Jie Chen, Ph.D.

Curriculum Vita

Updated on June 30, 2021

Mailing Address: Division of Biostatistics and Data Science, Department of Population Health Sciences, Medical College of Georgia, Augusta University, 1120 15th Street, AE - 1017, Augusta, GA 30912-4900

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Education

- Ph.D. in Statistics: August, 1995; Bowling Green State University, USA
- M.S. in Applied Statistics: June, 1990; The University of Akron, USA
- B.S. in Applied Mathematics: July, 1985; Chongqing University, P.R. China

Academic Positions

- August 2014 - Present: Professor of Biostatistics, Division of Biostatistics and Data Science, Department of Population Health Sciences (formerly Department of Biostatistics & Epidemiology), Medical College of Georgia, Augusta University

  Courses Taught:

  - STAT 9120 Theory of Linear Model
  - STAT 8640 Generalized Linear Models I
  - STAT 8620 Statistical Theory II
  - STAT 7110 Statistics Models and Methods
  - STAT 7020 Biostatistics II (on-line and in-class)
  - STAT 7910 Statistical Consulting Project
  - STAT 8870 Biostatistical Consulting in Research
  - STAT 8110 Introduction to Biostatistics
  - STAT 8890 Readings and Research
  - STAT 9300 Dissertation Research
- 2008 - 2015: Professor of Statistics, Department of Mathematics and Statistics, University of Missouri-Kansas City (UMKC)
  - Sept. 2014 - Aug. 2015: On-leave from UMKC
  - Jan. 2013 - Dec. 2013: Visiting Scientist, Bioinformatics Core, Stowers Institute for Medical Research, Kansas City, Missouri (on-leave from UMKC, funded by Stowers Institute, returned to UMKC in Jan. 2014)

  - Feb. 2012 - Aug. 2015: Secondary appointment - Clinical Professor of Department of Biomedical and Health Informatics, UMKC School of Medicine

- July, 2004 - December, 2006: Visiting Scientist, Bioinformatics Center, Stowers Institute for Medical Research, Kansas City, Missouri

- 2001 - 2008: Associate Professor, Department of Mathematics and Statistics, University of Missouri-Kansas City

- 1995 - 2001: Assistant Professor, Department of Mathematics and Statistics, University of Missouri-Kansas City

  Courses Taught from 1995 to 2014 at UMKC:

  - STAT 5537 Mathematical Statistics I (Graduate core courses)
  - STAT 5547 Mathematical Statistics II (Graduate core courses)
  - STAT 5565 Regression Analysis (Graduate core course)
  - STAT 5551 Applied Statistical Analysis (Graduate core course)
  - STAT 5572 Multivariate Analysis (Graduate core course)
  - STAT 5588 Theory of Linear Model (Doctoral core course)
  - STAT 5590 Special Topics: Clustering Analysis (Graduate independent reading course)
  - STAT 5590 Special Topics: Statistical Genetics (Graduate independent reading course)
  - STAT 5590 Special Topics: Biostatistics Topics (Graduate independent reading course)
  - STAT 5590 Special Topics: Statistical Change Point Analysis (Graduate independent reading course)
  - STAT 436 Intro to Mathematical Statistics I (Undergraduate Course)
  - STAT 235 Elementary Statistics (Undergraduate Course)

- 1990 - 1995: Teaching Fellow, Bowling Green State University

  Courses Taught: Introduction to Statistics, Calculus for Business

- 1988 - 1990: Graduate Research Assistant (Statistical Consulting Center), University of Akron

- 1985 - 1988: Lecturer, Southwest University of Finance and Economics, Chengdu, Sichuan, P.R. China

  Courses Taught: Linear Algebra, Mathematical Analysis, Calculus, Linear Programming, Probability and Statistics

Administrative Positions

- July 2017 - Present: Division Chief, Division of Biostatistics and Data Science, Department of Population Health Sciences, Medical College of Georgia, Augusta University

- July 2015 - January 2021: Graduate Program Director of the PhD Program in Biostatistics, Department of Population Health Sciences (formerly Department of Biostatistics & Epidemiology), Medical College of Georgia, Augusta University

- July 2015 - June 2021: Graduate Program Director of the MS Program in Biostatistics, Department of Population Health Sciences (formerly Department of Biostatistics & Epidemiology), Medical College of Georgia, Augusta University
- July 2008 - Aug. 2014: Department Chair (two full terms), Department of Mathematics and Statistics, University of Missouri-Kansas City, Kansas City, Missouri
- 2003 - May, 2008: Interdisciplinary Ph.D. Coordinator of the Department of Mathematics and Statistics, University of Missouri-Kansas City
- 2003 - August, 2007: Principal Graduate Advisor of the Department of Mathematics and Statistics, University of Missouri-Kansas City

Professional Memberships/National Offices

- Feb. 2016 - Jan. 2022: American Statistical Association (ASA) Representative to the Joint Committee on Women (JCW) in the Mathematical Sciences
- 2015 - Present: Member, Eastern North America Biometric Society (ENAR)
- 2015 - Present: Member, Association for Women in Mathematics (AWM)
- 2015 - Present: Member, Caucus of Women in Statistics (CWS)
- 2014 - Present: member of the Southern Regional Council of Statistics (SRCOS)
- 2013 - present: member of the Institute of Mathematical Statistics (IMS)
- 2009 - present: member of the American Mathematical Society (AMS)
- 2008 - present: member of the ASA Caucus of Academic Representatives
- 1999 - present: Life-time member of the International Chinese Statistical Association (ICSA)
- 1998 - 2000, 2014-2016: member of the International Indian Statistical Association (IISA)
- 1996 - present: member of ASA

Editorial Service

- May, 2021 - present: Associate Editor, *Frontiers in Statistics*
- January 1, 2017 - present: Editor-in-Chief, *Journal of Applied Stattistics*, Taylor & Francis, UK
- April, 2011 - present: Associate Editor, *Frontiers in Comuptational Genomics*, formerly *Frontiers in Bioinformatics and Computational Biology*
- July, 2006 - present: Reviewer, *Mathematical Reviews*
- August, 2005 - May, 2021: Associate Editor, *Journal of Probability and Statistical Science*

Awards and Honors

- April, 2021: Received the "Distinguished Service Award" given by Augusta University Graduate School for outstanding services to the graduate education at Augusta University.
- August, 2014: Elected as a Fellow of the American Statistical Association (ASA)
- 2010: Awarded University of Missouri President's Leadership Development Program (LDP) Certificate - Nominated by the Dean of the College of Arts and Sciences and the Provost of UMKC, and selected by the University of Missouri (UM) System to participate in the 2010 University of Missouri's Leadership Development Program (LDP), which is part of the UM President's Academic Leadership Institute. Being one of a select group of participants identified from throughout the UM System reflected participates' "potential to continue to make important professional contributions to the University community."
- Sept. 17 - 21, 2007: Lukcas Visiting Scholar, Department of Mathematics and Statistics, Bowling Green State University
- Apr. 23, 2004: Faculty honoree on Faculty and Staff Appreciation Day organized by the UMKC Activity and Program Council
- 2001: Faculty honoree at the 2001 UMKC Convocation and Awards Ceremony
- 2001: Promoted to Associate Professor with tenure
- 1995: Graduate Student Teaching Award, Bowling Green State University
- 1993 - 1994: Awarded Non-service Graduate Fellowship, Bowling Green State University

Research Interests

Statistical Change Point Analysis, Applied Statistics, Statistical Inference, Statistics in Bioinformatics, Biostatistics, Statistical Modeling of genomics data and DNA copy number experimental data, general data analysis, statistical consulting

Research Grants/Contracts

- 02/01/2020 - 01/31/2022: National Science Foundation (NSF), Principle Investigator, Project title: Second Annual Data Science Workshop: Emerging Data Science Methods for Complex Biomedical and Cyber Data.
- 05/01/2017 - 04/30/2022: National Institutes of Health, NIH Program Project Grant (PI: C. Isales), co-Investigator in Core A, Project title: Age Induced Impairment of Nutrient Signaling Results in Bone Loss.
- 01/01/2017 - present: Contract from Taylor & Francis Informa UK for Editor-in-Chief of the Journal of Applied Statistics
- 09/2012-08/2014: Faculty Research Grant, PI, awarded by University of Missouri Research Board (UMRB), Project title: Change Point Methods for the Estimation of CNV Regions in Next-Generation Sequencing Data.
- 12/2009-11/2010: Research grant, awarded by the Kansas City Area Life Science Research Institute, co-PI, Project title: Discovering the Etiology of Tetralogy of Fallot (PI: Dr. Doug Bittel, Children's Mercy Hospital and Clinics of Kansas City, MO)

- 5/2009-4/2010: Faculty Research Grant, PI, awarded by University of Missouri Research Board (UMRB), Project title: Statistical Approaches to the Identification of DNA Copy Number Variations
- 12/2004-11/2006: National Science Foundation (NSF) Grant, PI, Project title: Statistical Approaches to the Analysis of Genome-wide Measurements: Significance of Periodic Gene Expression and Correlations of Gene Content in Completely Sequenced Genomes,
- 1995 - 1996: Faculty Research Grant, PI, awarded by University of Missouri-Kansas City, Project title: Change Point Analysis with Applications

Refereed Journal Publications

I. Statistical methodology papers

1. Deng S, **Chen J**, Shi H, Integrative analysis of multiple types of genomic data using an accelerated failure time frailty model, *Computational Statistics*, 36(2), 1499-1532, 2021.
2. Coughlin SS, Yiğiter A, Xu H, Berman AE, **Chen J**, Early detection of change patterns in COVID-19 incidence and the implementation of public health policies: a multi-national study, *Public Health in Practice*, Volume 2, 2021, 100064, ISSN 2666-5352, https://doi.org/10.1016/j.puhip.2020.100064
3. Lee J and **Chen J**, A modified information criterion for tuning parameter selection in 1d fused LASSO for inference on multiple change points, *Journal of Statistical Computation and Simulation*, 90(8), 1496-1519, 2020.
4. Lee J and **Chen J**, A penalized regression approach for DNA copy number study using the sequencing data, *Statistical Applications in Genetics and Molecular Biology*, 30(18):4, 2019.
5. **Chen**, J. and Deng, S. (2018) Detection of Copy Number Variation Regions Using the DNA-Sequencing Data from Multiple Profiles with Correlated Structure, *Journal of Computational Biology*, **25**, 1128-1140.
6. Su Y, Shen X, **Chen J**, Isales CM, Zhao J, Shi X (2017). Differentially expressed genes in PPARg-deficient MSCs, *Molecular and Cellular Endocrinology*, **471**, 97-104.
7. Ji, T. and **Chen, J.** (2016). Statistical Methods for DNA Copy Number Variation Detection Using the Next Generation Sequencing Data. *Australian & New Zealand Journal of Statistics*, **58**, 473-491.
8. **Chen, J.** and Li, H. (2016). A Statistical Change-Point Analysis Approach for Modeling the Ratio of Next Generation Sequencing Reads. *Advances in the Mathematical Sciences, Association for Women in Mathematics*, Series 6, 283-300.
9. Ji, T. and **Chen, J.** (2015). Modeling the Next Generation Sequencing Read Count Data for DNA Copy Number Variant Study. *Statistical Applications in Genetics and Molecular Biology*, **14**, 361–374.
10. Ayten Yiğiter, J**Jie Chen**, Lingling An, and Nazan Danacioğlu (2015). An on-line CNV detection method for short sequencing reads, *Journal of Applied Statistics*, **42**:7, 1556 –1571
11. Paul J. Plummer and **Jie Chen** (2014). A Bayesian approach for locating change points in a compound Poisson process with application to detecting DNA copy number variations, *Journal of Applied Statistics*, **41**, 423–438.

12. Hua Li, Jim Vallandingham, and **Jie Chen** (2013). SeqBBS: A change-point model based algorithm and R package for searching CNV regions via the ratio of sequencing reads, refereed conference paper, *Proceedings of the 2013 IEEE International Workshop on Genomic Signal Processing and Statistics*, 46-49.

13. Beaulieu, Claudie, **Chen, Jie** and Sarmiento, Jorge L (2012). Change-point analysis as a tool to detect abrupt climate variations. *Philosophical Transactions A of the Royal Scoiety: Mathematical, Physical & Engineering Sciences*, **370**, 1228-1249.

14. Claudie Beaulieu, J. L. Sarmiento, S. E. Mikaloff Fletcher, **Jie Chen**, and D. Medvigy (2012). Identification and characterization of abrupt changes in the land uptake of carbon. *GLOBAL BIOGEOCHEMICAL CYCLES*, **26**: GB1007.

15. **Chen, Jie**, Yiğiter, A. and Chang, K.C. (2011). A Bayesian approach to inference about a change point model with application to DNA copy number experimental data. *Journal of Applied Statistics*, **38:9**, 1899-1913. First published on-line on 01 December 2010, DOI:10.1080/02664763.2010.529886.

16. Zhao J, **Chen Jie**, Yang TH, Holme P (2011). Pathogenesis of Axial Spondyloarthropathy in a Network Perspective, refereed conference paper, *2011 IEEE Conference on Systems Biology*, 2011, 41-46.

17. **Chen, Jie**, Yiğiter, A., Wang, Y.-P., and Deng, H.-W.(2010). A Bayesian Analysis for Identifying DNA Copy Number Variations using a Compound Poisson Process. *EURASIP Journal of Bioinformatics and Systems Biology.* vol. 2010, Article ID 268513, 10 pages. doi:10.1155/2010/268513.

18. **Jie Chen** and Yu-Ping Wang (2009). A Statistical Change Point Model Approach for the Detection of DNA Copy Number Variations in Array CGH Data. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **6**, 529-541.

19. **Chen, Jie** and Chang, K.-C. (2008). Discovering statistically significant periodic gene expression. *International Statistical Review*, **76**, 228-246.

20. **Chen, Jie** and Gupta, A.K. (2007). A Bayesian approach to the statistical analysis of a smooth-abrupt change point model. *Advances and Applications in Statistics*, **7**, 115-125.

21. Yu-Ping Wang, Maheswar Gunampally, **Jie Chen**, Douglas Bittel, Merlin G. Butler and Wei-Wen Cai (2007). A Comparison of Fuzzy Clustering Approaches for Quantification of Microarray Gene Expression. *Journal of VLSI Signal Processing*, published on-line first on August 17, 2007 at the SpringerLink DOI: 10.1007/s11265-007-0123-0.

22. **Jie Chen** and Yu-Ping Wang (2006). Detection of DNA copy number changes using statistical change point analysis, refereed conference paper, *Proceedings of the 2006 IEEE International Workshop on Genomic Signal Processing and Statistics*, 11-12.

23. **Chen, Jie**, Chen, J.T. and Gupta, A.K. (2006). Statistical Properties and a Likelihood Ratio Test for a Distorted Normal Model. *Far East Journal of Theoretical Statistics*, **18**, 145-160.

24. Earl F. Glynn, **Jie Chen**, and Arcady R. Mushegian (2006). Detecting periodic patterns in unevenly spaced gene expression time series using Lomb-Scargle periodograms. *Bioinformatics*, **22**, 310-316.

25. **Jie Chen** (2005). Identification of significant periodic genes in microarray gene expression data. *BMC Bioinformatics*, **6**:286.

26. Wang, Y., **Chen, Jie**, Wu, Q., and Castleman, K.R. (2005). Fast Frequency Estimation by Zero Crossings of Differential Spline Wavelet Transform. *EURASIP Journal on Applied Signal Processing*, **8**, 1251-1260.

27. **Jie Chen** and A. K. Gupta (2004). Statistical Inference of Covariance Change points in Gaussian Model. *Statistics*, **38**, 17-28.

28. Balakrishnan, N. and **Chen, Jie** (2004). Detecting a Change Point in a Sequence of Extreme Value Observations. *Journal of Probability and Statistical Science*, **2**, 55-64.

29. Nagar, D. K., **Chen, Jie**, and A. K. Gupta (2004). Distribution and Percentage Points of the Likelihood Ratio Statistic for Testing Circular Symmetry. *Computational Statistics and Data Analysis*, **47**, 79-89.

30. **Jie Chen**, Xi He, and Linheng Li (2004). Identifying the Patterns of Hematopoietic Stem Cells Gene Expressions using Clustering Methods: Comparison and Summary. *Journal of Data Science*, **2**, 297-309.

31. **Jie Chen** (2003). A Note on Change Point Analysis in a Failure Rate. *Journal of Probability and Statistical Science*,**1**, 135-140.

32. **Jie Chen** and N. Balakrishnan (2002). Locating a Change Point in a Gaussian Model when an Outlier is Present. *Journal of Applied Statistical Science*, **11**, 101-109, 2002.

33. **Jie Chen** and A. K. Gupta (2001). On Change Point Detection and Estimation. *Communications in Statistics-Simulation and Computation* , **30**, 665-697.

34. Logan, T. P., Gupta, A. K., and **Chen, Jie** (2000). On classification of multiple observations with application to marketing analysis. *American Journal of Mathematical Management Science*, **20**, no. 3-4, 387-402.

35. **Jie Chen** and A. K. Gupta (2000). Detecting Change Points for a Sequence of Random Vectors under Nonnormaility. *Random Operators and Stochastic Equations*, **8**, 127-142.

36. **Jie Chen** and A. K. Gupta (1999). Change Point Analysis of a Gaussian Model. *Statistical Papers*, **40**, 323-333.

37. A. K. Gupta, T. P. Logan, and **Jie Chen** (1999). A Variable Selection Technique in Discriminant Analysis with Application in Marketing Data. *Journal of Statistical Computation and Simulation*, **63**, 187-199.

38. **Jie Chen** (1998). Testing for a Change Point in Linear Regression Models. *Communications in Statistics-Theory and Methods*, **27**, 2481-2493.

39. **Jie Chen** and A. K. Gupta (1997). Testing and Locating Variance Change Points with Application to Stock Prices. *Journal of the American Statistical Association*, **92**, 739-747.

40. A. K. Gupta and **Jie Chen** (1996). Detecting Changes of Mean in Multidimensional Normal Sequences with Application to Literature and Geology. *Computational Statistics*, **11**, 211-221.

41. **Jie Chen** and A. K. Gupta (1995). Likelihood Procedure for Testing Change Point Hypothesis for Multivariate Gaussian Model. *Random Operators and Stochastic Equations*, **3**, 245-254.

II. Collaborative papers

42. Coughlin SS, **Chen J**, Cortes JE. Health care access and utilization among adult cancer survivors: Results from the National Institutes of Health "All of Us" Research Program. Cancer Medecine. 2021 May 3. doi: 10.1002/cam4.3924.

43. Rangachari P, **Chen J**, Ahuja N, Patel A, Mehta R. "Demographic and Risk Factor Differences between Children with "One-Time" and "Repeat" Visits to the Emergency Department for Asthma," Int. J. Environ. Res. Public Health 2021, 18, 486.

44. Lu X, Vick S, Chen Z, **Chen J**, Watsky MA. Effects of Vitamin D Receptor Knockout and Vitamin D Deficiency on Corneal Epithelial Wound Healing and Nerve Density in Diabetic Mice. Diabetes, 69(5):1042-1051, 2020.

45. Scott S, Byrd JK, Figueroa R, Williams H, **Chen J**, Lee J, Pucar D. 18F-fluorodeoxyglucose positron emission tomography/ computed tomography in predicting overall survival of oral cavity squamous cell carcinoma: Ongoing controversy, *World Journal of Nuclear Medicine*, 19(2): 111-117, 2020.

46. Chen L, Dong Y, **Chen J**, Huang Y, Zhu H. Epigenetics Predicts Serum 25-hydroxyvitamin D3 Response to Vitamin D3 Supplementation in African Americans, Molecular Nutrition & Food Research. DOI: 10.1002/mnfr.201900738. 64(1):e1900738, 2020.

47. Ellsworth SG, Rabatic BM, **Chen J**, Zhao J, Campbell J, Wang W, Stanton P, Matuszak M, Jolyy S, Kong FM (2017): Principal component analysis identifies patterns of cytokine expression in non-small cell lung cancer patients undergoing definitive radiation therapy, *PLOS ONE*, 12:9 e0183239.

48. Jin, J., Wang, W., Ten Haken, R. K., **Chen, J.**, Bi, N., Sadek, R., Zhang, H., Lawrence, T. S., Kong, F. (2015). Use a survival model to correlate single-nucleotide polymorphisms of DNA repair genes with radiation dose-response in patients with non-small cell lung cancer. *Radiotherapy and oncology : journal of the European Society for Therapeutic Radiology and Oncology*, **117**(1), 77-82.

49. Chatterjee, A., Ronghe, A., Singh. B., Bhat, N.K., **Chen, J** and Bhat, H.K. (2014) Natural antioxidants exhibit chemopreventive characteristics through the regulation of CNC-bZip transcription factors in estrogen-induced breast carcinogenesis. *J. Biochem. Mol. Toxicol.* **28**(12):529-538.

50. Zhao, Jing, **Chen, Jie**, Yang, Ting-Hong, and Holme, Petter (2012). Insights into the pathogenesis of axial spondyloarthropathy from network and pathway analysis. *BMC Systems Biology*, **6** (Suppl 1):S4.

51. James E. O'Brien, Jr, Nataliya Kibiryeva, Xin-Gang Zhou, Jennifer A. Marshall, Gary K. Lofland, Michael Artman, **Jie Chen**, and Douglas C. Bittel (2012). Noncoding RNA Expression in Myocardium From Infants With Tetralogy of Fallot. *Circulation: Cardiovascular Genetics*, **5**, 279-286.

52. Chiming Huang, Jennifer A. Titus, Richard L. Bell, Tamas Kapros, **Jie Chen** and Rosa Huang (2012). A Mouse Model for Adolescent Alcohol Abuse: Stunted Growth and Effects in Brain. *Alcoholism: Clinical and Experimental Research*, **36**, 1728–1737.

53. Douglas C Bittel, Merlin G Butler, Nataliya Kibiryeva, Jennifer A Marshall, **Jie Chen**, Gary K Lofland and James E O'Brien Jr. (2011). Gene expression in cardiac tissues from infants with idiopathic conotruncal defects. *BMC Medical Genomics*, 2011, **4:1**, doi:10.1186/1755-8794-4-1.

54. Le, J., Zhang, D., Menees, S., **Chen, Jie**, and Raghuveer, G.(2010). "Vascular Age" is Advanced in Children with Atherosclerosis Promoting Risk Factors. *Circulation: Cardiovascular Imaging*, **3**, 8-14.

55. Menees, S., Zhang, D., Le, J. **Chen, Jie** and Raghuveer, G.(2010). Variations in Carotid Artery Intima-media Thickness During the Cardiac Cycle in Children. *Journal of the American Society of Echocardiography*, **23**, 58-63.
56. Feng Zhang, Jianfeng Liu, **Jie Chen** and Hong-Wen Deng. (2008). HAPSIMU: a genetic simulation platform for population-based association studies. *BMC Bioinformatics*, **9**:331, published online first on August 5th, 2008 doi:10.1186/1471-2105-9-331.
57. Mary-Lee Dequéant, Earl Glynn, Karin Gaudenz, Matthias Wahl, **Jie Chen**, Arcady Mushegian, Olivier Pourquiè (2006). A Complex Oscillating Network of Signaling Genes Underlies the Mouse Segmentation Clock. *Science*, **314**, 1595-1598, 2006.
58. Koichi Akashi, Xi He, **Jie Chen**, Hiromi Iwasaki, Chao Niu, Brooke Steenhard, Jiwang Zhang, Jeff Haug, and Linheng Li (2003). Transcriptional Accessibility for Multi-Tissue and Multi-Hematopoietic Lineage Genes is Hierarchically Controlled During Early Hematopoiesis. *Blood*, **101**, 383-390.
59. Li,B., Pattenden, S.G., Lee, D., Gutièrrez, J., **Chen, Jie**, Seidel, C., Gerton, J. and Workman, J.L. (2005). Preferential occupancy of histone variant H2AZ at inactive promoters influences local histone modifications and chromatin remodeling. *Proceedings of the National Academy of Science*, **102**, 18385-18390.

Book Publication

1. **Jie Chen** and A. K. Gupta (2012). *Parametric Statistical Change Point Analysis - With Applications to Genetics, Medicine, and Finance*, second edition, Birkhauser, and copyrighted by Springer Science+Business Media LLC, New York.
2. **Jie Chen** and A. K. Gupta (2000). *Parametric Statistical Change Point Analysis*, Birkhauser, Boston.

Other Publications

(1). Book Chapter:

- **Chen J** (2021), Statistical Considerations on NGS Data for Inferring Copy Number Variations, Chapter 2 in the book *Deep Sequencing Data Analysis - Methods in Molecular Biology* (Noam Shomron (ed.)), vol. 2243, Springer Science+Business Media, LLC, part of Springer Nature 2021.
- **Chen, Jie** (2010). Change Point Methods in Genetics, in *Encyclopedia of Statistical Sciences* (Editors Kotz, S., Read, C.B., Balakrishnan, N. and Vidakovic, B.), John Wiley & Sons: Hoboken, NJ, USA.
- **Jie Chen** and Balakrishnan, N. (2003). Locating a Change Point in a Gaussian Model when an Outlier is Present, in *Focus on Applied Statistics* (Editor: Ahsanullah, M.), pp. 103-113. Nova Science Publishers, Inc., Hauppauge, New York.

(2). Non-refereed Conference Proceeding Paper/other paper:

- **Jie Chen**, Editorial, *Journal of Applied Statistics*, **48**(1), 1-3, 2021.
- **Jie Chen** (2017). Editorial, *Journal of Applied Statistics*, **44**(1), 1-2.

- **Jie Chen** and Y-P Wang (2007). Identification of DNA Copy Number Changes in aCGH Data, invited guest speaker paper in *Proceedings of The 4th Sino-International Symposium on Probability, Statistics, and Quantitative Management*, Vol. 4, pp. 11-20
- **Jie Chen** (2005). Change Point Analysis for Covariance Matrix in Multivariate Normal Models: An Application. Invited guest speaker paper in *Proceedings of the Second Sino-International Symposium on Probability, Statistics, and Quantitative Management*, Vol. 1, pp. 51-58

Invited Seminar Talks/Lectures (A selection)

1. Chen J “Detection of multiple change points in streaming data: Methods and Applications”, invited talk given at the Department of Biostatistics ZOOM seminar series of Spring 2021, School of Public Health and Health Professions, University at Buffalo, New York, April 15, 2021
2. Chen J “Statistical inference for multiple change points in streaming data,” invited Graduate Seminar in Probability & Statistics at Department of Mathematical Sciences, University of Wisconsin – Milwaukee, March 29, 2021
3. Chen J “Detection of Multiple Change Points: Methods and Applications,” Colloquium talk, Division of Biostatistics and Data Science, Population Health Sciences, Medical College of Georgia, Augusta University, on Feb. 8, 2019.
4. Chen J “Retrospective Multiple Change Points Detection: Method, Theory, and Application,” invited lecture at the Chinese Academy of Sciences, Beijing, China, on June 27, 2018.
5. Chen J “Bayesian approaches to change point analysis and their applications in CNV study,” invited seminar talk at Department of Epidemiology and Biostatistics, Arnold School of Public Health, University of South Carolina, on April 24, 2017.
6. “Change point analysis via Bayesian approach and its applications in the studies of DNA copy number variations,” invited lecture at School of Mathematical Sciences, Chongqing Normal University, Chongqing, China, December 12, 2016.
7. “An effective detection method for identifying DNA copy number variations using high throughput sequencing data,” invited lecture at School of Mathematical Sciences, Chongqing Normal University, Chongqing, China, December 13, 2016.
8. “Change point analysis via Bayesian approach and its applications in the studies of DNA copy number variations,” invited lecture at College of Mathematics and Statistics, Chongqing University, Chongqing, China, December 14, 2016.
9. ”Change point models in the Bayesian Perspective and their applications in CNV study,” Interdisciplinary Graduate Program in Statistics, University of Arizona, Tucson, AZ. April 6, 2016.
10. “Modeling genomics data of different platforms for the detection of CNV regions,” Department of Mathematics and Statistics Seminar, Georgia State University, Atlanta, GA., September 18, 2015.
11. “A short course in applied statistical modeling,” Chongqing University, Chongqing, China. June 22-24, 2015.
12. “On Statistical Modeling of Biological Data”, invited seminar talk, Department of Cancer Epidemiology, Cancer Institute/Hospital, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing, China, December 9, 2014.

13. “Change Point Analysis and its Applications”, invited seminar talk, Quality and Data Science Center, Academy of Mathematics & System Sciences, Chinese Academy of Sciences, Beijing, China, December 10, 2014.

14. “New methods for detecting DNA copy number variations using the next-generation sequencing data”, invited seminar talk, College of Bioengineering, Chongqing University, Chongqing, China, December 17, 2014.

15. “Change Point Analysis and its Applications”, invited seminar talk, College of Mathematics and Statistics, Chongqing University, Chongqing, China, December 18, 2014.

16. “New methods for detecting DNA copy number variations using the next-generation sequencing data”, invited seminar talk, College of Mathematical Sciences, Chongqing Normal University, Chongqing, China, December 18, 2014.

17. “Modeling next generation sequencing data for the detection of DNA structural changes”, Statistics seminar, H. Milton Stewart School of Industrial and Systems Engineering, Georgia Institute of Technology, Atlanta, Georgia, USA, September 17, 2013.

18. “Detecting CNV regions using genomics data of different platforms,” Graduate Seminar, College of Mathematics, Chongqing University, Chongqing, China, June 17, 2013, and invited lecture, Chongqing Medical University, Chongqing, China, June 19, 2013.

19. “A Bayesian approach for the identification of DNA copy number variations using the next generation sequencing data,” Invited lecture, International Workshop on the Perspectives on High-dimensional Data Analysis III of the Pacific Institute for the Mathematical Sciences (PIMS), University of British Columbia, Vancouver, Canada, May 23 - May 25, 2013.

20. “Statistical Change Point Analysis and its Applications,” Graduate Seminars of the College of Statistics, Southwest University of Finance and Economics, Chengdu, China, June 12, 2012; Graduate Seminars of the School of Mathematics and Statistics, Chongqing University, China, June, 6th, 2012, and Graduate Seminar of the Department of Mathematical Sciences, the Southwest Petroleum university, Chengdu, China, May 29th, 2012

21. “On Statistical Modeling of Biological Data,” UMKC School of Pharmacy, Division of Pharmacology and Toxicology Seminar Series, Hospital Hill campus, September 9th, 2010

22. “Modeling Various Molecular Biology Data,” Colloquia Talk Series of the School of Life Science at Chongqing University, Chongqing, China, June 30, 2010

23. “Introduction to Change Point Analysis and its Applications,” Colloquia Talk at the Department of Probability, Statistics, and Information Sciences, Fu Jen Catholic University, Taipei, Taiwan, June 2, 2010

24. “An overview of parametric statistical change point analysis and its various applications,” Invited lecture at the Department of Management, Kai Nan University, Taipei, Taiwan, June 2, 2010

25. “Analysis of the aCGH data for the Detection of DNA Copy Number Variations,” Invited lecture at the Special Scholars Lecture Series of School of Graduate Studies, Chongqing University, July 1st, 2009

26. “A Distorted Normal Model for the Gene Expression Data,” Colloquia talk, School of Mathematical Sciences, Sichuan University, Chengdu, Sichuan, China, June 28th, 2009

27. “Parametric Change-point Models for the Identification of DNA Copy Number Variations,” Statistics seminar, H. Milton Stewart School of Industrial and Systems Engineering, Georgia Institute of Technology, Atlanta, Georgia, USA, March 26th, 2009

28. “Statistical Approaches for the Detection of DNA Copy Number Variations in aCGH data,” School of Computing and Engineering Graduate Seminar, UMKC, March 13th, 2009

29. “Analyzing the aCGH data for DNA copy number changes,” Colloquia talk, University of Missouri-Columbia, Columbia, MO, USA, October 10, 2007

30. “Detecting periodically expressed genes for microarray experimental data,” Statistics Seminar, Bowling Green State University, Bowling Green, Ohio, September 19, 2007

31. “A Change point model approach for detecting significant DNA copy number changes in aCGH data,” Colloquia talk, Bowling Green State University, Bowling Green, Ohio, September 21, 2007

32. “Identification of DNA copy number changes in aCGH data using change-point model,” Colloquia talk given at Department of Applied Statistics and Information Science of Ming Chuan University, Taoyuan County, Taiwan, ROC, May 11, 2007

33. “Lomb-Scargle analysis of cell cycle gene expression data,” Colloquia talk given at Department of Statistics of TungHai University, Taichung, Taiwan, ROC, May 15, 2007, and Colloquia talk given at Department of Statistics and Information Science of Fu Jen Catholic University, Hsinchuang, Taipei Hsien, Taiwan, ROC, May 16,2007

34. “Detecting periodically expressed genes for microarray experimental data,” Colloquia talk given at Department of Statistics of Danjiang University, Taipei, Taiwan, ROC, May 16, 2007

35. “Identify Periodically Expressed Genes in Cell Cycle Gene Expression Data,” at the Biostatistics Club of the University of Kansas Medical Center, May 1st, 2006, Kansas City, Kansas, USA

36. “Statistical Analysis of Variance Change Points in Normal Models and it’s Potential to Gene Expression Analysis,” at the Bioinformatics Center of the Stowers Institute for Medical Research, Kansas City, Missouri, October 5, 2005

37. “On clustering analysis of Hematopoietic Stem Cell microarray data,” Colloquia talks at the Department of Statistics and Information Science, Fu Jen Catholic University, Taipei Hsien, Taiwan, ROC, May 29, 2005, and at Department of Mathematics, National Kaohsiung Normal University, Kaohsiung, Taiwan, ROC, June 1, 2005

38. “Statistical Methods for Identifying Periodic Genes in Microarray Experimental Data,” at the Bioinformatics Center of the Stowers Institute for Medical Research, Kansas City, Missouri, March 9, 2005

39. “A Statistical Model for Skewed Data,” at the Bioinformatics Center of the Stowers Institute for Medical Research, Kansas City, Missouri, November 10, 2004

40. “Inference on Variance Changes Points with Application to Stock Market,” Invited Lecture (90 minutes), at College of Mathematics, Chongqing University, Chongqing, China, June 25, 2002

41. “Variance Change Point Analysis in Normal Models,” Colloquia talk given at Department of Statistics, University of Missouri-Columbia, April 7, 2000

42. “Recent Statistical Methodology Development,” Graduate Seminar at College of Mathematics, Sichuan University, China, June 14, 1999

43. “Exploratory and Analytic Statistical Methods,” ”Statistics Development in the 21st Century,” ”Statistical Application in Economics,” and ”The Comparison of Change-Point and Outlier,” Invited lectures (4 hours) at the Summer Workshop organized by the Chengdu Statistical Association, Chengdu, China, June 17, 1999

Conference Presentations (A selection)

1. Chen J “Statistical Approaches for Retrospective Detection of Multiple Change Points with Applications,” **Keynote** speech at the 11th International Statistics Congress, Bodrum, Mugla, Turkey, October 4-8, 2019.

2. Chen J “Modeling multiple types of genomic data for predicting the survival time of cancer patients,” invited talk given in the session “Failure Time Analysis and Its Applications” at the 2018 ICSA China Conference with the Focus on Data Science, Qingdao, China, July 2-5, 2018.

3. Chen J “Statistical Modeling Approaches to Big Data Analytics,” invited panelist at the 2018 Research Symposium: Cyber Impact on Our Community, Country and Healthcare, in the session “Big Data Management/VINCI/HSR&D” on the campus of Charlie Norwood VAMC (Veterans Affairs Medical Center), Augusta, Georgia, May 17-18, 2018.

4. Lee, J and Chen, J “DNA Copy Number Variants Detection Using a Modified Information Criterion in the DNA-seq Data,” at 2018 Eastern North American Region (ENAR) of International Biometric Society (IBS) Spring Meeting, Hyatt Regency Atlanta, Georgia, March 24-27, 2018.

5. Deng S and Chen J “An Integrative Analysis of DNA Methylation and Copy Number Data for Biological Discovery,” topic contributed talk in the session “Modern Statistical Methods for Biological Discovery” at 2017 Joint Statistical Meetings, Baltimore, MD, USA, July 29th – August 3, 2017.

6. Chen J “Change-point detection for DNA-sequencing data with correlated structure,” invited talk at the Sixth International Workshop in Sequential Methodologies, University of Rouen Normandy, Rouen, France, June 20-23, 2017.

7. Chen J “Statistical Methods for identifying DNA copy number variations using NGS read-depth data,” invited talk at the 5th Workshop on Biostatistics and Bioinformatics, Georgia State University, Atlanta, GA, May 5-7, 2017.

8. “A new change point detection method for identifying DNA copy number variations using NGS read-depth data,” invited talk in the invited session entitled “Change-Point Detection and Related Topics” at the 10th ICSA International Conference, Shanghai, China, December 19-22, 2016.

9. “An on-line CNV detection method for the next generation sequencing data,” at the XXVIIIth International Biometric Conference, Victoria Convention Centre, Victoria, Canada, July 10 - 15, 2016.

10. “Modeling NGS read count data for CNV study,” Fourteenth Asia Pacific Bioinformatics Conference, San Francisco, CA. January 11, 2016.

11. “An On-line change point search method with application to CNV detection using DNA-seq data,” invited talk at the Institute of Mathematical Statistics (IMS) China International Conference on Statistics and Probability, Kunming, Yunnan, China, July 1 – 4, 2015.

12. “Statistical Change Point Analysis and its Application in Modeling the Next Generation Sequencing Data,” invited talk at the 2015 AWM (Association for Women in Mathematics) Research Symposium 2015, University of Maryland - College Park, College Park, April 11-12, 2015

13. “A new change point detection algorithm for identifying CNVs using short sequencing reads,” Invited talk, IMS-China International Conference on Statistics and Probability, Southwest University of Finance and Economics, Chengdu, China, July 1-4, 2013.

14. “Detecting CNV regions using genomics data of different platforms,” Invited talk, Cerner Conference on Frontiers in Biostatistical Methods, Kansas City, Missouri, USA, April 18, 2013.

15. “On the Detection of CNVs with Application to Cancer Cell Line Data,” Invited talk, The Second International Biostatistics Workshop of Jilin University, Changchun, Jilin, China, June 17th, 2012.

16. “On the analysis of next generation sequencing data for identifying CNV regions,” Contributed talk, the 2012 Joint Statistical Meetings, San Diego, California, USA, July 28 - August 2, 2012.

17. “A Homogenous Compound Poisson Change Point Model Approach for the Analysis of CNVs in Genomic Data,” Contributed talk, the 2010 Joint Statistical Meetings, Vancouver, Canada, August 1-6, 2010.

18. “Statistical Approaches for the Identification of DNA Copy Number Variations,” Invited talk, The 7th Sino-International Symposium on Probability, Statistics, and Quantitative Management, Jiaushi, Yilan County, Taiwan, ROC, June 5, 2010.

19. “Bayesian Approach For The Identification Of DNA Copy Number Changes In aCGH Data,” Contributed talk, the 2008 Joint Statistical Meetings, Denver, Colorado, August 2-7, 2008.

20. “Identification of DNA copy number changes in aCGH data using change-point model,” Invited guest speaker, the fourth Sino-International Symposium on Probability Statistics, and Quantitative Management, Taipei, Taiwan, ROC, May 12, 2007.

21. “On the detection of DNA copy number changes,” Contributed paper, Joint Statistical Meetings, August 6 - 10, 2006 Seattle, WA, USA

22. “Detection of DNA copy number changes using statistical change point analysis,” refereed conference paper invited as a podium presentation, 2006 IEEE International Workshop on Genomic Signal Processing and Statistics, College Station, Texas, USA, May 28 - May 30, 2006.

23. “Change point analysis for covariance matrix in multivariate normal models: an application,” Invited guest speaker, the Second Sino-International Symposium on Probability, Statistics, and Quantitative Management, May 28, 2005, Taipei, Taiwan, ROC.

24. “A Statistical Model for Microarray Gene Expression Data,” contributed paper, the Joint Statistical Meetings, August 3-7, 2003, San Francisco, USA

25. “Statistical Clustering Methods and Displays for DNA Microarray Data,” Contributed paper, Hawaii International Conference on Statistics and Related Fields, Honolulu, Hawaii, USA, June 5-9, 2002.

26. “On the Estimation of a Change Point in Failure Rate Models,” Invited talk, Second International Conference on Mathematical Methods in Reliability, Bordeaux, France, July 4-7, 2000.

27. “Testing and Locating Multiple Variance Change Points,” Invited talk, IISA International Conference, McMaster University, Hamilton, Canada, Oct. 10-11, 1998.

28. “Inference about Covariance Change Points with Application to Stock Market,” Contributed paper, 1998 Spring Meeting of the IBS-ENAR, joint with IMS and sections of ASA, Pittsburgh, PA, March 29-April 1, 1998.
29. “Inference about Variance Change Points,” Contributed paper, 1997 Spring Meeting of the IBS-ENAR, joint with IMS and sections of ASA, Memphis, Tennessee, March 23-march 26, 1997.
30. “On the Likelihood Procedure for Testing Change Point Hypothesis for Multivariate Gaussian Model,” Contributed paper, 230th Meeting of The IMS, Cleveland, Ohio, March 1994.

Special Workshops Attended

- “IMA Workshop: Organization of Biological Networks,” March 3 - March 7, 2008: I was invited (after application) to attend this one-week workshop sponsored by the NSF funded Institute for Mathematics and its Applications (IMA) on the campus of IMA, located in the University of Minnesota, Minneapolis, MN, from March 3rd to March 7th. This trip was completely funded by IMA.
- “IPAM: Next Generation Sequencing Technology and Algorithms for Primary Data Analysis,” October 3 to October 6, 2011, partially funded by the Institute for Pure and Applied Mathematics (IPAM), the University of California, Los Angeles.
- “IDEA Department Chairs Seminar,” November 7th - November 9th, 2012, St. Pete Beach, Florida. This trip was funded by the Provost of UMKC and by the Dean of the College of Arts and Sciences of UMKC.

Grant Review Service

- February, 2021: National Institutes of Health NAME study section, Bethesda, MD
- November, 2018: National Institutes of Health NHLBI study section, Bethesda, MD
- November, 2017: National Science Foundation, Divisions of Mathematical Sciences and Biological Sciences, Site Panelist, Alexandria, VA
- March, 2016: National Science Foundation, Division of Mathematical Sciences, Site Panelist, Washington D.C.
- January 2014: Ad hoc reviewer for the National Science Foundation on grant applications
- April and November, 2013: Reviewed two grant applications, respectively, for University of Missouri Research Board (UMRB)
- November, 2012: National Science Foundation, Division of Mathematical Sciences, Site Panelist, Washington D.C.
- April and November, 2012: Reviewed two grant applications, respectively, for University of Missouri Research Board (UMRB)
- June, 2011 - NIH Biomedical Computing and Health Informatics (BCHI) Study Section, Santa Monica, Los Angeles, California
- Dec., 2010 - Jan. 2011 Grant reviewer for the Office of Vice President for Research of Kuwait University for a research proposal submitted there

- April, 2010: Reviewed a grant application for University of Missouri Research Board (UMRB)
- Feb. 2009: Reviewed a grant application for the Sponsored Program of Research of Bowling Green State University, Bowling Green, Ohio
- April, 2009: Reviewed a grant application for University of Missouri Research Board (UMRB)
- Nov., 2007: Reviewed a grant application for University of Missouri Research Board (UMRB)
- April 2005: Reviewed three grant applications for University of Missouri Research Board (UMRB)

Served as Referee for the Following Journals

1. Annals of Applied Statistics
2. Annals of the Institute of Statistical Mathematics
3. Applied Mathematics Letters
4. Bioinformatics
5. Biometrika
6. BMC Bioinformatics
7. Canadian Journal of Statistics
8. Communication in Statistics - Simulation and Computation
9. Communications in Statistics-Theory and Methods
10. Computational Statistics
11. Computational Statistics and Data Analysis
12. Integral Transforms and Special Functions
13. International Journal on Artificial Intelligence Tools
14. International Statistical Review
15. IEEE Transactions on on Biomedical Engineering
16. IEEE Transactions on Signal Processing
17. Journal of Biomedicine and Biotechnology
18. Journal of Business and Economic Statistics
19. Journal of Applied Statistics
20. Journal of Probability and Statistical Science
21. Journal of the American Statistical Association
22. PLoS One

23. Statistica Neerlandica
24. Statistics and Computing
25. Statistical Applications in Genetics and Molecular Biology
26. Statistical Papers
27. Transactions on Pattern Analysis and Machine Intelligence (of the IEEE Computer Society)

Committee and Professional Services (A selection)

1. August 2020 - December 2020: Committee member, AU College of Sciences and Mathematics Search Committee for the Deparment Chair of Department of Mathematics
2. Feb, 2019 - Present: Co-Chair, Graduate Council Curriculum Subcommittee, Graduate School, Augusta University
3. October 2019 - Present: Co-Chair, Organizing Committee for the Second Annual Workshop "Emerging Data Science Methods for Complex Biomedical and Cyber Data"
4. Feb 2018-March 2019: Co-Chair, Organizing Committee for the Inaugural Workshop "Emerging Data Science Methods for Complex Biomedical and Cyber Data", workshop dates: March 29-30, 2019.
5. Contact person, GPC Collaboration with Math Dept for Accelerated BS/MS program in Math and Biostatistics, February 2017 - Present
6. Committee Chair of MS Data Science Program Initiative Committee, December 9, 2016 - May 2020
7. Chair of the Graduate Program Committee, Dept. of Biostatistics and Epidemiology, AU, July 2015 - 2021
8. Graduate Council member, Graduate School, Augusta University, July 2015 - present
9. UMKC Department contact person for the participating in the Celebration of the International Year of Statistics 2013 - Aprile, 2012 to present: Organized three events locally to celebrate the International Year of Statistics 2013:
10. Member, UMKC Chancellor's Diversity Council, 8-2011 - 12-2012
11. Member, Dean's Search Committee for the College of Arts and Sciences, UMKC, 8-2011 - 2-2012
12. Member, UMKC Provost's Program Advisory Committee - a 2020 Task Force Subcommittee, Spring semester 2011
13. External Reviewer, University of Nebraska-Omaha (UNO), Academic Planning Council Review on the Mathematics Department of UNO: As the external reviewer and the report writer, I provided a thorough review of the Mathematics Department of UNO and provided expert advice on the department's future development plan, 2-2010 - 3-2010
14. Member, Conference Technical Committee, IEEE 2008 World Congress on Computational Intelligence, December 2007 - 02-16-2008 (conference dates: June 1-6, 2008 in Hong Kong)

15. Member, UMKC Faculty Senate Standing Committee on Administrative Issues, 09-01-2007 - 08-20-2009

16. Member, UMKC Department of Mathematics and Statistics Search Committees, 01-02-2007 - 03-01-2007, 01-03-2006 - 03-31-2006, 01-05-2005 - 03-31-2005

17. Member, UMKC College of Arts and Sciences Curriculum Committee, 08-30-2006 - 08-29-2009

18. UMKC Department of Mathematics and Statistics Graduate Seminar Organizer, 08-21-2006 - 12-15-2006

19. Member, UMKC Internal Advisory Committee for SCE NSF funded educational grant, 07-25-2005 - 2008

20. Member, UMKC Graduate School's Preparing Future Faculty Fellowship Steering Committee, 08-25-2005 - 05-31-2010

21. Member, UMKC Bioinformatics Educational Initiative Committee, 01-04-2004 - 05-31-2004.

Graduate Students/Postdoctoral Fellows Advised

- Directed 5 Ph.D. Dissertations (2 at UMKC and 3 at Augusta University, students are employed at University of Central Missouri, Pharmaceutical Product Development, Inc., Incyte Corporation, and Emory University) and directed 1 MS Project (student is employed by Biostat Solutions, Inc.)
- Served 23 Ph.D committees (17 at UMKC and 6 at Augusta University)
- Served on 3 MS Committees at UMKC and 2 MS Committee at Augusta University
- Supervised 3 postdoctoral fellows (1 at UMKC and 2 at Augusta University)