

# Zhiye Guo

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

## EDUCATION

**University of Missouri – Columbia**

**Columbia, MO**

**Ph.D.** in Computer Science

Aug 2018-Expected graduation: Jul 2023

**Xiamen University**

**Xiamen, China**

**M.S.** in Electrical Engineering

Sep 2015 – Jun 2018

**B.S.** in Electrical Engineering and Automation

Sep 2011 – Jun 2015

## 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**

Aug 2018 – present

*University of Missouri – Columbia, Bioinformatics and Machine Learning Lab*

- ML/DL frame Development: Design and training deep learning algorithms applicable to computational biology
- Data Collection: Processed, curated and maintained protein data for different bioinformatics tasks
- Software development and maintenance: Released the deep learning-based software for protein structure prediction

**Software Engineer Intern | Advisor: Dr. Lei Wang**

Oct 2015 – Jun 2017

*Xiamen Weixintai Technology Co., Ltd.*

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

## RESEARCH PROJECTS

**CDPred: Protein inter-chain distance map prediction tool**

Jan 2021 – Jun 2022

- Designed and developed 2D attention-based deep learning architecture for protein inter-chain distance map prediction
- Reach SOTA in protein inter-chain distance prediction and complementary with AlphaFold2-Multimer on template-free inter-chain distance prediction
- Used by server MULTICOM\_qa which ranked No.1 in estimating the accuracy of protein quaternary structure models in the 15th Critical Assessment of Protein Structure Prediction (CASP15) competition
- GitHub: <https://github.com/BioinfoMachineLearning/CDPred>

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

Sep 2019 – Jun 2020

- Designed and developed multi-task residual convolutional network deep learning architecture to predict protein real-value inter-residue distance
- Server predictor MULTICOM-CONSTRUCT ranked No.5 in protein contact/distance prediction in the CASP14 competition
- GitHub: <https://github.com/multicom-toolbox/deepdist>

**DNSS2: Protein secondary structure prediction tool**

Nov 2018 – May 2019

- Designed and implemented six advanced one-dimensional deep learning networks for 3-state and 8-state secondary structure prediction

- Several deep learning architectures such as fractal networks, and convolutional residual memory networks are novel for protein secondary prediction
- GitHub: <https://github.com/multicom-toolbox/DNSS2>

### Resistance Welding Spot Defect Detection

Feb 2017 – Jul 2017

- Adopted the deep learning algorithm Convolutional Neural Networks to distinguish non-defective and defective products.
- Manually annotated the wrongly classified products and re-trained the convolutional neural networks.

### Detection System for Defective Automotive Relay on Assembly Line

Jun 2016 – Jan 2017

- Detected over 30 kinds of defects, including relay pin, shell, character, etc.
- 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: [http://xmvtc.cn/prod\\_detail-42.html](http://xmvtc.cn/prod_detail-42.html)

### Mold Visual Protector

Jan 2016 – May 2016

- Monitored the injection mold tool's core & cavity and reported abnormality
- Designed illuminant, and image processing algorithms and wrote detect 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*.
7. 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.