HOLLY (XINRAN) LI

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

OBJECTIVE: To obtain a full-time position in bioinformatics or computational biology (data analysis)

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: *Computational Molecular Biology and Genomics, Computational Methods for Biological Modeling and Simulation, 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, Zoology, Molecular Biology, Cell Biology, Modern Biotechnology.*

TECHNICAL SKILLS

Bioinformatics Techniques	Sequence alignment, Bioimage processing, Biological data mining
Programming Languages	Python, C, Java, Go, SQL, Perl, R, HTML, CSS, JavaScript, Matlab
Experimental Skills	IHC, PCR, ELISA, gene cloning, DNA/RNA/protein extraction/ligation, Bacterial culture, western blot, Electrophoresis, Cell culture/transformation

WORK EXPERIENCE

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

· Developed a Python program 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

Process a large-scale dataset using MapReduce   *Sep 2015, CMU*

· Use Elastic MapReduce and Hadoop to analyze hourly page view statistics from Wikipedia and filter out the most popular entries on the cloud

Machine Learning Tools   *Jan, 2015 - May, 2015, CMU*

· Implement decision trees, neural network, naive Bayes classifier, HMMs in Python to classifier data.

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

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

· 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.