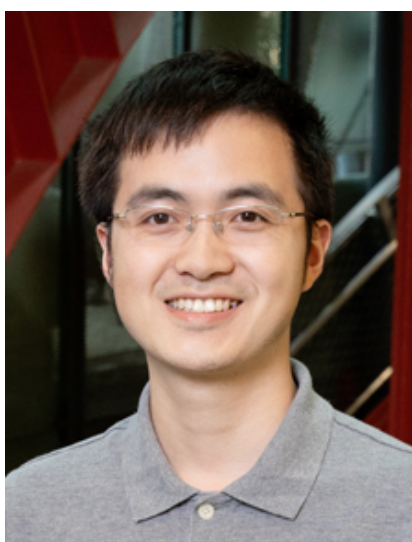# CAMPUS-WIDE COMPUTATIONAL BIOLOGY
BROWN BAG SEMINAR SERIES

"Predicting protein binding from limited annotations"

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Department of Computer Science

12.30pm-1pm, Friday Sept. 27th

1040 NCSA

Please bring your own food. Coffee and cookies will be provided!

Abstract: Many recent efforts to analyze signaling networks involve the construction of machine learning models to predict protein-peptide bindings. However, the training process usually requires a sufficient amount of data while the number of experimentally verified protein-peptide binding sites is often limited. In this talk, I will describe a generic framework to address this issue of data scarcity in protein binding prediction, using the prediction of kinase-specific phosphorylation sites as a demonstration of the framework's applicability. The framework uses an effective meta-learning training strategy to build a prediction model with robust transferability. I will show that this framework has better transferability than state-of-the-art methods and is effective in utilizing limited data to accurately predict phosphorylation sites for less-characterized kinases. Reference: https://doi.org/10.1101/519413

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