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 with a given ratio of neurons with values 1 or -1, using the function numpy.random.choice.

makeWeight calculates the interaction weights using numpy.fromfunction and a lambda 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. For each neuron in the network taken in a random order, we update its state using the dynamic function
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 $t_{max} = 100$ steps, to exit even if the model doesn't converge. 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

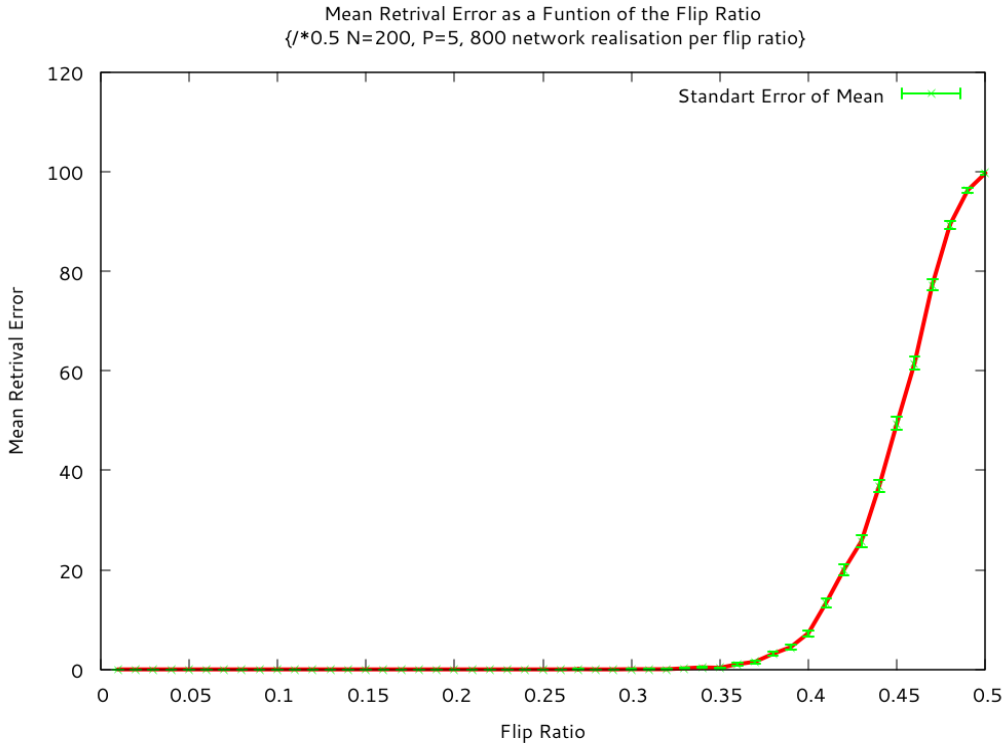
At this step we add two functions :

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 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. This error is small here because for each configuration (N, P, c), we averaged over 50 realisations. We could do this because the code was fast.
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, the threshold value is around $c = 0.35$. 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%.
We conclude that the Hopfield model works well only if the initial state of the Network is close to the target pattern. This is in accordance with the associative memory theory : since it is content addressed data, we need to start near the data we want to retrieve.

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. We create a network of N neurons and a growing number of patterns P.
We fix $c = 0.1$. For each P we try to retrieve all the patterns. When the mean error over all tries reaches 2% we stop and save the number of patterns created as P_{max}. We do this 10 times per N to have statistical average of P_{max} and we deduce $\alpha_{max} = P_{max}/N$. The error on the value of α_{max} is the variance of P_{max} divided by N.
To speed up the simulation, we start from $P = 0.1N$ because we are sure that a network with 500 neurons, for example, will be able to retrieve correctly at least 50 patterns. If this assumption was false, we would have known by analysing the output of the program.
The results are shown in table 1.3. As we could expect, we observe that the

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

Table 1: Capacity storage of a network of N neurons

capacity of the network increases with the number of neurons. 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 all N. Therefore, we should modify the model if we want to retrieve a sequence of patterns.

2 Exercise 2

2.1 Exercise 2.1 : Implementation

Most of the functions used for the first exercise will be reused in the second. Here we want to implement a particular type of Hopfield Network that have a component added : the Asymmetrical weights. 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 projection of the weights of a pattern on the next one.
- 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 $\overline{S}$ that will stabilize our transitions.

We add the following methods :

makeAssymetricWeight calculates the second set of weights that will be added to the standard ones according to the formula : $w_{ij}^L = \frac{\lambda}{N} \sum_{\mu=1}^{P} \xi_i^{\mu+1} \xi_j^{\mu}$

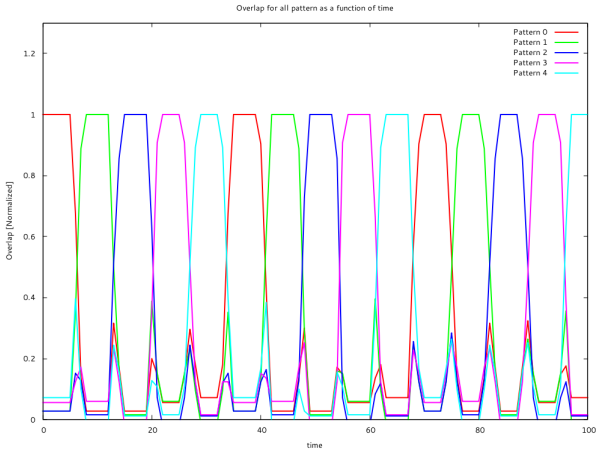
filterfunction The implementation of our filter function. We chose the Heaviside function : $G(t) = \frac{1}{\tau} \Theta(-t + \tau)$

dynamic It is a two step function that updates the state of the network at each time-step. Since we do synchronous update, all the variables are vectors.

1. Calculate the new $\overline{S}$ from the memory of all previous states, as $\overline{S} = \sum_{t'=0}^{t} G(t') S(t - t')$
2. Update the state of all the neurons in one step, according to the formula : $S_i = \text{sign}(\sum_{j=1}^{N} w_{ij} S_j + w_{ij}^L \overline{S})$ using the two weights matrix with the current and filtered state of the network.

The process is the same as in exercise 1. If we plot the overlap for all the patterns at every time step, we see that our network goes from one stored pattern to another (Figure 2.1)

Figure 2: Illustration of the sequential behaviour



2.2 Exercise 2.2 : λ range estimation

We consider that we have a *sequential behaviour* when all patterns μ are "visited", meaning that the overlap m^μ reaches the value 1 $\forall \mu$.
Keeping N=500,P=10 and τ=8 fixed, we simulate the network with different values of λ. The minimum value for which we can observe this behaviour is

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

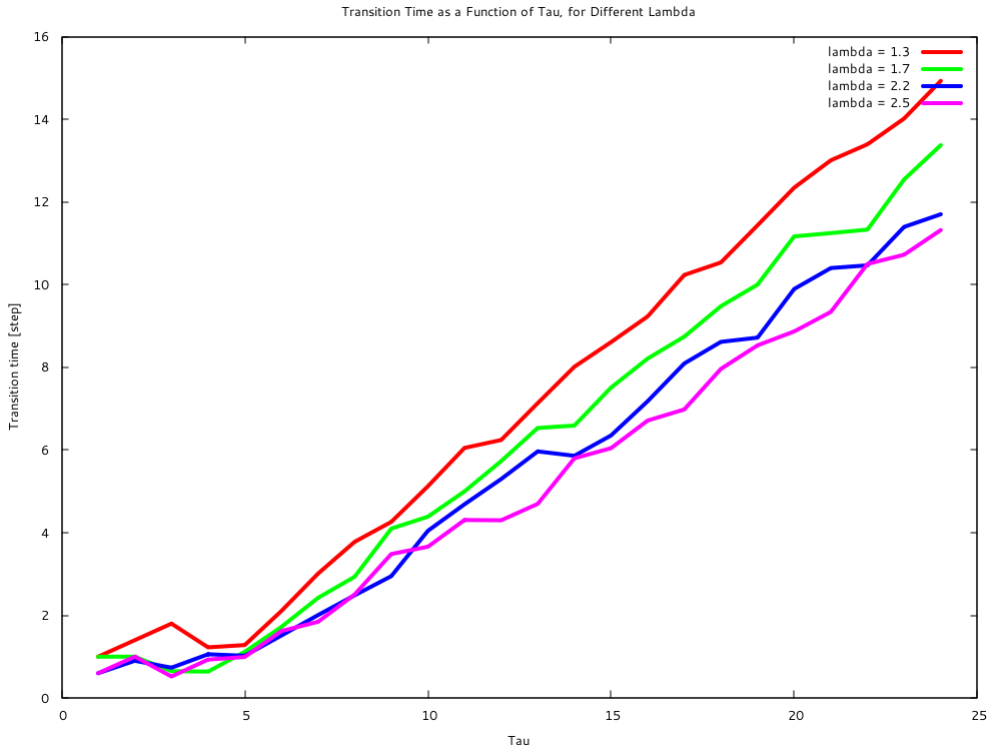
Due to the random generation of some variables, the value of λ_{min} is approximative. For values below this one, the network gets stuck in a particular pattern. This is in accordance with the new weights formula. When λ is very low, the additional term becomes negligible and we are back to the previous model, where we converged to one specific pattern.
For high values of λ, we observe that the network skips some patterns, meaning that the overlap m^μ increases but does not reach 1. Here the influence from the previous pattern is too strong, and the model becomes unstable. We found :

$$\lambda_{max} = 3.6$$

2.3 Exercice 2.3 : Estimation of the transition time

The transition time (that we defined as the time the network stays in a given frame with a overlap of 1) depends on the filter function parameter τ, and

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



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 results are displayed in Figure 2.3. If we discard the small values of $\tau < 5$, we see a linear behaviour, the transition time increasing with τ. This is what we wanted to obtain in this model, e.g., slowing down the transition time. Increasing λ shifts the curve downward. This behaviour is in accordance with what we observed in the previous section. The slope of the curve is fixed by other parameters.

2.4 Exercice 2.4 : Sequence Storage Capacity

By varying P with N fixed, we saw that increasing the number of patterns stored leads the network to never achieve an overlap of 1, or only for a few

patterns (with $N = 500$ and $P = 40$ for example, only one 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 set-up, 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 iteration (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

Comparing these results to the ones obtained with a non-sequential network model, we observe that the maximum load is significantly lower (divided by a factor ≈ 2.66). However the threshold value of $C_{stor} = 0.138$ is never exceeded. Therefore, this model allows the network to retrieve a sequence of patterns, but it reduces its storage capacity.

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.