



您现在的位置: 首页>师资队伍>副教授

师资队伍

院士

陈国良 院士 李国杰 院士

大师讲席

姚新 邵中 乔春明

教授

安虹 陈恩红 陈华平 陈小平
陈意云 冯新宇 顾乃杰 华蓓
黄刘生 蒋凡 李京 唐珂
王煦法 熊焰 许胤龙 杨寿保
岳丽华 赵保华 周学海

副教授

陈凯明 董兰芳 郭宇 韩文廷
何克东 黄章进 黄巍 吉建民
金培权 李金龙 李曦 刘贵全
芦建平 罗文坚 苗付友 邵晨曦
孙广中 **Thomas Weise** 田野 王上飞
王行甫 吴俊敏 邢凯 徐林莉
徐云 曾凡平 张信明 张昱
郑浩然 郑启龙

讲师

----讲师(含支撑岗位人员)名单----

博士后

-----博士后-----

学术活动

更多>>

- 北京林宙辰教授访问我院并做学术报告
题目: A Geometric Method for Optimal Design of Color Filter Arrays
时间: 11月20日下午3点

郑浩然

电话: (0551)63600432
E-Mail: hrzheng@ustc.edu.cn



主要研究方向:

智能计算及应用、机器学习与数据挖掘技术、计算机建模与仿真、生物信息学

郑浩然, 男, 1967年生, 博士, 副教授。1989年于西安交通大学自动控制专业获学士学位; 1992年于西安交通大学获模式识别与智能控制专业获硕士学位; 2000年于中国科学技术大学获信号与信息处理专业获博士学位, 2000年7月至2002年7月在中国科学技术大学计算机科学技术系人工智能中心做博士后研究, 出站后留校工作。主持和作为主要成员参加了国家自然科学基金项目两项, 国家973子课题两项、科学院知识创新工程子课题三项, 结合项目在国际知名学术刊物及国内外重要学术会议发表学术论文40多篇, 获国家发明专利一项。

获奖情况

- 2004年获王宽诚育才奖(二等奖);
- 2008年度安徽省优秀硕士学位论文奖(导师);
- 2010年获惠普信息科学青年教师奖。

主要论著

[01] Zhi Liang,* Hong Zhou, Zongxiao He, Haoran Zheng,* and Jiarui Wu,* , mirAct: a web tool for evaluating microRNA activity based on gene expression data, Nucleic Acids Research, 2011, Vol. 39, Web Server issue p.139 - 144 (通讯作者)

[02] Deguo Xia*,Haoran Zheng*, Zhiqiang Liu, Guisheng Li, Kai Zhao ,Lin Yang, MRSD: a web server for Metabolic Route Search and Design, Bioinformatics, Vol. 27 no. 11 2011, pages 1581 - 1582 (共同第一作者、通讯作者)

[03] Zhi Liang,* Hong Zhou, Zongxiao He1, Haoran Zheng,* and Jiarui Wu,* Expression levels of microRNAs are not associated with their regulatory activities, Biology Direct, 2011, 6:43 (通讯作者)

[04] Bin Rui, Tie Shen, Hong Zhou, Jianping Liu, Jiusheng Chen, Xiaosong Pan, Hanyan Liu, Jihui Wu, Haoran Zheng*, Yunyu Shi*, A systematic investigation of Escherichia coli central carbon metabolism in response to superoxide stress, BMC Systems Biology 2010, 4:122 (通讯作者)

[05] Jiusheng Chen, Haoran Zheng*, Haiyan Liu, Junqing Niu, Jianping Liu, Tie Shen, BinRui,Yunyu Shi, Improving metabolic flux estimation via evolutionary optimization for convex solution space ,Bioinformatics,2007, Vol.23No.9,p1115-1123 (通讯作者)

[06] Wen-bo Du ,Hao-ran Zheng*,Map-bin Hu , Evolutionary prisoner's dilemma game on weighted scale-free networks, Physica A 387 (2008) 3796-3800 (通讯作者)

[07] W. B. Du, X. B. Cao, H. R. Zheng* and H. Zhou, Evolutionary Games in Multi-agent Systems of Weighted Social Networks,International Journal of Modern Physics C, 20 (2009), pp. 701-710. (通讯作者)

[08] Zhiqiang Liu; Haoran Zheng*Deguo Xia; Guisheng Li; MetageGMRC: a web server for genome-scale metabolic reconstruction and comparison of metagenomes, The IEEE Fifth InternationalConference on Bio-Inspired Computing: Theories and Applications (BIC-TA 2010), p. 1155 - 1158.

[09] Deguo Xia; Haoran Zheng; Zhiqiang Liu; Guisheng Li; Kai Zhao; BCP-MG: A web server for predicting bacterial community of metagenome, The IEEE Fifth InternationalConference on Bio-Inspired Computing: Theories and Applications (BIC-TA 2010), p. 1138 - 1142.

[10] Qiwen Yu, Haoran Zheng. An Efficient Gene-Enzyme Identification Method in the Reconstruction of Metabolic Networks: Hybrid Participle Algorithm. The 1st International Conference on Information Science and Engineering. Nanjing, 2009:3587-3591.

[11] H.R. Zheng, H. Zhou, T. Shen and B. Rui, Flux Balance Analysis Within Physiologically Feasible Region, ICBBE 2009. 3rd International Conference on Bioinformatics and Biomedical Engineering.

地点：计算机学院6楼学术报告厅

- 美国伊利诺理工大学李向阳教授访问我院并做学术报告

题目：Large Scale Wireless Networking Systems: Theory, Experiences, and Lessons

时间：10月30日下午2:30

地点：计算机学院6楼学术报告厅

- 香港中文大学于旭教授访问我院并做学术报告

题目：Large Graph Query and Mining

时间：10月13日下午3点

地点：计算机学院6楼学术报告厅

- [12] J.-Q. Niu, K. Zhang and H. Zheng, An Agent-Based Modeling Approach at Molecular Scale for Biochemical Networks: Simulating from Stochastic Molecular Events, ICBBE 2009. 3rd International Conference on Bioinformatics and Biomedical Engineering.
- [13] K. Zhang, H. Zheng, X.-F. Yang, S.-Y. Han, H.-C. Hou, T.-C. Leng and N. Ding, Predicting Co-Complexed Protein Pairs Based on Communication Model Using Diverse Biological Data, Bioinformatics and Biomedical Engineering, ICBBE 2009. 3rd International Conference on Bioinformatics and Biomedical Engineering
- [14] Yang Xiao-fei, Zheng Hao-ran, Zhang Kuan, Han Si-yuan. "Integrating Genomic Data and Topological Metrics to Obtain Reliable Protein-Protein Interactions", The 6th International Conference on Fuzzy Systems and Knowledge Discovery (FSKD'09)
- [15] Tie Shen, Weiqun Shen, Ying Xiong, Haiyan Liu, Haoran Zheng, Hong Zhou, Bin Rui, Jianping Liu, Jihui Wu and Yunyu Shi, Increasing the accuracy of mass isotopomer analysis through calibration curves constructed using biologically synthesized compounds, Journal of Mass Spectrometry, 44 (2009), pp. 1066-1080.
- [16] Niu, Junqing; Zheng Haoran; Chen Jiusheng, et al. A Distributed-Based Stochastic Simulation Algorithm for Large Biochemical Reaction Networks. The 1st IEEE International Conference on Bioinformatics and Biomedical Engineering. Wuhan 2007:502-505.



中国科学技术大学
University of Science and Technology of China

CopyRight 2003-2011 中国科学技术大学计算机科学与技术学院 All Rights Reserved.

安徽省合肥市黄山路中国科学技术大学西区电三楼

通信地址：安徽省合肥市4号信箱 计算机科学与技术学院 邮政编码：230027