23 April 2025 ·

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Peer Review

Review of: "Predictive Coding Explains Asymmetric Connectivity in the Brain: A Neural Network Study"

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In this paper, the authors explore the contribution of neural feedback in a sensorimotor task using computational modeling. Specifically, they used convnets (CNN) and predictive coding networks to study the role of asymmetric feedback, inspired by recent neurophysiological evidence. They claim that "the performance-enhancing effect of
predictive coding under adverse conditions was optimal for medium-range asymmetric feedback."

I think the topic is very interesting and underexplored, so I appreciate the authors' willingness to investigate this and, in general, the field of deep predictive coding networks.

Unfortunately, I believe there are critical points that produce a mismatch between the authors' claims and the evidence shown to support them. Despite that, I believe the authors can easily realign claims and evidence by providing supplementary evidence and modifying some of the proposed ones. Here is a list of important points that I believe should be addressed:

1) The most important (and general) point regards the fact that the authors' way of conducting this work seems more aligned with the field of AI, defined as studying and designing models for performance purposes, than with computational neuroscience, defined as finding useful models of brain function. I believe their "biological realism" can be and should be improved to claim something about how biological circuits operate.

2) To be more specific, the evidence supporting the claims is rather anecdotal because the simulation experiments are very limited. The major point regards the fact that, as far as I understood it, the authors only trained one model instance per "condition" (either the range connection factor or the noise one). This is really problematic because all these results could be just driven by the weight initialization. To

 doi.org/10.32388/Z3YGMG

provide meaningful evidence, one should at least train multiple models and treat them as independent samples, similarly to how it is done in experimental neuroscience research with human or animal subjects.

3) From this, it follows another critical issue in this work. As far as I understood it, the authors performed statistics on the test set samples. This largely inflates the statistics (as evidenced by the very large F-values they reported, for example). A correct way of doing statistical analysis here would be to, as pointed out above, train multiple models and use them as samples (averaging across test set samples).

4) This is, of course, necessary but probably not really sufficient. Another critical point would be to show that the architectural choices are not driving the results (including hyperparameters). This is usually covered by performing architectural search or at least performing additional analyses with architectural variations.

5) Another point is to show that the models were trained properly. The authors reported, "The short and long backbone models were trained for 17 and 9 epochs, respectively." Why this discrepancy? The training stop criterion should be explicitly defined and should be selected to appropriately compare the different models.

6) Another very important point is how the authors defined and trained the predictive coding networks. They used the Predify library to retrain some pretrained feedforward networks by adding feedback layers. I think this is very problematic if one wants to make any claim about biological realism and comparison with biological systems. The problem is that Predify is meant for allowing already trained networks to be augmented with "predictive coding" principles, but again for performance purposes. It's not a good tool for modeling real brains, simply because it trains an already pretrained network. Of course, this is not how the brain operates. Actually, this is not even in principle how it is theorized by the predictive coding theories of brain function. A proper way to test asymmetrical feedback in bio-inspired models is to train an actual predictive coding network [1,2,3]. One of the most popular ones is PredNet, although it has been shown that its architecture does not follow exactly predictive coding principles, and this probably leads to poor representational alignment with biological systems [4,5].

7) In general, I found the paper difficult to read. I suggest better structuring of the sections, especially the methods and results, to improve readability. Also, the figures are low-quality and difficult to read properly.

References

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Declarations

Potential competing interests: No potential competing interests to declare.

doi.org/10.32388/Z3YGMG