

Fanchi Meng

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<http://fanchi.github.io/>

New grad in Software Engineering & Intelligent Systems, University of Alberta

Education

Jan-2014 to present: 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 random forest model that predicts disordered moonlighting regions (DMR) in proteins.
- Solves a binary classification problem.
- Trained on structured data with 22727 samples and 1588 features.
- Prediction accuracy = 0.82, AUC (area under the receiver operating characteristic curve) = 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 implementation](#) Java + MySQL

DFLpred

- A logistic regression model that predicts disordered flexible linker (DFL) regions in proteins.
- Solves a binary classification problem.
- Trained on structured data with 23154 samples and 2236 features + feature selection.
- 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 implementation](#) Java + MySQL

Page rank

- Implementation of page rank on Hadoop.
- Two MapReduce jobs.
- Given an initial page rank and transition matrix, it iteratively updates the page rank based on the previous page rank and transition matrix.
- [Project page](#) <https://github.com/fanchi/PageRank>

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
- Machine Learning: Weka, scikit-learn

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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