

# Zhou Xin

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## Education

*Bachelor of Biological Science*, School of Life Science, USTC, 2007-2011, GPA=3.21/4.3  
*Academic Master of Bioinformatics*, School of Life Science, USTC, 2011-2013, GPA=3.5/4.3

Thesis: *From local to global: a new perspective of Hepatitis B virus Genotyping framework* . 2013

## Research interests

Biology • Systems Biology, Genomics, Computational Biology, Bioinformatics

## Honors and awards

First Prize (rank 4th), 2006 National High School Mathematics League, Yunnan Division 2006  
Gold medal: The 2010 International Genetically Engineered Machine (iGEM) Foundation 2010  
CUDA Application Engineer 2012

## Publications

- (1) Zhao Lin, Zhou Xin et al. Integrating the environmental factor into the strategy updating rule to promote cooperation in evolutionary games Chinese Phys. B 2011 (2nd author)
- (2) Wang, Yu-Wei, Zhi Liang, Xin Zhou et al. High prevalence of mixed HBV infection contributes to genotype shift during antiviral therapy [under review] (8th author)

## Research Experiences

Title: *From local to global: a new perspective of Hepatitis B virus Genotyping framework*

School: *School of Life Science of USTC*

Year: 2011-2013

Description:

38 chronic hepatitis B virus(CHB) patients of 200 CHB patients were investigated genotype shift during adefovir dipivoxil(ADV)'s antiviral therapy. At the same time, we have detected that these patients' ADV antiviral efficiency decreased as well as their CHB virus' genotype has shifted from C-type dominating to B-type dominating, which is less sensitive to ADV via HBV's genome analysis, and this analysis was completed by next generation sequencing technology (454 pyro-sequencing and Solexa respectively).

In this project, I was devoting to: 1, constructing a framework of HBV genotyping based on sequence segments of proper length rather than traditional whole genome sequencing (such as K-mer), in my new framework, I applied independent component analysis (ICA) as a tool to extract each IC of the HBV's whole gene and simplified the sequencing content; 2, establishing a pipeline to eliminate the sequencing noise introduced by 2nd sequencing technique; 3, finding out the correlation-ship between CHB virus' genotype shift and immune and drug pressure.

Based on the genome variance of different HBV's subtype and their sensitivity to ADV's treatment and 2nd generation sequencing technology's ultra high resolution of DNA density, I have provided a rational explanation for genotype-shift and their decrease of antiviral efficiency, as well as built up a framework of virus genotype for personal medical treatment in the future.

Title: *small-RNA's role in gene's negative feedback transcriptional regulation*

School: *School of Life Science of USTC*

Year: *2011-2012*

Description:

Inspired by lacI and RyhB-Fe's regulation pattern, we constructed two different negative feedback circuits mediated by protein (transcript factor) and small RNA.

We constructed the reaction principles via these regulation patterns and compared the duration of signal's consuming in different systems. We set the moment when signal was input as the start point and calculate the relationship between signal's concentration and the time that the reaction has been on. At  $t = 0$ , the signal was input and the concentration of signal comes to  $S(mM)$ , and just because of the signal's input, it will activate a series of reactions and finally the signal will be decomposed clearly. Further, based on the logical model we re-wrote them to a set of ODE and calculated the speed of processing based on the law of mass action and Michaelis-Menten equation. We collected reaction parameters from many database such as *BRENDA* database and solved these ODEs via matlab. We found that the response time of signal in different regulation system is different. If we treat the system's response speed as an optimization of a biological system (especially in stress-response system), when the outside signal intensity baseline is lower than a certain threshold, the system with TF is better, otherwise, the system regulated by small RNA is better.

## Supervisors of master career

1st Supervisor Wu Jiarui [wujr@sibs.ac.cn](mailto:wujr@sibs.ac.cn) Professor

2nd Supervisor Liang Zhi [liangzhi@ustc.edu.cn](mailto:liangzhi@ustc.edu.cn) Assistant Professor

## Language

iBT=81: Reading=25, Listening=13, Speaking=18, Writing=25

2013

GRE=311+3: V=147, Q=164, AW=3

2012

## Skills

- Python, Perl, R and CUDA
- Basic molecular biology techniques
- Machine learning techniques

Last updated By ZHOU XIN: January 9, 2014 •