

Challenges and Issues in State-Of-The-Art Bio inspired Artificial Intelligence

TDT04 Advanced Bio-Inspired Methods

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1 Introduction

Researchers have shown the potential of Bio-Inspired AI in the past by introducing powerful methods like GA, NSGA-II, PSO and many more to tackle a wide range of problems such as complex optimisation or path-finding task. Despite the current predominant use of Deep Learning architectures in AI research and industry, Bio-AI methods are expected to remain of fundamental importance in future AI systems Del Ser et al. [DSOM⁺19]. Especially the combination of both fields is believed to be of high potential. As in every field of research however, there are challenges to face in future work to bring the field forward. In this essay, a state-of-the-art is conducted in which current challenges and issues of 8 recent papers from Bio-AI (Ji et al. [JLS⁺20], Kroos et al. [KP17], Miikkulainen [Mii21], Monsef et al. [MNJF19], Poulsen et al. [PTFR17], Sarkhey et al. [SZS15], Shah et al. [SK20], Suganuma et al. [SSN17]) are identified and reflected. An analysis of the literature reveals common threads, issues and challenges of which three important ones are addressed here. A first common challenge is **feature representation** in relation to Bio inspired methods, as it has a high impact on model choice and performance and thus is of high importance. A second identified challenge is **hyper-parameter optimization** which also determines performance. In the selected papers, issues in argumentation for certain parameter selections have been identified. Lastly, a look on **model performance analysis** will be taken, as it is of high importance to the field and issues with respect to comparability, objectivity and focus of measurement have been identified.

2 Feature Representation

This first identified challenge – feature representation – does not only appear in Bio-AI but in the entire field of Machine Learning (ML). Despite being addressed using Bio-AI methods Ji et al. [JLS⁺20], it is not directly an issue in the methods themselves but rather has a strong influence on model selection and design and thus is of central importance to the field. In Deep Learning, it is common that feature extraction is done by a model itself in the form of latent representations in e.g, Autoencoder motivated architectures. In state-of-the art Bio-AI on the other hand, feature extraction is often done manually (i.e., manually select feature extraction tools and methods, see Kroos et al. [KP17], Shah et al. [SK20], Poulsen et al. [PTFR17]). To do this efficiently, this procedure usually requires a deep understanding of the given problem as to select the most representative features. It is arguable

that this is problematic as one motivation of Bio-AI methods is to find solutions to a problem without requiring deeper understanding of a human operator in beforehand. For a deeper understanding of how this challenge is addressed in state-of-the-art Bio-AI, methods in the proposed papers are analyzed and reflected. An example of the influence of altering feature extraction methods can be found in Poulsen et al. [PTFR17]. Two feature representations for the same problem (i.e. aiming in a game) are explored and turn out to perform differently in the final algorithm. On the one hand it is good practice of the authors to explore different approaches, on the other hand this shows that there might be other representations unknown of that might outperform the proposed approaches. An automated or structured approach to find feature representations is lacking and thus remains a challenge for future work. In Kroos et al. [KP17] a heavy audio feature extraction is done using a two-step processing, breaking a large audio signal down to just a few representative features. Again, feature selection methods are chosen manually. It is hard to comprehend what information of the original signal is remained in the final representation and thus why the final algorithm performs as it does. This results in black-box testing, making it hard to optimize the approach without further understanding of the compression methods. Also here, a structured approach to feature extraction in Bio-AI is desirable. A similar problem occurs in Deep Learning and large efforts are spent to acquire better understanding of feature representations, which might also be important for future work in Bio-AI. Despite the importance of feature representation in Bio-AI, some works dispense or only briefly mention feature representation methods, see Mikkulainen [Mii21]. Others, like Shah et al. [SK20] heavily rely on feature representations, however lack to properly explain and argue their decisions. In Shah et al., multimodal feature extraction is performed however it remains a bit unclear why the specific approaches have been chosen. A structured approach to document, structure or even perform feature extraction might be helpful for the future field of Bio-AI. Interesting suggestions are provided by Ji et al. [JLS⁺20] by applying Bio-inspired methods to the problem.

3 Hyperparameter Optimization

Another challenge concerning Bio-AI is hyperparameter (HP) optimization. Common parameters in the field can be related to e.g., mutation mechanisms, crossover mechanisms, population initialization, population exploration and exploitation or member selection mechanisms. As in any other

ML field, the correct selection of HPs is crucial to the performance of a proposed algorithm altogether with the problem formulation. In Bio-AI however, compared to other fields, there is a much larger amount of possible HPs. This is due to the many mechanisms that apply in evolution. While there are known strategies to systematically find and select suitable HPs for a given problem, these approaches get exponentially less efficient with a growing amount of parameters which is especially painful in Bio-AI as it can be seen in state-of-the-art works, see Ji et al. [JLS⁺20] in which the authors had to make a compromise due to the vast amount of possible HPs combinations related to their problem using IBPSO. As a compromise solves the issue in the short term, the problem of optimization remains as it is hard to evaluate and compare models when using median parameter selections that might not be optimal for the compared candidates as can be seen in Ji et al.’s work. A more detailed discussion about optimization procedures can be found in [SSN17]. The authors also mention the lack of efficient approaches for HP optimization in Bio-AI is problematic as they might reduce flexibility of the models. While there is awareness with respect to the problem in the Bio-AI field, some works lack a proper explanation and argumentation of how and why they chose specific parameter constellations. In Poulsen et al. [PTFR17] for example, parameter values are dropped without further argumentation which makes it hard to better comprehend model performance. Besides of lacking model description in Miikkulainen [Mii21], there also is no mention of how and which parameters influence the possible outcomes. Kroos et al. [KP17] introduce J-NEAT building on top of NEAT while also introducing new HPs, making the algorithm more complex. It is however not stated of how the new parameters influence the performance in comparison to the old version. It is also not stated how to find optimal values for the newly introduced parameters. This in general obscures the understanding of model performance through HP selection and clearly is an issue. Probably not only in Bio-AI but in general. For future work it is arguable that it is important to introduce new methods to systematically find and document suitable HPs for given problems. This would also help to compare model performance, which is discussed in the next section.

4 Model Performance Analysis

To evaluate and compare different ML models, it is important to have measurements for model performance. Often times, authors state that their presented model ‘outperforms’ other versions. Commonly used metrics are

convergence speed, solution accuracy or error measures. In terms of future work the question must be posed, whether these measurements are sufficient, comparable and which other factors might also influence the evaluation of a given model. When comparing models, researchers try to recreate the same environment for each tested method, however, as we can already see in the previous section, this can be a challenging task given the varying nature of different approaches in terms of e.g., parameter selection for a given problem. Especially in Bio-AI there are often times multiple solutions for solving a similar problem, which indeed is mirrored from behavior in nature. Say, in nature, bees and ants have a similar goal which is described through exploration and exploitation of the environment. Their approaches to do so however clearly differ from one another. For their particular need and resources, they each however might have found an optimal solution. As stated in Del Ser et al. [DSOM⁺19] a clear distinction of efficacy and efficiency in Bio-AI should be made. Or better, the importance of efficiency should be weighted more in future Bio-AI. Considering the vast amount of necessary computational resources in fields such as Deep Learning, Bio-AI might yield some important advantages in terms of energy consumption and thus efficiency. These qualities should be considered more deeply in future research. In the state-of-the-art Bio-AI, clear challenges could be identified in these terms. As well Sarkhey et al. [SZS15], Ji et al. [JLS⁺20], Monsef et al. [MNJF19] and Kroos et al. [KP17] conduct detailed algorithm comparisons. It is noticeable that each of them approaches the comparison differently i.e., using different measures and focusing on other qualities of the compared algorithms. Kroos et al. for example solely focuses on error measures and does not consider model convergence speed or number of solutions. Sarkhey et al. presents plenty of tables and introduces various measurements without deeper describing them. Further they do not directly present measurement values but rather cascade the compared models in terms of measurement performance. Monsef et. al focuses on convergence speed and solution accuracy. In terms of energy efficiency only Suganuma et al. [SSN17] mentions the demanding computational power of their approach in using NEAT to evolve DCNNs for image classification. Shah et al. [SK20] demonstrates another issue. They state that their model outperforms existing models however they do not discuss or argue above that statement. It is intransparent how they came up with their conclusion. For future Bio-AI research especially the introduction of clear and uniform model evaluation measurements and the introduction of one or several efficiency measurements also in terms of energy consumption might be considered.

5 Conclusion

In this essay, 8 recent papers in the field of Bio-AI have been analyzed and three main challenges for future research have been identified, which they were **feature representation**, **hyperparameter optimization** and **model performance analysis**. All of them are of crucial importance in Bio-AI and turn out to be challenging fields in the state-of-the-art research that demand further work. Bio-AI has been recognized as a field of high potential in the future of AI research with plenty of advantages when compared to predominantly used approaches. For the field to further progress however, existing challenges and issues need to be tackled by researchers. Most of the here identified challenges do not only apply to Bio-AI but to the whole field of ML. Each field however needs to solve them according to their state of development and their need. It appears like most of the existing challenges are of structural rather than technical nature (which might however be reasoned in the incredibly limited technical understanding of the essay’s author). In general, a more structured approach rather than arbitrarily choosing and comparing values that seem suitable for the current task as well as communication among the researchers might already help for most of the stated problems. Addressing these challenges will not only contribute the development of the Bio-AI field but the AI research in general as it can be expected that Bio-AI and other ML methods will further merge in the future as can already be observed in the recently growing amount of work in e.g., neuroevolution, combining neural processing with evolutionary methods. For future terms, Bio-AI should make active use of one of its most valuable properties inherited from nature – efficiency in terms of resources – to counter the increasing amount of demanded computational power of state-of-the-art AI.

References

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