XINRAN LI

xinranli.github.io ⋄ (412) · 932 · 6740 ⋄ xinranli@cmu.edu

OBJECTIVE: To obtain a full-time position in bioinformatics or computational biology

EDUCATION

Carnegie Mellon University (CMU) *Pittsburgh, PA*
M.S. in Computational Biology *Aug 2014 – Dec 2015(expected)*
Honor: Merit Fellowship (Tuition Scholarship) from Department of Biological Sciences
Selected Courses: *Applied Cell and Molecular Biology, Java For Application Programmer, Data Structure for Application Programming, Machine Learning, Bioimage Informatics, Programming for Scientists, Network Science*

Sun Yat-sen University (SYSU) *Guangzhou, China*
B.S. in Biological Science *Sep 2010 – June 2014, China*
Honor: Best software tool project and gold award in 2013 iGEM (International Genetic Engineering Machine) world competition held in MIT, Boston (SYSU-Software team member) *Nov, 2013, MIT*
Selected Courses: *Bioinformatics, Biostatistics, Genetics, Microbiology, Physiology, Oncology, Biochemistry, Organic Chemistry, Inorganic Chemistry, Ecology.*

TECHNICAL SKILLS

Bioinformatics Techniques	Sequence alignment, Bioimage processing, Biological data mining
Programming Languages	Python, Java, Go, Perl, R, HTML, CSS, JavaScript, Matlab
Experimental Skills	IHC, PCR, ELISA, gene cloning, DNA extraction, DNA ligation, Bacterial culture, western blot, Electrophoresis, Cell culture, Cell transformation
Operating Systems	Windows, Linux/Unix, Mac

WORK EXPERIENCE

Philips Research *May 2015 – Aug 2015*
Research Intern of Clinical Informatics Solutions and Services(CISS) *Briarcliff Manor, NY*

· Developed a program in Python to predict antibiotic resistant genes by mapping SNPs to corresponding genes in *Enterococcus faecalis* chromosome and classify potential mutations into synonymous and non-synonymous.

· Implemented statistical method to estimate correlation between putative antibiotic resistant genes to clinical profiles based on P-values of Chi-Square test using R.

SELECTED PROJECTS

Bioimage Processing *Oct, 2014 - May 2015, CMU*

· Used Matlab to perform noise filtering, feature detection, image segmentation and simulation of microphotographs.

Networks visualization of snc RNA and RNA-Binding Protein interaction *Oct, 2014, CMU*

· Applied R to visualize small-noncoding RNA and RNA-Binding proteins interactions network.

Analysis of CRISPR/Cas9-induced DNA Sequences Differences *Mar, 2014 - Jun, 2014, SYSU*

· Developed a program in Perl to analyze CRISPR/Cas9 edited DNA sequence of *CD274* gene and *B2M* gene in two different human cell lines and estimated CRISPR/Cas9 gene-editing efficiency.

Computer Aided Synbio Tool for Synthetic Biology (Team project) *Mar, 2013 - Nov 2013, SYSU*

· Developed a software which enables regulatory networks simulation, gene circuits design, modeling, vector design to address specific technical challenges in synthetic biology by mathematical modeling.

· Designed icons, software UI, website graphic interfaces and illustrative postboard.