**个人简历**

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**个人简介：**

李晋，39岁，博士，长期从事生物信息学的教学与科研工作。本人具有统计学、信息学、计算机、药学和遗传学等学术背景。目前主要研究方向为药物基因组学和药物信息学（Pharmacogenomics and Pharmacoinformatics）和癌症系统生物学(Cancer Systems Biology)，特别是药物-药物组合预测（Drug-drug combination prediction）、癌症风险通路挖掘(Cancer risk pathway mining)、表达数量性状挖掘(Expression QTL)、基因-基因互作(Gene-Gene Interaction)等。主持在研国家自然科学基金地区项目一项，海南省自然科学基金一项，完成国家自然科学基金青年项目一项，黑龙江省自然科学基金一项，黑龙江省教育厅、卫生厅各一项。在Science translational medicine、European journal of human genetics、Frontiers in Genetics、genes、Scientific reports、Bioinformatics等杂志发表SCI收录学术论文35篇，被引用900余次，其中第一作者10篇。长期承担概率论与数理统计、生物统计学、多元统计分析、统计遗传学等多门课程的教学工作。

**工作经历**

2020.11-至今 海南医学院 教授、博士生导师

2018.4-2020.10 美国俄亥俄州立大学 博士后

2016.12-2018.3 美国印第安纳大学 博士后

2014.9-2020.10 哈尔滨医科大学 副教授、硕士生导师

2009.9-2014.8 哈尔滨医科大学 讲师

2004.6-2009.8 哈尔滨医科大学 助教

**学习经历**

2012.3-2016.7 哈尔滨工业大学 生命科学与技术学院 计算机科学与技术学院 生物医学工程 博士 导师：郭茂祖教授

2006.8-2009.6 哈尔滨医科大学 生物信息科学与技术学院   
生物物理学 硕士 导师：李霞教授

2000.8-2004.6 吉林大学数学学院 统计学 学士

**在研科研课题**

1. 2023.1-2026.12《基于生物通路和子通路分析的个性化乳腺癌药物组合筛选》 国家自然科学基金地区项目（32260155，33万） 主持

2. 2021.1-2025.12 《基于多组学数据的个性化癌症药物组合筛选》 海南医学院科研启动经费 （50万） 主持

3. 2021.4-2023.12 《整合多组学数据的细胞系特异药物协同作用预测研究》 海南省自然科学基金面上项目 （5万） 主持

**已完成科研课题**

1. 2014.1-2016.12《面向人类复杂疾病的EQTL模块挖掘及其META分析方法研究》 国家自然科学基金青年项目（61300116，23万） 主持 已结题

2. 2014.1-2016.12 《全基因组meta-eQTL模型挖掘人类复杂疾病风险模块》 黑龙江省自然科学基金（5万） 主持 已结题

3. 2013.1-2015.12 《基于基因-基因共调控网络挖掘类风湿性关节炎风险基因》

黑龙江省教育厅面上项目（2万） 主持 已结题

4. 2012.1-2013.12 《复杂疾病相关基因功能类挖掘方法研究及平台建设》

黑龙江省卫生厅项目 主持 已结题

**SCI学术论文**

**已发表第一作者或并列第一作者论文**

1. Wang, L;…; **Li, Jin\*,** *DysPIA: A novel Dysregulated Pathway Identification Analysis method.* Frontiers in Genetics, 2021,12: 647653..
2. **Li, Jin,** et al., *Essentiality and Transcriptome-Enriched Pathway Scores Predict Drug-Combination Synergy.* Biology,2020.9.
3. Wang, L.;**Li, Jin,** et al., *Identification of Alternatively-Activated Pathways between Primary Breast Cancer and Liver Metastatic Cancer Using Microarray Data*. Genes, 2019.10(10): p. 753.
4. **Li, Jin**, et al., *eSNPO: An eQTL-based SNP Ontology and SNP functional enrichment analysis platform.* Scientific reports, 2016. **6**: p. 30595.
5. **Li, Jin**, et al., *A gene-based information gain method for detecting gene-gene interactions in case-control studies.* European journal of human genetics, 2015. **23**(11): p. 1566-1572.
6. **Li, Jin**, et al., *Mining disease genes using integrated protein–protein interaction and gene–gene co‐regulation information.* FEBS open bio, 2015. **5**(1): p. 251-256.
7. **Li, Jin**, et al., *Relationship of common expression quantitative trait loci genes to the immune system.* Genetics and Molecular Research, 2013. **12**(4): p. 6546-6553. （
8. Jiang, Y.; **Li, Jin** et al., *HGPGD: the human gene population genetic difference database.* PloS one, 2013. **8**(5): p. e64150.
9. **Li, Jin**, et al., *DBGSA: a novel method of distance-based gene set analysis.* Journal of human genetics, 2012. **57**(10): p. 642-653.
10. Wang, L.; **Li, Jin** et al., *A novel stepwise support vector machine (SVM) method based on optimal feature combination for predicting miRNA precursors.* African Journal of Biotechnology, 2011. **10**(74): p. 16720-16731.

**已发表其他论文：**

1. Zeng, Z. et.al, Identifying novel therapeutic targets in gastric cancer using genome-wide CRISPR-Cas9 screening, Oncogene, 2022 41(14):2069-2078.
2. Yu,H, et al., *Conditional transcriptional relationships may serve as cancer prognostic markers,* BMC Medical Genomics, 2021, 14,101.
3. Zhang, X, et al., *A pan-cancer study of class-3 semaphorins as therapeutic targets in cancer*, BMC Genomics, 2020.4.
4. Lin X. et al.,*Genome-wide analysis of aberrant enhancer DNA methylation in human osteoarthritis*, BMC Medical Genomics, 2020, 1.
5. Zhang, X, et al., *Identification of a subtype of hepatocellular carcinoma with poor prognosis based on expression of genes within the glucose metabolic pathway*, Cancers, 2019 14;11(12).
6. Liu, E, et al., *A Fast and Furious Bayesian Network and Its Application of Identifying Colon Cancer to Liver Metastasis Gene Regulatory Networks*. IEEE/ACM transactions on computational biology and bioinformatics, 2019.10.
7. Sun, X., et al., *A PET imaging approach for determining EGFR mutation status for improved lung cancer patient management*, Science translational medicine,2018. 10(431): p. eaan8840. （SCI影响因子：17.16）
8. Xu, J., et al., *EWAS: epigenome-wide association study software 2.0*, Bioinformatics, 2018.34(15): p. 2657-2658.
9. Zhang, T., et al., *Core signaling pathways in ovarian cancer stem cell revealed by integrative analysis of multi-marker genomics data*. PloS one, 2018. 13(5): p. e0196351.
10. Lv, W., et al.,*The drug target genes show higher evolutionary conservation than non-target genes*, Oncotarget,2017, 7(4): p. 4961.
11. Lv, H., et al., *Genome-wide haplotype association study identify the FGFR2 gene as a risk gene for Acute Myeloid Leukemia.* Oncotarget, 2017. 8(5): p. 7891.
12. Zhang, M., et al., *Genome-wide pathway-based association analysis identifies risk pathways associated with Parkinson’s disease.* Neuroscience, 2017. 340: p. 398-410.
13. Zhang, M., et al., *Integrative analysis of genome-wide association studies and gene expression analysis identifies pathways associated with rheumatoid arthritis.* Oncotarget, 2016. 7(8): p. 8580.
14. Xuan, P., et al., *Prediction of potential disease-associated microRNAs based on random walk.* Bioinformatics, 2015. 31(11): p. 1805-1815.
15. Shang, Z., et al., *Genome-wide haplotype association study identify TNFRSF1A, CASP7, LRP1B, CDH1 and TG genes associated with Alzheimer's disease in Caribbean Hispanic individuals.* Oncotarget, 2015. 6(40): p. 42504.
16. Zhang, R., et al., *Genes with stable DNA methylation levels show higher evolutionary conservation than genes with fluctuant DNA methylation levels.* Oncotarget, 2015. 6(37): p. 40235.
17. Jiang, Y., et al., *MCPerm: a Monte Carlo permutation method for accurately correcting the multiple testing in a meta-analysis of genetic association studies.* PloS one, 2014. 9(2): p. e89212. citation:
18. Lv, H., et al., *Association between polymorphisms in the promoter region of interleukin-10 and susceptibility to inflammatory bowel disease.* Molecular biology reports, 2014. 41(3): p. 1299-1310.
19. Zhang, M., et al., *Pathway-based association analysis of two genome-wide screening data identifies rheumatoid arthritis-related pathways.* Genes and immunity, 2014. 15(7): p. 487-494.
20. Teng, Z., et al., *Computational prediction of protein function based on weighted mapping of domains and GO terms.* BioMed research international, 2014. 2014.
21. Zhang, R., et al., *RADB: a database of rheumatoid arthritis-related polymorphisms.* Database, 2014.
22. Xuan, P., et al., *Prediction of microRNAs associated with human diseases based on weighted k most similar neighbors.* PloS one, 2013. 8(8): p. e70204.
23. Zhang, R., et al., *Association between the IL7R T244I polymorphism and multiple sclerosis: a meta-analysis.* Molecular biology reports, 2011. 38(8): p. 5079-5084.
24. Sun, P., et al., *Assessing the patterns of linkage disequilibrium in genic regions of the human genome.* The FEBS journal, 2011. 278(19): p. 3748-3755.
25. Chen, X., et al., *A sub-pathway-based approach for identifying drug response principal network.* Bioinformatics, 2010. 27(5): p. 649-654.

**会议特邀学术报告**

1. *Identification of Alternatively-Activated Pathways between Primary Breast Cancer and Liver Metastatic Cancer Using Microarray Data,* 2019 International Conference on Intelligent Biology and Medicine (ICIBM 2019), Columbus, Ohio, USA, 2019.6.9-11.
2. *Pathway-based drug combinatory synergy prediction using gene expression and essentiality data,* 2020 AACR Annual meeting, Cancer Research 80 (16 Supplement), 4397-4397