Sheng Wang

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Professional Preparation

Institute of Theoretical Physics, Chinese Academy of Sciences	China	Bioinformatics	PhD 2010
School of Life Sciences, Shanghai Jiao Tong University	China	Biotechnology	B.S. 2005

Appointments

2017-now	Research Scientist, King Abdullah University of Science and Technology
2014-2017	Research Professional, Department of Human Genetics, University of Chicago
2011-2014	Postdoctoral Research Fellow, Toyota Technological Institute at Chicago
2010-2011	Postdoctoral Research Associate, Institute of Computing Technology, Chinese Academy of Sciences

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Top10 Selected Publications (†corresponding author, *co-first author)

- **S Wang***, Z Li*, Y Yu, J Xu†. “Folding membrane proteins by deep transfer learning”. *Cell Systems* **5**(3), (2017)

- **S Wang**, S Sun, J Xu†. “Analysis of deep learning methods for blind protein contact prediction in CASP12”. *Proteins* **82**(s2), (2017)

- J Skinner*, **S Wang***, J Lee, C Ong, R Sommese, S Sivaramakrishnan, W Koelmel, M Hirschbeck, H Schindelin, C Kisker, K Lorenz, T Sosnick†, M Rosner†. “Conserved salt-bridge competition triggered by phosphorylation regulates the protein interactome”. *PNAS* **114**(51), (2017)

- M Shao*†, J Ma*, **S Wang***†. “DeepBound: Accurate Identification of Transcript Boundaries via Deep Convolutional Neural Fields”. *Bioinformatics* **33**(14), (2017)

- **S Wang***, S Sun*, Z Li, R Zhang, J Xu†. “Accurate De Novo Prediction of Protein Contact Map by Ultra-Deep Learning Model”. *PLoS Computational Biology* **13**(1), (2017)

- **S Wang†**, J Ma, J Xu†. “AUCpreD: proteome-level protein disorder prediction by AUC-maximized deep convolutional neural fields”. *Bioinformatics* **32**(17), (2016)

- **S Wang†***, W Li*, R Zhang, S Liu, J Xu†. “CoinFold: a web server for protein contact prediction and contact-assisted protein folding”. *Nucleic Acids Research* **44**(W1), (2016)

- **S Wang**†*, W Li*, S Liu, J Xu†. "RaptorX-Property: a web server for protein structure property prediction". *Nucleic Acids Research* **44**(W1), (2016)

- **S Wang**†, J Peng, J Ma, J Xu†. "Protein Secondary Structure Prediction using Deep Convolutional Neural Fields". *Scientific Reports* **6**, (2016).

- **S Wang**, J Peng, J Ma, J Xu†. "Protein structure alignment beyond spatial proximity". *Scientific Reports* **3**, (2013).

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Synergistic Activities

- Completed a series of NIH and NSF grants (including **NIH-R01GM08973**, **NSF-DBI0960390**, **NSF-CCF1149811**, **NSF-DBI1262603**) as the main developer and contributor. The major resultant of these grants is the protein structure prediction server **RaptorX**, which has accumulated ~40,000 users and processed ~250,000 jobs. This work has been published in *Nature Protocol* and cited by ~500 times (according to Google Scholar, the same below).

- Developed a new machine learning method, denoted as AUC-maximized **DeepCNF**, for learning from class imbalanced data. This work has been accepted in a variety of leading conferences including **ECCB** 2016, **ECML** 2016, and **IJCAI BOOM** 2016. The resultant Web Server, denoted as RaptorX-Property which has been published in *Nucleic Acids Research*, has processed ~28,000 jobs. All related works has been cited by ~120 times.

- Developed a brand-new system **RaptorX-Contact** for de novo contact-assisted protein modeling, which has been published in *PLoS Computational Biology* and *Cell Systems*. This work was **officially ranked 1st** in contact prediction in the worldwide protein structure prediction (CASP) competition round XII, which was latter invited for publication in *Proteins*. The resultant Web Server, published in *Nucleic Acids Research*, has processed ~11,000 jobs. All relevant works has been cited by ~100 times.

- Developed a novel protein structure alignment algorithm **DeepAlign**, which has been published in *Scientific Reports* and been cited by ~70 times. The resultant Web Server has processed ~5,000 jobs.

- Won the following awards: Warren DeLano Award for Structural Bioinformatics and Computational Biophysics in **ISMB 3DSIG** 2012 and **ISMB 3DSIG** 2014, Best Paper Award in **RECOMB** 2014, Best Poster Award in **IJCAI BOOM** 2016, Best Paper Award in **APBC** 2018.

- **Reviewer** for the following journals: Nucleic Acid Research, Bioinformatics, Proteins, BMC Bioinformatics, Journal of Molecular Biology, Scientific Reports, PLoS ONE, Oncotarget, Molecular BioSystems**[Top 10 reviewers]**, Journal of Computer-Aided Molecular Design (JCAM), Journal of Bioinformatics and Computational Biology (JBCB), Advances in Protein Chemistry & Structural Biology (APCSB), Statistical Methods in Medical Research (SMM), IEEE-TCBB, etc.