Songpeng Zu

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EDUCATION

2011.09–present **PhD Candidate**, *Bioinformatics Laboratory*, Tsinghua University.
Graduate Major GPA: 90.84/100

- Applied Stochastic Processes
- Basic Functional Analysis
- Statistic Inference
- Probabilistic Graph
- Pattern Recognition
- Design of Bioinformatics Algorithms

2007.09–2011.07 **Bachelor**, *School of Life Science*, Tsinghua University.
Undergraduate Major GPA: 86.32/100

- Linear Algebra and Analytic Geometry
- Advanced Calculus
- Biostatistics
- Biochemistry
- Cell Biology
- Genetics
- General Physics (required for Physics major)
- Organic Chemistry (required for Chemistry major)

RESEARCH INTERESTS

- Statistical learning theory and application
- Computational Chemistry
- Network Polypharmacology

RESEARCH EXPERIENCE

2013.03–present Prediction of drug-protein interactions by integrating large-scale ligand-protein interactions with genomic information

2013.07 Identification of HIV-1 subtypes and drug resistance by genomic data analysis

2011.12–2013.01 Inference of the interactions between drug chemical substructures and protein domains from incomplete data by EM algorithm

2010.12–2011.06 Molecular dynamics simulations of compound-protein interactions

WORK EXPERIENCE

2013.09–present TA of Probabilistic Graphical Models

2011.08–2012.12 Undergraduate Affair Counselor(for scholarship and financial aid assessment)

2008.09 Internship in Novozymes China Investment Company

2008.08 2008 Beijing Olympic Games volunteer

AWORD

2013 Tsinghua Scholarship for Overseas Graduate Studies

2012 Tsinghua Excellent Undergraduate Affair Counseior

2010 Tsinghua Zhongying Tang Scholarship

OTHER INFORMATION

Softwares Matlab, R, Perl, and C/C++

Hobbies Football and the international ballroom dance

PAPER UNPUBLISHED

SUDO: Globally Inferring the Interactions between Drug Chemical Substructures and Protein domains from Incomplete Drug Target Interactions Data

Songpeng Zu*, Ting Chen and Shao Li.

In this work, we constructed a probalisitic model and estimated the parameters by EM algorithm to decipher the possible mechanisms that govern drug-protein interactions from incomplete data.