Physics and Computer Science Department
Xavier University of Louisiana
New Orleans, LA, 70125

Phone: 504-520-6700
E-mail: kzhang@xula.edu

Kun (Karen) Zhang

Professional Experiences

- **Aug. 2018 – present, Professor of Computer Science,** Physics and Computer Science Department, Xavier University of Louisiana
- **Aug. 2013 – Jul. 2018, Associate Professor,** Computer Science Department, Xavier University of Louisiana
- **Aug. 2016 – May 2017, Interim Dept. Head,** Computer Science Department, Xavier University of Louisiana
- **Apr. 2019 – present, Lead of Bioinformatics Core,** Xavier RCMI Center for Cancer Research
- **Sept. 2014 – Mar. 2019, Lead of Bioinformatics Facility and Co-Director of Cell Molecular and Bioinformatics Core,** Xavier RCMI Center for Cancer Research
- **2017- Present, affiliated faculty**, Center of Genomics and Bioinformatics, Tulane University
- **2014 - Present, affiliated faculty**, Center for Research and Scientific Computing, Tulane University
- **2007 – Present, affiliated faculty,** Tulane Cancer Center;
- **May. 2007 – July. 2013, Assistant Professor,** Computer Science Department, Xavier University of Louisiana
- **2000 – 2006,**
  - **Research Assistant**, Department of Electrical Engineering and Computer Science, Tulane University
  - **Teaching Assistant**, Tulane A.B. Freeman Business School, Tulane University

Education:

- Ph.D., M.S. Computer Science (Machine Learning and Data Mining), Tulane University

Research Interest

- Bioinformatics, Big Data Analytics/Data Mining/Data Analysis, Statistical Machine Learning/Pattern Recognition, and Database Management System, with the objective of making the technology more useful for challenging real-world applications in biology, medicine and other scientific data management and decision-making.

Research Projects

- **Awarded Grants**
  1. "**Event Detection for Streaming Analytics: An Intelligent Mathematical Paradigm**", **ARO, DOD**
     - Principal Investigator
     - Awarded funds: $660,000, 7/2020-7/2023
  2. "A Data-driven Pan-cancer Study of Biological Bases of Cancer Health Disparities", NIH RCMI Research Project

- **Principal Investigator**
- Awarded funds: $1,421,285, 4/2019 – 3/2023

3. NIH RCMI Program at Xavier University of Louisiana (Principal Investigator: Dr. Guangdi Wang, Chemistry Department, Xavier University of Louisiana)
   - **Lead of Bioinformatics Core**
   - Awarded funds: $710,010, 4/2019 – 3/2023

4. "Detecting Race-Relevant Molecular Biomarkers with Clinical Utilities Using Multi-Omics Data across Tumor Types", NIH INBRE LBRN Full Research Project
   - **Principal Investigator**
   - Awarded funds: $448,086, 5/2018 – 3/2021

5. "Trans-Omics Integration of Multi-Omics Studies for Male Osteoporosis", U19AG055373, (Principal Investigator: Dr. HongWen Deng, Tulane University)
   - **Co-investigator & Site PI**
   - Awarded funds: $43,840, 4/2017-3/2022

6. "Noncoding RNAs in Herpesvirus Biology and AIDS malignancies (Core B)", NIH PAR-13-321 (P01), (Principal Investigator: Dr. Erik Flemington, Tulane University)
   - **Co-investigator & Site PI**
   - Awarded funds: $129,940, 2/2017-1/2022

7. "A Pan-Cancer Analysis of Racial Disparities in tumor Driver Mutations and Clinical Outcomes", Pilot project, Xavier BUILD, RCMI, and LCRC programs
   - **Principal Investigator**
   - Awarded funds: $35,257, 4/2016 – 3/2017

8. "A Mathematical and Computational Framework for Anomaly Detection in Data Streams", Department of Defense, U.S. Army Research Office, Basic and Applied Scientific Research.
   - **Principal Investigator**
   - Awarded funds: $594,000, 8/2015 – 8/2018

9. NIH RCMI Program at Xavier University of Louisiana (Principal Investigator: Dr. Guangdi Wang, Chemistry Department, Xavier University of Louisiana)
   - **Lead of Bioinformatics Facility and Co-Director of Cell Molecular and Bioinformatics Core**
   - Awarded funds: $746,520, 9/2014 – 3/2019

10. "An Integrated Framework to Access and Mine Distributed Heterogeneous Data Streams with Uncertainty", the Department of Defense (DOD), U.S. Army Research Office, Basic and Applied Scientific Research
    - **Principal Investigator**
    - Awarded funds: $463,100, 1/2012 – 1/2015

11. Louisiana Cancer Research Consortium Seed Grant, "Gene Expression, Somatic Mutations and Survival Outcomes: a Go-Term Driven Predictive Tree (Rule) Model and the Open Source Software",
    - **Principal Investigator**, Awarded funds: $25,000 (direct cost), 7/2014 - 6/2015

12. "A Hybrid Data Mining Framework for Efficient Characterization of Insertion Preferences of Retrotransposons", NIH RCMI Program,

- **Principal Investigator** of Pilot Project
- Awarded funds: $725,105, 9/2009 – 7/2014

13. "Louisiana's Cyber Connectivity via LONI", NSF RII C2,
   - **Senior Personnel**
   - 7/2010 – 8/ 2013

14. "A Verification-Driven Learning Model that Enriches CS and Related Undergraduate Programs", NSF Cpath program, (Principal Investigator: Dr. Shengru Tu, UNO)
   - **Co-Investigator & Site Co- Principal Investigator**
   - Awarded funds: $44,982, 9/2009 – 9/2012

15. "Enhancement of microRNA Research through Bioinformatics Tool Development", **NIH INBRE Program, Louisiana Biomedical Research Network (LBRN),**
   - **Principal Investigator** of Pilot Project
   - Awarded funds: $155,198, 5/2010 – 4/2012

16. "A Data Mining Framework to Predict Alu Insertion Sites", Louisiana Board of Regents Research Competitiveness Subprogram,
   - **Principal Investigator**
   - Awarded funds: $107,489, 6/2008 – 6/2012

17. "New Informatics Paradigm for Reconstructing Signaling Pathways in Human Disease", **NIH 1R21LM010137-01, Administrative Supplements, sub-awarded from the University of New Orleans,** (Principal Investigator: Dr. Dongxiao Zhu)
   - **Co-Investigator & Site Principal Investigator**
   - Awarded funds: $76,412, 7/2010 – 8/2011

18. "Analysis of Epstein Barr virus type III latency on cellular miRNA gene expression", **NIH R01 CA130752, Administrative Supplements, sub-awarded from Tulane Cancer Center,** (Principal Investigator: Dr. Erik Flemington)
   - **Co-Investigator & Site Principal Investigator**
   - Awarded funds: $57,049, 6/2009 – 9/2010

19. "Divide-Conquer Based Approach for Direct Frequent Sequential Pattern Mining", **Faculty Summer Research Program, NIH INBRE Program, Louisiana Biomedical Research Network**
   - **Principal Investigator**
   - Awarded funds: $9,772, 5/2009 - 8/2009

20. "Efficient Characterization of Alu Insertion Sites via Model-Based Search Tree", **Faculty Summer Research Program, NIH INBRE Program, Louisiana Biomedical Research Network**
   - **Principal Investigator**
   - Awarded funds: $18,269, 6/2008 - 8/2008

21. "Cancers and Alu Insertions – a preliminary study from data mining perspective", Louisiana Cancer Research Consortium Start-up support, Xavier University of Louisiana
   - **Principal Investigator**
   - Awarded funds: $18,000, 11/2007 -11/2008

22. "Empirical comparison of popular data mining algorithms at the presence of sample selection bias", Faculty-Student Undergraduate Research/Creative Collaborations

Sponsored by the Center of Undergraduate Research at Xavier University of Louisiana

- **Principal Investigator**
- Awarded funds: $2,500, 6/2007 -5/2008

Awards and Recognition

- Full project talks winner, "Detecting Race-Relevant Molecular Biomarkers with Clinical Utilities using Multi-omics Data across Tumor Types", 2021 LBRN 19th Annual Meeting Awards

- Recipient of "Expert" Ranking of the Bioinformatics for Precision Oncology Program, organized by Pine-biotech Company, Tulane University, LSU center for computation & technology, Loyola University New Orleans, University of Haifa, Tauber Bioinformatics Research Center, 2019; Completed and certified in the following courses,
  - i. Introduction to Bioinformatics; Transcriptomics 1, 2, 3, 4; Introduction to Genomics; Genomics 1; Epigenetics 1

- Recipient of Outstanding Scientific Achievement, Louisiana Cancer Research Consortium Annual Scientific Retreat, 2018

- Certificate of CCAS Department Head Leadership Workshop, July 2016

- The research of Dr. Kun Zhang is the Louisiana Board of Regents daily feature for March 6th, 2012. (http://web.laregents.org/category/daily/)

- Recipient of Top-10 Data Mining Case Studies, IEEE 10th International Conference on Data Mining, 2010

- Junior Faculty recipient of 2010 Norman C. Francis Excellence in Scholarship Award, Xavier University of Louisiana

- Crown Winner of IEEE 8th International Conference on Data Mining Contest, 2008

- Best Application Paper Award, IEEE 6th International Conference on Data Mining, 2006

- Student Travel Award: IEEE 6th International Conference on Data Mining 2006, Sponsored by IBM Research & Microsoft

- Research/Teaching Assistant Scholarships, School of Engineering, Tulane University, 2000-2006

Publications (* Corresponding author)

- **Submitted Manuscripts**
  1. "Polygenic Basis for Racial Disparity in Prostate Cancer", submitted to **Cancer Epidemiology, Biomarkers Prev.**
  2. "Deciphering the increased prevalence of TP53 mutations in metastatic prostate cancers", submitted to **PLOS Computational Biology**
  3. "Uncovering Personalized Driver Genes via Bayesian Network Integration", submitted to **Bioinformatics**
  4. "CSRDA: Cost-sensitive Regularized Dual Averaging for Handling Imbalanced and High-dimensional Streaming Data", submitted to **the 2021 IEEE International Conference on Data Mining**

5. "A Fast and Interpretable Cost-sensitive Sparse Online Learning Framework for Streaming Data Classification and Online Anomaly Detection", submitted to **Knowledge and Information Systems**

- **2021**

6. Chen Z, Fang Z, Sheng V, Zhao J, Fan W, Edwards A, **Zhang K***, "Adaptive Robust Local Online Density Estimation for Streaming Data", **Int J Mach Learn Cybern.** 2021 Jun;12(6):1803-1824. doi: 10.1007/s13042-021-01275-y. Epub 2021 Feb 3. PMID: 34149955

7. Chen Z, Cao B, Edwards A, Deng H, **Zhang K***, "A deep imputation and inference framework for estimating personalized and race-specific causal effects of genomic alterations on PSA", **J Bioinform Comput Biol.** 2021 Jul 2:2150016. doi: 10.1142/S0219720021500165. Online ahead of print. PMID: 34225568

8. Chen Z, Zhang W, Deng H, **Zhang K*,** Effective Cancer Subtype and Stage Prediction via Dropfeature-DNNs, **IEEE/ACM Trans Comput Biol Bioinform**, 2021 Feb 12;PP. doi: 10.1109/TCBB.2021.3058941.PMID: 33577454 DOI: 10.1109/TCBB.2021.3058941

9. Zhang W, Dong Y, Sartor O, **Zhang K*,** "Comprehensive Analysis of Multiple Cohort Datasets Deciphers the Utility of Germline Single-Nucleotide Polymorphisms in Prostate Cancer Diagnosis", **Cancer Prev Res**. 2021 Apr 17. doi: 10.1158/1940-6207.CAPR-20-0534. Online ahead of print. PMID: 33866309

10. Gallegos KM, Patel JR, Llopis SD, Walker RR, Davidson AM, Zhang W, **Zhang K**, Tilghman SL, "Quantitative Proteomic Profiling Identifies a Potential Novel Chaperone Marker in Resistant Breast Cancer", **Front Oncol.** 2021 Feb 25;11:540134. doi: 10.3389/fonc.2021.540134. eCollection 2021. PMID: 33718123

11. Ma T, Bai S, Qi Y, Zhan Y, Ungerleider N, Zhang DY, Neklesa T, Corey E, Dehm SM, **Zhang K**, Flemington EK, Dong Y, "Increased transcription and high translation efficiency lead to accumulation of androgen receptor splice variant after androgen deprivation therapy", **Cancer Lett.** 2021 Apr 28;504:37-48. doi: 10.1016/j.canlet.2020.12.037. Epub 2021 Feb 6. PMID: 33556543

12. Walker RR, Gallegos KM, Bratton MR, Lemieux KP, **Zhang K,** Wang G, Davidson AM, Tilghman SL, "Acquisition of Letrozole Resistance Through Activation of the p38/MAPK Signaling Cascade", **Anticancer Res.** 2021 Feb;41(2):583-599. doi: 10.21873/anticanres.14810. PMID: 33517263

13. Lu Y, Li M, Lee GY, Zhao N, Chen Z, Edwards A, **Zhang K*,** "Seeking the exclusive binding region of phenylalkylamine derivatives on human T-type calcium channels via homology modeling and molecular dynamics simulation approach", **Pharmacol Res Perspect.** 2021 May;9(3):e00783. doi: 10.1002/prp2.783. PMID: 33984189

14. Qu G, Xiao L, Hu W, Wang J, **Zhang K**, Calhoun V, Wang Y, "Ensemble manifold regularized multi-modal graph convolutional network for cognitive ability prediction", **IEEE Transactions on Biomedical Engineering**, 10.1109/TBME.2021.3077875

- **2020**

15. Z. Chen, A. Edwards, C. Hicks and **K. Zhang***, "Inferring Personalized and Race-specific Causal Effects of Genomic Aberrations on Gleason Scores: A Deep Latent Variable Model", **Frontiers in Oncology**, 13 March 2020

16. W. Zhang, Y. Dong, **K. Zhang***, Gene Expression Analysis Reveals a Pitfall in the Molecular Research of Prostate Tumors Relevant to Gleason Scores", **Proceedings of AACR 2020 annual meeting**

17. W. Zhang, Y. Dong, **K. Zhang***, Gene Expression Analysis Reveals a Pitfall in the Molecular Research of Prostate Tumors Relevant to Gleason Scores", **J Bioinform Comput Biol.** 18(5):2050032. doi: 10.1142/S0219720020500328. Epub 2020 Sep 16. PMID: 3293828

18. W. Zhang, Y. Dong, Oliver Sartor, E. Flemington, **K. Zhang***, "SEER and Gene Expression Data Analysis Deciphers Racial Disparity Patterns in Prostate Cancer Mortality and the Public Health Implication", **Scientific Reports**, 2020 Apr 22;10(1):6820. doi: 10.1038/s41598-020-63764-4.

19. Lan R, Jin B, Liu YZ, Zhang K, Niu T, You Z. "Genome and transcriptome profiling of FBXW family in human prostate cancer", **Am J Clin Exp Urol**. 2020 Aug 15;8(4):116-128. eCollection 2020. PMID: 32929407

- **2019**

20. S. Mei and **K. Zhang***(2019),"A Multi-Label Learning Framework for Drug Repurposing", **Pharmaceutics.** 2019 Sep 9;11(9). pii: E466. doi: 10.3390/pharmaceutics11090466, PMID: 31505805

21. S. Mei and **K. Zhang***(2019),"Neglog: Homology-Based Negative Data Sampling Method for Genome-Scale Reconstruction of Human Protein-Protein Interaction Networks", **Int J Mol Sci.** 2019 Oct 12;20(20). pii: E5075. doi: 10.3390/ijms20205075, PMID: 31614890

22. S. Mei and **K. Zhang***(2019),"A Computational Framework for Predicting Direct Contacts and Substructures within Protein Complexes", **Biomolecules.** 2019 Oct 25;9(11). pii: E656. doi: 10.3390/biom9110656, PMID: 31717703

23. W. Zhang, E. Flemington, H. Deng, **K. Zhang***, "Epigenetically silenced candidate tumor suppressor genes in prostate cancer: identified by modelling the stratified promoter methylation profiles over tumor samples and applied to progression prediction", **Cancer Epidemiology Biomarkers & Prevention**, 2019 Jan; 28(1):198-207, PMID: 30262601

24. Q. Zhou, B. Yu, C. Anderson, ZP. Huang, J. Hanus, W. Zhang, Y. Han, PS. Bhattacharjee, S. Srinivasan, **K. Zhang**, DZ. Wang, S. Wang. "LncEGFL7OS regulates human angiogenesis by interacting with MAX at the EGFL7/miR-126 locus." **Elife**. 2019 Feb 11;8. pii: e40470. doi: 10.7554/eLife.40470

25. J. Lu, Y. Chen, Z. Ao, J. Shen, C. Zeng, X. Lin, L. Peng, R. Zhou, X. Wang, C. Peng, H Xiao, **K. Zhang** and H. Deng, "System network analysis of genomics and transcriptomics data identified type 1 diabetes associated pathway and genes", **Genes and Immunity**, volume 20, pages 500–508 (2019)

26. Z. Chen, A. Edwards, Y. Gao and **K. Zhang***, "Learning Discriminative Subregions and Pattern Orders for Facial Gender Classification", **Image and Vision Computing**, Elsevier, 2019, Volume 89, Pages 144-157

27. S. Bai, S. Cao, L Jin, M. Kobelski, B. Schouest, X. Wang, N. Ungerleider, M. Baddoo, W. Zhang, E. Corey, R. Vessella, X. Dong, **K. Zhang**, X. Yu, EK Flemington and Y. Dong (2019), "A Positive Role of c-Myc in Regulating Androgen Receptor and its Splice Variants in Prostate Cancer", **Oncogene**. 2019 Jun; 38(25):4977-4989. doi: 10.1038/s41388-019-0768-8. Epub 2019 Feb 28.

28. Cao S, Ma T, Ungerleider N, Roberts C, Kobelski M, Jin L, Concha M, Wang X, Baddoo M, Nguyen HM, Corey E, Fazli L, Ledet E, Zhang R, Silberstein JL, Zhang W, **Zhang K**, Sartor O, Dong X, Flemington EK, Dong Y. "Circular RNAs add diversity to androgen receptor isoform repertoire in castration-resistant prostate cancer", **Oncogene**. 2019 Aug 13. doi: 10.1038/s41388-019-0947-7

29. Xian P, Ge D, Wu VJ, Patel A, Tang WW, Wu X, **Zhang K**, Li L, You Z."PD-L1 instead of PD-1 status is associated with the clinical features in human primary prostate tumors." **Am J Clin Exp Urol.** 2019 Jun 15;7(3):159-169. eCollection 2019.

30. Z.Duan, H. Miller, X. Fu,D. Ge,B. Jin, A. Moustafa, R. Lan, **K. Zhang**, Z. Chen, and Z. You, "Th17 cells promote tumor growth in an immunocompetent orthotopic mouse model of prostate cancer", **Am J Clin Exp Urol.** 2019; 7(4): 249–261,PMC6734037

- **2018**

31. *S. Mei*, E. Flemington and **K. Zhang***, "Transferring knowledge of bacterial protein interaction networks to predict pathogen targeted human genes and immune signaling pathways: a case study on M. tuberculosis", **BMC Genomics**, 201819:505,https://doi.org/10.1186/s12864-018-4873-9

32. Z. Chen, Z. Fang, J. Zhao, W. Fan, A. Edwards, K. Zhang*, "Online density estimation over streaming data: A local adaptive solution". **In Proceedings of the IEEE International Conference on Big Data**, Seattle, Washington, December 2018, pages 201-210

33. *W. Zhang*, E. Flemington, **K. Zhang***, "Driver gene mutations based clustering of tumors: methods and applications", **Bioinformatics,** Volume 34, Issue 13, 1 July 2018, Pages i404–i411, https://doi.org/10.1093/bioinformatics/bty232

34. Z. Fang, et al. **K. Zhang**, et al.,"SPIN1 promotes tumorigenesis by blocking the uL18 (universal large ribosomal subunit protein 18)-MDM2-p53 pathway in human cancer", **Elife**, 2018

- **2017**

35. W. Zhang, A. Edwards, E. Flemington, **K. Zhang***, "Racial disparities in clinical outcomes and tumor mutation burden, and the association between tumor mutation burden and cancer incidence rate", **Scientific Reports,** volume 7, Article number: 13639 (2017), Nature Publishing group

36. W. Zhang, A. Edwards, E. Flemington, **K. Zhang***, "Significant prognostic features and patterns of somatic TP53 mutations in human cancers", **Cancer Informatics**, 2017:16 1176935117691267

37. Z. Chen, Z. Fang, W. Fan, A. Edwards, **K, Zhang***, "CSTG: An Effective Framework for Cost-sensitive Sparse Online Learning", **Proceedings of the 17th SIAM International Conference on Data Mining,**

38. S. Mei, E. Flemington and **K. Zhang***, "A computational framework for distinguishing direct versus indirect interactions in human functional protein-protein interaction networks", **Integr Biol (Camb).** 2017 May 19. doi: 10.1039/c7ib00013h

39. S. Tilghman, J. Pratt, S. Llopis, A.Davidson, R. Walker, P. Carriere, I. Davenport, W. Zhang and **K. Zhang**, "Proteomic Characterization of Aromatase Inhibitor Resistant Mammospheres Reveal The Presence of a Novel Nuclear Chaperone", **Cancer Research, Experimental and Molecular Therapeutics**

- **2016**

  40. S. Mei and **K. Zhang***, "Multi-label l_2-regularized logistic regression for predicting activation/inhibition relationships in human protein-protein interaction networks", **Scientific Reports**, 2016 Nov 7;6:36453. doi: 10.1038/srep36453. Nature Publishing group

  41. S. Mei and **K. Zhang***, "Computational discovery of Epstein-Barr virus targeted human genes and signaling pathways", **Scientific Reports**. Article number: 30612 (2016), Nature Publishing group

  42. W. Zhang, E. Flemington, **K. Zhang***, "Mutant TP53 disrupts age-related accumulation patterns of somatic mutations in multiple-cancer types" **Cancer Genetics**, 2016 Sep;209(9):376-380. doi: 10.1016/j.cancergen.2016.07.001. Epub 2016 Jul 9.

  43. Q. Zhang, S. Liu, K. Parajuli, W. Zhang, **K. Zhang**, Z. Mo, J. Liu, Z. Chen, S. Yang, A. Wang, L. Myers, Z You, "Interleukin-17 promotes prostate cancer via MMP7-induced epithelial-to-mesenchymal transition", **Oncogene**, Nature Publishing group

  44. S. Yang, D. Mercante, **K. Zhang*** and Z. Fang*, "An Integrated Approach for RNA-seq Data Normalization", **Cancer Informatics,** 2016 Jun 27;15:129-41. doi: 10.4137/CIN.S39781. PMID: 27385909

  45. W. Zhang, A. Edwards, Z. Fang, E. Flemington and **K. Zhang***, "Integrative genomics and transcriptomics analysis reveals potential mechanisms for good prognosis of patients with human papillomavirus infected head and neck carcinomas", **Scientific Reports**, 6, Article number: 24927 (2016), doi:10.1038/srep24927, Nature Publishing group

  46. W. Zhang, A. Edwards, W. Fan, E. Flemington and **K. Zhang***, "The Modularity and Dynamicity of miRNA-mRNA Interactions in High-Grade Serous Ovarian Carcinomas and the Prognostic Implication", **Computational Biology and Chemistry**, NIHMS764499

  47. S. Liu, Q. Zhang, C. Chen, D. Ge, Y. Qu, R. Chen, Y. Fan, N. Li, W. Tang, W. Zhang, **K. Zhang**, A. Wang, B. Rowan, S. Hill, O. Sartor, A. Abdel-Mageed, L. Myers, Q. Lin, Z. You, "Hyperinsulinemia enhances interleukin-17-induced inflammation to promote prostate cancer development in obese mice through inhibiting glycogen synthase kinase 3-mediated phosphorylation and degradation of interleukin-17 receptor", **Oncotarget.**7296, DOI: 10.18632

- **2015**

  48. Cao S, Moss W, O'Grady T, Concha M, Strong MJ, Wang X, Yu Y, Baddoo M, **Zhang K**, Fewell C, Lin Z, Dong Y, Flemington EK., "New non-coding lytic transcripts derived from the Epstein Barr virus latency origin of replication oriP are hyper-edited, bind the paraspeckle protein, NONO/p54nrb, and support lytic viral transcription", **J Virol.** 2015 Apr 29. pii: JVI.00608-15. PMID: 25926645

  49. X. Wu, W. Fan, J. Peng, **K. Zhang**, Y. Yu, "Iterative sampling based frequent itemset mining for big data", **International Journal of Machine Learning and Cybernetics**, March 2015, DOI 10.1007/s13042-015-0345-6

  50. W. Zhang, A. Edwards, P. Deininger and **K. Zhang***, "The duplication and intragenic domain expansion of human C2H2 zinc finger genes are associated with transposable

elements and relevant to the expression-based clustering", **Proceedings of the 7th international conference on Bioinformatics and Computational Biology (BICoB)**

- **2014**

51. K. Wu, **K. Zhang***, W. Fan, A. Edwards and P. Yu, "RS-Forest: A Rapid Density Estimator for Streaming Anomaly Detection", **Proceedings of the 14th IEEE International Conference on Data Mining**, pp. 600 - 609

52. W. Zhang, A. Edwards, E. Flemington, **K. Zhang***, "Somatic Mutations Favorable to Patient Survival Are Predominant in Ovarian Carcinomas", **PLoS ONE** 9(11): e112561. doi:10.1371/journal.pone.0112561

53. K. Wu, A. Edwards, W. Fan, J. Gao and **K. Zhang***, "Classifying Imbalanced Data Streams via Dynamic Feature Group Weighting with Importance Sampling", **Proceedings of the 14th SIAM International Conference on Data Mining,** pp. 722-730, doi: 10.1137/1.9781611973440.83

- **2013**

54. W. Zhang, A. Edwards, W. Fan, Z. Fang, P. Deininger and **K. Zhang***, "Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data", **BMC Genomics**, **14**:584, doi:10.1186/1471-2164-14-584

55. W. Zhang, A. Edwards, E. Flemington and **K. Zhang***, "Inferring polymorphism-induced regulatory gene networks active in human lymphocyte cell lines by weighted linear mixed model analysis of multiple RNA-Seq datasets", **PLOS ONE**, 10.1371/journal.pone.0078868

56. M. Strong, T. O'Grady, Z. Lin, G. Xu, M. Baddoo, C. Parsons, **K. Zhang**, CM Taylor and E. Flemington. "Epstein-Barr Virus and Human Herpesvirus 6 Detection in a non-Hodgkin's Diffuse Large B-Cell Lymphoma Cohort using RNA-Seq". **J Virol.** 2013, Sep 18. PMID: 24049168.

57. S. Yang, S. Pounds, **K. Zhang***, and Z. Fang*, "PAIR: Paired Allelic log-Intensity-Ratio based normalization algorithm for SNP-CGH arrays", **Bioinformatics**. 2013 Feb 1;29(3):299-307. PMID: 23196989, (Journal Impact Factor: 5.323)

58. Fang Z, Du R, Edwards A, Flemington EK, **Zhang K***, "The Sequence Structures of Human MicroRNA Molecules and Their Implications". **PLoS ONE** 8(1): e54215. doi:10.1371/journal.pone.005421, PMID: 23349828, (Journal Impact Factor: 4.41)

59. J. Peng and **K. Zhang**, "A Margin Technique for Dimension Reduction with Applications to Hyperspectral Imagery", **International Conference on Advanced Computer Science and Electronics Information** (ICACSEI 2013), May 2013

- **2012**

60. W. Zhang, A. Edwards, W. Fan, EK Flemington, **K. Zhang***, "miRNA-mRNA Correlation-Network Modules in Human Prostate Cancer and the Differences between Primary and Metastatic Tumor Subtypes". **PLoS ONE** 7(6): e40130. doi:10.1371/journal.pone.0040130 (Journal Impact Factor: 4.41)

61. W. Zhang, A. Edwards, D. Zhu, EK Flemington, P. Deininger, **K. Zhang***, "miRNA-Mediated Relationships between Cis-SNP Genotypes and Transcript Intensities in

Lymphocyte Cell Lines". **PLoS ONE** 7(2): e31429. doi:10.1371/journal.pone.0031429, (Journal Impact Factor: 4.41)

62. **K. Zhang***, W. Fan, A. Edwards, A. Orgah and P. Deininger, "Analysis And Characterization Of Alu Insertion Sites: A Statistical Method And A Data Mining Solution", Book Chapter, **Sequence and Genome Analysis III - Emerging Methods, Techniques and Applications**; iConcept Press Ltd

- **2011**

63. W. Zhang, A. Edwards, W. Fan, P. Deininger and **K. Zhang*,** "Alu Distribution and Mutation Types of Cancer Genes", **BMC Genomics**, 2011, March, 12:157, doi:10.1186/1471-2164-12-157, PMID:21429208, (Journal Impact Factor: 4.07)

64. N. Deng, A. Puetter, **K. Zhang**, K. Johnson, Z. Zhao, C. Taylor, EK. Flemington and D. Zhu, "Isoform-level microRNA-155 Target Prediction Using RNA-seq", **Nucleic Acids Research**. 2011 May; 39(9): e61. Epub 2011 Feb 11, (Journal Impact Factor: 8.026)

- **2010**

65. W. Zhang, A. Edwards, W. Fan, D. Zhu and **K. Zhang***, "svdPPCS: an Effective Singular Value Decomposition-Based Method For Conserved And Divergent Co-Expression Gene Module Identification", **BMC Bioinformatics** 2010, 11:338 doi:10.1186/1471-2105-11-338, (Journal Impact Factor: 3.03)

66. H. Chen, Z. Zhao, **K. Zhang** and D. Zhu, "New Aspects on Haplotype Inference from SNP Fragments", Book Chapter, **A Practical Guide to Bioinformatics Analysis**, published by iConcept Press Ltd

67. G. Xu, C. Fewell, C. Taylor, N. Deng, D. Hedges, X. Wang, **K. Zhang**, H. Zhang, Q. Yin, J. Cameron, M. Lacey, Z. Lin, D. Zhu and E. Flemington "Transcriptome and Targetome Analysis in mir-155 Expressing Cells Using RNA-seq", **RNA.** 2010 Aug; 16(8):1610-22. Epub 2010 Jun 28. (Journal Impact Factor: 6.051)

68. W. Fan, E. Zhong, J. Peng, O. Verscheure, **K. Zhang**, J. Ren, R. Yan and Q. Yang, "Generalized and Heuristic-Free Feature Construction for Improved Accuracy", **Proceedings of 2010 SIAM International Conference on Data Mining.** Pages 629 - 640. Acceptance rate < 23%

69. A. Edwards and **K. Zhang**, "A Programming Remediation Plan", **Journal of Computing Sciences in Colleges**, Volume 25 Issue 5, pp. 41-47,

- **2009**

70. **K. Zhang***, W. Fan, P. Deininger, A. Edwards, Z. Xu and D. Zhu, "Breaking the Computational Barrier: A Divide-Conquer And Aggregate Based Approach For Alu Insertion Site Characterization", **Int. J. Computational Biology and Drug Design**, Vol. 2, No. 4, pp. 302–322

71. W. Fan and **K. Zhang**, "Bagging", **Encyclopedia of Database Systems**, pp. 206-210, Springer

72. E. Zhong, W. Fan, J. Peng, **K. Zhang**, J. Ren, D. Turaga and O. Verscheure, "Cross Domain Distribution Adaptation via Kernel Mapping", **Proceedings of the15th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining (KDD09)**, pp. 1027-1036, Paris. Acceptance rate < 9%

- **2008**

  73. W. Fan, **K. Zhang**, H. Cheng, J. Gao, X. Yan, J. Han, P. S. Yu, O. Verscheure, "Direct Mining of Discriminative and Essential Graphical and Itemset Features via Model-based Search Tree", **Proceedings of the 14th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining (KDD08),** pp. 230-238, Las Vegas. Acceptance rate < 9%

  74. **K. Zhang** and W. Fan, "Forecasting Skewed Biased Stochastic Ozone Days: Analyses, Solutions And Beyond", **Knowledge and Information System (KAIS),** 14(3), pp. 299-326, Springer, (Journal Impact Factor: 2.225)

  75. E. Zhong, S. Xie, W. Fan, J. Ren, J. Peng, and **K. Zhang**, "Graph-based Iterative Hybrid Feature Selection", **Proceedings of the 8th IEEE International Conference on Data Mining (ICDM08)**, pp. 1133-1138. Acceptance rate < 15%

  76. A. Lopez, **K. Zhang** and F. Lopez, "Cultural Representations of Gender Among U. S. Computer Science Undergraduates: Statistical and Data Mining Results", **Proceedings of the ACM SIGCSE 2008 technical symposium on computer science education**, pp. 407- 411, Portland

  77. A. Lopez, **K. Zhang** and F. Lopez, "Gender and Race: Stereotyping, Coping Self-efficacy and Collective Self-esteem in the CSET Undergraduate Pipeline", **Proceedings of the 38th ASEE/IEEE Frontiers in Education Conference**, Saratoga Springs, NY

- **2006**

  78. **K. Zhang**, W. Fan, B. Buckles, X. Yuan and Z. Xu, "Discovering Unrevealed Properties of Probability Estimation Trees: On Algorithm Selection and Performance Explanation", **Proceedings of the 6th IEEE International Conference on Data Mining (ICDM06)**, pp. 741-752. Acceptance rate < 9%

  79. **K. Zhang**, W. Fan, X. Yuan, I. Davidson and X. Li, "Forecasting Skewed Biased Stochastic Ozone Days: Analyses and Solutions", **Proceedings of the 6th IEEE International Conference on Data Mining (ICDM06)**, pp. 753 – 764. Acceptance rate < 9%,

  80. W. Fan and **K. Zhang**, "Pulmonary Embolism Prediction through Random Decision Trees", **KDDCUP2006**

- **2005**

  81. **K. Zhang**, Z. Xu, J. Peng and B. Buckles, "Learning Through Changes: an Empirical Study of Dynamic Behaviors of Probability Estimation Trees", **Proceedings of the 5th IEEE International Conference on Data Mining (ICDM05)**, pp. 817-820. Acceptance rate <15%

  82. C. Barbu, **K. Zhang**, J. Peng and B. Buckles, "Boosting In Classifier Fusion VS. Fusing Boosted Classifiers", **Proceedings of the IEEE International Conference on Information Reuse and Integration**, pp. 332 – 337. Acceptance rate < 30%

  83. **K. Zhang**, Z. Xu and B. Buckles, "Oblique decision tree induction using multi-membered evolution strategies", **Proceedings of the SPIE International Conference on Defense and Security**, Volume 5812, pp. 263-270. Acceptance rate < 35%

11

84. P. Zhang, J. Peng, **K. Zhang** and R. Sims, "Empirical comparison of robustness of classifiers on IR imagery", **Proceedings of the SPIE International Conference on Defense and Security,** Volume 5807, pp. 370-379. Acceptance rate $< 30\%$

- **2004**
   85. Z. Xu, **K. Zhang** and B. Buckles, "DNA sequence classification using support vector machine", **Proceedings of the 8th World Multiconference on Systemic, Cybernetics and Informatics**, Orlando.

Presentations and Invited Talk

1. "Detecting Race-Relevant Molecular Biomarkers with Clinical Utilities Using Multi-Omics Data across Tumor Types", LBRN annual meeting, 2019 - 2021
2. "Epigenetically silenced candidate tumor suppressor genes in prostate cancer: identified by modelling the stratified promoter methylation profiles over tumor samples and applied to progression prediction", LBRN Conference on Biology and Bioinformatics, Apr. 2019
3. Tumor Grade, Patient Age and Geographical Area Related Racial Disparity Patterns in Prostate Cancer Mortality: Epidemiological Implications and the Underlying Molecular Biology", LCRC retreat, May 2019
4. "Data Science – from Concepts to Practice", oral presentation, Xavier NEH Seminar Aug. 2018
5. "Driver gene mutations based clustering of tumors: methods and applications", oral presentation, ISMB conference, Jul. 2018
6. "Xavier RCMI Bioinformatics Facility – Progress Review", RCMI EAC Meeting, June., 2018
7. "Cancer Bioinformatics: Challenges and Methods", oral presentation, LCRC retreat, May 25th, 2018
8. "Epigenetically silenced candidate tumor suppressor genes in prostate cancer: identified by modelling the stratified promoter methylation profiles over tumor samples and applied to progression prediction", poster presentation, LCRC retreat, May 2018
9. "Driver gene mutations based clustering of tumors: methods and applications", poster presentation, LBRN Conference on Biology and Bioinformatics, Apr. 2018
10. "CSTG: An Effective Framework for Cost-sensitive Sparse Online Learning", Proceedings of the 17th SIAM International Conference on Data Mining, 2017
11. "Racial disparities in clinical outcomes and tumor mutation burden, and the association between tumor mutation burden and cancer incidence rate", the LCRC Retreat, 2017
12. "The Modularity and Dynamicity of miRNA-mRNA Interactions in High-Grade Serous Ovarian Carcinomas and the Prognostic Implication", Computational Biology and Chemistry", Fourth Annual LBRN Computational Biology and Bioinformatics Conference, 2016
13. "Integrative genomics and transcriptomics analysis reveals potential mechanisms for good prognosis of patients with human papillomavirus infected head and neck carcinomas", the LCRC Retreat, 2016
14. "Xavier RCMI Bioinformatics Facility – Progress Review", RCMI EAC Meeting, Mar., 2016
15. "The Modularity and Dynamicity of miRNA-mRNA Interactions in High-Grade Serous Ovarian Carcinomas and the Prognostic Implication", Computational Biology and Chemistry", Asian Pacific Bioinformatics Conference, 2016
16. "Xavier RCMI Bioinformatics Facility – Progress Review", RCMI EAC Meeting, Sep., 2015
17. "Ovarian carcinomas: somatic mutations and patient survival", LCRC annual scientific retreat, Apr. 2015

18. "Xavier RCMI Bioinformatics Facility – An Overview", LCRC seminar series, College of Pharmacy, Xavier University of Louisiana, April, 2015
19. "Xavier RCMI Bioinformatics Facility – An Update", RCMI EAC Meeting, Jan., 2015
20. "The duplication and intragenic domain expansion of human C2H2 zinc finger genes are associated with transposable elements and relevant to the expression-based clustering", the 7th international conference on Bioinformatics and Computational Biology (BICoB), Mar. 2015
21. "RS-Forest: A Rapid Density Estimator for Streaming Anomaly Detection", the 14th IEEE International Conference on Data Mining, Dec. 2014
22. "Somatic mutations favorable to patient survival are predominant in ovarian carcinomas", the International NIH Symposium on Minority Health and Health Disparities, Dec. 2014
23. "The duplication and intragenic domain expansion of human C2H2 zinc finger genes are associated with transposable elements and relevant to the expression-based clustering", LCRC annual scientific retreat, March, 2014
24. "The duplication and intragenic domain expansion of human C2H2 zinc finger genes are associated with transposable elements and relevant to the expression-based clustering", the Advanced Computational Biology symposium, Howard University, March 26th, 2014
25. "The duplication and intragenic domain expansion of human C2H2 zinc finger genes are associated with transposable elements and relevant to the expression-based clustering", LCRC seminar series, College of Pharmacy, Xavier University of Louisiana, April, 2014
26. "Alu Insertion Site Characterization & Beyond", RCMI Annual Meeting, NIH RCMI program, College of Pharmacy, Xavier University of Louisiana. May, 2014
27. "Alu distribution and mutation types of cancer genes", 2nd Annual High Performance Computing User Symposium-LSU, June, 2013
28. "miRNA-mediaed relationships between cis-SNP genotypes and transcript intensities in lymphocyte cell lines", 2nd Annual High Performance Computing User Symposium-LSU, June, 2013
29. "Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data", 2nd Annual High Performance Computing User Symposium-LSU, June, 2013
30. "Alu Insertion Site Characterization & Beyond", RCMI Annual Meeting, NIH RCMI program, College of Pharmacy, Xavier University of Louisiana. May, 2013
31. "Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data", LCRC annual scientific retreat, March, 2013
32. "Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data", the 13th RCMI International Symposium on Health Disparities. December, 2012
33. "Inferring the expression variability of human transposable element-derived exons by linear model analysis of deep RNA sequencing data", LCRC/RCMI seminars, College of Pharmacy, Xavier University of Louisiana. May, 2012
34. "Alu Insertion Site Characterization & Beyond", RCMI Annual Meeting, NIH RCMI program, College of Pharmacy, Xavier University of Louisiana. April, 2012
35. "Enhancement of microRNA research through bioinformatics tool development", Louisiana Biomedical Research Network Annual Retreat, NIH INBRE program. January, 2012
36. "Alu distribution and mutation types of cancer genes", Southeast Regional IDeA Meeting. September, 2011
37. "miRNA-mediated relationships between cis-SNP genotypes and transcript intensities in lymphocyte cell lines", Southeast Regional IDeA Meeting. September, 2011
38. "SNP-involved, miRNA-mediated relationships between cis-SNP genotypes and transcript intensities in lymphocyte cell lines", Dr. Erik Flemington Lab, Tulane Cancer Center. February, 2011

39. "miRNA-mediated relationships between cis-SNP genotypes and transcript intensities in lymphocyte cell lines", Louisiana Biomedical Research Network Annual Retreat, NIH INBRE program. January, 2011
40. "Top-10 Data Mining Case Studies: forecasting skewed biased stochastic Ozone Days: analyses, solutions and beyond", the 10th IEEE International Conference on Data Mining. December, 2010.
41. "A divide-conquer and aggregate based approach for Alu insertion site characterization", the 12th RCMI International Symposium on Health Disparities. December, 2010
42. "Generalized and heuristic-free feature construction for improved accuracy", SIAM International Conference on Data Mining. April, 2010
43. "A divide-conquer and aggregate based approach for Alu insertion site characterization", Louisiana Biomedical Research Network Annual Retreat, NIH INBRE program. January, 2010
44. "A divide-conquer and aggregate based approach for Alu insertion site characterization", LCRC/RCMI seminars, College of Pharmacy, Xavier University of Louisiana, 2010
45. "Direct mining of discriminative and essential frequent patterns via model-based search tree", the Department of Computer Science, University of New Orleans. October, 2009
46. "Efficient characterization of Alu insertion sites via model-based search tree", Louisiana Cancer Research Consortium Annual Scientific Retreat. March, 2009
47. "Efficient characterization of Alu insertion sites via model-based search tree", Louisiana Biomedical Research Network Annual Retreat, NIH INBRE program. January, 2009
48. "Direct mining of discriminative and essential graphical and itemset features via model based search tree", the 14th ACM SIGKDD International Conference on Knowledge Discovery & Data Mining. August, 2008.
49. "Decision trees, regularized least squares and their applications to automatic target recognition", SPIE Defense and Security. April, 2007
50. "Forecasting skewed biased stochastic ozone days: analyses and solutions", the 6th IEEE International Conference on Data Mining. December, 2006
51. "Discovering unrevealed properties of probability estimation trees: on algorithm selection and performance explanation", the 6th IEEE International Conference on Data Mining. December, 2006
52. "Learning through changes: an empirical study of dynamic behaviors of probability estimation trees", the 5th IEEE International Conference on Data Mining. November, 2005
53. "Oblique decision tree induction using multi-membered evolution strategies", SPIE Defense and Security, 2005

Professional Services

- Member of ACM (Association for Computing Machinery)
- Member of ISCB (International Society for Computational Biology)
- Reviewer or Review Editorial Board for the following journals
    - 2019 — : Nature Biotechnology
    - 2018 — : Briefings in Bioinformatics
    - 2015 — : Frontiers Oncology
    - 2014 — : Information Fusion
    - 2013 — : OMICS: A Journal of Integrative Biology
    - 2012 — : ACM Transactions on Knowledge Discovery from Data
    - 2011 — : Frontiers Journal Series
    - 2010 — : Knowledge and Information Systems (KAIS)

- External Reviewer for Tulane University's Oliver Fund Scholar competition, 2018
- Organizer of the International Workshop on Big Data, Streams and Heterogeneous Source Mining: Algorithms, Systems, Programming Models and Applications, 2012-2018 (http://big-data-mining.org/)
- NSF Panelist for Division of Undergraduate Education, 2017
- Session Chair of the SIAM International Conference on Data Mining (SDM17).
- Local arrangement Co-chair of the IEEE International Conference on Data Mining (ICDM 2017)
- Program Committee Member or Reviewer for the following national or international conferences including
    - The 21st IEEE International Conference on Data Mining, 2021
        - Reviewed 8 out of 800+ papers submitted internationally
    - The 35th AAAI Conference on Artificial Intelligence, 2021
        - Reviewed 7 out of 1000+ papers submitted internationally
    - The 20th IEEE International Conference on Data Mining, 2020
        - Reviewed 8 out of 900+ papers submitted internationally
    - The 34th AAAI Conference on Artificial Intelligence, 2020
        - Reviewed 7 out of 1000+ papers submitted internationally
    - The 33rd AAAI Conference on Artificial Intelligence, 2019
        - Reviewed 6 out of 1000+ papers submitted internationally
    - The 19th IEEE International Conference on Data Mining, 2019
        - Reviewed 8 out of 900+ papers submitted internationally
    - The 28th ACM International Conference on Information and Knowledge Management, 2019
        - Reviewed 7 out of 800+ papers submitted internationally
    - The 18th IEEE International Conference on Data Mining, 2018
        - Reviewed 8 out of 900+ papers submitted internationally
    - The 1st IEEE International Conference on Artificial Intelligence and Knowledge Engineering, 2018
        - Reviewed 3 out of 60+ papers submitted internationally
    - The 17th IEEE International Conference on Data Mining, 2017
        - Reviewed 17 out of 700+ papers submitted internationally
    - The SIAM International Conference on Data Mining (SDM17), 2017
        - Reviewed 9 out of 400+ papers submitted internationally
    - The 16th IEEE International Conference on Data Mining, 2016
        - Reviewed 10 out of 900+ papers submitted internationally
    - The SIAM International Conference on Data Mining (SDM16), 2016
        - Reviewed 7 out of 500+ papers submitted internationally
    - The 15th IEEE International Conference on Data Mining, 2015
        - Reviewed 7 out of 800+ papers submitted internationally
    - The ECML/PKDD 2015 CONFERENCE,
        - Reviewed 3 out of 500+ papers submitted internationally
    - The SIAM International Conference on Data Mining (SDM15), 2015
        - Reviewed 10 out of 500+ papers submitted internationally
    - The SIAM International Conference on Data Mining (SDM14), 2014
        - Reviewed 4 out of 500+ papers submitted internationally

- o The ECML/PKDD 2014 CONFERENCE
  - ▪ Reviewed 3 out of 500+ papers submitted internationally
- o The 14th IEEE International Conference on Data Mining, 2014
  - ▪ Reviewed 7 out of 900+ papers submitted internationally
- o The 13th IEEE International Conference on Data Mining, 2013
  - ▪ Reviewed 10 out of 900+ papers submitted internationally
- o The NIH RCMI 2012 International Health Disparities Symposium, 2012
  - ▪ Reviewed 10 abstracts submitted nationally
- o Supervised Undergraduate Research Experiences Program, Louisiana Board of Regents. 2012
  - ▪ Reviewed 4 CS proposals submitted within the state
- o The 11th IEEE International Conference on Data Mining, 2011
  - ▪ Reviewed 8 out of 900+ papers submitted internationally
- o The European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML PKDD), 2011
  - ▪ Reviewed 7 out of 700+ papers submitted internationally
- o The 10th IEEE International Conference on Data Mining, 2010
  - ▪ Reviewed 7 out of 800+ papers submitted internationally
- o The ACM SIGKDD International Conference on Data Mining, 2010
  - ▪ Reviewed 8 out of 700+ papers submitted internationally
- o FSDM-2010: International Workshop on Feature Selection for Data Mining
  - ▪ Reviewed 4 out of 300+ papers submitted internationally
- o The 8th IEEE International Conference on Data Mining, 2008
  - ▪ Reviewed 8 out of 900+ papers submitted internationally
- o The Data Streaming Mining and Management Workshop, the 7th IEEE International Conference on Data Mining, 2007
  - ▪ Reviewed 9 out of 300+ papers submitted internationally
- o Reviewer for ACM SIGKDD 2006, IEEE CVPR 2005