

Peijue Zhang

602A, Graduate Living Center,
Georgia Institute of Technology,
Atlanta, GA, 30318,
The United State
404-998-0806
pzhang1992@gatech.edu

EDUCATION:

Georgia Institute of Technology, Atlanta, US September 2015-Present
Bioinformatics Program
GPA(Fall 2015) : 4.0/4.0

Sun Yat-Sen University, Guangzhou, China September 2011-July 2015
Bachelor of Science in Biotechnology
GPA : 3.8/4.00

Shenzhen Experimental School, Shenzhen, China September 2008-June 2011

RELEVANT COURSEWORK:

Programming for Bioinformatics; CS for Bioinformatics; Genomics and Applied Bioinformatics;
Organic Chemistry; Biochemistry; Biostatistics; Histology and Embryology; Cell Biology;
Genetics; Biotechnics; Bioinformatics

Course in Spring 2016: Computational Genomics; Biostatistics; Introduction to Database Systems

Skills:

Computer language : Perl, Shell, MySQL
Software : Matlab, WinBUGs/OpenBUGs, Mathematica
Working Environment : Linux, Windows, Mac OS

RESEARCH PROJECTS AND REPORTS:

Spring 2016 Course report
“Genome Assembly of 36 *Haemophilus influenzae*”: using multiple tools to assemble 36 raw
sequencing data of *Haemophilus influenzae* from CDC;
Link: http://compngenomics2016.biology.gatech.edu/index.php/Genome_Assembly_Group

Spring 2016 Advisor : Eva K. Lee, Georgia Institute of Technology
“Network of antibiotics interaction and auto-prescribing for multi-disease patient”: building
network of drug-drug interaction and drug-disease relationship to automatically generate
prescription for multi-disease patient;

September 2015 - Present Advisor : Eva K. Lee, Georgia Institute of Technology
“Environmental risk evaluation of antibiotics in sewage”: building multiple models to predict the environmental concentration of target antibiotics(main target drugs: Ciprofloxacin and Doxycycline) and evaluate their potential of causing environmental hazard;

Fall 2015 Course report
“In silico prediction of clinical pathogenicity by CADD scoring of exome variants found in genome of a Male belonging to the Chinese Dai Minority”: finding the SNPs in one human genome and using annotation tools to select unusual significant SNPs then conducting pathogenicity evaluation;
Link: <https://gtbinf.wordpress.com/2015/12/07/in-silico-prediction-of-clinical-pathogenicity-by-cadd-scoring-of-exome-variants-found-in-genome-of-a-male-belonging-to-the-chinese-dai-minority/>

Fall 2015 Course report
“Differential Gene Expression Analysis of Influenza A virus strains”: finding the differentially expressed genes in the tissues infected by different strains of Influenza A viruses and identifying the pathways in the tissues that are significantly changed;
Link: <https://gtbinf.wordpress.com/2015/11/02/differential-gene-expression-analysis-of-influenza-a-virus-strains/>

Fall 2014 Course report
“An analysis of the trend of adamantane resistance among H1N1 influenza virus isolated from China between 1956 and 2011”: did statistical analyses on one or multiple amino acid substitutions at positions 26, 27, 30, 31 or 34 in the transmembrane domain of the M2 protein of H1N1 influenza virus, finally obtained the drug resistance trend of H1N1 in recent decades in China;

2013 - 2015 Advisor : Jianzhong Liu, Sun Yat-Sen University
Producing lysine with engineering *corynebacterium glutamicum*: induce the engineering bacteria to produce lysine by manipulating some key genes in metabolic pathway of *corynebacterium glutamicum*;

Fall 2012 Course report
“The confidence level of Chinese consumers toward GM food”: after digging into several survey researches investigating the confidence of Chinese people in GM food, and doing statistical analyses, found out the confidence level of Chinese consumers toward GM food and the differences among Northern, Central and Southern China;

2012 - 2014 Advisor : Wensheng Shu, Sun Yat-Sen University
Experimenting with microbial fuel cell (MFC) to process acid mine drainage (AMD): build a MFC system with sulfate reducing bacteria and iron-oxidizing bacteria to precipitate metal ions and generate power at the same time;