Zhiye Guo

573-529-0448 | xmuzhiyeguo@gmail.com | Linkedin | Github

Machine Learning • Deep Learning • Computational Biology• Computer Vision• Robotics

EDUCATION

University of Missouri – Columbia

Ph.D. in Computer ScienceXiamen UniversityM.S. in Electrical EngineeringB.S. in Electrical Engineering and Automation

TECHNICAL SKILL

Programming Languages: Python, C++, C# **Tools/Frameworks**: PyTorch, TensorFlow, NumPy, Pandas, Halcon, OpenCV, Version Control {Git}

PROFESSIONAL EXPERIENCE

Graduate Research Assistant | Advisor: Dr. Jianlin Cheng University of Missouri – Columbia, Bioinformatics and Machine Learning Lab

- Developed deep learning algorithms applicable to computational biology, and processed, curated, and maintained protein data for various bioinformatics tasks.
- Designed and trained deep learning algorithms, resulting in the release of five deep learning-based software for protein structure prediction.

Software Engineer Intern | Advisor: Dr. Lei Wang

Xiamen Weixintai Technology Co., Ltd.

- Developed machine vision software for detecting products in industrial production lines.
- Designed optical experiment platforms and imaging processing algorithms for automotive delay defect detection and developed deep learning algorithms to improve the accuracy of defect detection for highly reflective objects.

RESEARCH PROJECTS

CDPred: Protein inter-chain distance map prediction tool

- Designed and developed a 2D attention-based deep learning architecture for protein inter-chain distance map prediction.
- Achieved State-of-the-Art performance in protein inter-chain distance prediction and complemented Alphafold2-Multimer on template-free inter-chain distance prediction.
- Contributed to the No.1 ranking of server MULTICOM_qa in the prestigious 15th Critical Assessment of Protein Structure Prediction (CASP15) competition by providing remarkable accuracy in predicting the quality of quaternary structure of proteins.
- Open-sourced on GitHub: <u>https://github.com/BioinfoMachineLearning/CDPred</u>

DeepDist: Protein real-value inter-residue distance prediction tool

- Designed and developed a multi-task residual convolutional network deep learning architecture to predict protein real-value inter-residue distance.
- Contribution to server predictor MULTICOM-CONSTRUCT's No.5 ranking in protein contact/distance prediction in the CASP14 competition.
- Open-sourced on GitHub: <u>https://github.com/multicom-toolbox/deepdist</u>

DNSS2: Protein secondary structure prediction tool

- Designed and implemented six advanced one-dimensional deep learning networks for 3-state and 8-state secondary structure prediction.
- Developed novel deep learning architectures such as fractal networks and convolutional residual memory

Columbia, MO Aug 2018-Expected graduation: Jul 2023 Xiamen, China Sep 2015 – Jun 2018 Sep 2011 – Jun 2015

Oct 2015 – Jun 2017

Aug 2018 – present

Jan 2021 – Jun 2022 ter-chain distance map

Nov 2018 – May 2019

Sep 2019 – Jun 2020

networks for protein secondary prediction.

• Open-sourced on GitHub: <u>https://github.com/multicom-toolbox/DNSS2</u>

Resistance Welding Spot Defect Detection

- Adopted the deep learning algorithm Convolutional Neural Networks to distinguish non-defective and defective products.
- Thoroughly scrutinized and annotated the erroneously classified products, and painstakingly re-trained the convolutional neural networks to ensure outstanding detection accuracy.

Detection System for Defective Automotive Relay on Assembly Line

- Developed a comprehensive system that detects over 30 types of defects in automotive relays, including relay pin, shell, and character defects.
- Designed experimental platform, illuminant, and image processing algorithm, and developed application software.
- Designed algorithm for image segmentation, image enhancement, image filtering, deviation model, and character recognition.
- Product web: <u>http://xmvtc.cn/prod_detail-42.html</u>

Mold Visual Protector

Jan 2016 – May 2016

- Monitored the injection mold tool's core and cavity and reported abnormalities.
- Designed illuminant and image processing algorithms and wrote detection software.
- Selected infrared light and polaroid to filter out the emissive light.

PUBLICATIONS

- 1. **Guo, Z.**, Liu, J., Skolnick, J. and Cheng, J., 2022. Prediction of inter-chain distance maps of protein complexes with 2D attention-based deep neural networks. *Nature Communications*, 13(1), pp.1-10.
- 2. **Guo, Z.**, Wu, T., Liu, J., Hou, J. and Cheng, J., 2021. Improving deep learning-based protein distance prediction in CASP14. *Bioinformatics*, *37*(19), pp.3190-3196.
- 3. **Guo**, **Z**., Wu, T., Hou, J. and Cheng, J., 2021. DeepDist: real-value inter-residue distance prediction with deep residual convolutional network. *BMC bioinformatics*, 22(1), pp.1-17.
- 4. **Guo**, Z., Hou, J. and Cheng, J., 2021. DNSS2: improved ab initio protein secondary structure prediction using advanced deep learning architectures. *Proteins: Structure, Function, and Bioinformatics*, 89(2), pp.207-217.
- 5. **Guo**, Z., Ye, S., Wang, Y. and Lin, C., 2017, July. Resistance welding spot defect detection with convolutional neural networks. *In International Conference on Computer Vision Systems* (pp. 169-174). Springer, Cham.
- 6. Mahmud, S., **Guo**, **Z**., Quadir, F., Liu, J. and Cheng, J. 2022, Multi-head attention-based U-Nets for predicting protein domain boundaries using 1D sequence features and 2D distance maps. *BMC Bioinformatics*.
- Liu, J., Wu, T., Guo, Z., Hou, J. and Cheng, J., 2022. Improving protein tertiary structure prediction by deep learning and distance prediction in CASP14. *Proteins: Structure, Function, and Bioinformatics*, 90(1), pp.58-72.
- 8. Wu, T., Liu, J., **Guo**, **Z**., Hou, J. and Cheng, J., 2021. MULTICOM2 open-source protein structure prediction system powered by deep learning and distance prediction. *Scientific reports*, *11*(1), pp.1-9.
- 9. Chen, C., Wu, T., **Guo**, Z. and Cheng, J., 2021. Combination of deep neural network with attention mechanism enhances the explainability of protein contact prediction. *Proteins: Structure, Function, and Bioinformatics*, *89*(6), pp.697-707.
- 10. Chen, X., Liu, J., **Guo**, **Z**., Wu, T., Hou, J. and Cheng, J., 2021. Protein model accuracy estimation empowered by deep learning and inter-residue distance prediction in CASP14. *Scientific Reports*, *11*(1), pp.1-12.
- 11. Hou, J., Wu, T., **Guo**, Z., Quadir, F. and Cheng, J., 2020. The MULTICOM protein structure prediction server empowered by deep learning and contact distance prediction. In *Protein Structure Prediction* (pp. 13-26). Humana, New York, NY.
- 12. Soltanikazemi, E., Quadir, F., Roy, R.S., **Guo**, Z. and Cheng, J., 2022. Distance-based reconstruction of protein quaternary structures from inter-chain contacts. *Proteins: Structure, Function, and Bioinformatics*, *90*(3), pp.720-731.

Feb 2017 – Jul 2017

Jun 2016 – Jan 2017