

EXPERIENCE *(All at Stanford University)*

- 10/2014 – present* **Web Design and Development** (Project Leader, Designer, and Developer)
RNA Mapping Database (<http://rmdb.stanford.edu>):
- Redesigned server front-end completely with interactivity, data visualization and prediction services, which aided data sharing for a 30,000-user community with 100,000+ data points
 - Created cross-platform interface for EteRNA cloud lab, user dashboard and login system
 - Fixed bugs of previous code, optimized performance, improved database management
- Primer Design Server** (<http://primerize.stanford.edu>):
- Implemented server back-end from scratch: MATLAB process, CherryPy framework, and query management, which enables quantitative refinement and speeds up design by 10x
 - Designed server front-end user interface and detailed tutorial page
 - Administered domain hosting and routine maintenance
- 09/2014 – present* **Translational Bioinformatics and Computational Biology** (Coursework)
- Performed genome-wide association study (GWAS) on microarray datasets for Parkinson's disease searching for significant SNP hits and GO term enrichment using R
 - Mined clinical records for integrative drug-lab measurement relations using R and MySQL
 - Implemented sequence alignment algorithm with affine gaps using dynamic programming, K-means clustering and KNN classification for machine learning of leukemia patient data
 - Implemented molecular dynamic (MD) simulation of protein folding dynamic in Python
 - Built chemoinformatics network of ligand similarity and drug feature of diabetes targets.
- 01/2013 – 01/2015* **Software Development for Academic Application** (Graduate Student Research)
- Programmed massive parallel synthesis code and high-throughput data processing pipeline, which semi-automate high-dimensionality data for quantitative analysis
 - Developed graphical output codes in MATLAB, which are in daily use by entire lab
 - Built interface with other RNA modeling software, automated RNA diagram coloring
 - Simplified code structure, debugged and administered public RNA analysis server
 - Curated and organized lab MATLAB repositories and documented packages
 - Automated fluorescence intensity quantitation, image manipulation, spindle selector, tip-tracking visualizer in MATLAB, which improved productivity by 10x
- 02/2012 – present* **RNA Biochemistry and Structure** (Graduate Student Research)
- Established quantitative method for data normalization, which is adopted as standard in field
 - Developed robust structural validation using systematic mutagenesis and multi-dimensional high-throughput RNA mapping technique with next-generation sequencing (NGS)
 - Validated structure of first RNA element for flu virus packaging, and successfully attenuated virulence

SKILLS

- **Programming and design:** fluent in MATLAB, R, Python, MySQL, JavaScript, C++, HTML5, CSS3, and LaTeX; familiar with Java, Git, and Linux shell.
- **Communication:** efficient in writing, documentation, and time management; extremely detail-oriented.
- **Attitude:** self-motivated, self-disciplined, independent and hardworking. Fast and enthusiastic learner.

EDUCATION

- 09/2011 – present* **Stanford University, Ph.D in Biochemistry** (expected 2016) *Stanford, CA*
- *09/2011 – 08/2014* Stanford Graduate Fellow
- 09/2007 – 07/2011* **China Agricultural University, B.S in Molecular Biology** *Beijing, China*
- *11/2010* Chancellor Scholarship, National Scholarship for *summa cum laude*
 - *12/2009* “Triple Excellent” Student of University, Scholarship for *magna cum laude*