

Bibliography for James Dai in chronological order

Publications in refereed journals and invited commentary

† Senior and corresponding author.

1. Kane RL, Wall M, Potthoff S, Stromberg K, **Dai Y**, Meyer ZJ. The effect of alcoholism treatment on medical care use. *Medical Care*. 2004; 42(4):395-402.
2. Eberly LE, Neaton JD, Thomas AJ, **Dai Y**. Multiple-stage screening and mortality in the Multiple Risk Factor Intervention Trial. *Journal of the Society for Clinical Trials*. 2004; 1(2):148-61.
3. Polyak SJ, Sullivan DG, Austin MA, **Dai JY**, Shuhart MC, Lindsay KL, Bonkovsky HL, Di Bisceglie AM, Lee WM, Morishima C, Gretch DR, Halt-C Trial Group. Comparison of amplification enzymes for Hepatitis C Virus quasispecies analysis. *Virology Journal*. 2005; 2:41. PMCID: PMC1090623.
4. Wall MM, **Dai Y**, Eberly LE. GEE estimation of a misspecified time-varying covariate: an example with the effect of alcoholism treatment on medical utilization. *Statistics in Medicine*. 2005; 24(6):925-39.
5. **Dai JY**, Ruczinski I, LeBlanc M, Kooperberg C. Imputation methods to improve inference in SNP association studies. *Genetic Epidemiology*. 2006; 30(8):690-702.
6. Storey JD, **Dai JY**, Leek JT. The optimal discovery procedure for large-scale significance testing, with applications to comparative microarray experiments. *Biostatistics*. 2007; 8(2):414-32.
7. **Dai JY**, LeBlanc M, Kooperberg C. Semiparametric estimation exploiting covariate independence in two-phase randomized trials. *Biometrics*. 2009; 65(1):178-87. PMCID: PMC2892338.
8. **Dai JY**, LeBlanc M, Smith NL, Psaty B, Kooperberg C. SHARE: an adaptive algorithm to select the most informative set of SNPs for candidate genetic association. *Biostatistics*. 2009; 10(4):680-93. PMCID: PMC2742496.
9. Kooperberg C, LeBlanc M, **Dai JY**, Rajapakse I. Structures and Assumptions: Strategies to Harness Gene x Gene and Gene x Environment Interactions in GWAS. *Statistical Science*. 2009; 24(4):472-88. PMCID: PMC2904990.
10. **Dai JY**, DeFrances MC, Zou C, Johnson CJ, Zarnegar R. The Met proto-oncogene is a transcriptional target of NF kappaB: implications for cell survival. *Journal of Cellular Biochemistry*. 2009; 107(6):1222-36. PMCID: PMC2868332.
11. Reid SE, **Dai JY**, Wang J, Sichalwe BN, Akpomiemie G, Cowan FM, Delany-Moretlwe S, Baeten JM, Hughes JP, Wald A, Celum C. Pregnancy, contraceptive use, and HIV acquisition in HPTN 039: relevance for HIV prevention trials among African women. *Journal of Acquired Immune Deficiency Syndromes*. 2010; 53(5):606-13. PMCID: PMC2845724.

12. Lumley T, Shaw PA, **Dai JY**. Connections between Survey Calibration Estimators and Semiparametric Models for Incomplete Data. *International Statistical Review*. 2011; 79(2):200-20. PMCID: PMC3699889.
13. Huang Y, Ballinger DG, **Dai JY**, Peters U, Hinds DA, Cox DR, Beilharz E, Chlebowski RT, Rossouw JE, McTiernan A, Rohan T, Prentice RL. Genetic variants in the *MRPS30* region and postmenopausal breast cancer risk. *Genome Medicine*. 2011; 3(6):42. PMCID: PMC3218816.
14. **Dai JY**, Gilbert PB, Masse BR. Partially hidden Markov model for time-varying principal stratification in HIV prevention trials. *Journal of American Statistical Association*. 2012;107:52-65. PMCID: PMC3649016.
15. **Dai JY**, Logsdon B, Huang Y, Hsu L, Reiner A, Prentice R, Kooperberg C. Simultaneously testing for marginal genetic association and gene-environment interaction. *American Journal of Epidemiology*. 2012;176:164-173. PMCID: PMC3499112.
16. Hsu L, Jiao So J, **Dai JY**, Hutter CM, Peters U, Kooperberg C. Powerful cocktail methods for detecting genome-wide gene-environment interaction. *Genetic Epidemiology*. 2012;36:183-194. PMCID: PMC3654520.
17. **Dai JY**, Hughes JP. A unified procedure for meta-analytic evaluation of surrogate endpoints in randomized clinical trials. *Biostatistics*. 2012;13(4):609-624. PMCID: PMC3616754.
18. **Dai JY**, Kooperberg C, LeBlanc M, Prentice RL. Two-stage testing procedures with independent filtering for genome-wide gene-environment interaction. *Biometrika*. 2012; 99(4):929-944. PMCID: PMC3629859.
19. Logsdon B, Carty CL, Reiner AP, **Dai JY**, Kooperberg CL. A novel variational Bayes multiple locus Z-statistic for genome-wide association studies with Bayesian model averaging. *Bioinformatics*. 2012;28(13):1738-1744. PMCID: PMC3381972.
20. Hughes JP, **Dai JY**. Comments on “A sequential Phase 2b trial design for evaluating vaccine efficacy and immune correlates for multiple HIV vaccine regimens” by Gilbert PB, Grove D, Gabriel E, Huang Y, Gray G, Hammer SM, Buchbinder SP, Kublin J, Corey L and Self SG. *Statistical Communications in Infectious Disease*. 2012, 3(1): Article 4.
21. **Dai JY**, Gilbert PB, Hughes JP, Brown E. Estimating PrEP efficacy for HIV prevention among participants with a threshold level of drug concentration. *American Journal of Epidemiology*. 2013; 177(3):256-263. PMCID: PMC3577049.
22. McGowan I, Hoesley C, Cranston RD, Andrew P, Janocko L, **Dai JY**, Carballo-Diequez A, Kunjara Na Ayudhya R, Piper J, Hladik F, Mayer K. A Phase 1 Randomized, Double Blind, Placebo Controlled Rectal Safety and Acceptability Study of Tenofovir 1% gel (MTN-007). *PLoS One*. 2013;8(4) :e60147. PMCID: PMC3616022.
23. Pandey JP, Namboodiri AM, Bu S, Tapsoba JDD, Sato A, **Dai JY**. Immunoglobulin genes and the acquisition of HIV infection in a randomized trial of recombinant adenovirus HIV vaccine. *Virology*. 2013;441(1):70-4. PMCID: PMC3750738.

24. **Dai JY**, Li SS, Gilbert PB. Case-only methods for competing risks models with application to assessing differential vaccine efficacy by viral and host genetics. *Biostatistics*. 2014; 15(1):196-203. PMCID: PMC3862206.
25. Logsdon BA, **Dai JY**, Auer PL, Ganesh SK, Smith NL, Wilson JG, Tracy RP, Graubert T, Lange LA, Rich SS, Lettre G, Carlson C, Jackson R, O'Donnell C, Wurfel M, Nickerson D, Reiner AP, Kooperberg C. A variational Bayes discrete mixture test for rare variant association. *Genetic Epidemiology*. 2014; 38(1):21-30. PMCID: PMC4030763.
26. Tapsoba JD, Kooperberg C, Reiner AP, Wang CY, **Dai JY**[¶]. Robust estimation for secondary trait association in case-control genetic studies. *American Journal of Epidemiology*. 2014;179(10):1264-72. PMCID: PMC4010189.
27. **Dai JY**, Chan KC, Hsu L. Testing concordance of instrumental variable effects in generalized linear models with application to Mendelian randomization. *Statistics in Medicine*. 2014; 33(23):3986-4007. NIHMSID: NIHMS594539.
28. Li SS, Gilbert PB, Tomaras GD, Kijak G, Ferrari G, Thomas R, Zolla-Pazner S, Montefiori D, Liao X, Nabel G, Pinter A, Evans DT, Gottardo R, **Dai JY**, Janes H, Morris D, Fong Y, Edlefsen PT, Li F, Frahm N, Alpert MD, Rerks-Ngarm S, Pitisuttithum P, Kaewkungwal J, Nitayaphan S, Robb ML, O'Connell RJ, Haynes BF, Michael NL, Kim JH, McElrath MJ, Geraghty D. Association of a FCGR2C polymorphism with vaccine efficacy and correlates of HIV-1 infection risk in the RV144 trial. *Journal of Clinical Investigation*. 2014;124(9):3879-3890.
29. Holmes MV, Dale CE, Zuccolo L, . . . , **Dai JY**, . . . , Keating B, Dudbridge F, Casas JP on behalf of the InterAct Consortium. Association between alcohol and cardiovascular disease: Mendelian randomization analysis based on individual participant data. *British Medical Journal*. 2014;349:g4164.
30. Liu S*, **Dai JY***, Yao L, Li X, Reid B, Self S, Ma J, Chang Y, Feng S, Tapsoba JD, Sun X, Sun XB. Esophageal adenocarcinoma and its rare association with Barrett's esophagus in Henan, China. *PLoS ONE*. 2014; DOI: 10.1371/journal.pone.0110348.
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31. **Dai JY**, Zhang X. Mendelian randomization studies for a continuous exposure under case-control sampling. *American Journal of Epidemiology*. 2015;181(6):440-449.
32. Marrazzo JM, Ramjee G, Richardson BA, Gomez K, Mgodi N, Nair G, Palanee T, Nakabiito C, van der Straten A, Noguchi L, Hendrix CW, **Dai JY**, Ganesh S, Mkhize B, Taljaard M, Parikh UM, Piper J, Masse B, Grossman C, Rooney J, Schwartz JL, Watts H, Marzinke MA, Hillier SL, McGowan IM, Chirenje ZM, for the VOICE Study Team. Tenofovir-Based preexposure prophylaxis for HIV infection among African women. *New England Journal of Medicine*. 2015;372(6):509-18.
33. Mgodi NM, Kelly C, Gati B, Greenspan S, **Dai JY**, Bragg V, Livant E, Piper JM, Nakabiito C, Magure, T, Marrazzo JM, Chirenje ZM, Riddler SA for the MTN-003B protocol team. Factors

- associated with bone mineral density in healthy African women. *Archives of Osteoporosis*. 2015;10:206. doi: 10.1007/s11657-015-0206-7.
34. Hladik F, Burgener A, Ballweber L, Gottardo R, Vojtech L, Fourati S, **Dai JY**, Cameron M, Strobl J, Hughes S, Hoesley C, Andrew P, Johnson S, Piper J, Friend D, Ball T, Cranston R, McElrath JM, McGowan I. Mucosal effects of tenofovir 1% gel. *eLife* 2015; 10.7554/eLife.04525.
 35. **Dai JY**, Tapsoba JDT, Buas MF, Onstad L, Levine DM, Risch HA, Chow WH, Bernstein L, Ye W, Lagergren J, Bird NC, Corley DA, Shaheen NJ, Wu AH, Hardie LJ, Reid BJ, Whiteman DC, Vaughan TL. A newly identified susceptibility locus near FOXP1 modifies the association of gastroesophageal reflux with Barrett's esophagus. *Cancer Epidemiology, Biomarker & Prevention*. 2015; 24(11):1739-47.
 36. Wang X, Li X, Paulson TG, Reid BJ, Kooperberg C, **Dai JY**. Copy number alterations detected by whole-exome and whole-genome sequencing of esophageal adenocarcinoma. *Human Genomics*. 2015; 9:22; DOI: 10.1186/s40246-015-0044-0.
 37. **Dai JY**, Zhang X, Wang CY, Kooperberg C. Augmented case-only design for randomized clinical trials with failure time endpoints. *Biometrics*. 2016; 72(1):30-8.
 38. **Dai JY**, Hendrix C, Richardson B, Cliff K, Marzinke M, Chirenje M, Marrazzo J, Brown ER. Pharmacological measures of adherence and risk of HIV acquisition in the VOICE study. *Journal of Infectious Diseases*. 2016;213(3):335-42.
 39. Mirembe BG, Kelly C, Mgodi N, Greenspan S, **Dai JY**, Mayo A, Piper J, Akello CA, Kiweewa FM , Magure T, Nakabiito C, Marrazzo JM, Chirenge ZM and Riddler SA for the MTN-003B Protocol team. Bone Mineral Density Changes among Healthy African Pre-menopausal women participating in a Tenofovir based HIV Pre-Exposure Prophylaxis Study: The MTN-003B Study. *JAIDS*. 2016;71(3):287-294.
 40. Cheng Y, **Dai JY**, Kooperberg C. Group association test using hidden Markov models. *Biostatistics*. 2016: 17(2):221-234.
 41. **Dai JY**, Tapsoba JDT, Buas MF, the BEACON Consortium, Risch H, Vaughan TL. Constrained score statistics identify genetic loci interacting with multiple risk factors in Barrett's esophagus. *American Journal of Human Genetics*: 2016;99(2):352-365.
 42. Beigi RH, Noguchi L, Montgomery E, Biggio J, Hendrix CW, Marzinke M, **Dai JY**, Pan J, Ayudhya R, Schwartz J, Isaacs K, Piper JM, Watts DH. A randomized safety and pharmacokinetic trial of daily Tenofovir 1% gel in term and near term pregnancy. *Journal of the International AIDS Society*. 2016;19(1):20990.
 43. Noguchi LM, Montgomery ET, Biggio JR, Hendrix CW, Bogen DL, Hillier S, **Dai JY**, Piper JM, Marzinke MA, Dezzutti CS, Isaacs SK, Schwartz JL, Watts DH, Beigi RH. Detectable tenofovir levels in breast-feeding infants of mothers exposed to topical tenofovir. *Antimicrobial Agents and Chemotherapy*. 2016;60(9):5616-5619.

44. Wang X, **Dai JY**[¶]. TwoPhaseInd: an R package for estimating gene-treatment interactions and discovering predictive markers in randomized clinical trials. *Bioinformatics*. 2016;32(21):3348-3350.
45. Cheng Y, **Dai JY**, Paulson TG, Wang X, Li X, Reid BJ, Kooperberg C. Quantification of multiple tumor clones using gene array and sequencing data. *Annals of Applied Statistics*. 2017;11(2):967-991.
46. **Dai JY**, Liang J, LeBlanc M, Prentice RL, Janes H. Case-only approach to identifying markers predicting treatment effects on the relative risk scale. *Biometrics*. 2017;74(2):753-763.
47. Tsilidis KK, **Dai JY**, Peters U. Mendelian randomization analysis identifies body mass index and fasting insulin as potential causal risk factors for pancreatic cancer risk. *Journal of National Cancer Institute*. 2017;109(9):djqx043.
48. Montgomery ET, Noguchi LM, **Dai JY**, Pan J, Biggio J, Hendrix C, Isaacs K, Watts DH, Schwartz JL, Piper J, Beigi R. Acceptability of and adherence to an antiretroviral-based vaginal microbicide among pregnant women in the United States. *AIDS Behav*. 2018;22(2):402-411.
49. Justman JE, Nair G, Hendrix CW, Piper JM, Marzkinke MA, **Dai JY**, et al. Pharmacokinetics and pharmacodynamics of Tenofovir reduced-glycerin 1% gel in the rectal and vaginal compartments in women: a cross-compartmental study with directly observed dosing. *JAIDS*. 2018;78(2):175-82.
50. Neumeyer S, Banbury BL, Arndt V, Berndt SI, Bezieau S, Bien SA, Buchanan DD, Butterbach K, Caan BI, Campbell PT, Casey G, Chan AT, Chanock SJ, **Dai JY**, et al. Mendelian Randomization study of age at menarche and age at menopause and the risk of colorectal cancer. *British Journal of Cancer* 2018;118:1639-1674.
51. **Dai JY**, Peters U, Wang X, Kocarnik J, Chang-Claude J, Slattery ML, Chan A, Lemire M, Berndt SI, Casey G, Song M, Jenkins MA, Brenner H, Thrift AP, White E, Hsu L. Diagnostics of pleiotropy in Mendelian randomization studies: global and individual tests for direct effects. *American Journal of Epidemiology*. 2018;187(12):2672-2680.
52. **Dai JY**, Wang X, Ma J, Wei B, Zhang C, Sun X, Self S, Yao L, Odze RD, Vaughan T, Guo Y. Whole-genome sequencing of esophageal adenocarcinoma in China reveals distinct mutation signatures and genomic alterations. *Communication Biology*. 2018;1:174|DOI: 10.1038/s42003-018-0182-8.
53. Cheng Y, **Dai JY**, Wang X, Kooperberg C. Identifying disease-associated copy number variations by a doubly penalized regression model. *Biometrics*. 2018;74(4):1341-1350.
54. Zhao SS, Leonardson A., Geybels M, McDaniel A, Yu M, Kolb S., Zong H., Carter K, Siddiqui J, Cheng A, Wright J, Pritchard C, Lance R, Troyer D, Fan J, Ostrander E, **Dai JY**, Tomlins S, Feng Z, and Stanford J. A Five-CpG DNA Methylation Score has Prognostic Value for Metastatic Progression in Men Treated for Localized Prostate Cancer. *Prostate*. 2018;78:1084-1091.

55. Wang X, **Dai JY**, Albanes D, Arndt V, Berndt SI, Bezieau S, Brenner H, et al. Mendelian randomization of C-reactive protein on colorectal cancer risk. *International Journal of Epidemiology*. 2018. DOI: 10.1093/ije/dyy244.
56. **Dai JY**, LeBlanc M, Goodman PJ, Lucia MS, Thompson IM, Tangen CM. Case-only methods identified genetic loci predicting a subgroup of men with reduced risk of high-grade prostate cancer by finasteride. *Cancer Prevention Research*. 2019;12(2):113-120.
57. Wang CY, **Dai JY**. Best linear inverse probability weighted estimation for two-phase designs and missing covariate regression. *Statistics in Medicine*. 2019;38(15):2783-96.
58. **Dai JY**, LeBlanc M. Case-only trees and random forests for exploring gene-treatment interactions in randomized clinical trials. *Journal of Royal Statistical Society, Series C*. 2019;68(5):1371-1391.
59. **Dai JY**, Wang B, Wang X, Cheng A, Kolb S, Wright JL, Stanford JL. Physical activity is associated with lower risk of metastatic-lethal prostate cancer outcomes and hypomethylation in the CRACR2A gene. *Cancer Epidemiology, Biomarker and Prevention*. 2019;28(2):258-264.
60. Vaughan TL, Onstad L, **Dai JY**. Interactive Decision Support for Esophageal Adenocarcinoma Screening and Surveillance. *BMC Gastroenterology*. 2019. 19(1):109. doi: 10.1186/s12876-019-1022-0.
61. Cheng A, Zhao S, Wright JL, Kolb S, Karnes RJ, Jenkins RB, Davicioni E, Feng Z, Fan J-B, **Dai JY**, Stanford JL. A four-gene transcript score to predict metastatic progression in men treated for localized prostate cancer: development and validation studies. *Prostate*. 2019;79(14):1589-1596. doi: 10.1002/pros.23882
62. **Dai JY**, Wang X, Wang B, Sun W, Jordahl KM, Kolb S, Nyame YA, Wright JL, Ostrander EA, Feng Z, Stanford JL. DNA methylation and *cis*-regulation of gene expression by prostate cancer risk SNPs. *PLOS Genetics* 16(3):e1008667. (2020). <http://doi/10.1371/journal.pgen.1008667>.
63. **Dai JY**, Stanford JL, LeBlanc M. A multiple-testing procedure for high-dimensional mediation analyses. *Journal of American Statistical Association: Theory and Methods*. 2020. DOI: [10.1080/01621459.2020.1765785](https://doi.org/10.1080/01621459.2020.1765785)
64. Middha P, Lindström S, Behrens S, ..., **Dai JY**, ..., Easton DF, Milne RL, Chang-Claude J on behalf of Breast Cancer Association Consortium. An assessment of interactions between 205 breast cancer susceptibility loci and 13 established risk factors in relation to breast cancer risk in the Breast Cancer Association Consortium. *International Journal of Epidemiology*. 2020. 49(1):216-230.
65. Wang X, Crasso CS, Jordahl KM, Kolb S, Nyame YA, Wright JL, Ostrander EA, Troyer DA, Lance R, Feng Z, **Dai JY**, Stanford JL. Copy number alterations are associated with metastatic lethal progression in prostate cancer. *Prostate Cancer and Prostatic Diseases*. 23, 494-506 (2020). PMID: 32071439. <http://doi.org/10.1038/s41391-020-0212-8>.

66. Middha P, Mavaddat N, Choudhury P, ..., **Dai JY**, ..., Easton DF, Milne RL, Garcia-Closas M, Chang-Claude J. Combined associations of a polygenic risk score and classical risk factors with breast cancer risk. *Journal of National Cancer Institute*. 2021; 113(3):329-337.
67. Dighe S, Chen J, Yan L,, **Dai JY**,, Vaughan TL, Madeleine MM, Hardie LJ, Buas MF. Germline variation in the insulin-like growth factor pathway and risk of Barrett's esophagus and esophageal adenocarcinoma. *Carcinogenesis*. 2021;42(3):369-377.
68. Karlsson Q, Brook MN, Dadaev T,, Stanford JL, **Dai JY**,, Eeles RA, Kote-Jarai Z. Rare germline variants in ATM predispose to prostate cancer: A PRATICAL Consortium study. *European Urology Oncology*. 2021;S2588-9311(20)30209-1. doi: 10.1016/j.euo.2020.12.001
69. Zhang H, Cai R, **Dai JY**, Sun W. EMeth: An EM algorithm for cell type decomposition based on DNA methylation data. *Sci Rep* 2021;11:5717.
70. Hua X, **Dai JY**, Lindström S,, Chan AT, Peters U, and Newcomb PA. Genetically predicted circulating C-reactive protein concentration and colorectal cancer survival: A Mendelian randomization study. *Cancer Epidemiology, Biomarkers & Prevention* 2021;30(7):1349-1358.
71. Liao JB, Gwin WR, Urban RR, Hitchcock-Bernhardt KM, Coveler AL, Higgins D, Childs JS, Shakalia H, Swensen RE, Stanton SE, Tinker AV, Wahl TA, Ancheta RG, McGonigle KF, **Dai JY**, Disis ML, Goff BA. Pembrolizumab with low dose carboplatin for recurrent platinum resistant ovarian, fallopian tube, and primary peritoneal cancer: survival and immune correlates. *Journal of ImmunoTherapy of Cancer* 2021;0:e003122. Doi:10.1136/jitc-2021-003122.
72. Chen J, Ali MW, Yan L, Dighe SG, **Dai JY**, Vaughan TL, Casey G, Buas MF. Prioritization and functional analysis of GWAS risk loci for Barrett's esophagus and esophageal adenocarcinoma. *Human Molecular Genetics* 2022;31(3):410-422.
73. Huang Y, Hua X, Labadie JD, Harrison TA, **Dai JY**, Lindstrom S,, Chan AT, Peters U, and Newcomb PA. Genetic variants associated with circulating C-reactive protein levels and colorectal cancer survival: Sex- and lifestyle factors- specific associations. *International Journal of Cancer* 2022;150(9):1447-1454.
74. Wang X, Jordahl KM, Zhu C, Livingstone J, Rhie SK, Wright JL, Grady WM, Boutros PC, Stanford JL, **Dai JY**[¶]. Methylation subtypes of primary prostate cancer predict poor prognosis. *Cancer Epidemiology, Biomarker and Prevention* 2022;31(7):1473-1482.
75. Ali MW, Chen J, Yan Li, Wang X, **Dai JY**, Vaughan TL, Casey G, Buas MF. A risk variant for Barrett's esophagus and esophageal adenocarcinoma at chr8p23.1 affects enhancer activity and implicates multiple gene targets. *Human Molecular Genetics*. 2022;31(23):3975-3986.
76. Wang X, Gharahkhani P, Levin DM, Fitzgerald RC, ..., Whiteman DC, MacGregor S, Schumacher J, Vaughan TL, Buas MF, and **Dai JY**[¶]. eQTL set-based association analysis identifies novel susceptibility loci for Barrett's esophagus and esophageal adenocarcinoma. *Cancer Epidemiology, Biomarker and Prevention*. 2022;31(9):1735-1745.

77. FitzGerald LM, Jung C, Wong EM, Joo JE, Bassett JK, Dowty JG, Wang X, **JY Dai**, Stanford JL, O'Callaghan NO, Nottle T, Pedersen J, Giles GG, Southey MC. Detection of differentially methylated CpGs between tumor and adjacent benign cells in diagnostic prostate cancer samples. Submitted to *Scientific Report*.
78. Ghezelayagh TS, Wu ES, Barber EL, Dao MD, Zsiros E, Urban RR, Gray HJ, Goff BA, Shah CA, Neubauer NL, **Dai JY**, Tanyi JL, Liao JB. Timing and duration of bevacizumab treatment and survival in patients with recurrent ovarian, fallopian tube, and peritoneal cancer: a multi-institution study. *Eur J Gynaecol Oncol*. 2023 Feb;44(1):17-25.
79. FitzGerald LM, Jung C, Wong EM, Joo JE, Bassett JK, Dowty JG, Wang X, **JY Dai**, Stanford JL, O'Callaghan NO, Nottle T, Pedersen J, Giles GG, Southey MC. Detection of differentially methylated CpGs between tumor and adjacent benign cells in diagnostic prostate cancer samples. Submitted to *Scientific Report*.
80. Ma C, Wang X, **Dai JY**, Turman C, Kraft P, Stopsack KH, Loda M, Pettersson A, Mucci LA, Stanford JL, Penney KL. Germline genetic variants associated with somatic TMPRSS2-ERG fusion status in prostate cancer. Revised for *Cancer Epidemiology, Biomarker and Prevention*.

Book chapters

Dai JY, Hsu L, Kooperberg C. **Handbook of Statistical Methods for Case-Control Studies**. Chapter 25: Two-stage testing for genome-wide gene-environment interactions. Chapman & Hall/CRC 2018.

Kooperberg C, **Dai JY**, Hsu L. **Statistical approaches to gene × environment interactions for complex phenotypes**. Chapter 2: Two-stage procedures for the identification of Gene × Environment and Gene × Gene interactions in genome wide association studies. MIT Press 2016.

arXiv deposit

Dai JY, Chen H, Wang X, Huang Y, Sun W, Stanford J, Grady W, Feng Z. Incorporating increased variability in detecting aberrant cancer DNA methylation. [arXiv:2302.14826](https://arxiv.org/abs/2302.14826).

Chen H, LeBlanc ML, **Dai JY**[¶]. Augmented learning of heterogeneous treatment effects in randomized clinical trials via gradient boosting trees. [arXiv:2302.01367](https://arxiv.org/abs/2302.01367).

Wang X, Ming Yu, Grady W, Ziding F, Sun W, **Dai JY**[¶]. DMseg: a Python algorithm for *de novo* detection of differential methylation region in methylome studies. [arXiv:2306.15032](https://arxiv.org/abs/2306.15032).