

Fanchi Meng

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PhD candidate in Software Engineering & Intelligent Systems, University of Alberta

Education

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

DMRpred: a machine learning model that predicts disordered moonlighting regions (DMR) in proteins. This model gives probability and binary classification results on if a residue belongs to a DMR. On blind test dataset, this method obtained accuracy of 0.82 and AUC (area under the receiver operating characteristic curve) of 0.86, and is statistically significantly better than the second best method (accuracy = 0.74, AUC = 0.82).

Web server <http://biomine.cs.vcu.edu/servers/DMRpred/>

Back end Java + MySQL

Machine learning model Random forest

DFLpred: a machine learning model that predicts disordered flexible linker (DFL) regions in proteins. I improved the AUC by 35% when compared with the second-best other method, and improved the sensitivity by 1.3 times at the low range of false positive rates (≤ 0.1). This model is published in high impact journal and is actively used by the research community.

Web server <http://biomine.cs.vcu.edu/servers/DFLpred/>

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

Back end Java + MySQL

Machine learning model Logistic regression

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

Skills

- Programming languages: Java, Python, Matlab
- Big data: Hadoop Map-Reduce
- Predictive modelling tool: Weka

Publications

- **Meng F.** and Kurgan L., *DFLpred: High-throughput prediction of disordered flexible linker regions in protein sequences*, Bioinformatics, vol. 32, pp. i341-i350, 2016. [link](#)
- **Meng F.**, Uversky V. and Kurgan L., *Computational Prediction of Intrinsic Disorder in Proteins*, Current Protocols in Protein Science, supp. 88, pp. 2.16.1-2.16.14, 2017. [link](#)

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