HOLLY LI

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

Education

Carnegie Mellon University Pittsburgh, PA

M.S. Computational Biology

AUG 2014
MAY 2016
(EXPECTE)

Honor Department Merit Fellowship (Tuition Scholarship)

Selected Courses Computational Molecular Biology and Genomics |Computational Methods for Biological Modeling and Simulation | Applied Cell and Molecular Biology | Machine Learning | Bioimage Informatics |Programming for Scientists | Java for Application Programmer

Sun Yat-sen University Guangzhou, China

B.S. Biological Science

SEP 2010
JUN 2014

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)

Selected Courses Higher Mathematics | Bioinformatics | Biostatistics | Genetics, Neurology | Microbiology | Physiology | Oncology | Biochemistry | Organic/Inorganic Chemistry | Ecology| Zoology |Molecular Biology |Cell Biology | Modern Biotechnology.

Skills

Programming

Python
Java
Perl
SQL
Go
R
HTML
PHP
CSS
C#
C
JavaScript
MATLAB
Shell

Lab Skills

IHC
PCR
ELISA
Flow cytometry
Gene cloning
Bacterial culture
Western blot
Electrophoresis
Cell culture
Plasmid Extraction

Work Experience

Philips Research Briarcliff Manor, NY

Research Intern of Clinical Informatics Solutions and Services(CISS)

MAY 2015
AUG 2015

Analyzing clinical high-throughput NGS data using Python script to identify putative genetic mutations that might cause non-conservative change in biological function and are responsible for antibiotic resistance in bacterial pathogens (*Enterococcus faecalis)* genome.

Validated the results by statistical methods using R.

Selected Project

Biological Problem Modeling and Simulation

Simulated different biological problems using different mathematical models and algorithms. Such as simulation of neuron spiking based on refined HC-LIF models, molecule dynamics simulations based on Markov models, infectious decrease epidemic simulation based on SIR model, etc.

Biological/Clinical data mining and processing

Processed bioimage data by noise filtering, feature detection, object segmentation and simulation of microphotographs using computational methods and visualized biological interactions network between small non-coding RNA(snc-RNA) and RNA-binding proteins using MATLAB and R.

Analysis of CRISPR/Cas9 Gene Edit Efficiency

Designed algorithm and wrote Perl script to analyze CRISPR/Cas9 edited DNA sequence of *CD274* gene and *B2M* gene in different human cell lines and estimated CRISPR/Cas9 gene-editing efficiency by alignment between NGS samples and reference genome.

Generalized Data Mining Platform

Implemented both front-end and back-end machine learning algorithms such as Random Forest, Neural Network, Hidden Markov Model of a web based data mining platform.