



Dr Jiangning Song

Senior Research Fellow

Head, Structural Bioinformatics Laboratory



Monash Biomedicine Discovery Institute
Infection and Immunity Program

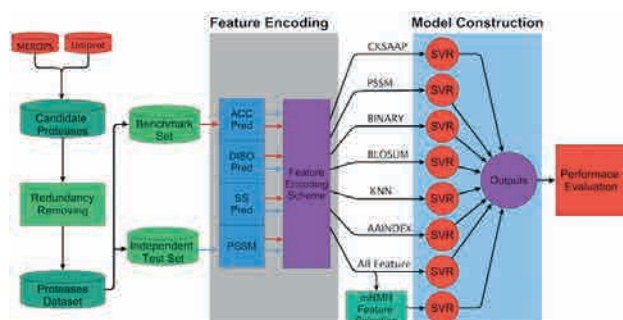
EMAIL jiangning.song@monash.edu

TELEPHONE +61 3 9902 9304

Structural bioinformatics is the branch of bioinformatics concerned with the analysis and prediction of the three-dimensional structure of biological macromolecules on a genomic scale by developing computational methods. Machine-learning techniques have recently provided cost-effective solutions to challenging problems that were previously considered difficult to address. Our research focus is to develop heterogeneous biological feature-integrated approaches and tools based on machine learning and data mining to further our understanding of biological systems. We are motivated to investigate, develop and apply cutting-edge bioinformatics methodologies to understand and address a range of open and challenging problems in genomics, molecular biology and systems biology. The developed bioinformatics algorithms and tools can be used as powerful means to facilitate high-throughput screening (HTS), guide rational drug design and address emerging challenges in precision pharmacology. To date, bioinformatics tools we developed include Cascleave, Cascleave 2.0, APIS, PROSPER, hCKSAAP_UbSite, Crystals, Procleave, Periscope, GlycoMine, PROSPER 2.0, Bastion4 and DeepCleave.

Research Projects

1. Computational modelling and experimental validation of types III, IV and VI secretion effector proteins in Gram-negative pathogens
2. Reconstruction of structural interaction networks at the host-pathogen synapse
3. Comparative genome-scale metabolic modelling of *Klebsiella pneumoniae*
4. Predicting the effects of noncoding variants de novo in the human personal genome
5. A machine-learning-based method to link protein post-translational modification stoichiometry and functional phenotype



The flowchart of our developed PROSPER 2.0 web server.

Selected significant publications:

1. Chen Z, Zhou Y, Zhang Z, **Song J.** 2015. Towards more accurate prediction of ubiquitination sites: a comprehensive review of current methods, tools and features. *Briefings in Bioinformatics*. 16(4):640-657.
2. Li F, Li C, Wang M, Webb GI, Zhang Y, Whisstock JC, **Song J.** 2015. GlycoMine: a machine learning-based approach for predicting N-, C- and O-linked glycosylation in the human proteome. *Bioinformatics*. 31(9):1411-1419.
3. Chang CCH, Tey BT, **Song J,** Ramanan RN. 2015. Towards more accurate prediction of protein folding rates: a review of the existing web-based bioinformatics approaches. *Briefings in Bioinformatics*, 16(2): 314-324.
4. Wang M., Zhao X.M., Tan H., Akutsu T., Whisstock JC, **Song J.** 2014. Cascleave 2.0, a new approach for predicting caspase and granzyme cleavage targets. *Bioinformatics*. 30(1): 71-80.
5. **Song J,** Tan H, Shen H, Mahmood K, Boyd SE, Webb GI, Akutsu T, Whisstock JC. 2010. Cascleave: towards more accurate prediction of caspase substrate cleavage sites. *Bioinformatics*, 26(6): 752-760.