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### Introduction

Deep learning models are successful at reproducing the input-output map of sensory areas (retina, V1, V4, IT). However, can these models generate experimentally testable mechanistic hypotheses of internal biological computations?

We show that model reduction on artificial networks can generate new experimentally testable hypotheses

- Deep learning mostly concerns the accuracy of the input-output mapping
- Neuroscience aims to understand the internal computational mechanisms of generating the output given sensory stimuli.



L. McIntosh, N. Maheswaranathan et al. NeurIPS (2016)

## Are the artificial network's computational mechanisms for generating neural responses the same as those in the brain?



• generalize to wide arrays of visual stimuli

# From deep learning to mechanistic understanding in neuroscience: the structure of retinal prediction (9)

What can deep learning models tell us about the inner-workings of the brain? We combine "in-silico neurophysiological experiments" and "interpretation tools" to perform model reduction, yielding new experimentally testable mechanisms.

Model reduction: Identifying *important* sub-circuits Average over uniform directions and keep only important units



Compare with existing circuit modes and the state of the

### Integrated Gradients: How important is a neuron?



(i) Apply chain rule to evaluate importance of hidden layer neurons

$$\mathbf{r}(t) = \sum_{\substack{x,y,c \\ \text{channel}}} \left| \int_{0}^{1} d\alpha \frac{\partial \mathcal{F}}{\partial z_{cxy}^{[1]}} \right|_{s(t,\alpha)} \right| \begin{array}{c} (W_{cxy}^{[1]} \circledast s) = \sum_{\substack{x,y,c \\ \text{filter stimulus}}} \left| \mathcal{G}_{cxy}(s) \right| (W_{cxy}^{[1]} \circledast s) = \sum_{\substack{x,y,c \\ \text{channel}}} \left| \mathcal{G}_{cxy}(s) \right| \left| W_{cxy}^{[1]} \circledast s \right|_{s(t,\alpha)} \right|$$

(ii) Exploit stimulus invariances to reduce dimensionality.  $r(t) = \sum_{c=1}^{8} \left( \sum_{m=1}^{36} \sum_{m=1}^{36} \mathcal{G}_{cxy}(s) \right) \cdot \left( W_c^{[1]} \circledast s \right) \equiv \sum_{c=1}^{8} \mathcal{G}_c(s) \cdot \left( W_c^{[1]} \circledast s \right) \equiv \sum_{c=1}^{8} \mathcal{A}_c.$ 

• testable by neurophysiology experiments





Higher frequency -> Cell-type 2 responds more strongly -> shifts response earlier

### Model reduction on artificial network yielded three experimentally verified mechanisms and a new testable hypothesis.



**I. Latency coding:** Dual ON-OFF bipolar pathways model consistent with (i) pharmacological experiments, (ii) existing theory **2. Motion anticipation:** Dual pathways are necessary and inhibitory cell type is necessary. Qualitatively consistent with a recently proposed theory. 3. Motion reversal: ON/OFF reversal along space explains existence of the burst. Inhibitory pathway explains the fixed latency. Qualitatively consistent with a recently proposed theory **4. Omitted Stimulus Response:** Derived a new & only theory that agrees with all experimental facts. The model predicts existence of two types of ON bipolar cells (one only active in high frequency regime with earlier peak, the other always active with later peak) both sending inputs to the same ganglion cell.



A "new and only" model that captures "predictive latency" One ON-bipolar pathway is always active, while the other is only active in high-frequency





Q1. What computational mechanism causes the large amplitude burst? Q2. How is the latency of the peak proportional to the period of the flashes?