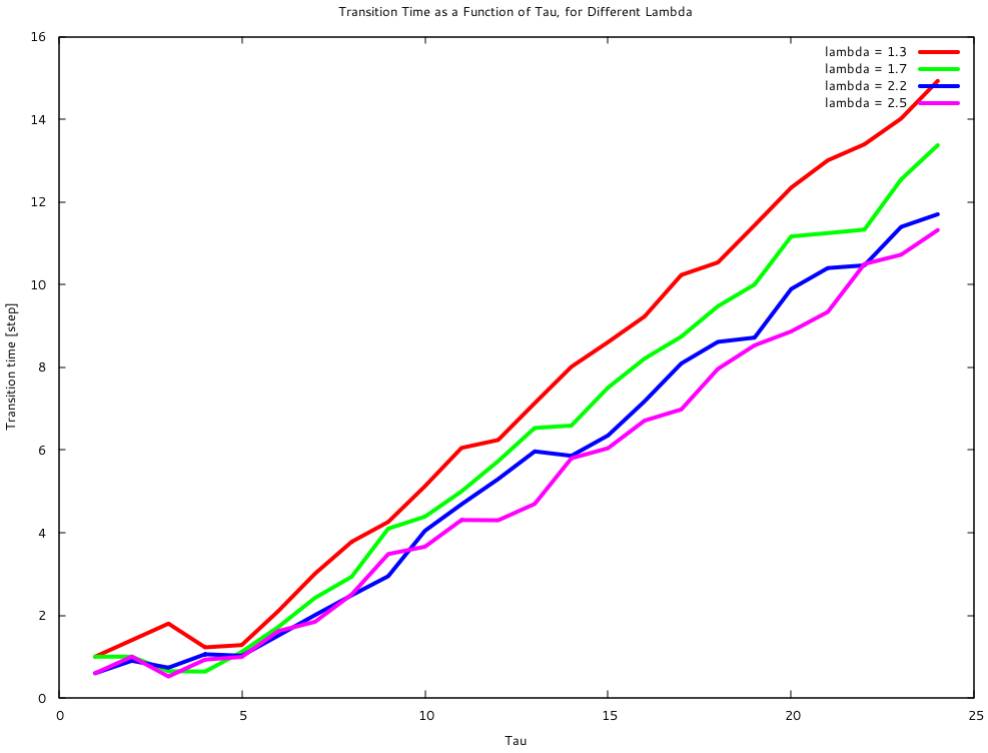


Figure 3: Mean retrieval error as a function of the flip ration $c \in [0.01, 0.51]$.



$$\lambda_{max} = 3.6$$

2.3 Exercice 2.3 : Estimation of the transition time

The transition time (i.e the time the network stay in a given frame with a overlap of 1 before trying t catch another) depend on τ, the filter function parameter and on λ.

We run our network 5 times for each configuration ($\lambda \in [1.3, 1.7, 2.2, 2.5]$ and $\tau \in [1, 25]$), saving the transition time on a file to plot it with gnuplot. The result is displayed in Figure 2.3. If we discart the small value of $\tau < 5$, we see a linear behaviour, the transition time increasing with τ. The slope is fixed by other parameters, and λ gives a shift of downward to the curve curve.

2.4 Exercice 2.4 : Sequence Storage Capacity

By varying P with N fixed, we saw that increasing the number of pattern stored lead the network to never acheive an overlap of 1, or only for a few pattern (with $N = 500$ and $P = 40$ for example, only pattern, the 4, was retrieved correctly). If we print the overlap we see that for a high P, the mean overlap is considerably lower (only 22 out of 400 iteration sees their overlap over 0.7 for $N = 500$ and $P = 50$, this number was 375 with the same setup, for $P = 10$). So transition from fully recovered patterns are our control behaviour to test the number of pattern we can store.

We fixed all the parameter of our network, except the number of pattern P and the size of the network N. We then moved P until one of the pattern stored was missed during an interation (this is our criterion but several can be chosen, like a threshold with the transition time between two pattern that get very long with P). The results are displayed on Table 2.4. Again due to the randomness of the process we show here statistical average, but on too few sample to be sure.

N	250	500	1000
P_{max}	15	33	52
α_{max}	0.06	0.066	0.052

Table 2: Sequence storage capacity of a network of N neurons

We can compare those results to the one for a non-sequencial network. Our maximum load is significantly lower, divided by a factor ≈ 2.66.

References

[1] W. Gerstner, W. Kistler, R. Naud, L. Paninski, *Neuronal Dynamics : from single neurons to networks and models of cognition*, Cambridge University Press, 2014.