Protein structure prediction using AI and quantum computers

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Abstract

This work seeks to combine the combined advantage of leveraging these emerging areas of Artificial Intelligence and quantum computing in applying it to solve the specific biological problem of protein structure prediction using Quantum Machine Learning algorithms. The CASP dataset from ProteinNet was downloaded which is a standardized data set for machine learning of protein structure. Its large and standardized dataset of PDB entries contains the coordinates of the backbone atoms, corresponding to the sequential chain of N, C_alpha, and C' atoms. This dataset was used to train a quantum-classical hybrid Keras deep neural network model to predict the structure of the proteins. To visually qualify the quality of the predicted versus the actual protein structure, protein contact maps were generated with the experimental and predicted protein structure data and qualified. Therefore this model is recommended for the use of protein structure prediction using AI leveraging the power of quantum computers.

The code is provided in the following Github repository

<https://github.com/bengeof/Protein-structure-prediction-using-AI-and-quantum-computers>

Introduction

The past few years have seen a surge in the application of data-driven AI methods to solve complex problems in biology [1-3]. The areas of application include genomics, proteomics, and drug discovery[4-10]. These have led to tremendous advances in research in biological science. Another emerging area from which life science research can leverage advances is through quantum computing[11-15]. Therefore this work seeks to combine the combined advantage of leveraging these emerging areas of Artificial Intelligence and quantum computing in applying it to solve the specific biological problem of protein structure prediction using Quantum Machine Learning algorithms. Quantum machine learning algorithms are machine/deep learning algorithms that leverage the power of quantum computers. Fault-tolerant quantum computers may be far off, however solving real-world quantum-chemistry problems on near-term quantum devices is possible through the PennyLane [16] which provides an interface to use any of the quantum hardware provided by any of the quantum hardware providers such as IBM, Google, or Microsoft. Classical data is encoded into quantum states through amplitude encoding techniques to reflect the quantum state/wave-function of the quantum circuit. The circuit parameters are then optimized to produce the solution. These quantum layers are introduced between classical Keras layers to turn classical Keras-based deep neural network into a quantum-classical hybrid deep neural network to solve data-driven AI problems through leveraging the power of quantum computers.

Methods

The CASP dataset from ProteinNet was downloaded. ProteinNet is a standardized data set for machine learning of protein structure [17]. Its large and standardized dataset of PDB entries contains the coordinates of the backbone atoms, corresponding to the sequential chain of N, C_alpha, and C' atoms. This dataset was used to train a quantum-classical hybrid Keras deep neural network model whose model configuration is shown below in Fig. 1. A classical convolutional deep neural network inspired in part by Wang et. al. [18] along with introducing quantum Keras layers to make a hybrid model was built and the summary of input dimension, hidden layers, and output dimension of the network is shown in Fig.1.

The code is provided in the following Github repository

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Fig.1 - Model Configuration

Layer (type)	Output Shape	Param #
embedding_1 (Embedding)	(None, 128, 3)	63
conv1d_10 (Conv1D)	(None, 128, 64)	648
dropout_8 (Dropout)	(None, 128, 64)	0
conv1d_11 (Conv1D)	(None, 128, 64)	12352
max_pooling1d_3 (MaxPooling1D)	(None, 64, 64)	0
conv1d_12 (Conv1D)	(None, 64, 64)	12352
dropout_9 (Dropout)	(None, 64, 64)	0
conv1d_13 (Conv1D)	(None, 64, 64)	12352
max_pooling1d_4 (MaxPooling1D)	(None, 32, 64)	0
conv1d_14 (Conv1D)	(None, 32, 128)	24784
dropout_10 (Dropout)	(None, 32, 128)	0
conv1d_15 (Conv1D)	(None, 32, 128)	49280
max_pooling1d_5 (MaxPooling1D)	(None, 16, 128)	0
conv1d_16 (Conv1D)	(None, 16, 128)	49280
dropout_11 (Dropout)	(None, 16, 128)	0
conv1d_17 (Conv1D)	(None, 16, 128)	49280
conv1d_18 (Conv1D)	(None, 16, 32)	4128
conv1d_19 (Conv1D)	(None, 16, 4)	132
lambda_3 (Lambda)	(None, 16, 16, 8)	0
conv2d_transpose_13 (Conv2DT	(None, 16, 16, 64)	576
conv2d_transpose_14 (Conv2DT	(None, 16, 16, 64)	4168
conv2d_transpose_15 (Conv2DT	(None, 16, 16, 128)	73856
dropout_12 (Dropout)	(None, 16, 16, 128)	0
conv2d_transpose_16 (Conv2DT	(None, 32, 32, 128)	147584
conv2d_transpose_17 (Conv2DT	(None, 32, 32, 128)	147584
dropout_13 (Dropout)	(None, 32, 32, 128)	0
conv2d_transpose_18 (Conv2DT	(None, 64, 64, 128)	147584
conv2d_transpose_19 (Conv2DT	(None, 64, 64, 64)	73792
dropout_14 (Dropout)	(None, 64, 64, 64)	0
conv2d_transpose_20 (Conv2DT	(None, 128, 128, 64)	36928
conv2d_transpose_21 (Conv2DT	(None, 128, 128, 64)	36928
dropout_15 (Dropout)	(None, 128, 128, 64)	0
conv2d_transpose_22 (Conv2DT	(None, 128, 128, 64)	36928
conv2d_transpose_23 (Conv2DT	(None, 128, 128, 64)	4168
conv2d_transpose_24 (Conv2DT	(None, 128, 128, 64)	4168
conv2d_transpose_25 (Conv2DT	(None, 128, 128, 1)	65

Results and Discussion

With the trained model, predictions were carried out. To visually qualify the quality of the predicted versus the actual protein structure, protein contact maps were generated with the actual and predicted protein structure data. The predicted and the actual contact map for two instances of prediction for a random seed is shown below in Fig.2

Fig. 2 – Protein contact maps

The convergence of the model is depicted in the figure below

Fig. 3 – Loss function convergence

Conclusion

This work seeks to combine the combined advantage of leveraging these emerging areas of Artificial Intelligence and quantum computing in applying it to solve the specific biological problem of protein structure prediction using Quantum Machine Learning algorithms. The CASP dataset from ProteinNet was downloaded which is a standardized data set for machine learning of protein structure. Its large and standardized dataset of PDB entries contains the coordinates of the backbone atoms, corresponding to the sequential chain of N, C_{alpha}, and C' atoms. This dataset was used to train a quantum-classical hybrid Keras deep neural network model to predict the structure of the proteins. To visually qualify the quality of the predicted versus the actual protein structure, protein contact maps were generated with the experimental and predicted protein structure data and qualified. Therefore this model is recommended for the use of protein structure prediction using AI leveraging the power of quantum computers.

Reference

1. Tang, Binhua, Zixiang Pan, Kang Yin, and Asif Khateeb. "Recent advances of deep learning in bioinformatics and computational biology." *Frontiers in genetics* 10 (2019): 214
2. Mamoshina, Polina, Armando Vieira, Evgeny Putin, and Alex Zhavoronkov. "Applications of deep learning in biomedicine." *Molecular pharmaceuticals* 13, no. 5 (2016): 1445-1454.
3. Akay, Altug, and Henry Hess. "Deep learning: current and emerging applications in medicine and technology." *IEEE journal of biomedical and health informatics* 23, no. 3 (2019): 906-920.
4. Zou, James, Mikael Huss, Abubakar Abid, Pejman Mohammadi, Ali Torkamani, and Amalio Telenti. "A primer on deep learning in genomics." *Nature genetics* 51, no. 1 (2019): 12-18.
5. Ramsundar, Bharath, Peter Eastman, Patrick Walters, and Vijay Pande. *Deep learning for the life sciences: applying deep learning to genomics, microscopy, drug discovery, and more*. "O'Reilly Media, Inc.", 2019.
6. Eraslan, Gökçen, Žiga Avsec, Julien Gagneur, and Fabian J. Theis. "Deep learning: new computational modelling techniques for genomics." *Nature Reviews Genetics* 20, no. 7 (2019): 389-403.
7. Chen, Hongming, Ola Engkvist, Yinhai Wang, Marcus Olivecrona, and Thomas Blaschke. "The rise of deep learning in drug discovery." *Drug discovery today* 23, no. 6 (2018): 1241-1250.

8. Jing, Yankang, Yuemin Bian, Ziheng Hu, Lirong Wang, and Xiang-Qun Sean Xie. "Deep learning for drug design: an artificial intelligence paradigm for drug discovery in the big data era." *The AAPS journal* 20, no. 3 (2018): 1-10.
9. Dana, Dibyendu, Satishkumar V. Gadhiya, Luce G. St Surin, David Li, Farha Naaz, Quaisar Ali, Latha Paka et al. "Deep learning in drug discovery and medicine; scratching the surface." *Molecules* 23, no. 9 (2018): 2384
10. Urban, Gregor, Kevin Bache, Duc TT Phan, Agua Sobrino, Alexander K. Shmakov, Stephanie J. Hachey, Christopher CW Hughes, and Pierre Baldi. "Deep learning for drug discovery and cancer research: Automated analysis of vascularization images." *IEEE/ACM transactions on computational biology and bioinformatics* 16, no. 3 (2018): 1029-1035.
11. Cao, Yudong, Jhonathan Romero, and Alán Aspuru-Guzik. "Potential of quantum computing for drug discovery." *IBM Journal of Research and Development* 62, no. 6 (2018): 6-1.
12. Outeiral, Carlos, Martin Strahm, Jiye Shi, Garrett M. Morris, Simon C. Benjamin, and Charlotte M. Deane. "The prospects of quantum computing in computational molecular biology." *Wiley Interdisciplinary Reviews: Computational Molecular Science* 11, no. 1 (2021): e1481.
13. Barzen, Johanna, Frank Leymann, Michael Falkenthal, Daniel Vietz, Benjamin Weder, and Karoline Wild. "Relevance of Near-Term Quantum Computing in the Cloud: A Humanities Perspective." *Cloud Computing and Services Science* 1399 (2021): 25.
14. Alexeev, Yuri, Dave Bacon, Kenneth R. Brown, Robert Calderbank, Lincoln D. Carr, Frederic T. Chong, Brian DeMarco et al. "Quantum computer systems for scientific discovery." *PRX Quantum* 2, no. 1 (2021): 017001.
15. Li, Junde, Mahabubul Alam, Congzhou M. Sha, Jian Wang, Nikolay V. Dokholyan, and Swaroop Ghosh. "Drug Discovery Approaches using Quantum Machine Learning." *arXiv preprint arXiv:2104.00746* (2021).
16. Bergholm, V., Izaac, J., Schuld, M., Gogolin, C., Alam, M.S., Ahmed, S., Arrazola, J.M., Blank, C., Delgado, A., Jahangiri, S. and McKiernan, K., 2018. PennyLane: Automatic differentiation of hybrid quantum-classical computations. *arXiv preprint arXiv:1811.04968*
17. AlQuraishi, Mohammed. "ProteinNet: a standardized data set for machine learning of protein structure." *BMC bioinformatics* 20, no. 1 (2019): 1-10
18. Wang, Sheng, Siqi Sun, Zhen Li, Renyu Zhang, and Jinbo Xu. "Accurate de novo prediction of protein contact map by ultra-deep learning model." *PLoS computational biology* 13, no. 1 (2017): e1005324.