

# HOLLY (XINRAN) LI

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

## EDUCATION

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### Carnegie Mellon University (CMU)

Pittsburgh, PA

M.S. in Computational Biology

Aug 2014 – May 2016 (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, Neurology, Microbiology, Physiology, Oncology, Biochemistry, Organic/Inorganic Chemistry, Ecology, Zoology, Molecular Biology, Cell Biology, Modern Biotechnology.*

## TECHNICAL SKILLS

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### 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, flow cytometry, gene cloning, biomolecule extraction, Bacterial culture, western blot, Electrophoresis, Cell culture/transformation

## WORK EXPERIENCE

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### 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

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### Biological Modeling and Simulation

Jan, 2015 - May, 2015, CMU

- Implemented several mathematical modeling algorithms in Python to simulate biological problems.

### 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.

### 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