Zhenyu Jia, Ph.D.

CURRICULUM VITAE

CONTACT

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EDUCATION

BS	Biochemistry	Wuhan University, China	1994-1998
	Molecular Biology	Chinese Academy of Sciences, China	1998-1999
MS	Statistics	UC Riverside	2003-2005
PhD	Genetics, Genomics & Bioinformatics	UC Riverside	2002-2006

EXPERIENCES

Research Assistant	Institute of Biophysics, CAS, China	1999-2001
Teaching Assistant	UC Riverside	2005-2006
Statistical Consulting	UC Riverside	2004-2007
Postdoctoral Scholar	UC Riverside	2006-2007
Specialist	UC Irvine	2007-2008
Statistical Consulting	UC Irvine	2007-present
Project Scientist	UC Irvine	2008-2013
Assistant Professor	U Akron	2013-present

PUBLICATIONS (* Corresponding author; [1] Co-First author)

1. Jia, Z. and Xu, S. (2005) Clustering expressed genes on the basis of their association with a quantitative phenotype. *Genetical Research*, 86:193-207.
2. Jia, Z. (2006) Mixture Models for Microarray Data Analysis. *Ph.D. Thesis (Major Professor: Xu, S.) --University of California, Riverside*
3. Xu, S. and Jia, Z. (2007) Genome-wide Analysis of Epistatic Effects for Quantitative Traits in Barley. *Genetics*, 175:1955-1963.
4. Jia, Z. and Xu, S. (2007) Mapping Quantitative Trait Loci for Expression Abundance. *Genetics*, 176:611-623.
5. Jia, Z.* and Xu, S. (2008) Bayesian Mixture Model Analysis for Detecting Differentially Expressed Genes. *The International Journal of Plant Genomics*, Volume 2008, Article ID 892927, 12 pages.
6. Jia, Z.*, Tang, S., Mercola, D. and Xu, S. (2008) Detection of Quantitative Trait Associated Genes Using Cluster Analysis. *EvoBIO 2008, Lecture Notes in Computer Science 4973, E. Marchiori and J.H. Moore (Eds.)*, 83-94.
7. Jia, Z.*, Wang, Y., Koziol, J., McClelland, M. and Mercola, D. (2008) A New Bi-Model Classifier for Predicting Outcomes of Prostate Cancer Patients. *in JSM Proceedings, Biometrics Section. Denver, CO: American Statistical Association.*
8. Arora, S., Wang, Y., Jia, Z., Vardar-Sengul, S., Munawar, A., Doctor, K., Birrer, M., McClelland, M., Adamson, E. and Mercola, D. (2008) Egr1 Regulates the Coordinated Expression of Numerous EGF Receptor Target Genes as identified by ChIP on chip of Prostate Cancer Cells. *Genome Biology*, 9:R166.
9. Koziol, J., Feng, A., Jia, Z., Wang, Y., Goodison, S., McClelland, M. and Mercola, D. (2009) The Wisdom of the Commons: Ensemble Tree Classifiers for Prostate Cancer Prognosis. *Bioinformatics*, 25:54-60.
10. Jia, Z.*, Wang, Y., Ye, K., Li, Q., Tang, S., Xu, S. and Mercola, D. (2009) Association Study between Gene Expression and Multiple Relevant Phenotypes with Cluster Analysis. *EvoBIO 2009, Lecture Notes in Computer Science 5483, C. Pizzuti, M.D. Ritchie, and M. Giacobini (Eds.), 1-12*
11. Koziol, J. and Jia, Z.* (2009) The Concordance Index C and the Mann-Whitney Parameter Pr[X>Y] with Randomly Censored Data. *Biometrical Journal*, 51:467-474.
12. Cheng, C., Bettahi, I., Cruz-Fisher, M., Pal, S., Jain, P., Jia, Z., Holmgren, J., Harandi, A. and de la Maza, L.(2009) Effective vaccination against Chlamydia trachomatis using the major outer membrane protein adjuvanted with CpG oligodeoxynucleotide coupled to the nontoxic B subunit of cholera toxin. Vaccine, 27:6239-6246.

13. Cao, J.N., Gollapudi, S., Sharman, E.H., Jia, Z., Gupta, S .(2010) Age-related Alterations of Gene Expression Patterns in Human CD8+ T cells. Aging Cell, 9:19-31.
14. Ye, K., Jia, Z., Wang, Y., Flicek, P., Apweiler, R. (2010) Mining Unique-m Substrings from Genomes. Journal of Proteomics & Bioinformatics, 3:99-103.
15. Xia, X.[1], Jia, Z.[1], Porwollik, S., Long, F., Hömme, C., Ye, K., Müller-Tidow, C., McClelland, M., Wang, Y. (2010) Evaluating Oligonucleotide Properties for DNA Microarray Probe Design. Nucleic Acids Research, 38:11 e121.
16. Wang, Y.[1], Xia, X.[1], Jia, Z.[1], Sawyers, A., Yao, H., Wang-Rodriquez, J., Mercola, D., McClelland, M. (2010) In silico estimates of tissue components in surgical samples based on expression profiling data. Cancer Research, 70:6448-6455.
17. Basu, A., Banerjee, H., Rojas, H., Martinez, S., Roy, S., Jia, Z., Lilly, M., De León, M., and Casiano, C. (2011) Differential Expression of Peroxiredoxins in Prostate Cancer: Consistent Upregulation of PRDX3 and PRDX4. The Prostate, 71:755-765.
18. Jia, Z.[1], Wang, Y.[1], Sawyers, A., Yao, H., Rahmatpanah, F., Xia, X., Xu, Q., Pio, R., Turan, T., Koziol, J., Goodison, S., Carpenter, P., Wang-Rodriquez, J., Simoneau, A., Meyskens, F., Sutton, M., Lernhardt, W., Beach, T, Monforte, J., McClelland, M. and Mercola, D. (2011) Diagnosis of Prostate Cancer Using Differentially Expressed Genes in Stroma. Cancer Research, 71:2476-2487.
19. Chen, X., Xu, S., Wang, Y., McClelland, M., Jia, Z.* and Mercola, D.* (2011) Identification of Biomarkers for Prostate Cancer Prognosis Using a Novel Two-step Cluster Analysis. Lecture Notes in Bioinformatics, 7036:63-74.
20. Jia, Z.*, Rahmatpanah, F., Chen, X., Lernhardt, W., Wang, Y., Xia, X., Sawyers, A., McClelland, M.* and Mercola, D.* (2012) Expression changes in the stroma of prostate cancer predict subsequent relapse. PLoS ONE, 7(8): e4137.
21. Chen, X., Xu, S., McClelland, M., Rahmatpanah, F., Sawyers, A., Jia, Z.*, Mercola, D*. (2012) An Accurate Prostate Cancer Prognosticator Using a Seven-Gene Signature Plus Gleason Score and Taking Cell Type Heterogeneity into Account. PLoS ONE, 7(9): e45178.
22. Lee, C., Zhang, Q., Zi, X., Dash, A., Soares, M., Rahmatpanah, F., Jia, Z., McClelland, M., Mercola, D. (2012) TGF-β mediated DNA methylation in prostate cancer. Transl Androl Urol, 1(2):78-88.
23. Jia, Z.[1]*, Wang, Y.[1], Hu, Y., McLaren, C., Yu, Y., Ye, K., Xia, X., Koziol, J., Lernhardt, W., McClelland, M. and Mercola, D. (2013) A Sample Selection Strategy to Boost the Statistical Power of Signature Detection in Cancer Expression Profile Studies. Anti-Cancer Agents in Medicinal Chemistry, 13(2):203-11.
24. Pio, R., Jia, Z., Baron, V., Merola, D. (2013) Early Growth Response Gene 3 (Egr3) is highly over-expressed in non-relapsing prostate cancer but not in relapsing prostate cancer. PLos ONE, 8(1):e54096.
25. Rahmatpanah, F., Jia, Z.*, Chen, X., Jones, F., McClelland, M. and Mercola, D. (2012) Expression of HER2 in Breast Cancer Promotes a Massive Reorganization of Gene Activity and Suggests a Role for Epigenetic Regulation. J Data Mining Genomics Proteomics 3:e102. doi:10.4172/2153-0602.1000e102

AWARDS

1. Outstanding freshman scholarship, Wuhan University, China, 1994
2. Wuhan university fellowship, Wuhan University, China, 1995-1997
3. Tong-yi fellowship, Wuhan University, China, 1997-1998
4. Excellent graduate student scholarship, CAS, China, 1998-1999
5. Dean's fellowship, UC Riverside, 2002-2003
6. Ecology and Evolution Summer Fellowship, UC Riverside, Summer 2003
7. Travel Award, EvoStar 08 in Naples, Italy, 2008
8. Faculty Career Development Award, University of California, Irvine, 2008-2009
9. Travel Award, EvoStar 09 in Tubingen, Germany, 2009
10. Scholarship, AACR Cancer Biostatistics Workshop, Sonoma, CA, 2009
11. Bridging Fund award (Co-PI), UC Irvine Chao Family Comprehensive Cancer Center, UC Irvine, 2012

PATENTS

1. Gene Expression Signatures Useful for the Diagnosis and Prognosis of Prostate Cancer. (2009), pending
2. The Prostate Cancer Tumor Microenvironment Exhibits Numerous Differentially Expressed Gene Changes Useful for Diagnosis of Prostate Cancer without Tumor Cells. (2010), pending

PROFESSIONAL ACTIVITIES

• Member, American Statistical Association (ASA), 2006 – present
• Member, American Association for Cancer Research (AACR), 2008 – present
• Member, Pervasive Adaption (PARADA), 2008 – present
• Editorial Board Member, Journal of Data Mining in Genomics & Proteomics, 2010 – present

• Statistical consultant: *UC Riverside, UC Irvine, Sidney Kimmel Cancer Center, Proveri Inc., Agendia Inc., Biostatistics Shared Resource, UCI, Vaccine Research Institute of San Diego, UC San Diego, and San Diego State University*
• Journal Review: *Journal of Biotechnology*; *Bioinformatics*; *Genetics Research*; *Biotechnology Advances; Journal of Proteomics & Bioinformatics; Cancer Letters; Proteomics; Current Proteomics; Journal of Proteomics; Biotechnology and Applied Biochemistry; Electrophoresis; Biometrical Journal; Neurocomputing; Proteome Science; Lecture Notes in Computer Science(EvoBIO); ICPR; PLoS Computational Biology; Computer Methods and Programs in Biomedicine; Journal of Translational Medicine; BMC Bioinformatics; Nucleic Acids Research*
• Conference Program Committee: EvoStar (EvoBIO), 2009 – present
• Conference Program Committee: International Association for Pattern Recognition (ICPR), 2010 - present
• Sidney Kimmel Cancer Center 2007, "Mixture Models for Microarray Data Analysis", Invited Talk
• University of California, Irvine 2007, "Mixture Models for Microarray Data Analysis", Invited Talk
• EvoStar 08 in Naples, Italy 2008, "Detection of Quantitative Trait Associated Genes Using Cluster Analysis", Oral Presentation
• University of California, Riverside, 2008, "A New Bi-Model Classifier for Predicting Outcomes of Prostate Cancer Patients", Invited Talk
• SPECS Investigators Meeting, University of Vanderbilt, Nashville, 2008, "A New Bi-Model Approach for the Development of a Classifier for Predicting Outcomes for Prostate Cancer Patients", Oral Presentation
• SPECS Investigators Meeting, Vandervilt University, Nashville 2008, "The Prostate Cancer Tumor Microenvironment Exhibits Numerous Differentially Expressed Gene Changes Useful for Diagnosis of Prostate Cancer", Oral Presentation
• SPECS Annual Meeting, Laguna Beach, 2009, "A New Bi-Model Approach for the Development of a Classifier for Predicting Outcomes for Prostate Cancer Patients", Oral Presentation
• EvoStar 09 in Tubingen, Germany 2009, "Association Study between Gene Expression and Multiple Relevant Phenotypes with Cluster Analysis", Oral Presentation
• Biostatistics Shared Resource, Chao Family Comprehensive Cancer Center, University of California, Irvine, 2009, “Genomics Data Analysis Using R”, Tutorials
• Department of Epidemiology, University of California, Irvine, 2010, "Diagnosis of prostate cancer without tumor cells using differentially expressed genes in stroma adjacent to tumors", Invited Talk
• SPECS Annual Meeting, UC Irvine, 2010, "Diagnosis of Prostate Cancer without Tumor Cells Using Differentially Expressed Genes in Stroma near Tumors", Oral Presentation
• Baylor College of Medicine, Houston, TX, 2010, "Diagnosis of prostate cancer using differentially expressed genes in stroma", Invited Talk
• Department of Computer Science, University of California, Irvine, 2010, "Diagnosis of prostate cancer using differentially expressed genes in stroma", Invited Talk
• JSM 10 in Vancouver, Canada, 2010, "The Use of Nomogram Predictions as Comparators for Adjuvant Treatment Studies in Prostate Cancer", Oral Presentation
• The University of Texas MD Anderson Cancer Center, Department of Bioinformatics and Computational Biology, 2011, "Diagnosis and Prognosis of Prostate Cancer Using Gene Expression Signatures", Invited Talk
• 2nd International Conference on Proteomics & Bioinformatics, Las Vegas, July 2-4, 2012, "The use of nomogram predictions as comparators in a phase II prostate cancer adjuvant treatment trial", Invited Talk
• 1st Chinese Young Chemical Physicists Forum, Guiyang, China, July 28-30, 2012, "Identification of gene signatures in tumor microenvironment that are useful for prostate cancer diagnosis and prognosis", Invited Talk