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廖波

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教师介绍



廖波

教授, 博士生导师, 教育部新世纪优秀人才。主要从事智能与生物信息处理、数据挖掘与机器学习、大数据技术等研究。承担国家级项目5项, 省部重点或一般项目8项, 参与国家级或省部级I 获得Scopus信息科学青年科学之星, 湖南省自然科学二等奖, 辽宁省自然科学三等奖, 湖南省秀学术论文一等奖。指导学生获得湖南省优秀学位论文5篇。获得湖南大学天语教师奖、科研标兵称号。目前已在国际SCI杂志上发表学术论文100余篇, SCI累计引用他引1200多次。h指数为

中文名：

廖波

学历：

英文名：

职称：

所属机构：[省研究生培养创新基地](#) [信息工程系](#) [学院领导](#)

学习与工作经历

学习经历：

1999.09-2001.07大连理工大学 计算数学

2001.09-2004.06大连理工大学 计算数学

2004.06-2006.05 中国科学院研究生院 生物信息处理

工作经历：

2004.06-2006.05 中国科学院研究生院博士后。

2005年来湖南大学工作至今。

研究领域

1. 大数据技术
2. 数据挖掘与机器学习
3. 图像处理
4. 智能与生物信息处理

主讲课程



博士学位课程 “计算机科学中的数学方法”

留学博士学位课程 “Mathematical methods on computer science”

研究生学位课程 “模糊数学原理及应用”、“组合数学”、“生物信息学基础”和“生物信息处理”

留学生学位课程 “High Scientific Computing”

研究生选修课程 “计算分子生物学”

本科生必修课程 “离散数学”、“大学信息技术基础”

本科生选修课程 “生物信息学中的计算机技术”

学术兼职

Nature 杂志顾问团专家成员,国际SCI杂志MATCH Communications in Mathematical and in Computer Chemistry,Current Computer-Aided Drug Design和International Journal of Data Mining and Bioinformatics的编委,国际杂志的编委:International Journal of Analyzing Methods of Components and Combinatorial Biology in Mathematics ; Biostatistics, Bioinformatics and Biomathematics ; International Journal of Engineering and Industries ; Journal of Next Generation Information Technology,Bioinformatics和IEEE-ACM Transactions on Computational Biology and Bioinformatics等20余家国际SCI杂志审稿人,计算机学报和计算机研究与发展等权威期刊的审稿人。教育部高等学校科学研究优秀成果奖评审专家,国家自然科学基金和霍英东奖励基金评审专家。

科研状况

近五年主持的主要科研项目：

- [1] 国家自然科学基金面上项目（61672214）：面向生物大数据分析的正则化方法及应用研究,2017.1-2020.12
- [2] 国家自然科学基金面上项目（61370171）：大规模SNP数据挖掘及其在复杂疾病分析中的应用研究,2013.9-2017.12
- [3] 国家自然科学基金面上项目（60973082）：蛋白质组信息分析及应用算法研究，2010.1-2012.12
- [4] 国家自然科学基金面上项目(11171369):肿瘤基因表达谱数据分析及应用算法研究，2012.1-2015.12
- [5] 新世纪优秀人才项目（NCET-10-0365）:肿瘤基因表达谱数据分析模型及应用算法研究, 2011.1-2013.12
- [6] 湖南省科技计划重点项目（2012FJ2012）：肿瘤数字基因表达谱数据挖掘方法及其致病机理研究, 2012-2015
- [7] 国家自然科学基金面上项目(10571019):数学方法在计算分子生物学中的应用, 2006.1-2008.12
- [8] 湖南省科技计划(2009FJ3195)项目:生物信息学方法在肿瘤蛋白质组学研究中的应用，2009.1-2011.12
- [9]湖南省自然科学基金面上项目（07JJ5080):一种特征基因提取算法及其在血吸虫基因组分析中的应用，2007.1-2009.12

获奖情况:

- [1] 09年获得湖南省自然科学奖二等奖一项，排名第一
- [2] 09年获得Scopus信息科学青年科学之星，全国10人获奖,其中有杰青和千人等。
- [3] 2010年入选教育部新世纪优秀人才计划
- [4] 2012年获得辽宁省自然科学三等奖, 排名第二
- [5] 2010年获得湖南省自然科学优秀论文一等奖一项，排名第一
- [6] 2007年获湖南大学天语奖
- [7] 2011年获湖南大学优秀教师和科研标兵称号
- [8] 2011,2013 湖南省优秀硕士学位论文指导教师

近三年代表作

- 1、 Bo Liao, Benyou Liao, Xingming Sun, Qingguang Zeng, A Novel method for similarity analysis and protein subcellular localization prediction, *Bioinformatics*,2010,26(21):2678-2683
- 2、 Bo Liao, Xiong Li, Wen Zhu, Zhi Cao, A Novel Method to Select Informative SNPs and Their Application in Genetic Association Studies, *IEEE/ACM TRANSACTIONS ON Computational Biology and Bioinformatics* , 2012,9(5):1529-1534
- 3、 Bo Liao, Xiong Li, Lijun Cai, Zhi Cao,Wen Zhu, Informative SNPs selection based on two-locus and multilocus linkage disequilibrium: Criteria of Max-Correlation and Min-Redundancy, *IEEE/ACM TRANSACTIONS ON Computational Biology and Bioinformatics*,2013,10(3):688-695
- 4、 Bo Liao, Yun Li, Yan Jiang, et al, Using Multi-Instance Hierarchical Clustering Learning System to Predict Yeast Gene Function, *Plos One*,2014,9(3): e90962
- 5、 Bo Liao,Yan Jiang,Wei Liang,Wen Zhu,Lijun Cai,Zhi Cao , Gene selection using locality sensitive Laplacian score , *IEEE/ACM TRANSACTIONS ON Computational Biology and Bioinformatics*,2014,11(6):1146-1156
- 6、 Liao B, Jiang Y, Yuan G, Zhu W, Cai L, et al. Learning a Weighted Meta-Sample Based Parameter Free Sparse Representation Classification for Microarray Data. *PLoS ONE* , 2014 , 9(8): e104314
- 7、 Bo Liao , Xiong Li, et al. A hierarchy clustering method of selecting kernel SNPs to unify informative SNPs and tag SNPs , *IEEE/ACM TRANSACTIONS ON Computational Biology and Bioinformatics*,2015,12(1):113-122
- 8、 Bo Liao ,Yan Jiang, et al. On efficient feature ranking methods for High-throughput data analysis *IEEE/ACM TRANSACTIONS ON Computational Biology and Bioinformatics*,2015 , 12 (6) : 1374-1384.
- 9、 Ying Liang,Kunlong Qiu,Bo Liao*,Wen Zhu,Xuanlin Huang,Lin Li,Xiangtao Chen , Keqin Li , seeksv: an accurate tool for somatic structural variation and virus integration detection , *Bioinformatics* , 2016 , doi:10.1093/bioinformatics/btw591
- 10、 Changlong Gu, Bo Liao*, Xiaoying Li , Keqin Li , Network Consistency Projection for Human miRNA-Disease Associations Inference , *Scientific Reports* 6:36054.
- 11、 Wei Liu, Wen Zhu, Bo Liao*, Xiangtao Chen , Gene Regulatory Network Inferences Using a Maximum-Relevance and Maximum-Significance Strategy , *PLoS ONE* , 2016 , 11(11): e0166115.
- 12、 Min Chen, Xingguo Lu, Bo Liao*, Zejun Li, Lijun Cai, Changlong Gu , Uncover miRNA-Disease Association by Exploiting Global Network Similarity , *PLoS ONE* , 2016 , 11(12): e0166509.
- 13、 Quang-Huy Duonga,Bo Liao,Philippe Fournier-Vigerc,Thu-Lan Dama , An efficient algorithm for mining the top-k high utility itemsets, using novel threshold raising and pruning strategies , *Knowledge-Based Systems* , 2016 , 104 , 106-122.
- 14、 Lihong Peng , Bo Liao* , Wen Zhu , Yan Jiang , Wei Liang , Keqin Li,Predicting Drug-Target Interactions with Multi-Information Fusion , *IEEE Journal of Biomedical and Health Informatics*, 2016 , DOI 10.1109/JBHI.2015.2513200.

学术论文

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2. Chunxin Yuan, Bo Liao, Tianming Wang, New 3D graphical representation of DNA sequences and their numerical characterization, *Chemical Physic Letters*, 2003, 379:412-417.
3. Bo Liao, Tianming Wang, Analysis of similarity of DNA sequences based on 3D graphical representation, *Chemical physics letters*, 2004, 388:195-200.
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8. Bo Liao, Tianming Wang, Analysis of similarity of DNA sequences based on non-overlapping triplets of nucleotide bases, *Journal of Chemical Information and Computer Science*, 2004, 44:1666-1670.
9. Bo Liao, Tianming Wang, Kequan Ding, On A Six-Dimensional Representation of RNA Secondary Structures, *Journal of Biomolecular Structure Dynamics*, 2004, 22:455-464.
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11. Bo Liao, Mingshu Tan, Kequan Ding, A 4D representation of DNA sequences and its application, *Chemical Physic Letters*, 2005, 402:380-383.
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88. Liao Zhong Li, Liao Bo, Qingguang Zeng, Xing Li, A Novel Two-Stage Approach for Epistasis Detection in Genome Wide Case Control Studies, *Biochemical Genetics*, 2014, 52(9-10) :403-414
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