

Protein Structure and Function Prediction

SPEAKER Dr Jianyi YANG

Associate Professor
School of Mathematical Sciences
Nankai University
China

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VENUE CS Seminar Room, Y6405
6th Floor, Yellow Zone
Yeung Kin Man Academic Building
City University of Hong Kong
83 Tat Chee Avenue
Kowloon Tong

ABSTRACT

The success of DNA sequencing techniques makes the number of known protein sequences far exceeds that of structurally and/or functionally known proteins. Traditional experimental protein structure and function determination techniques are often too expensive and slow to meet with the increasing requirements of genome-wide research, and furthermore, do not work for all proteins. Development of accurate structure and function modeling algorithms represents an efficient, and probably the only solution to the problem. Following the "sequence-to-structure-to-function" paradigm, we have developed the I-TASSER pipeline for automated protein structure prediction and structure-based function annotation. Over the last decade, I-TASSER has been consistently ranked as the No. 1 method for protein structure prediction in the 7-12th community-wide CASP (Critical Assessment of protein Structure Prediction) experiments. The COFACTOR and COACH methods, both included in the I-TASSER pipeline, have demonstrated considerable success in community-wide ligand-binding site predictions and been ranked as the top function annotation methods in the 9-10th CASP and the CAMEO (Continuous Automated Model Evaluation) experiments, respectively. These results demonstrated the significant advantage of the I-TASSER pipeline over other state-of-the-art methods, which are now ready to use in genome-wide protein structure and function prediction.

BIOGRAPHY

Jianyi Yang received his Ph.D. degree from Nanyang Technological University in 2012. Dr Yang joined the Yang Zhang Lab in the University of Michigan as a Postdoctoral Research Fellow in 2011, and was promoted to a Research Investigator in 2014. He is now an Associate Professor in the School of Mathematical Sciences, Nankai University, China. His research interests include structural bioinformatics, machine learning and data mining. He has over 30 publications in top international journals such as Nature Methods, Nucleic Acids Research, and Bioinformatics. He is an Associate Editor of the journal BMC Bioinformatics. Dr Yang was elected by the National Thousand Young Talents Program in 2016. More information can be found at the website of his lab: <http://yanglab.nankai.edu.cn/>.

All are welcome!



In case of questions, please contact Dr WONG Ka Chun at Tel: 3442 8618, E-mail: kc.w@cityu.edu.hk, or visit the CS Departmental Seminar Web at <http://www.cs.cityu.edu.hk/news/seminars/seminars.html>.

