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## Work Experience

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### \*\*\* Research Institute | Biological Foundation Model Design Oct 21, 2024 — Present

- **Single cell foundation model: in-context learning single cell foundation model (53m, 300m, 600m, 2B) Training model with observation and perturbation data**
  1. Design model architecture, modeling cells on group level  
From data preprocessing to model design, to downstream benchmark (based on scGPT), The model performs better than scGPT, Transcriptformer, UCE.
  2. In-context learning in single cell data, explore scaling law in single cell data.
  3. Model implementation: PyTorch → PyTorch Lightning. Attention acceleration with FlashAttention and FlexAttention.  
Loss function design and multi-classification head design.
  4. Built downstream multi-task evaluation pipeline: batch-effect correction, cell classification, perturbation prediction; designed new tasks for single-cell foundation models.
  5. Model parallel acceleration: FSDP, data parallelism, checkpointing.
  6. Mentored interns to deliver independent projects.
- **BindCraft protein design: used BindCraft to design binder proteins; ~5% of designs exhibited strong binding affinity.**

Designed antigen ligands with constrained binding sites and generated corresponding binders via BindCraft, in collaboration with the experimental team.

## Education

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Wageningen University | M.Sc. in Bioinformatics GPA: 7.5/10 Sep 1, 2022 — Aug 21, 2024  
Course grades: Computational Biology (8.5/10), Molecular Systems Biology (7.5/10), Machine Learning (7.5/10), Advanced Statistics (8/10)

Deep Learning (8/10), Software Engineering (7.5/10), Genomics (8/10)

- **Protein structure and sequence embeddings (sgBERT, gBERT): combined protein structure and sequence via attention to obtain protein embeddings; preliminary exploration of multi-modal fusion.**

Independent design: protein structure representation, Transformer model implementation, evaluated on protein structure classification.  
[ChunZhuo/sgBERT: Two BERT-like models for protein structure and protein structure with sequence](#)
- **Protein-protein interface false-positive prediction: applied harmonic functions to enforce equivariance, integrated into a graph neural network to model interaction interfaces, and predicted whether a binding event is a false positive.**

Benchmarked protein-interaction prediction models on the alanine-scanning task, from classical docking software (HADDOCK) to machine-learning models (linear regression, random forest) to graph neural networks (DeepRank-GNN).  
Independent design: extended DeepRank-GNN by incorporating an equivariant graph neural network.  
[ChunZhuo/SEGIN: Add SE feature into DeepRank](#)
- **Coursework: sequence assembly → differential gene expression → protein domain analysis; plant GNSR gene analysis.**

Gene regulatory network analysis.  
Java software development: parking-lot entry system.

Northwest A&F University | B.Sc. in Horticulture (Agriculture) GPA: 3.51 Sep 1, 2018 — Jul 30, 2022  
Course grades: Advanced Mathematics (91/100), Linear Algebra (94/100), Probability

## Curriculum vitae

Theory (92/100), Fundamental Biochemistry (91/100), Organic Chemistry (94/100)

- Kiwifruit shoot-tip cryotherapy for virus elimination.  
RT-PCR; plant tissue culture.

### Skills

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IELTS: 7.0 (Speaking 7.0) GRE: 320

Python: pytorch, pytorch lightning, R, Java, C++