Hierarchical architectures for spiking Winner-Take-All networks

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SCIENCE
PASSION
TECHNOLOGY

Outline

Goals

- Further the understanding of the network model
- Simulate feedback found in the visual cortex
- Show connection between Bayesian inference and network model

Biological background

- Spiking neural networks
- Winner-Take-All networks
- Modular structure of the brain
- Hierarchical structure of the brain
- Feedback mechanisms in cortical hierarchies

Kanizsa square, Lee TS (2003)

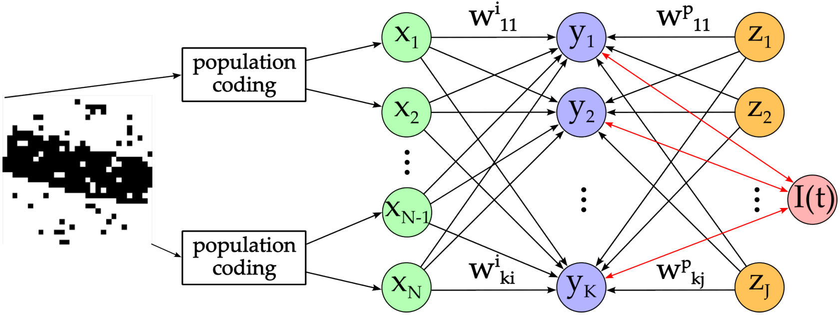
Biological background

- Probabilistic brain
- Synaptic plasticity

Theoretical background

- Bayesian inference gives the probability of an hypothesis given related evidence
- $P(H|E) = \frac{P(E|H)P(H)}{P(E)}$
- Network model of Nessler et al. (2013) used and expanded
- Nessler et al. (2013) claimed that synaptic weights converge towards the log of probability

The network


population coding
population coding
x_1
x_2
x_{N-1}
x_N
w^i_{11}
w^i_{ki}
y_1
y_2
y_K
w^p_{11}
w^p_{kj}
z_1
z_2
z_J
I(t)

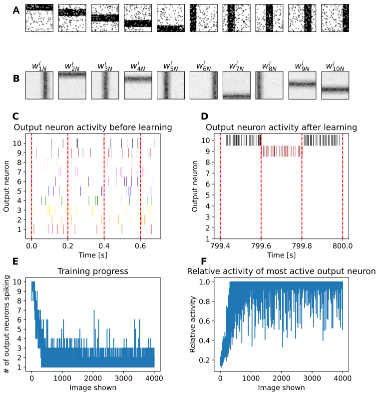
Methodology

- Simulation was performed in Python
- Simulation step size was 1 ms
- Pixels of input images and the prior had a noise level of 10%

Ambiguous visual stimuli 1

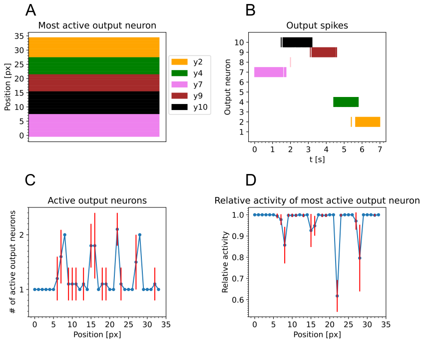
- Network learned to group horizontal and vertical bars into 10 groups
- After training ambiguous images with 1 horizontal and 1 vertical bar were shown
- Network was able to focus on individual bars, due to prior neurons

Ambiguous visual stimuli 2

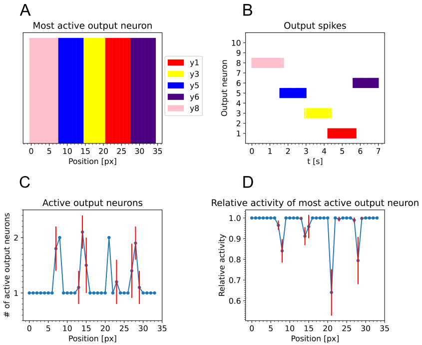


Training plot

Ambiguous visual stimuli 3

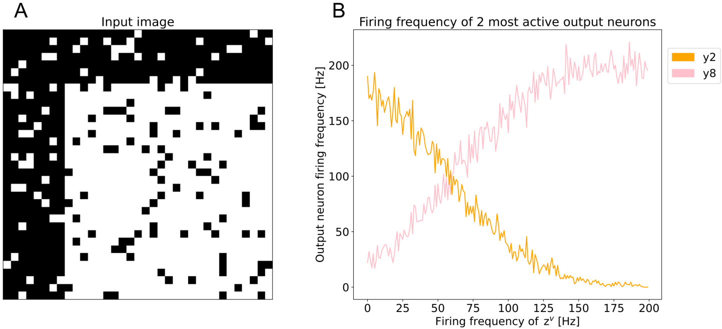


Horizontal validation



Vertical validation

Ambiguous visual stimuli 4

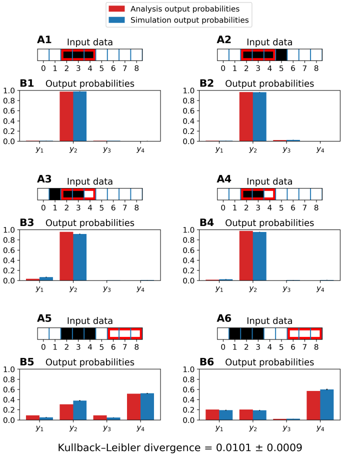


Variable prior activity

Analysis and simulation of the network 1

- usage of smaller 1-D images to make network easier to analyse
- Mathematical derivation of Bayesian likelihood, prior and posterior
- Derived synaptic weights from Bayesian likelihood and prior
- Simulated network with those weights and fitted hyperparameters
- Compared Bayesian posterior to output of the simulation

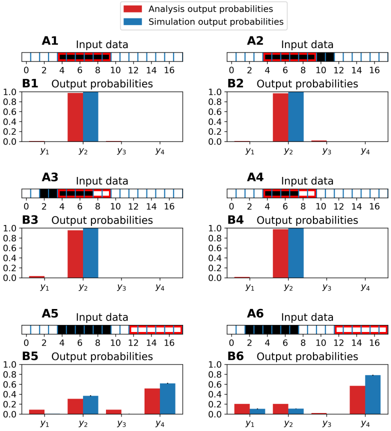
Analysis and simulation of the network 2



Transferability of hyperparameters 1

- Input size and prior neuron firing rate was doubled
- Network was simulated with same hyperparameters of smaller network, to check if they are applicable to any network size

Transferability of hyperparameters 2



Kullback–Leibler divergence = 0.2392 ± 0

Training with predetermined hyperparameters 1

- Determined hyperparameters were used to train weights
- Trained weights were compared to analytically determined weights

Training with predetermined hyperparameters 2

A Learned $P^{X|Y}$

0.52	0.49	0.53	0.06	0.1	0.08	0.12	0.11	0.06
0.09	0.07	0.49	0.49	0.51	0.09	0.09	0.09	0.06
0.07	0.08	0.08	0.06	0.51	0.5	0.52	0.07	0.1
0.11	0.1	0.12	0.07	0.09	0.06	0.53	0.46	0.51

B Calculated $P^{X|Y}$

0.9	0.9	0.9	0.1	0.1	0.1	0.1	0.1	0.1
0.1	0.1	0.9	0.9	0.9	0.1	0.1	0.1	0.1
0.1	0.1	0.1	0.1	0.9	0.9	0.9	0.1	0.1
0.1	0.1	0.1	0.1	0.1	0.1	0.9	0.9	0.9

C Learned $P^{Y|Z}$

1.14	0.02	0.02	0.02
0.03	1.17	0.03	0.01
0.02	0.02	1.15	0.02
0.02	0.03	0.03	1.17

D Calculated $P^{Y|Z}$

0.9	0.03	0.03	0.03
0.03	0.9	0.03	0.03
0.03	0.03	0.9	0.03
0.03	0.03	0.03	0.9

Analysis of model

- Analysed impact of hyperparameters
  - Firing rate of input neurons
  - Firing rate of prior neurons
  - Decay time constant
- Connection between model and Bayesian inference was shown
  - Network outputs spike according to Bayesian posterior
  - Trained weights converge towards the log of their respective probabilities

Conclusion

- Thesis provided insight to hierarchical spiking Winner-Take-All network model
- Showed that the network model can simulate effects like attention and changing beliefs through feedback
- Provided ideas on how to further analyse and improve the model

Sources

- Lee TS, Mumford D. (July 2003). “Hierarchical Bayesian inference in the visual cortex.” In: J Opt Soc Am A Opt Image Sci Vis. DOI: doi:10.1364/josaa.20.001434
- Nessler, Bernhard et al. (Apr. 2013). “Bayesian Computation Emerges in Generic Cortical Microcircuits through Spike-Timing-Dependent Plastic ity.” In: PLOS Computational Biology 9.4, pp. 1–30. doi: 10.1371/journal. pcbi.1003037. url: https://doi.org/10.1371/journal.pcbi.1003037