

Ten Simple Rules for Deep Learning in Biology

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Introduction

Deep learning (DL), a subfield of machine learning (ML) that focuses on deep artificial neural networks, is exploding in popularity and is increasingly being used for biological data analysis [1]. However, DL itself remains an active area of research, and the complexity of this field poses a large barrier of entry to those who would like to correctly utilize state-of-the-art DL technology in biological research applications. While much has been written about the impressive results of DL in biology, there is a comparative dearth of literature articulating best practices for its use, with most instructional literature focusing on ML, rather than DL [2].

To fix this problem, we solicited input from a diverse community of researchers, who wrote this manuscript collaboratively using the GitHub version control platform [3] and Manubot [4]. In the course of our discussions, several themes became clear: the importance of understanding and applying ML fundamentals as a baseline for utilizing DL, the necessity for extensive model comparisons and careful evaluation, and the need for critical thought in interpreting results generated by means of DL, among others. Ultimately, the rules we established range from high-level guidance to the implementation of best practices, and it is our hope that they will provide actionable, DL-specific advice for both new and experienced DL practitioners alike who would like to employ DL in biological research. By increasing the accessibility of DL techniques to biology, we aim to improve the overall quality and reproducibility of DL in the literature, enabling these powerful methods to be properly utilized to generate new scientific insights.

Rule 1: Concepts that apply to machine learning also apply to deep learning

Rule 2: Use traditional methods to establish performance baselines

Rule 3: Understand the complexities of training deep neural networks

Rule 4: Know your data and your question

Rule 5: Choose an appropriate neural network architecture and data representation

Rule 6: Tune your hyperparameters extensively and systematically

Rule 7: Address deep neural networks' increased tendency to overfit the dataset

Rule 8: Do not necessarily consider a DL model as a black box

Rule 9: Interpret predictions in the correct manner

Rule 10: Don't share models trained on sensitive data

One of the greatest opportunities for deep learning in biology is the ability for deep learning techniques to incorporate representation learning to extract information that can not readily be

captured by traditional methods [5]. The abundance of features for each training example means that the representation learning of the deep learning models can capture information-rich abstractions of data during the training process. Therefore with both deep learning and traditional machine learning models (e.g. k -nearest neighbors models, which learn by memorizing the full training data), it is imperative not to share models trained on sensitive data. Applying deep learning to images of cats from the internet does not pose significant ethical, legal, or privacy problems; this is not the case when dealing with classified, confidential, trade secret, or other types of biological data that cannot be shared. For example, adversarial training techniques such as model inversion attacks can be used to exploit model predictions to recover recognizable images of people's faces used for training [6]. These risks are even more significant in deep learning compared to traditional machine learning techniques due to the greater representational capacity of the models. This is achieved by the large number of model weights, even in a relatively small project, that allow deep learning to model high-dimensional non-linear relationships among data. It is this enhanced modeling capacity that allows the model to learn more robust and nuanced features of specific data, leading to the danger of revealing the underlying sensitive data. When training deep learning models on sensitive data, be sure not to share the model weights directly, and use privacy preserving techniques [7] such as differential privacy [8,9] and homomorphic encryption [10,11] to protect sensitive data.

Conclusion

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