

JIE PENG

CURRICULUM VITAE

Contact Information

Work Address: Department of Statistics
University of California, Davis, CA 95616
Phone: (530)-752-0958
Email: jiepeng@ucdavis.edu
Homepage: <http://anson.ucdavis.edu/~jie>
Google Scholar: [Link](#)
Github: [Link](#)

Education

2000-2004 Stanford University, Stanford, CA Ph.D. Statistics
1996-2000 Peking University, Beijing, China BS Mathematics

Positions

04/2016 -	Member	UC Davis Genome Center
07/2015 -	Professor	Department of Statistics
07/2010 - 06/2015	Associate Professor	Department of Statistics University of California, Davis
09/2004 - 06/2010	Assistant Professor	Department of Statistics University of California, Davis

Publications

Journals Published

1. **Peng, J.** and D. Siegmund. Mapping quantitative traits with random and with ascertained sibships (2004). Proceedings of the National Academy of Sciences, 101 (21): 7845-7850. [\[pdf\]](#)
2. **Peng, J.** and D. Siegmund. The admixture model in linkage analysis (2005). Journal of Statistical Planning and Inference, 130 (1-2): 317-324. [\[pdf\]](#)
3. **Peng, J.**, H.-K. Tang, and D. Siegmund. Genome scans with gene-covariate interaction (2005). Genetic Epidemiology, 29 (3): 173-184. [\[pdf\]](#)
4. Tang, H., **J. Peng**, P. Wang, and N. Risch. Estimation of individual admixture: analytical and study design considerations (2005). Genetic Epidemiology, 28 (4): 289-301. [\[pdf\]](#)
5. **Peng, J.** and D. Siegmund. QTL mapping under ascertainment (2006). The Annals of Human Genetics, 70 (6): 867-881. [\[pdf\]](#)
6. **Peng, J.**, P. Wang, and H. Tang. Controlling for false positive findings of trans-hubs in e-QTL mapping (2007). BMC Proceedings, 1 (Suppl 1): S157. [\[pdf\]](#)

7. Tang, H., **J. Peng**, P. Wang, M. Coram, and L. Hsu. Combining multiple family-based association studies (2007). *BMC Proceedings*, 1 (Suppl 1): S162. [\[pdf\]](#)
8. **Peng, J.** and H.G. Müller. Distance-based clustering of sparsely observed stochastic processes, with applications to on-line auctions (2008). *The Annals of Applied Statistics*, 2(3): 1056-1077. [\[pdf\]](#)
9. Paul, D. and **J. Peng**. Consistency of restricted maximum likelihood estimators of principal components (2009). *The Annals of Statistics*, 37(3): 1229-1271. [\[pdf\]](#)
10. **Peng, J.**, P. Wang, N.F. Zhou, and J. Zhu. Partial correlation estimation by joint sparse regression models (2009). *Journal of the American Statistical Association*, 104 (486): 735-746. [\[pdf\]](#), [\[supplementary\]](#)
11. **Peng, J.** and D. Paul. A geometric approach to maximum likelihood estimation of the functional principal components from sparse longitudinal data (2009). *Journal of Computational and Graphical Statistics*, 18(4): 995-1015. [\[pdf\]](#)
12. **Peng, J.**, J. Zhu, A. Bergamaschi, W. Han, D.Y. Noh, J.R. Pollack, and P. Wang. Regularized multivariate regression for identifying master predictors with application to integrative genomics study of breast cancer (2010). *The Annals of Applied Statistics*, 4(1): 53-77. [\[pdf\]](#), [\[supplementary\]](#)
13. Jin, J., **J. Peng**, and P. Wang. A generalized fourier approach to estimating the null parameters and proportion of nonnull effects in large-scale multiple testing (2010). *Journal of Statistical Research*, 44(1): 103-127. [\[pdf\]](#)
14. Paul, D., **J. Peng**, and P. Burman. Semiparametric modeling of autonomous nonlinear dynamical systems with application to plant growth (2011). *The Annals of Applied Statistics*, 5(3): 2078-2108. [\[pdf\]](#), [\[supplementary\]](#)
15. Wang, R., **J. Peng**, and P. Wang. SNP set analysis for detecting disease association using exon sequence data (2011). *BMC Proceedings*, 5(Suppl 9). [\[pdf\]](#)
16. Paul, D. and **J. Peng**. Principal components analysis for sparsely observed correlated functional data using a kernel smoothing approach (2011). *Electronic Journal of Statistics*, 5: 1960-2003. [\[pdf\]](#)
17. Chitwood, D.H., L.R. Headland, D.L. Filiault, R. Kumar, J.M. Jiménez-Gómez, A.V. Schragar, D.S. Park, **J. Peng**, N.R. Sinha and J.N. Maloof. Native environment modulates leaf size and response to simulated foliar shade across wild tomato species (2012). *PLoS ONE*, 7(1): e29570. [\[pdf\]](#)
18. Chitwood, D.H., L.R. Headland, R. Kumar, **J. Peng**, J.N. Maloof, and N.R. Sinha. The developmental trajectory of leaflet morphology in wild tomato species (2012). *Plant Physiology*, 158(3): 1230-1240. [\[pdf+html\]](#)
19. Viswanath, V., E. Fletcher, B. Singh, N. Smith, D. Paul, **J. Peng**, J. Chen, and O. Carmichael. Impact of DTI smoothing on the study of brain aging (2012). *34th Annual International Conference of the IEEE Engineering in Medicine and Biology Society*, 34: 94-97. [\[pdf\]](#)

20. Nguyen, T., **J. Peng**, and J. Jiang. Fence methods for backcross experiments (2012). *Journal of Statistical Computation and Simulation*, 84(3): 644-662. [[pdf](#)]
21. Kumar, R., Y. Ichihashi, S. Kimura, D.H. Chitwood, L.R. Headland, **J. Peng**, J.N. Maloof, and N.R. Sinha. A high-throughput method for Illumina RNA-Seq library preparation (2012). *Frontiers in Plant Science*, 3(202): 1-10. [[html](#)]
22. Carmichael, O., J. Chen, D. Paul, and **J. Peng**. Diffusion tensor smoothing through weighted Karcher means (2013). *Electronic Journal of Statistics*, 7(0): 1913-1956. [[pdf](#)], [[supplementary](#)]
23. Li, S., L. Hsu, **J. Peng**, and P. Wang. Bootstrap inference for network construction with an application to a breast cancer microarray study (2013). *The Annals of Applied Statistics*, 7(1): 391-417. [[pdf](#)], [[supplementary](#)]
24. Koenig, D., J.M. Jiménez-Gómez, S. Kimura, D. Fulop, D.H. Chitwood, L.R. Headland, R. Kumar, M. F. Covington, U.K. Devisetty, A.V. Tat, T. Tohge, A. Bolger, K. Schneeberger, S. Ossowski, C. Lanz, G. Xiong, M. Taylor-Teeples, S. M. Brady, M. Pauly, D. Weigel, B. Usadel, A. R. Fernie, **J. Peng**, N.R. Sinha, and J.N. Maloof. Comparative transcriptomics reveals patterns of selection in domesticated and wild tomato (2013). *Proceedings of the National Academy of Sciences*, 110(28): 2655-2662. [[pdf+html](#)]
25. Chitwood, D., R. Kumar, L.R. Headland, A. Ranjan, M.F. Covington, Y. Ichihashi, D. Fulop, J. M. Jiménez-Gómez, **J. Peng**, J.N. Maloof, and N.R. Sinha. A quantitative genetic basis for leaf morphology in a set of precisely defined tomato introgression lines (2013). *The Plant Cell*, 25(7): 2465-2481. [[pdf+html](#)]
26. **Peng, J.**, D. Paul, and H.G. Müller. Time-warped growth processes, with applications to the modeling of boom-bust cycles in house prices (2014). *The Annals of Applied Statistics*. Volume 8, Number 3, 1561-1582. [[pdf](#)], [[supplementary](#)]
27. Ichihashi, Y., J.A. Aguilar-Martínez, M. Farhi, D.H. Chitwood, R. Kumar, L.V. Millon, **J. Peng**, J.N. Maloof, and N.R. Sinha. Evolutionary developmental transcriptomics reveals a gene network module regulating inter-specific diversity in plant leaf shape (2014). *Proceedings of the National Academy of Sciences*, 111(25): E2616-21. [[pdf](#)]
28. Chitwood, DH, Ranjan, A, Kumar, R, Ichihashi, Y, Zumstein, K, Headland, LR, Ostria-Gallardo, E, Aguilar-Martínez, JA, Bush, S, Carriedo, L, Fulop, D, Martinez, CC, **J Peng**, Maloof, JN, Sinha, NR. Resolving distinct genetic regulators of tomato leaf shape within a heteroblastic and ontogenetic context (2014). *The Plant Cell*, 26(9): 3616-29. [[pdf](#)]
29. Wong, R.K.W., T.C.M. Lee, D. Paul, and **J. Peng**. Fiber direction estimation, smoothing and tracking in diffusion MRI (with Discussion) (2016). *The Annals of Applied Statistics*, 10(3): 1137-1156. [[pdf](#)]
30. Wong, R.K.W., T.C.M. Lee, D. Paul, and **J. Peng**. Rejoinder: Fiber direction estimation, smoothing and tracking in diffusion MRI (2016). *The Annals of Applied Statistics*, 10(3): 1166-1169. [[pdf](#)]

31. Paul D., **J. Peng**, and P. Burman. Nonparametric estimation of dynamics of monotone trajectories (2016). The Annals of Statistics, Vol. 44, No. 6, 2401-2432. [[pdf](#)]
32. An C., Ichihashi Y., **J. Peng**, Sinha N.R., Hagiwara N. (2016). Transcriptome dynamics and potential roles of Sox6 in the postnatal heart. PloS One 11(11): e0166574. [[html](#)].
33. Choi Y., Coram M., **J. Peng**, and Tang H. A Poisson Log-Normal model for constructing gene covariation network using RNA-seq data (2017). Journal of Computational Biology, 24(7):721-731. [[DOI: 10.1089/cmb.2017.0053](#)]
34. Zhou S., Paul D., and **J. Peng**. Modeling subject-specific nonautonomous dynamics (2018). Statistica Sinica, 28: 423-447. [[doi:10.5705/ss.202016.0113](#)]
35. Yan H., Carmichael O., Paul D., and **J. Peng**. Estimating fiber orientation distribution from diffusion MRI with spherical needlets (2018). Medical Image Analysis, Vol. 46: 57-72. [[html](#)].
36. Petralia F., Wang L., **J. Peng**, Yan A., Zhu J., and Wang P. A new method for constructing tumor specific gene co-expression networks based on samples with tumor purity heterogeneity (2018). Bioinformatics, 34(13):i528 - i536. [[html](#)].
37. Conley C., Ozbek U., Wang P., and **J. Peng**. Characterizing functional consequences of DNA copy number alterations in breast and ovarian tumors by spaceMap (2018). Journal of Genetics and Genomics, 45(7):361 - 371. [[html](#)]
38. Yang J. and **J. Peng**. Estimating time-varying graphical models (2020). Journal of Computational and Graphical Statistics, 29(1): 191-202 [[html](#)]
39. Li H., Aue A., Paul D., **J. Peng**, and Wang, P. An adaptable generalization of Hotelling's T^2 test in high dimension (2020). The Annals of Statistics, 48(3): 1815-1847. [[html](#)]
40. Chowdhury S., Wang R., Yu Q., Huntoon C.J., Karnitz L.M., Kaufmann S.H., Gygi S.P., Birrer M.J., Paulovich A.G., **J. Peng**, and Wang P. DAGBagM: Learning directed acyclic graphs of mixed variables with an application to identify prognostic protein biomarkers in ovarian cancer (2021). [[html](#)]

Submitted

1. Hwang S., Lee T.C.M., Paul D., and **J. Peng**. Estimating Fiber Orientation Distribution with Application to Study Brain Lateralization Using HCP D-MRI Data (2021). *Submitted*. [[pdf](#)] [arXiv:2004.04258v2](#)
2. Chowdhury S., Ferri-Borgogno S., Yang P., Wang W., **J. Peng**, Mok S., and Wang P. Learning directed acyclic graphs for ligands and receptors based on spatially resolved transcriptomic analysis of ovarian cancer (2021). *Submitted*. [[html](#)]
3. Li H., Aue A., Paul D., and **J. Peng**. Testing high-dimensional general linear hypotheses under a multivariate regression model with spiked noise covariance (2022). *Submitted*.

Preprints

1. Yang, J. and **J. Peng** (2019). Estimating spatially-smoothed fiber orientation distribution. [pdf] [arXiv:1910.07712](#).
2. Wang R. and **J. Peng**. Learning directed acyclic graphs via bootstrap aggregating (2014). [pdf] [arXiv:1406.2098](#)

Book Chapters

1. Hsu, L., **J. Peng**, and Wang P. Learning network from high dimensional array data. Fu, W.J., (ed), *Frontiers in Computational and Systems Biology* (2010), Vol. 15 (Ch 7), Springer, pp. 133-156.
2. Paul D. and **J. Peng**. Statistical analysis of diffusion MRI (2020). Ghosh, S.K., Datta, S., and Kundu, S., (ed), *IISA Series on Statistics and Data Science*, Springer. *In Press*

Professional Services

Editorial and Advisory Boards

2022-	Area Editor of <i>Annals of Applied Statistics</i>
2014 -	Associate Editor of <i>Journal of Computational and Graphical Statistics</i>
2013 -	Action Editor of <i>Journal of Machine Learning Research</i>
2013 - 2015	Guest Editor of a special issue of <i>Statistics and Its Interface</i>
2010 - 2013	Advisory Board of <i>Bioinformatics Core, Genome Center, UC Davis</i>
2005 - 2007	Regional Advisory Board of <i>WNAR</i>

Software Development

1. R package `fpca`, <http://cran.r-project.org/>, co-developer: Debashis Paul
2. R package `space`, <http://cran.r-project.org/>, co-developer: Pei Wang
3. R package `remmap`, <http://cran.r-project.org/>, co-developer: Pei Wang
4. R package `binco`, <http://cran.r-project.org/>, co-developers: Shuang Li and Pei Wang
5. R package `dynamics`, <https://github.com/jie108/dynamics>, co-developer: Debashis Paul
6. R package `dagbag`, <https://github.com/jie108/dagbag>, co-developer: Ru Wang
7. R package `spaceMap`, <https://topherconley.github.io/spacemap/>, co-developer: Chris Conley, Pei Wang
8. R package `PLNet`, <https://github.com/jie108/PLNet>, co-developer: Yoonha Choi, Hua Tang
9. R package `TSNet`, <https://github.com/jie108/TSNet>, co-developer: Francesca Petralia, Li Wang, Pei Wang

10. R package `loggle`, <http://cran.r-project.org/>, co-developer: Jilei Yang
11. R scripts `DiST`, <https://github.com/jie108/DiST>, co-developer: Raymond Wong
12. Python scripts `NARM`, https://github.com/jie108/FOD_Narm_codes, co-developer: Jilei Yang
13. R package `dagbagM`, <https://github.com/jie108/dagbagM>, co-developer: Shrabanti, Chowdhury
14. D-MRI analysis pipeline codebase `BJS`, <https://github.com/vic-dragon/BJS>, co-developer: Seung Yong Hwang
15. R package `dagbagST`, <https://github.com/jie108/DagBagST>, co-developer: Shrabanti, Chowdhury