NAME: Yong Chen

PHOTO

[PRESENT POSITIONS]

Associate Professor of Biostatistics (with tenure) at The University of Pennsylvania (Penn).

Director of Computing, Inference and Learning Lab at University of Pennsylvania (https://penncil.med.upenn.edu)

Senior Fellow at the Institute of Biomedical Informatics at Penn.

Senior Scholar at the Center for Evidence-based Practice at Penn School of Medicine.

member at the Applied Mathematics & Computational Science Program, Penn Arts & Sciences.

[FORMER POSITIONS] Assistant Professor of Biostatistics at the University of Pennsylvania

[DEGREES] Ph.D. in Biostatistics

[FIELDS OF MAJOR STATISTICAL ACTIVITIES] Statistical inference, evidence synthesis and data integration, electronic health record data, drug safety.

[SELECTED PUBLICATIONS] (selected from 120 peer-reviewed publications)

1. Bai, R, Moran, G, Antonelli, J, Chen, Y and Boland, M. (May, 2020) Spike-and-Slab Group Lassos for Grouped Regression and Sparse Generalized Additive Models. Journal of the American Statistical Association (in press).

2. Huang, J, Ning, Y, Reid, N and Chen, Y (Jan., 2020), On specification tests for composite likelihood inference, Biometrika (accepted).

3. Chen, Y, Ning, J, Ning, Y, Liang, K-Y and Bandeen-Roche, K. (2017) On pseudolikelihood inference for semiparametric models with boundary problems . Biometrika, 104 (1): 165–179.

4. Ning, J, Chen, Y, Cai, C, Huang, X and Wang, MC. (2015) On the Dependence Structure of Bivariate Recurrent Event Processes: Inference and Estimation, Biometrika 102(2): 345-358.

5. Chen, Y, Huang, J, Ning, Y, Liang, K-Y and Lindsay, B. (March, 2018) A conditional test for composite likelihood with boundary constraints. Biometrika 105 (1), 225-232.

6. Hong, C, Ning, Y, Wang, S, Wu, H, Carroll, RJ and Chen, Y. (2017) PLMT: A novel pseudolikelihood based EM test for homogeneity in generalized exponential tilt mixture models, Journal of the American Statistical Association 112 (50).(This paper won 2015 JSM Biometrics section Byar Awards)

7. Chen, Y and Liang, KY. (2010) On the asymptotic behaviour of the pseudolike ratio test statistic with boundary problemslihood, Biometrika, 97 (3), 603-620.

8. Ning, J, Cai, C, Chen, Y, Huang, X and Wang, MC. (Jan., 2020) Semiparametric Modelling and Estimation of Covariate-Adjusted Dependence between Bivariate Recurrent Events, Biometrics (in press).

9. Duan, R, Ning, Y, Wang, S, Lindsay, B, Carroll, R, and Chen, Y (Dec., 2019) A fast score test for generalized mixture models, Biometrics (in press) (This paper won 2018 ENAR Distinguished Student Paper Award)

10. Hong, C, Salanti, G, Morton, S, Riley, R, Chu, H, Kimmel, S, and Chen, Y (September 2019) Testing small study effects in multivariate meta-analysis, Biometrics (in press; discussion paper).

11. Wang, L, Chai, X, Chen, Y, and Chen, J (August 2019) Novel Two-Phase Sampling Designs for Studying Binary Outcomes, Biometrics (in press).

12. Duan, R, Cao, M, Ning, Y, Zhu, M, Zhang, B, McDermott, A, Chu, H, Zhou, X, Moore, J, Ibrahim, J, Scharfstein, D, Chen, Y (July, 2019), Global identifiability of latent class models with applications to diagnostic test accuracy studies: a Grobner basis approach, Biometrics (in press).

13. Hong, C, Ning, Y, Wei, P, Cao, Y and Chen, Y. (2017) A semiparametric model for vQTL mapping, Biometrics 73(2): 571-581.

14. Liu, Y, Chen, Y and Chu H. (2015) A unification of models for meta-analysis of diagnostic accuracy studies without a gold standard, Biometrics.

15. Ma, X, Lian, X, Chu, H, Ibrahim, J, and Chen, Y (Jan., 2018) A Bayesian hierarchical model for network meta-analysis of diagnostic tests, Biostatistics.

16. Ning, J†, Chen, Y† and Piao, J (July, 2017) Maximum likelihood estimation and EM algorithm of Copas selection model for publication bias correction. Biostatistics, 18(3): 495–504.

17. Chen, Y, Ning, J and Cai, C. (2015) Regression analysis of longitudinal data with irregular and informative observation times, Biostatistics, 16(4): 727-739.

18. Hong, C, Duan, R, Zeng, L, Hubbard, R, Lumley, T, Riley, R, Chu, H, Kimmel, S and Chen, Y (2020) Galaxy plot: a new visualization tool of bivariate metaanalysis studies, American Journal of Epidemiology (in press).

19. Liu, YL, Huang, J, Urbanowicz, R, Chen, K, Manduchi, E, Greene, C, Scheet, P, Moore, JH., and Chen, Y. (August 2019) Embracing study heterogeneity for finding genetic interactions in large-scale research consortia. Genetic Epidemiology (in press).

20. Shen, W, Liu, S, Chen, Y and Ning, J. (December 2018) Regression analysis of longitudinal data with outcome-dependent sampling and informative censoring . Scandinavian Journal of Statistics (Dec. 26, 2018).

21. Hubbard, R, Huang, J, Harton, J, Oganisian, A, Choi, G, Utidjian, L, Eneli, I, Bailey, L, Chen, Y (September 2018) A Bayesian latent class approach for EHR-based phenotyping, Statistics in Medicine 38:74–87.

22. Li, R, Chen, Y, Ritchie, M and Moore, J. (Oct, 2019) Polygenic prediction of disease risks in electronic health record data. Nature Reviews Genetics (in press).

23. Duan, R, Boland, MB, Liu, ZX, Liu, Y, Chang, H, Xu, H, Chu, H, Schmid, C, Forrest, C, Holmes, J, Schuemie, M, Berlin, J.A. and Chen, Y. (Oct, 2019) Learning from Electronic Health Records Across Multiple Sites: A Communication-efficient and Privacy-preserving Distributed Algorithm. Journal of the American Medical Informatics Association (in press).

24. Tong, J, Huang, J, Wang, X, Moore, J, Hubbard, R and Chen, Y. (Sep. 2019) An augmented estimation procedure for EHR-based association studies accounting for differential misclassification. Journal of the American Medical Informatics Association.

25. Li, R, Duan, R, Kember, R, Regeneron Genetic Center, Rader, D, Damrauer, S, Moore, J and Chen, Y. (July, 2019) A regression framework to uncover pleiotropy in large-scale electronic health record data. Journal of the American Medical Informatics Association 26, 1083-1090.

26. Li, R, Chen, Y and Moore, J (April 2019). Integration of genetic and clinical information to improve imputation of data missing from electronic health records. Journal of the American Medical Informatics Association.

27. Chen, Y, Wang, J, Chubak, J, Hubbard, R (2018) Inflation of type I error rates due to differential misclassification in EHR-derived outcomes: Empirical illustration using breast cancer recurrence, Pharmacoepidemiology & Drug Safety 28(2):264-268

28. Huang, J, Duan, R, Hubbard, R, Wu, Y, Moore, JH, Xu, H, and Chen, Y (March 2018), PIE: A prior knowledge guided integrated likelihood estimation method (PIE) for bias reduction in association studies using electronic health records data,, Journal of the American Medical

Informatics Association. Volume 25, Issue 3, Pages 345–352. (selected as one of the top 5 best papers by the IMI Yearbook Section on Clinical Research Informatics from 741 papers published in 2017)

29. Duan, R, Zhang, X, Du, J, Huang, J, Tao, C, and Chen, Y (2017). [Post-marketing Drug Safety Evaluation using Data Mining Based on FAERS](). International Conference on Data Mining and Big Data (pp. 379-389). Springer, Cham.

30. Huang, J, Zhang, X, Du, J, Duan, R, Yang, L, Moore, JH, Chen, Y, Tao, C (2017), [Comparing difference of adverse effects among multiple drugs using FAERS data](), Stud Health Technol Inform 245:1268.

31. Duan, R, Cao, M, Wu, Y, Huang, J, Denny, J, Xu, H and Chen, Y. (2016) [An Empirical Study for Impacts of Measurement Errors on EHR based Association Studies](), AMIA annual symposium proceedings, 10:1764-1773 (This paper won the first prize of "Best of Student Papers in Knowledge Discovery and Data Mining (KDDM)"Awards)

[ICSA ACTIVITIES]

Life-time member of ICSA

Serve as Member of Membership Committee of ICSA during 2017 – 2019

Organize invited talk sessions at ICSA in 2016, and ICSA International Conference in 2019

Teach short course at ICSA in 2016 and 2017

Review for Statistica Sinica

Organized invited talk sessions at the ENAR (2014, 2016, 2017, 2019) and JSM (2018, 2020).

[PROFESSIONAL COMMITTEES]

Serve as Council of Sections Representative during 2020-2022 for the ASA Biometrics Section

Member of Philadelphia Chapter of ASA, 2015 – present

Member of the Scientific Merit Reviewing Committee: Patient-Centered Outcomes Research Institute (PCORI) - Large Pragmatic Trial Panel. March 2015 – present

Member of the Scientific Merit Reviewing Committee: Small Business Health Informatics (NIH). June 2018 - present

[HONORS AND AWARDS]

- 2020. Elected Fellow, [American Statistical Association]()
- 2019. [Distinguished Faculty member]() at the Department of Biostatistics, Epidemiology and Informatics, the Perelman School of Medicine, University of Pennsylvania
- 2018. [Best paper award]() by the International Medical Informatics Association (IMIA) Yearbook Section on Clinical Research Informatics
- 2018. Elected Member, [International Statistical Institute]()
- 2018. Elected Member, [Society for Research Synthesis Methodology]()

- 2015. Institute of Mathematical Statistics IMS Travel Award
- 2010. Margaret Merrell Award for excellence in research, Department of Biostatistics, The Johns Hopkins University.
- 2005 — 2010. Sommer Scholar, the Bloomberg School of Public Health, the Johns Hopkins University

[STATEMENT]

I am deeply honored to be nominated. I have been actively engaged in various ICSA conferences and related activities over the past years. I look forward to working closely with the ICSA leadership, and making contributions to reach the goals and expand the impacts of ICSA in biomedical sciences.