

# Fanchi Meng

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PhD student in Software Engineering & Intelligent Systems, University of Alberta  
Looking for an intern job in software engineering in 2017

## Education

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**Jan-2014 to Mar-2018 (expected):** PhD in Software Engineering & Intelligent Systems (GPA 3.8/4.0)

Department of Electrical and Computer Engineering, University of Alberta, Canada

**Sep-2006 to June-2013:** Bachelor & Master in Computer Science and Technology (GPA 81.6/100, 87.5/100)

College of Information Engineering, Northwest A&F University, China

## Projects

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**DFLpred:** a novel computational tool that predicts one of the major functions of disordered proteins, flexible linkers. It solves a binary classification problem that predicts if a given residue in an input sequence is a flexible linker or not. I improved the prediction performance by 35% when compared with the second-best other method, measured by the Area Under the Receiver Operating Characteristic curve (AUC), and improved the sensitivity by 1.3 times at the low range of false positive rates ( $\leq 0.1$ ).

Web server <http://biomine-ws.ece.ualberta.ca/DFLpred/>

Package <https://fanchi.github.io/DFLpred/>

Back end Java

Training model Logistic regression

**pcDETECT:** a web server that integrates two existing predictive models to predict if a given protein sequence can pass the four steps of the crystallization pipeline. It is the first web server that allows users to run fast predictions for large dataset, and slower but more accurate predictions for small dataset. I also benchmarked the prediction performance of all other available tools.

Web server <http://biomine-ws.ece.ualberta.ca/pcDETECT/>

Back end Java

Data analysis Python

A full list and details of my projects can be found at <https://sites.ualberta.ca/~fanchi/projects.html>

## Skills

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- Programming languages: Java, Python, Matlab
- Predictive modelling tool: Weka

## Publications

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- **F. Meng** and L. Kurgan, *DFLpred: High-throughput prediction of disordered flexible linker regions in protein sequences*, Bioinformatics, vol. 32, pp. i341-i350, 2016. [link](#)
- **F. Meng**, C. Cai, and H. Yan, *A Biclustor-Based Bayesian Principal Component Analysis Method for Microarray Missing Value Estimation*, IEEE Journal of Biomedical and Health Informatics, vol. 18, pp. 863-871, 2014. [link](#)

A full list of my publications can be found at <https://sites.ualberta.ca/~fanchi/publications.html>