



# Liguang Zhu

*Data Scientist*

## Highlights

- Strong skills in analytics and solution prototyping with R, Python and Weka.
- Extensive experience in cross-disciplinary research, analytics and predictive modeling.
- Experienced in AWS, Microsoft Azure, high performance computing, and grid computing.
- Experienced in SQL, NoSQL, and data warehousing.
- Exposed to Hadoop and its ecosystem

## Experience

### Mar 2010 - Present, Clatyon School of IT, Monash University Researcher & PhD

Specialise in data science disciplines including machine learning, probabilistic modeling, predictive modeling, and graph theory.

- Played a key role in researching and prototyping of a novel feature engineering algorithm: Subsumption Resolution.
- Independently researched various predictive models on highly imbalanced biological data and implemented a tool for enzyme specificity prediction.
- Leading the design and development of a novel protein design pipeline by study high dimensional biological data.
- Designed one of the most stable protein molecules: FN3con.
- Designed a pharmaceutically promising molecule that challenges the current understanding of structure-folding relationship of proteins.
- Coordinated with research groups in different disciplines such as data science, structural biology, protein production unit, and chemical engineering.

### Nov 2016 - Mar 2017, South East Water Data Scientist Intern

Responsible for exploring statistical and machine learning solutions to risk prediction and budget modeling of the gravity sewerage system.

- Utilised customer retention analysis for system failure modeling.
- Utilised customer segmentation analysis to reduce selection-bias.
- Explored and analysed datasets with various machine learning techniques such as classification, clustering, and association rule discovery.
- Sourced multiple datasets of CCTV inspections, historical renewal programs, and system failure records from data warehouses.
- Designed and implemented a budget optimisation software to maximise ROI.
- Utilised *Tableau* for visual analytics and reporting.

Liguang (Leon) Zhu  
leon.l.zhu@gmail.com  
+61 433 082 233

**Sep 2012 - Present, Monash University**

**Teaching Associate**

Responsible for delivering, facilitating, and managing tutorials, discussion, and practical laboratories.

- Advanced algorithms and data structures
- Business intelligence and data warehousing
- Introduction to data science
- Introduction to computer science
- programming foundations in Python

**Sep 2010 - Dec 2010, School of Biological Science, Monash University**

**Research Assistant**

Responsible for the development and deployment of a portable database system on customised data collection devices for ecology research.

**Sep 2010 - Dec 2012, Fleet Software & Services Pty Ltd**

**Freelancer Data Science Consultant**

Involved in the design and development of a value prediction system based on historical fleet exchange data.

- Managed data cleaning and predictive modeling.
- Minimised the average prediction error to \$600.

**Education**

**2012 - present, Monash University**

**Doctorate of Philosophy**

**2008 - 2010, Monash University**

**Master of Computer Science (Minor Thesis in Data Science)**

**2003 - 2007, Beijing Jiaotong University, China**

**Bachelor of Engineering in Computer Science with Honours**

**References**

Provide upon request.

## Publications

- B. Porebski, S. Keleher, J. Hollins, A. Nickson, **L. Zhu**, et. al. (2016) *Smoothing a rugged protein folding landscape by sequence-based redesign*. Scientific Report, 6, Art. no. 33958.
- B.T. Porebski, A.A. Nickson, D.E. Hoke, M.R. Hunter, **L. Zhu**, S. McGowan, G.I. Webb, and A.M. Buckle. (2015). *Structural and dynamic properties that govern the stability of an engineered fibronectin type III domain*. Protein Engineering, Design and Selection. 28(3): 67-78. Oxford University Press.
- **L. Zhu**, B.T. Porebski, A.M. Buckle, G.I. Webb. (2013). *A probabilistic approach to In Silico protein design*. QMB E3: Enzyme Engineering and Evolution. Queenstown, New Zealand.
- B.T. Porebski, **L. Zhu**, D.E. Hoke, W. Dai, S. Keleher, N.A. Borg, S.P. Bottomley, G.I. Webb, A.M. Buckle. (2013). *A structural, biophysical and computational investigation of two sequence-based protein engineering methods*. Poster session presented at: The 38th Lorne Conference on Protein Structure and Function. Lorne, Victoria.
- F. Zheng, G.I. Webb, P. Suraweera, and **L. Zhu**. (2012). *Subsumption Resolution: An Efficient and Effective Technique for Semi-Naive Bayesian Learning*. Machine Learning 87(1): 93-125. Springer Netherlands.