

CURRICULUM VITAE
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Date of Birth: January 10, 1969

Place of Birth: Taipei, Taiwan

Educational Background: Ph.D. majored in *Biostatistics*, 1997
Graduate Institute of Public Health,
National Taiwan University, Taipei, Taiwan
M.B.A. majored in *Statistics*, 1993
Graduate Institute of Statistics,
National Chengchi University, Taipei, Taiwan
B.S. majored in *Electrical Engineering*, 1991
Department of Electrical Engineering,
National Taiwan University, Taipei, Taiwan

Professional Positions:

Distinguished Research Fellow, Institute of Statistical Science, Academia Sinica,
Taipei, Taiwan, 2020-present

Research Fellow, Institute of Statistical Science, Academia Sinica,
Taipei, Taiwan, 2009-2020

Adjunct Professor, Institute of Public Health, National Yang-Ming University,
Taipei, Taiwan, 2011-present

Adjunct Professor, Department of Mathematics, National Taiwan Normal University,
Taipei, Taiwan, 2010-present

Associate Research Fellow, Institute of Statistical Science, Academia Sinica,
Taipei, Taiwan, 2003-2009

Assistant Research Fellow, Institute of Statistical Science, Academia Sinica,
Taipei, Taiwan, 2000-2003

Assistant Professor, Department of Mathematics, National Taiwan Normal University,
Taipei, Taiwan, 1999-2000

Mandatory Army Service, Department of Public Health, National Defense Medical
Center, Taipei, Taiwan, 1997-1999.

Lecturer, Graduate Institute of Epidemiology, National Taiwan University,
Taipei, Taiwan, 1996-97

Honors and Awards:

- Wu Ta-Yu Memorial Award of National Science of Council, ROC (2004)
- Academia Sinica Research Award for Junior Research Investigators (2010)
- Academia Sinica Investigator Award (2014)
- Outstanding Research Award of Ministry of Science & Technology (National Science Council) (2010, 2013, 2016)
- Academic Award of Ministry of Education, ROC (2018)

Academic Service:

Co-Editor: *Biometrics*, 2014-2016

Editorial Board Member: *Spatial Statistics*, 2021- present

Mathematical Reviews/MathSciNet Reviewer, 2017- present

Associate Editor: *Biometrics*, 2006-2014

Associate Editor: *Statistica Sinica*, 2006-present

Associate Editor: *Annals of the Institute of Statistical Mathematics*, 2009 - present

Associate Editor: *Sankhya (The Indian Journal of Statistics) Series B*, 2012-2013

Referee: *Annals of Statistics, Australian & New Zealand Journal of Statistics,*

Biometrics, Biometrical Journal, Bernoulli, Biometrika, BMC Bioinformatics, BMC Genetics, Canadian Journal of Statistics, Computational Statistics and Data Analysis, Genetic Epidemiology, Human Genetics, IEEE Transactions on Signal Processing, Journal of Data Science, Journal of Multivariate Analysis, Journal of Statistical Planning and Inference, Journal of the American Statistical Association, Journal of the Chinese Statistical Association, Journal of the Formosan Medical Association, Journal of the Royal Statistical Society Series B, Metron (International Journal of Statistics), Lifetime Data Analysis, PLoS One, Scandinavian Journal of Statistics, Statistica Sinica, Statistics in Medicine

Membership in Professional Organization:

International Biometric Society, International Chinese Statistical Association

*Publications:**(A) Refereed Journal Paper (published/accepted):*

1. Chen, Y.-H. (1994). Classes of life distribution and renewal counting process. *Journal of Applied Probability*, **31**, 1110-1115.
2. Chen, Y.-H., and Chen, H. (1999). Incomplete covariates data in generalized linear models. *Journal of Statistical Planning and Inference*, **79**, 247-258.
3. Chen, Y.-H., and Chen, H. (2000). A unified approach to regression analysis under double sampling design. *Journal of the Royal Statistical Society, Ser B*, **62**, 449-460.
4. Chen, Y.-H. (2000). A robust imputation method for surrogate outcome data. *Biometrika*, **87**, 711-716.
5. Chen, Y.-H. (2002). Cox regression in cohort studies with validation sampling. *Journal of the Royal Statistical Society, Series B*, **64**, 51-62.
6. Chen, Y.-H. and Tsai, C.-C. P. (2002). A new method for estimation of the attenuation relationship with variance components. *Bulletin of the Seismological Society of America*, **92**, 1984-1991.
7. Chen, Y.-H. and Wang, M. (2002). Sample size and optimal designs in stratified comparative trials to establish the equivalence of treatment effects among two ethnic groups. *Journal of Biopharmaceutical Statistics*, **12**, 553-566.
8. Chatterjee, N., Chen, Y.-H., and Breslow, N. E. (2003). A pseudoscore estimator for regression problems with two-phase sampling. *Journal of the American Statistical Association*, **98**, 158-168.
9. Chen, Y.-H. (2004). New approach to association testing in case-parent designs under informative parental missingness. *Genetic Epidemiology*, **27**, 131-140.
10. Chen, Y.-H. (2006). Computationally efficient Monte Carlo EM algorithms for generalized linear mixed models. *Journal of Statistical Computation and Simulation*, **76**, 817-828.
11. Chen, Y.-H. and Lin, H.-W. (2006). Regression analysis under two-stage sampling designs: A brief review and perspective. *Journal of the Chinese Statistical Association*, **44**, 79-90.
12. Wu, J.-F., Chen, C.-H., Hsieh, R.-P., Shih, H.-H., Chen, Y.-H., Li, C.-R., Chiang, C.-Y., Shau, W.-Y., Ni, Y.-H., Chen, H.-L., Hsu, H.-Y. and Chang, M.-H. (2006). HLA typing associated with hepatitis B E antigen seroconversion in children with chronic hepatitis B virus infection: a long-term prospective sibling cohort study in Taiwan. *Journal of Pediatrics*, **148**, 647-651.
13. Tsai, C.-C. P., Chen, Y.-H. and Liu, C.-H. (2006). The path effect in ground motion variability: an application of the variance component technique. *Bulletin of the Seismological Society of*

America, 96, 1170-1176.

14. Chen, Y.-H. and Kao, J.-T. (2006). Multinomial logistic regression approach to haplotype association analysis in population-based case-control studies. *BMC Genetics*, 7:43.
15. Chatterjee, N. and Chen, Y.-H. (2007). Maximum likelihood inference on a mixed marginally and conditionally specified regression model for genetic epidemiologic studies with two-phase sampling. *Journal of the Royal Statistical Society, Ser B*, 69, 123-142.
16. Chatterjee, N. and Chen, Y.-H. (2007). A semiparametric pseudo-score method for analysis of two-phase studies with continuous phase-I covariates. *Lifetime Data Analysis*, 13, 607-622.
17. Chen, Y.-H., Chatterjee, N., and Carroll, R. J. (2008). Retrospective analysis of haplotype-based case-control studies under a flexible model for gene-environment association. *Biostatistics*, 9, 81-99.
18. Chen, Y.-H. and Lin, H.-W. (2008). Simple association analysis combining data from trios/sibships and unrelated controls. *Genetic Epidemiology*, 32, 520-527.
19. Chen, Y.-H., Lin, H.-W, and Liu H. (2009). Two-stage analysis for gene-environment interaction utilizing both case-only and family-based analysis. *Genetic Epidemiology*, 33, 95-104.
20. Chen, Y.-H., Chatterjee, N., and Carroll, R. J. (2009). Shrinkage estimators for robust and efficient inference in haplotype-based case-control studies. *Journal of the American Statistical Association*, 104, 220-233.
21. Chen, Y.-H. (2009). Weighted Breslow-type and maximum likelihood estimation in semiparametric transformation models, *Biometrika*, 96, 591-600.
22. Chen, Y.-H., Wu, Y.-C., and Wang, M. (2009). A Bayesian approach to evaluating regional treatment effect in a multiregional trial, *Journal of Biopharmaceutical Statistics*, 19, 900-915.
23. Tung, Y.-C., Chang, G.-M., and Chen, Y.-H. (2009). Associations of physician volume and weekend admissions with ischemic stroke outcome in Taiwan: a nationwide population-based study, *Medical Care*, 47, 1018-1025.
24. Chen, Y.-H. and Zucker, D. M. (2009). Case-cohort analysis with semiparametric transformation models, *Journal of Statistical Planning and Inference*, 139, 3706-3717.
25. Chatterjee, N., Chen, Y.-H., Luo, S., and Carroll, R. J. (2009). Analysis of case-control association studies: SNPs, Imputation and haplotypes. *Statistical Science*, 24, 489-502.
26. Lin, H.-W. and Chen, Y.-H. (2010). Association analysis under population stratification: a two-stage procedure utilizing population- and family-based analyses. *Human Heredity*, 69,160-170.

27. Chen, Y.-H. (2010). Semiparametric marginal regression analysis for dependent competing risks under an assumed copula. *Journal of the Royal Statistical Society, Ser B*, 72, 235-251.
28. Wen, C.-C. and Chen, Y.-H. (2011). Nonparametric maximum likelihood analysis of clustered current status data with the gamma frailty Cox model. *Computational Statistics and Data Analysis*, 55, 1053-1060.
29. Chen, Y.-H. (2012). Maximum likelihood analysis of semi-competing risks data with semiparametric regression models, *Lifetime Data Analysis*, 18, 36-57.
30. Chen, Y.-H. and Wang, M. (2012). Assessing dose-region profile of drug efficacy: A multiregional trial strategy, *Journal of Biopharmaceutical Statistics*, 22, 894-902.
31. Emura, T., Chen, Y.-H., Chen, H.-Y. (2012). Survival prediction based on compound covariate under Cox proportional hazard models, *PLoS ONE*, 7, e47627.
32. Wen, C.-C. and Chen, Y.-H. (2012). Conditional score approach to errors-in-variable current status data under the proportional odds model, *Scandinavian Journal of Statistics*, 39, 635-644.
33. Shen, C.-W. and Chen, Y.-H. (2012). Model selection for generalized estimating equations accommodating drop-out missingness, *Biometrics*, 68, 1046-1054.
34. Wen, C.-C. and Chen, Y.-H. (2013). A frailty model approach for regression analysis of bivariate interval-censored survival data, *Statistica Sinica*, 23, 383-408.
35. Kor, C. T., Cheng, K. F. and Chen, Y.-H. (2013). A method for analyzing clustered interval censored data based on Cox's model, *Statistics in Medicine*, 32, 822-832.
36. Wen, C.-C. and Chen, Y.-H. (2013). Assessing age-at-onset risk factors with incomplete covariate current status data under proportional odds models, *Statistics in Medicine*, 32, 2001-2012.
37. Chen, Y.-H., Chatterjee, N., and Carroll, R. J. (2013). Using shared genetic controls in studies of gene-environment interactions, *Biometrika*, 100, 319-338.
38. Shen, C.-W. and Chen, Y.-H. (2013). Model selection of generalized estimating equations with multiply imputed longitudinal data, *Biometrical Journal*, 55, 899-911.
39. Choi, S., Huang, X., and Chen, Y.-H. (2014). A class of semiparametric transformation models for survival data with a cured proportion, *Lifetime Data Analysis*, 20, 369-386.
40. Wen, C.-C. and Chen, Y.-H. (2014). A functional inference approach for interval-censored data with covariate measurement error, *Statistica Sinica*, 24, 1301-1307.
41. Wen, C.-C. and Chen, Y.-H. (2014). Semiparametric analysis of incomplete current status outcome data under transformation models, *Biometrics*, 70, 335-345.
42. Guo, C.-Y., Chen, Y.-J., Chen, Y.-H. (2014). The logistic regression model for gene-gene and

- gene-environment interactions using both case-parent trios and unrelated case-controls, *Annals of Human Genetics*, 78, 299-305.
43. Lu, W., Liu, M., and Chen, Y.-H. (2014). Testing goodness-of-fit for the proportional hazards model based on nested case-control data, *Biometrics*, 70, 845-851.
 44. Lin, H.-W. and Chen, Y.-H. (2014). Adjustment for missing confounders in studies based on observational databases: Two-stage calibration combining propensity scores from primary and validation data, *American Journal of Epidemiology*, 180, 308-317.
 45. Shen, C.-W. and Chen, Y.-H. (2015). Model selection for marginal regression analysis of longitudinal data with missing observations and covariate measurement error, *Biostatistics*, 16(4):740-753.
 46. Emura, T. and Chen, Y.-H. (2016). Gene selection for survival data under dependent censoring, a copula-based approach, *Statistical Methods in Medical Research*, 25, 2840–2857.
 47. Hsu, M.-J. and Chen, Y.-H. (2016). Optimal linear combination of biomarkers for multi-category diagnosis, *Statistics in Medicine*, 35(2), 202-213.
 48. Wen, C.-C. and Chen, Y.-H. (2016). Joint analysis of current count and current status data, *Journal of Multivariate Analysis*, 143, 153-164.
 49. Chatterjee, N., Chen, Y.-H., Maas, P., Carroll, R. (2016). Constrained maximum likelihood estimation for model calibration using summary-level information from external big-data sources, *Journal of the American Statistical Association (Discussion Paper)*, 111, 107-117; (*Rejoinder*), 130-131.
 50. Huang, C.-H. and Chen, Y.-H. (2017). Regression analysis for bivariate gap time with missing first gap time data, *Lifetime Data Analysis*, 23(1), 83-101.
 51. Huang, C.-H., Chen, Y.-H., Chuang, Y.-W. (2017). Semiparametric regression analysis of recurrent gap times in the presence of competing risks, *Statistica Sinica*, 27, 1059-1077.
 52. Huang, C.-H., Li, B., Chen, C.-M., Wang, W., Chen, Y.-H. (2017). Subdistribution regression for recurrent events under competing risks: with application to shunt thrombosis study in dialysis patients, *Statistics in Biosciences*, 9, 339-356. doi:10.1007/s12561-016-9161-0. <https://doi.org/10.1007/s12561-016-9161-0>.
 53. Yang, C.-C., Chen, Y.-H., Chang, H.-Y. (2017). Joint regression analysis of marginal quantile and quantile association: application to longitudinal body mass index in adolescents, *Journal of the Royal Statistical Society, Ser C*, 66, 1075-1090.
 54. Yen, T.-J., Yen, Y.-M., Chen, Y.-H., Hwang, J.S. (2017). Estimating network structure from time to event data, *The Annals of Applied Statistics*, 11, 1429-1457.

55. Chen, Y.-H. (2017). Discussion on “Dissecting multiple imputation from a multi-phase inference perspective: what happens when God's, imputer's and analyst's models are uncongenial?”, *Statistica Sinica*, 27, 1559.
56. Yang, C.-C., Chen, Y.-H., Chang H.-Y. (2017). Composite marginal quantile regression analysis for longitudinal adolescent body mass index data, *Statistics in Medicine*, 36, 3380-3397.
57. Lai, E.-Y., Chen, Y.-H., Wu, K.-P. (2017). A knowledge-based T^2 statistic to perform pathway analysis for quantitative proteomic data. *PLOS Computational Biology*, 13(6): e1005601. <https://doi.org/10.1371/journal.pcbi.1005601>.
58. Shen, C.-W. and Chen, Y.-H. (2018). Joint model selection of marginal mean regression and correlation structure for longitudinal data with missing outcome and covariates. *Biometrical Journal*, 60, 20-33.
59. Shen, C.-W. and Chen, Y.-H. (2018). Model selection for semiparametric marginal mean regression accounting for within-cluster subsampling variability and informative cluster size. *Biometrics*, 74, 934-943.
60. Wen, C.-C. and Chen, Y.-H. (2018). Pseudo and conditional score approach to joint analysis of current count and current status data. *Biometrics*, 74, 1223-1231.
61. Wang, J.-H. and Chen, Y.-H. (2018). Overlapping group screening for detection of gene-gene interactions: application to gene expression profiles with survival trait. *BMC Bioinformatics*, 19:335.
62. Tseng, C.-H., Chen, Y.-H. (2019). Penalized approach for data missing not at random, *Statistical Methods in Medical Research*, 28(1), 134-150.
63. Wen, C.-C. and Chen, Y.-H. (2019). Sample size determination for semiparametric analysis of current status data. *Statistical Methods in Medical Research*, 28(8):2247-2257.
64. Chao, S.-H. and Chen, Y.-H. (2019). A novel regression analysis method for randomly truncated strong motion data. *Earthquake Spectra*, 35, 977-1001.
65. Wen, C.-C., Chen, Y.-H., Chi-Hong Tseng (2020). Joint analysis of panel count and interval-censored data using distribution-free frailty analysis. *Biometrical Journal*, 62, 1164-1175.
66. Hsu, C.-Y., Chen, Y.-H., Yu, R.-R., Hung, T.-W. (2020). Assessing wage status transition and stagnation using quantile transition regression. *The Annals of Applied Statistics*, 14(1), 160-177.
67. Wang, J.-H., and Chen, Y.-H. (2020). Interaction screening by Kendall's partial correlation for ultrahigh-dimensional data with survival trait. *Bioinformatics*, 36(9), 2763-2769.

68. Huang, C.-H., Chen, Y.-H., Wang, J.-L., Wang, M. (2020). Semiparametric copula-based analysis for treatment effects in the presence of treatment switching. *Statistics in Medicine*, 39(22), 2936-2948.
69. Chen, Y.-H. and Wang, H. (2020). The association between depression and gastroesophageal reflux based on phylogenetic analysis of miRNA biomarkers. *Current Medicinal Chemistry*, 2020, 27, 1-12.
70. Chen, Y.-H. and Wang, H. (2020). Exploring diversity of COVID-19 based on substitution distance. *Infection and Drug Resistance*, 2020(13), 3887–3894.
71. Wen, C.-C. and Chen, Y.-H. (2020) Discrete time survival data with longitudinal covariates. *Statistics in Medicine*, 39, 4372-4385.
72. Chao, S.-H, Lin, C.-M., Kuo, C.-H., Huang, J.-Y., Wen, K.-L., Chen, Y.-H. (2020) Implementing horizontal-to-vertical fourier spectral ratios and spatial correlation in a ground motion prediction equation to predict site effects. *Earthquake Spectra*, accepted.
73. Shen, C.-W., Chen, Y.-H., and Chen, C.-S. (2021) A distribution-free model selection criterion for anisotropic spatial correlations. *Spatial Statistics*, 41, 100476.
74. Liu, T.-W, Chen, Y.-H., Guo, C.-Y. (2021) A Novel cross-validation strategy for artificial neural networks using distributed-lag environmental factors. *PLoS ONE*, 16(1): e0244094.
75. Chen, Y.-H. and Wang, H. (2021). The association between migraine and depression based on miRNA biomarkers and cohort studies. *Current Medicinal Chemistry*, to appear.
76. Wang, J.-H, and Chen, Y.-H. (2021) Network-adjusted Kendall's Tau measure for feature screening with application to high-dimensional survival genomic data. *Bioinformatics*, to appear.
77. Hsu, C.-Y., Wen, C.-C., Chen, Y.-H. (2021). Quantile function regression analysis for interval censored data, with application to salary survey data. *Japanese Journal of Statistics and Data Science*, to appear.
78. Guo, C.-Y., Huang, H.-Y., Kuo, P.-C., Chen, Y.-H. (2021). Extensions of the distributed lag non-linear model (DLNM) to account for cumulative mortality. *Environmental Science and Pollution Research*, to appear.
79. Wu, W.-T., Pan, C.-Y., Chang, S.-L., Chen, Y.-H., Tung, C.-J., Lin, P. (2021). Study Protocol for radiation exposure and cancer risk assessment- The Taiwan Nuclear Power Plants and Epidemiology Cohort Study (TNPECS). *Journal of Epidemiology*, to appear.

(B) Conference Paper:

1. Chen, Y.-H. (1993). Classes of life distribution and renewal counting process. 1993 Taipei International Statistical Symposium (invited paper session), December 1993 (Taipei).
2. Chen, Y.-H., and Chen, H. (1997). Estimation in the generalized linear models with mis-measured covariates. In Proceedings of Contemporary Multivariate Analysis and Its Applications (K.T. Fang and F. J. Hickernell, eds.), May 1997 (Hong Kong).
3. Chen, Y.-H., and Chen, H. (1997). Incomplete covariates data in generalized linear models. The IMS Asian and Pacific Regional Meeting (invited paper session), July 1997 (Taipei).
4. Chen, Y.-H. and Tsai, C.-C. P. (2001). Variance components estimation with Taiwan seismic data. The 3rd Cross Strait Statistics and Probability Conference (invited paper session), April 2001 (Taipei).
5. Chen, Y.-H. (2001). Cox regression in cohort studies with validation sampling. The Fifth ICSA International Conference (invited paper session), August, 2001 (Hong Kong).
6. Chen, Y.-H. (2002). A pseudo score estimator for regression problems with two-phase sampling. 2002 Taipei International Statistical Symposium and Bernoulli Society EAPR Conference (invited paper session), July 2002 (Taipei).
7. Chen, Y.-H. (2002). Estimation in generalized linear mixed models using multiple imputation. 2002 International Conference on Applied Statistics, Actuarial Science and Financial Mathematics, Dec 2002 (Hong Kong).
8. Chen, Y.-H. (2004). Incorporating incomplete parental genotype information in sibling-case-control studies gene-environmental independence. 2004 Taipei Symposium on Statistical Genomics (invited paper session), December 2004 (Taipei).
9. Chen, Y.-H. (2006). Haplotype association analysis in population-based case-control study. Conference on Probability and Statistics, January 2006 (Calcutta)
10. Chen, Y.-H. (2006). A model for relaxing gene-environment independence assumption in retrospective analysis of haplotype-based case-control studies. The 5th Cross Strait Statistics and Probability Conference (invited paper session), July 2006 (Chu-Nan).
11. Chen, Y.-H. (2008). Two-stage genetic association studies correcting for population stratification. 2008 Joint Meeting of Indian Statistical Institute, The Institute of Statistical Mathematics, Institute of Statistical Science Academia Sinica. June 2008 (Taipei).
12. Chen, Y.-H. (2008). An iteratively reweighted algorithm for NPMLE in semiparametric transformation models. 2008 Southern Taiwan Statistical Conference (invited paper session),

June 2008 (Hualien).

13. Chen, Y.-H. (2008). Shrinkage estimators for robust and efficient inference in haplotype-based case-control studies. 2008 Joint Statistical Meetings (invited paper session), July 2008 (Denver).
14. Chen, Y.-H. (2009). Statistical issues in genetic association studies: Robustness and efficiency. The 1st Institute of Mathematical Statistics Asia Pacific Rim Meeting (invited paper session), June 2009 (Seoul).
15. Chen, Y.-H. (2010). Two stage genetic association correcting for population stratification. The 1st Joint Biostatistics Symposium (invited paper session), July 2010 (Beijing).
16. Chen, Y.-H. (2010). Missing covariate with high dimensional surrogates. The eighth ICSA International Conference (invited paper session), December 2010 (Guangzhou).
17. Chen, Y.-H. (2011). Model selection for generalized estimating equations accommodating dropout missingness. IMS-China International Conference on Statistics and Probability, July 2011 (Xian).
18. Chen, Y.-H. (2012). Survival prediction with high dimensional covariates. IMS-Asia Pacific Rim Meeting 2012, July 2012 (Tsukuba, Japan).
19. Chen, Y.-H. (2013). Survival prediction under dependent censoring: a copula-based approach. The 9th ICSA International Conference, December 2013 (Hong Kong, China).
20. Chen, Y.-H. (2014). Semiparametric analysis of incomplete current status outcome data under transformation models. The 4th International Biostatistics Workshop of Jilin University (Invited Speech), June 2014.
21. Chen, Y.-H. (2014). The 23rd South Taiwan Statistics Conference (Keynote Speech), June 2014 (Hualien, Tawan).
22. Chen, Y.-H. (2014). Semiparametric analysis of incomplete current status outcome data under transformation models. The XXVII International Biometric Conference (Invited Session), July 2014 (Florence, Italy).
23. Chen, Y.-H. (2015). Using shared genetic controls in studies of gene-environment interactions. 2015 Joint Statistical Meetings (Invited Session), August 2015 (Seattle, USA).
24. Chen, Y.-H. (2016). Constrained maximum likelihood estimation for model calibration using summary-level information from external big-data sources. Workshop on Recent Developments in Empirical Likelihood Methodology (Invited Session), June 2016 (Singapore)
25. Chen, Y.-H. (2016). Constrained maximum likelihood estimation for model calibration using summary-level information from external big-data sources. Cross Strait Probability and

statistics Conference (Keynote Speaker), August 2016 (Chengdu, China)

26. Chen, Y.-H. (2016). Joint regression analysis of marginal quantile and quantile association: application to longitudinal body mass index in adolescents. The 10th ICSA International Conference (Invited Speaker), December 2016 (Shanghai, China).
27. Chen, Y.-H. (2017). Joint regression analysis of marginal quantile and quantile association: application to longitudinal body mass index in adolescents. The ISI-ISM-ISSAS Joint Statistical Meeting (Invited Speaker), February 2017 (New Delhi, India).
28. Chen, Y.-H. (2017). Semiparametric regression analysis of recurrent gap times in the presence of competing risks. The 2017 IMS China International Conference on Statistics and Probability, June 2017 (Naning, China).
29. Chen, Y.-H. (2017). Optimal Linear Combination of Biomarkers for Multi-category Diagnosis. Workshop on Design of Health Care Studies. July 2017 (Singapore).
30. Chen, Y.-H. (2017). Semiparametric Analysis of Incomplete Current Status Outcome Data under Transformation Models. The International Indian Statistical Association 2017 Conference. December 2017 (Hyderabad, India).
31. Chen, Y.-H. (2018). Constrained maximum likelihood estimation for model calibration using summary-level information from external big-data sources. Workshop on complex big data and statistical machine learning, March 2018 (Shanghai, China)
32. Chen, Y.-H. (2019). Semiparametric copula-based analysis for treatment effects in the presence of treatment switching. The 11th ICSA International Conference. December 2019 (Hungzhou, China)

(C) *Book/Book Chapter:*

1. Chen, Y.-H. and Tzeng, J.-Y. (1999). Chinese Edition of *Primer of Biostatistics*, 4th ed. (by Glantz, S. A.), Taipei: Ho-Chi.
2. Emura, T., Chen, Y.-H. (2018). *Survival Analysis with Dependent Censoring, Copula-Based Approaches* (Springer Briefs in Statistics, JSS Research Series in Statistics), New York: Springer.
3. Wang, J.-H., Pan, C.-H., Chen, Y.-H., Chang, I.-S. (2020). Non-parametric maximum likelihood estimation for case-cohort and nested case-control designs with competing risks data, editor(s): Yichuan Zhao, Ding-Geng Chen, *Statistical Modeling in Biomedical Research, Emerging Topics in Statistics and Biostatistics*, New York: Springer.

(D) Unpublished Papers:

1. Shih, J.-H. and Chen, Y.-H. (2020). Characterizing Archimedean copula, manuscript.
2. Shih, J.-H. and Chen, Y.-H. (2021). A new modeling framework for competing risks data, manuscript.
3. Hsu, S.-Y. and Chen, Y.-H. (2021). Causal data fusion using propensity scores, manuscript.

Courses Taught:

1. Mathematical Statistics (NTNU Math. Dept., NYMU Institute of Public Health)
2. Introduction to Statistical Learning and Data Mining (NYMU Institute of Public Health)
3. Statistical Learning and Data Mining (NYMU Institute of Public Health)
4. Bayesian Statistics ((NTNU Math. Dept.)
5. Biostatistical Methods III (Longitudinal Data Analysis) (NYMU Institute of Public Health)
6. Statistical Methods I, II (Linear and Generalized Linear Models, Multivariate Data Analysis) (NTNU Math. Dept.)
7. Elementary Probability and Statistics (NTNU Math. Dept.)
8. Elementary Biostatistics (NTU Medical School)