

## Haonan Wu

Ph.D. Student/Research Assistant  
Computer Science and Engineering at Penn State  
State College, PA, USA

### CONTACT INFORMATION

---

Email: [hvw5426@psu.edu](mailto:hvw5426@psu.edu)  
Tel: +1 (814) 7696989  
Linkedin: <https://www.linkedin.com/in/haonan-wu-2a7006193/>  
Web: <https://wu-haonan.github.io/>

### EDUCATION

---

#### The Pennsylvania State University (PSU), USA

Ph.D. in Computer Science and Engineering  
Supervisor: Prof. Paul Medvedev

Aug. 2023 - present

**Research Topics:** Theoretical and Algorithmic Bioinformatics

#### Shandong University (SDU), PRC

Master of Science in Operational Research and Cybernetics

Sep. 2020 - Jun. 2023

**GPA:** 92.17/100

**Relevant Coursework:** Graphs and Digraphs, Combinatorial Optimization, Analysis and Design of Algorithms, Modern Functional Analysis, Elements of Modern Algebra, Mathematical Analysis

#### Shandong University (SDU), PRC

Bachelor of Science in Biotechnology

Sep. 2016 - Jun. 2020

**GPA:** 90.65/100

**Relevant Coursework:** Biochemistry, Cell Biology, Molecular Biology

### WORK EXPERIENCE

---

#### The Pennsylvania State University

*Research Assistant in Department of Computer Science and Engineering*

Supervisor: Supervisor: Prof. Paul Medvedev

State College, USA

Jan. 2024 – present

Developing bioinformatics theories and algorithms.

### RESEARCH INTERESTS

---

- Bioinformatics and computational biology
- Algorithmic and Theoretical Bioinformatics
- Graph theory
- Deep Learning

### RESEARCH EXPERIENCE

---

#### A k-mer-based estimator of the substitution rate between repetitive sequences

2025

We relax the non-repetitive assumption and propose a novel estimator for the mutation rate. We derive theoretical bounds on our estimator's bias. Our experiments show that it remains accurate for repetitive genomic sequences, such as the alpha satellite higher order repeats in centromeres. We demonstrate our estimator's robustness across diverse datasets like the HOR region of the centromere.

Softwares:

- [https://github.com/medvedevgroup/Repeat-Aware\\_Substitution\\_Rate\\_Estimator](https://github.com/medvedevgroup/Repeat-Aware_Substitution_Rate_Estimator)
- [https://github.com/Wu-Haonan/Repeat-Aware\\_mutation\\_rate\\_estimator](https://github.com/Wu-Haonan/Repeat-Aware_mutation_rate_estimator)
- [https://github.com/Wu-Haonan/Repeat-Aware\\_phylogenetic\\_distance\\_estimator](https://github.com/Wu-Haonan/Repeat-Aware_phylogenetic_distance_estimator)

#### Spatom: a graph neural network for structure-based protein-protein interaction site prediction

2023

We propose Spatom, a novel framework for PPI site prediction. This framework first defines a weighted digraph for a protein structure to precisely characterize the spatial contacts of residues, then performs a weighted digraph convolution to aggregate both spatial local and global information and finally adds an improved graph attention layer to drive the predicted sites to form more continuous region(s). We tested it on a diverse set of challenging protein-protein complexes and demonstrated the best performance among all the compared methods.

## Softwares:

- Web server: <http://liulab.top/Spatom/server>
- Source code: <https://github.com/Wu-Haonan/Spatom>

## PEER-REVIEWED PUBLICATIONS

---

### Preprints

- **Haonan Wu**, Antonio Blanca, and Paul Medvedev, A k-mer-based estimator of the substitution rate between repetitive sequences, *bioRxiv* 2025.06.19.660607; doi: <https://doi.org/10.1101/2025.06.19.660607>

### Journals

- **Haonan Wu**, Jiyun Han, Shizhuo Zhang, Gaojia Xin, Chaozhou Mou, Juntao Liu, Spatom: a graph neural network for structure-based protein-protein interaction site prediction, *Briefings in Bioinformatics*, Volume 24, Issue 6, November 2023, bbad345, <https://doi.org/10.1093/bib/bbad345>

### Conference proceedings

- WABI

## PROFESSIONAL SERVICE

---

### Peer-Reviewer

RECOMB 2025, ISMB 2025, ACM-BCB 2025

### Short courses

- Deep-learning workshop, School of Mathematics and Statistics, SDU, China Winter 2022  
Handouts of the course.

### Undergraduate Mentor

- Inorganic and Analytical Chemistry, School of Marine, SDU, China Fall 2018
- Probability and Mathematical Statistics II, School of Marine, SDU, China Spring 2019

## TALKS & POSTER

---

### Talks

- WABI 2025, University of Maryland, MD, USA
- Graphs and Digraphs, School of Mathematics, SDU, China Spring 2022  
Topic: Applications of Digraph in bioinformatics and computational biology
- Sequence and Assembly Seminar, School of Mathematics and Statistics, SDU, China  
Topic: Introduction of Single Molecular Sequence and assembly algorithms for long-reads

### Posters

- WABI 2025, University of Maryland, MD, USA (Link)
- Rao Prize Conference 2025, Penn State University, PA, USA (Link)

## OTHER EXPERIENCES

---

**Explored the possible reason for abundance of oxides on the Martian surface** Jun. 2017 - Oct. 2018  
Planetary Lab, Space Science School, SDU with Dr. Zhongchen Wu

## SKILLS

---

- **Programming:** Python, MATLAB, C++, experience programming in Linux server
- **Package:** Pytorch, scikit-learn
- **Scripting Language:** L<sup>A</sup>T<sub>E</sub>X
- **Language:** Chinese (native speaker), English (working language)

## REFERENCES

---

**Prof. Paul Medvedev**

***Professor***

*Department of Computer Science and Engineering*

*Department of Biochemistry and Molecular Biology*

***Director***

*Center for Computational Biology and Bioinformatics @ the Genome Sciences Institute of the Huck*

*The Pennsylvania State University, PA, USA*

E-mail: pzm11@psu.edu

Web Page: <https://medvedevgroup.com/principal-investigator/>

Google Scholar: [https://scholar.google.com/citations?user=Gwd6p\\_8AAAAJ](https://scholar.google.com/citations?user=Gwd6p_8AAAAJ)

**Prof. Antonio Blanca**

***Associate Professor***

*Department of Computer Science and Engineering*

*The Pennsylvania State University, PA, USA*

E-mail: azb1015@psu.edu

Web Page: <https://www.cse.psu.edu/~azb1015/>

Google Scholar: <https://scholar.google.com/citations?user=tl6ib-MAAAAAJ&hl=en>