Curriculum Vitae
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Education

Yale University, PhD in Statistics, December 1995.
Dissertation topic: *A Spatial-Temporal Model for Real Estate Price Indices*.
Advisor: John Hartigan.

The University of Chicago, Master of Sciences in Statistics, June 1989.
Masters thesis topic: *Temporal Models for Rainfall Deposition*.
Advisor: Michael Stein.

The University of Chicago, Bachelor of Sciences in Mathematics, June 1987.
Fulfilled degree requirements for Bachelor of Arts in Statistics.

Professional Experience

Department of Statistical Science, Duke University,
Research Professor, September 2017 to present.
Associate Research Professor, September 2007 to August 2017.

Institute of Statistics and Decision Sciences, Duke University,
Assistant Research Professor, September 2006 to September 2007.
Adjunct Assistant Professor and Research Scientist Fall 1998 to December 2000.
Visiting Assistant Professor Fall 1996 to Summer 1998.

Department of Biostatistics and Bioinformatics and
Institute of Statistics and Decision Sciences, Duke University,
Assistant Research Professor, December 2000 to August 2006.

Department of Statistics, Virginia Polytechnic and State University
Visiting Assistant Professor, Spring 1996.

Department of Statistics, Yale University
System Administrator, Fall 1993 to Fall 1995.

Case, Shiller, Weiss, Inc.
A Cambridge, Massachusetts real estate economics firm.
Summer Intern, Summer 1993.

National Cancer Institute
Summer Fellowship, Division of Cancer Etiology. Summer 1992.
Summer Fellowship, Division of Cancer Etiology. Summer 1988.

Price Waterhouse

Quantitative Methods Consulting Group, Washington D.C.
Senior Consultant, Spring 1991 to Fall 1991.
Staff Consultant, Fall 1989 to Spring 1991.

Publications

Benjamin–Neelon SE, **Iversen Jr ES**, Clancy SM, Hoyo C, Bennett GG, Kravitz RM, Ostbye T (2019). Early child care and weight status in a cohort of predominantly black infants in the US. *Childhood Obesity*. DOI: 10.1089/chi.2019.0127. PMID: 31618046.

Reid BM, Permuth JB, Chen YA, Fridley BL, **Iversen Jr ES**, Chen Z, Jim H, Vierkant RA, Cunningham JM, Barnholtz–Sloan JS, Narod S, Risch H, Schildkraut JM, Goode EL, Monteiro AN, Sellers TA (2019). Genome–wide analysis of common copy number variation and epithelial ovarian cancer risk. *Cancer Epidemiology, Biomarkers and Prevention*. 28(7):1117–1126. DOI: 10.1158/1055–9965.EPI–18-0833. PMID: 30948450.

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Hart SN, Hoskin T, Shimelis H, Moore RM, Feng B, Thomas A, Lindor NM, Polley EC, Goldgar DE, **Iversen Jr ES**, Monteiro ANA, Suman VJ, Couch, FJ (2019). Comprehensive annotation of BRCA1 and BRCA2 missense variants by functionally validated sequence–based computational prediction models. *Genetics in Medicine*. 21(1):71–80. https://doi.org/10.1038/s41436–018–0018–4. PMID: 29884841.

Iversen Jr ES, McCarthy JM, Burdett KB, Lipton G, Phillips G, Dressman H, Ross J, Chao N (2018). Bridging the gaps: using an NHP model to predict single dose radiation absorption in humans. *International Journal of Radiation Biology*. 0(0):1–10. DOI: 10.1080/09553002.2018.1532614. PMID: 30371121.

Guidugli L, Shimelis H, Masica DL, Pankratz VS, Lipton GB, Singh N, Hu C, Monteiro ANA, Lindor NM, Goldgar DE, Karchin R, **Iversen Jr ES**, Fergus J. Couch FJ (2018). Assessment of the clinical relevance of BRCA2 missense variants by functional and computational approaches. *American Journal of Human Genetics*. 102:233–248. DOI: 10.1016/j.ajhg.2017.12.013. PMID: 29394989.

Earp M, Tyrer JP, Winham SJ, Lin HY, Chornokur G, Dennis J, Aben KKH, Anton–Culver H, Antonenkova N, Bandera EV, Bean YT, Beckmann MW, Bjorge L, Bogdanova N, Brinton LA, Brooks–Wilson A, Bruinsma F, Bunker CH, Butzow R, Campbell IJ, Carty K, Chang–Claude J, Cook LS, Cramer DW, Cunningham JM, Cybulski C, Dansonka–Mieszkowska A, Despierre E, Doherty JA, Dork T, du Bois A, Durst M, Easton DF, Eccles DM, Edwards RP, Ekici AB, Fasching PA, Fridley BL, Gentry–Maharaj A, Giles GG, Glasspool R, Goodman MT, Gronwald J, Harter P, Hein A, Heitz F, Hildebrandt MAT, Hillemanns P, Hogdall CK, Hogdall E, Hosono S, **Iversen Jr ES**, Jakubowska A, Jensen A, Ji BT, Jung AY, Karlan BY, Kellar M, Kiemeney LA, Lim BK, Kjaer SK, Krakstad K, Kupryjanczyk J, Lambrechts D, Lambrechts S, Le ND, Lele S, Lester J, Levine DA, Li Z, Liang D, Lissowska J, Lu K, Lubinski J, Lundvall L, Massuger LFAG, Matsuo K, McGuire V, McLaughlin JR, McNeish I, Menon U, Milne RL, Modugno F, Moysich K B, Ness RB, Nevanlinna H, Odunsi K, Olson SH, Orlow I, Orsulic S, Paul J, Pejovic T, Pelttari LM, Permuth JB, Pike MC, Poole EM, Rosen B, Rossing NA, Rothstein JH, Runnebaum IB, Rzepecka IK, Schernhammer E, Schwaab I, Shu XO, Shvetsov YB, Siddiqui N, Sieh W, Song H, Southey MC, Spiewankiewicz B, Sucheston–Campbell L, Tangen IL, Teo SH, Terry KL, Thompson PJ, Thomsen L, Tworoger SS, van Altena AM, Vergote I, Vestrheim–Thomsen LC, Vierkant RA, Walsh CS, Wang–Gohrke S, Wentzensen N, Whittemore AS, Wicklund KG, Wilkens LR, Woo YL, Wu AH, Wu X, Xiang YB, Yang H, Zheng W, Ziogas A, Lee AW, Pearce CL, Berchuck A, Schildkraut JM, Ramus SJ, Monteiro ANA, Narod SA, Sellers TA, Gayther SA, Kelemen LE, Chenevix–Trench G, Risch HA, Pharoah PDP, Goode El, Phelan CM (2018). Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*. 13(7): e0197561. https://doi.org/10.1371/journal.pone.0197561.

Kelemen LE, Earp M, Fridley BL, Chenevix–Trench G and on behalf of Australian Ovarian Cancer Study Group, Fasching PA, Beckmann MW, Ekici AB, Hein A, Lambrechts D, Lambrechts S, Els VN, Vergote I, Rossing MA, Doherty JA, Chang–Claude J, Behrens S, Moysich KB, Cannioto R, Lele S, Odunsi K, Goodman MT, Shvetsov YB, Thompson PJ, Wilkens LR, Dork T, Antonenkova N, Bogdanova N, Hillemanns P, Runnebaum IB, Andreas du B, Harter P, Heitz F, Schwaab I, Butzow R, Pelttari LM, Nevanlinna H, Modugno F, Edwards RP, Kelley JL, Ness RB, Karlan BY, Lester J, Orsulic S, Walsh C, Kjaer SK, Jensen A, Cunningham JM, Vierkant RA, Giles GG, Bruinsma F, Southey MC, Hildebrandt MA, Liang D, Lu K, Wu X, Sellers TA, Levine DA, Schildkraut JM, **Iversen Jr ES**, Terry KL, Cramer DW, Tworoger SS, Poole EM, Bandera EV, Olson SH, Orlow I, Liv C, Vestrheim T, Bjorge L, Krakstad C, Tangen IL, Kiemeney LA, Aben KK, Massuger LFAG, van Altena AM, Pejovic T, Bean Y, Kellar M, Cook LS, Le ND, Brooks–Wilson A, Gronwald J, Cybulski C, Jakubowska A, Lubinski J, Wentzensen N, Brinton LA, Lissowska J, Hogdall E, Engelholm SA, Hogdall C, Lundvall L, Nedergaard L, Pharoah PDP, Dicks E, Song H, Tyrer JP, McNeish I, Siddiqui N, Carty K, Glasspool R, James P, Campbell IG, Eccles D, Whittemore AS, McGuire V, Rothstein JH, Sieh W, Narod SA, Phelan CM, McLaughlin JR, Risch HA, Anton–Culver H, Ziogas A, Menon U, Gayther SA, Gentry–Maharaj A, Ramus SJ, Wu AH, Pearce CL, Lee AW, Pike MC, Kupryjanczyk J, Podgorska A, Plisiecka–Halasa J, Sawicki W, Goode EL, Berchuck A and the Ovarian Cancer Association Consortium (2018). rs495139 in the TYMS–ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. *International Journal of Molecular Sciences*. 19(9):2473. DOI: 10.3390/ijms19092473.

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Benjamin–Neelon SE, Ostbye T, Bennett GG, Kravitz R, Clancy SM, Stroo M, **Iversen Jr ES**, Hoyo C (2017). Cohort profile for the Nurture observational study examining associations of multiple caregivers on infant growth in the Southeastern United States. *BMJ Open*. 7:e013939. DOI: 10.1136/bmjopen–2016–013939. PMID: 28179416.

Sosa–Pagan J, **Iversen Jr ES**, Grandl J (2017). TRPV1 temperature activation is specifically sensitive to strong decreases in amino acid hydrophobicity. *Scientific Reports*. 7(1):549. DOI: 10.1038/s41598–017–00634–4. PMID: 28373693.

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Hampras SS, Sucheston–Campbell LE, Cannioto R, Chang–Claude J, Modugno F, Dork T, Hillemanns P, Preus L, Knutson KL, Wallace PK, Hong CC, Friel G, Davis W, Nesline M, Pearce CL, Kelemen LE, Goodman MT, Bandera EV, Terry KL, Schoof N, Eng KH, Clay A, Singh PK, Joseph JM, Aben KK, Anton–Culver H, Antonenkova N, Baker H, Bean Y, Beckmann MW, Bisogna M, Bjorge L, Bogdanova N, Brinton LA, Brooks–Wilson A, Bruinsma F, Butzow R, Campbell IG, Carty K, Cook LS, Cramer DW, Cybulski C, Dansonka–Mieszkowska A, Dennis J, Despierre E, Dicks E, Doherty JA, du Bois A, Durst M, Easton D, Eccles D, Edwards RP, Ekici AB, Fasching PA, Fridley BL, Gao YT, Gentry–Maharaj A, Giles GG, Glasspool R, Gronwald J, Harrington P, Harter P, Hasmad HN, Hein A, Heitz F, Hildebrandt MA, Hogdall C, Hogdall E, Hosono S, **Iversen Jr ES**, Jakubowska A, Jensen A, Ji BT, Karlan BY, Kellar M, Kelley JL, Kiemeney LA, Klapdor R, Kolomeyevskaya N, Krakstad C, Kjaer SK, Kruszka B, Kupryjanczyk J, Lambrechts D, Lambrechts S, Le ND, Lee AW, Lele S, Leminen A, Lester J, Levine DA, Liang D, Lissowska J, Liu S, Lu K, Lubinski J, Lundvall L, Massuger LF, Matsuo K, McGuire V, McLaughlin JR, McNeish I, Menon U, Moes–Sosnowska J, Narod SA, Nedergaard L, Nevanlinna H, Nickels S, Olson SH, Orlow I, Weber RP, Paul J, Pejovic T, Pelttari LM, Perkins B, Permuth–Wey J, Pike MC, Plisiecka–Halasa J, Poole EM, Risch HA, Rossing MA, Rothstein JH, Rudolph A, Runnebaum IB, Rzepecka IK, Salvesen HB, Schernhammer E, Schmitt K, Schwaab I, Shu XO, Shvetsov YB, Siddiqui N, Sieh W, Song H, Southey MC, Tangen IL, Teo SH, Thompson PJ, Timorek A, Tsai YY, Tworoger SS, Tyrer J, van Altena AM, Vergote I, Vierkant RA, Walsh C, Wang–Gohrke S, Wentzensen N, Whittemore AS, Wicklund KG, Wilkens LR, Wu AH, Wu X, Woo YL, Yang H, Zheng W, Ziogas A, Gayther SA, Ramus SJ, Sellers TA, Schildkraut JM, Phelan CM, Berchuck A,

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Chen S, **Iversen Jr ES**, Friebel T, Finkelstein D, Weber BL, Eisen A, Peterson LE, Schildkraut JM, Isaacs C, Peshkin BN, Corio C, Leondaridis L, Tomlinson G, Dutson D, Kerber R, Amos CI, Strong LC, Berry DA, Euhus DM, Parmigiani G. (2006). Characterization of BRCA1 and BRCA2 Mutations in a Large United States Sample. *Journal of Clinical Oncology.* 24(6):863–71. DOI: 10.1200/JCO.2005.03.6772. PMCID: PMC2323978.

Iversen Jr ES, Chen S (2005). Population–Calibrated Gene Characterization: Estimating Distributions of Age at Onset Associated with Breast Cancer Susceptibility Genes. *Journal of the American Statistical Association.* 100:399–409.

Rich JN, Hans C, Jones B, **Iversen Jr ES**, McClendon RE, Rasheed BKA, Dobra A, Dressman HK, Bigner DD, Nevins JR and West M (2005). Gene Expression Profiling and Genetic Markers in Glioblastoma Survival. *Cancer Research* 65(10):4051–4058.

Berchuck A, **Iversen Jr ES**, Lancaster JM, Pittman J, Luo J, Lee P, Murphy S, Dressman HK, Febbo PG, West M, Nevins JR, Marks JR (2005). Patterns of Gene Expression That Characterize Long–Term Survival in Advanced Stage Serous Ovarian Cancers. *Clinical Cancer Research* 11(10):3686–3696.

Zhou X, **Iversen Jr ES**, Parmigiani G (2005). Classification of missense mutations of disease genes. *Journal of the American Statistical Association*, 100:51–60. DOI: 10.1198/016214504000001817. PMCID: PMC2311507.

Berchuck A, **Iversen Jr ES**, Lancaster J, Dressman HK, West M, Nevins JR and Marks JR (2004). Prediction of optimal versus suboptimal cytoreduction of advanced stage serous ovarian cancer using microarrays. *American Journal of Obstetric Gynecology*, 190(4):910–25.

Seo DM, Wang T, Dressman H, Herderick EE, **Iversen Jr ES**, Dong C, Vata K, Milano CA, Rigat F, Pittman J, Nevins JR, West M, and Goldschmidt-Clermont PJ (2004). Gene expression phenotypes of atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, 24(10):1922 – 1927.

Pittman J, Huang E, Dressman H, Horng CF, Cheng SH, Tsou MH, Chen CM, Bild A, **Iversen Jr ES**, Liao M, Huang AT, Nevins JR, West M (2004). Integrated modeling of clinical and gene expression information for personalized prediction of disease outcomes. *PNAS*, 101, 8431–8436. DOI: 10.1073/pnas.0401736101. PMCID: PMC420411.

Iversen Jr ES and Luo J (2003). Molecular and Genetic Modeling of Disease Risk. *2003 Proceedings of the American Statistical Association, Risk Section [CD-ROM]*, Alexandria, VA: American Statistical Association.

Huang E, Cheng SH, Dressman H, Pittman J, Tsou MH, Horng CF, Bild A, **Iversen Jr ES**, Liao M, Chen CM, West M, Nevins JR and Huang AT (2003). Gene expression predictors of breast cancer outcomes (with commentary). *The Lancet*, 361:1590–1596.

Berry DA, **Iversen Jr ES**, Gudbjartsson DF, Hiller E, Garber J, Peshkin BN, Lerman C, Watson P, Lynch H, Hilsenbeck S, Rubinstein WS, Hughes K and Parmigiani G (2002). BRCAPRO validation, sensitivity of genetic testing of BRCA1/BRCA2, and prevalence of other breast cancer susceptibility genes. *Journal of Clinical Oncology*. 20:2701-12.

Iversen Jr ES. (2001). Spatially disaggregated real estate indices. *Jour. Bus. & Econ. Stat*, 19:341–357.

Iversen Jr ES, Parmigiani G, Berry D, Schildkraut J (2000). Genetic susceptibility and survival: application to breast cancer. *Journal of the American Statistical Association*, 95:28–42.

Iversen Jr ES, Parmigiani G, Berry D (1999). Validating Bayesian prediction models: a case study in genetic susceptibility to breast cancer. In *Case Studies In Bayesian Statistics*, Volume IV, Gatsonis *et al.*, eds. New York: Springer Verlag.

Parmigiani G, Berry D, **Iversen Jr ES**, Müller P, Schildkraut J, and Winer E (1999). Modeling risk of breast cancer and decisions about genetic testing. In *Case Studies In Bayesian Statistics*, Volume IV, Gatsonis *et al.*, eds. New York: Springer Verlag.

Claus EB, Schildkraut J, **Iversen Jr ES**, Berry DA, Parmigiani G (1998). The effect of BRCA1 and BRCA2 on the association between breast cancer risk and family history, *Journal of the National Cancer Institute* 90:1824–1829.

Schildkraut J, **Iversen Jr ES**, Parmigiani G, Berry, D (1997). Prognostic Significance of Estimated BRCA1 and BRCA2 mutation status in women diagnosed with breast cancer, *Genetic Epidemiology*, 14:538.

Iversen Jr ES, Lees JM (1996), A statistical technique for validating velocity models, *Bull. Seismol. Soc. Am.* 86(60), 1853-1862.

Invited Talks

Evidence–based Network for the Interpretation of Mutant Alleles (ENIGMA) Consortium meeting, Springdale, Utah, April 2019. "Multifactorial VarCall Model Update."

Evidence–based Network for the Interpretation of Mutant Alleles (ENIGMA) Consortium meeting, Springdale, Utah, April 2019. "A VarCall Model for a Mouse ES Cell–Based Functional Assay."

Policies and Regulatory Pathways to FDA licensure: Radiation Countermeasures and Biodosimetry Devices meeting, Rockville, Md, October 2018. "Bridging the Gaps: Using an NHP Model to Predict Single Dose Radiation Absorption in Humans."

Evidence–based Network for the Interpretation of Mutant Alleles (ENIGMA) Consortium meeting, Edinburgh, Scotland, June 2018. "Multifactorial VarCall Models."

Evidence–based Network for the Interpretation of Mutant Alleles (ENIGMA) Consortium meeting, Santiago de Compostela, Spain, September 2017. "New VarCall Analysis of BRCA1 Variants."

Evidence–based Network for the Interpretation of Mutant Alleles (ENIGMA) Consortium meeting, Limassol, Cyprus, January 2017. "The BRCA1 and BRCA2 VarCall VUS Classification Models."

Ovarian Cancer Association Consortium Investigators Meeting, El Escorial, Spain, April 2013. "Ovarian Cancer Consortia Risk Model Update."

Ovarian Cancer Association Consortium Investigators Meeting, El Escorial, Spain, April 2013. "Ovarian Cancer Consortia Risk Model Update."

Department of Biostatistics, University of Miami, November 2012. "Functional Annotation Signatures as Prior Information in Genetic Association Studies."

Ovarian Cancer Association Consortium Investigators Meeting, Quebec City, Ontario, September 2012. "Models for Genetic Association Given Consortium Data."

Ovarian Cancer Association Consortium Investigators Meeting, Quebec City, Ontario, September 2012. "DNA Repair Pathway Analysis."

Ovarian Cancer Association Consortium Investigators Meeting, Chicago, IL, March 2012. "Ongoing Analysis of the NCOCS iCOGS Candidates."

Methods of Analysis of GxE Interactions in Complex Disease: The Genes, Environment and Health Initiative Investigators Meeting, Bethesda, MD, January 2010. "Bayesian Models, Model Selection and Prior Specification for Gene–Environment Association Studies."

Methods of Analysis of GxE Interactions in Complex Disease: The Genes, Environment and Health Initiative Investigators Meeting, Bethesda, MD, January 2009. "Bayesian Models and Prior Choice for Gene–Environment Association Studies."

SAS, Inc., November 2008. "Four Examples of Modern Applied Bayesian Analysis."

Methods of Analysis of GxE Interactions in Complex Disease: The Genes, Environment and Health Intitiative Investigators Meeting, Bethesda, MD, May 2008. "Bayesian Modeling and Optimal Design for Studies of Gene–Environment Association."

Joint Statistical Meetings, Salt Lake City, July 2007. "A Bayesian Branching Process Model for Loss of Cell Cycle Synchrony."

Ovarian Cancer Association Consortium Spring Meeting, April 2006. "Analysis, Study Design and Power Issues of Special Relevance to the OCAC."

National Institute of Environmental Health Sciences, March 2006. "Study Design and Inference for Genome-wide and Pathway Association Studies."

Johns Hopkins University, Expression Analysis Working Group, December 2005. "Model Search and Combination for High Dimensional Genomic Assay Data."

Statistical Methods in Molecular Epidemiology. 13$^{\text{th}}$ EUROTOX Training and Discussion Session. Bochum, Germany, September 2005. "Sample Selection, Study Design and Statistical Inference for Studies of the Genetic and Environmental Etiology of Cancer."

Vanderbilt/UAB/Duke Inter–SPORE Workshop on Statistical Methods in Proteomics and Genomics, April 2005. "Model Search and Combination for High Dimensional Genomic Assay Data."

University of Alabama at Birmingham, Cancer Center Biostatistics, November 2004. "Array Based Predic-

tion of Survival Outcome: Model Search and Combination."

Johns Hopkins University, Biostatistics Seminar Series, February 2004. "Gene Characterization with High Risk Family Data."

North Carolina State University, Environmental Statistics Working Group, October 2001. "Assessing Evidence for Gene–Environment Interactions Given High Risk Family Data."

Cancer Genetics Network Steering Committee Meeting, Irvine, CA, June 2001. "Ascertainment Corrected Analysis of Family Data."

North Carolina State University, Biomedical Statistics Working Group, March 2001. "Population–calibrated estimation of cancer penetrance among BRCA1/2 mutation carriers."

Simon Fraser University, March 2001. "Modeling Inherited Susceptibility to and Prognosis After Breast Cancer."

National Institute of Environmental Health Sciences, February 2001. "Modeling Inherited Susceptibility to and Prognosis After Breast Cancer."

Cancer Genetics Network Steering Committee Meeting, Philadelphia, November 1999. "New Ideas for Handling Issues in the Analysis of Modifier of Penetrance Studies."

Joint Statistical Meetings, Baltimore, August 1999. "Analysis of Case–Control Studies With a View Towards Absolute Risk Prediction."

Teaching

Duke University

Introduction to Statistical Consulting (STA 470). A participatory introduction to statistical consulting in conjunction with the campus–wide consulting service offered by the Department of Statistical Science. Fall 2019, Spring 2020.

Statistical Methods for Computational Biology (STA 613/CBB 540). Introduction to methods of statistical inference and stochastic modeling underlying common tools in functional genomics and computational molecular biology. Spring 2020.

Introduction to Statistical Consulting/Statistical Consulting Workshop (STA 470/851). A participatory introduction to statistical consulting in conjunction with the campus–wide consulting service offered by the Department of Statistical Science. Spring 2014, Fall 2014, Spring 2015, Fall 2015, Spring 2016, Fall 2016, Spring 2017, Fall 2017, Spring 2018, Fall 2018, Spring 2019.

Independent Study (STA493). An extended statistical consulting project to identify and characterize trends in educational attainment data. Spring 2017.

Case Studies in Cancer Molecular and Genetic Epidemiology (STA 790). Introduction to statistical methods in cancer clinical and genetic epidemiology through case studies. Spring 2013.

Statistical Methods for Computational Biology (STA 270/BGT 200). Introduction to methods of statistical inference and stochastic modeling underlying common tools in functional genomics and computational molecular biology. Fall 2002, Fall 2003, Fall 2004.

Advanced Modeling and Scientific Computing (STA 376), an introduction to advanced statistical modeling and modern computational and numerical methods useful in implementing statistical analyses. Fall 1998, Spring 2000, Spring 2001, Spring 2002.

Statistics and Data Analysis in Economics (STA 110B), an undergraduate first course in Statistics for Economics majors. Fall 1996, Spring 1997, Fall 1997, Spring 1998, Spring 1999, Fall 1999.

Virginia Polytechnic and State University

Methods of Statistical Computing (STAT 4004), an introduction to computational aspects of data analysis from algorithms to computing environments. Spring 1996.

Statistical Computing (STAT 5304), a survey of fundamental topics in numerical computing, Monte Carlo methods, resampling methods, and computer intensive tools for statistical inference. Spring 1996.

Student Advising

Computational Biology & Bioinformatics (CBB) rotation advisor for Devang Thakkur, PhD Student in CBB, Summer 2019.

Honors thesis advisor for Mao Hu, BS Statistical Science, Spring 2015.

Statistical Science masters thesis supervisor for Michael Mayhew (Computational Biology and Bioinformatics, 2014).

Statistical Science masters thesis supervisor for Jianling Zhong (Computational Biology and Bioinformatics, 2017).

Committee member for Yingbo Li, Ph.D. in Statistical Science, Spring 2013.

Supervisor for Weizi Huang, MS in Computational Biology and Bioinformatics Summer 2010. Research topic: incorporating functional annotation data into models for gene–environment assocation.

Co–supervisor (with M. Clyde) of Melanie Wilson, PhD in Statistical Science Spring 2010. Research topic: prior distributions for model selection and model averaging.

Committee member for Haige Shen, Ph.D. in Computational Biology and Bioinformatics, Fall 2007.

Committee member for Jen–Hwa Chu, Ph.D. in Statistical Science, Summer 2007.

Co–supervisor (with M. Clyde) of Jingqin Luo, Ph.D. in Statistics and Decision Sciences, Fall 2006. Research topic: Bayes Classification and Prediction via Compositional Shrinkage Regressions.

Committee member for Yingjun Cao, M.S. in Electrical and Computer Engineering, Spring 2003.

Co–supervisor (with G. Parmigianni) of Kathy Zhou, Ph.D. in Statistics and Decision Sciences, December 2002. Research topic: Disease Causality of Missense Mutations.

Masters thesis supervisor for Philippe Luedi, M.S. in Statistics and Decision Sciences, Summer 2002.

Committee member for Maria DeIorio, Ph.D. in Statistics and Decision Sciences, Fall 2001. Research topic: Markov Random Fields at Multiple Resolutions and an ANOVA Model for Dependent Random Measures.

Committee member for Daniel Gudbjartsson, Ph.D. in Statistics and Decision Sciences, Fall 2000. Research topic: Multipoint Linkage Analysis Based on Allele Sharing Scores.

Committee member for Xiaolan Ye, M.S. in Statistics and Decision Sciences, Spring 2000.

Committee member for Hongjun Wang, M.S. in Statistics and Decision Sciences, Spring 1999.

Professional Affiliations

American Statistical Association,

International Society for Bayesian Analysis,

American Society for Human Genetics, and

American Association for Cancer Research.

Professional Service

Editorial Roles:

Associate Editor, *Journal of the American Statistical Association*, 2009 – 2012.

Editorial Board, *Medical Decision Making*, 12/2003 – 12/2006.

Referee for:

Journal of the American Statistical Association, *Biometrika*, *Biostatistics*, *Mathematical Biosciences*, *Journal of Statistical Planning and Inference*, *Statistics in Medicine*, *Medical Decision Making*, *Journal of Epidemiology and Biostatistics*, *Journal of the National Cancer Institute*, *British Journal of Cancer*, *European Journal of Human Genetics*, *Human Mutation*, *Genetics in Medicine*, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, and *Real Estate Economics*.

NIH Invited Planning Workshops:

'Next Generation Analytic Tools for Large Scale Genetic Epidemiolgoy Studies of Complex Diseases,' September 2010.

'Gene–Environment Interplay in Common Complex Diseases: Forging an Integrative Model,' January 2010.

'Workshop on Genetic Susceptibility to Prostate Cancer,' April 2001.

NIH Review Panels:

'Bridging the Gap: Cancer Mechanism to Population Science U01,' April 2014.

'Tumor Microenvironment Network,' June 2011.

'SPORE in Gynecologic, Breast and Skin Cancers,' February 2010.

'P01 Singlet,' October 2008.

'Tumor Microenvironment Network,' September 2006.

'Population Based Prevention Studies P01 Review Cluster,' January 2005.

'Molecular Carcinogenesis P01 Review,' September 2004.

'Population Based Prevention Studies P01 Review Cluster,' June 2004.

Non–NIH Review Panels:

French ARC 'Breast Cancer Risk Assessment Models,' November 2013.

Duke Cancer Prevention, Detection and Control Program Panel, June 2011.

Duke Cancer Prevention, Detection and Control Program Panel, June 2010.

California Breast Cancer Research Program Review Panel, August 2009.

Duke Clinical & Translational Science Award (CTSA) Panel, July 2009.

Duke Clinical & Translational Science Award (CTSA) Panel, February 2008.

Service to Professional Associations:

Publications Officer, Risk Section, American Statistical Association, 2006.

Organizer: Special Contributed Session on Risk Assessment, Spring 2001 meeting, Biometrics Society (ENAR).

Research Support

Ongoing

5P50-CA116201-13 Couch (PI) 09/01/19 – 08/31/20
Mayo Clinic/NIH Iversen (PI of Duke subcontract)
MAYO Clinic Breast SPORE — Project1: Cancer Risks for Mutations in Breast Cancer Genes
The goal of the proposed research is to develop and characterize multi–factorial models for classifying variants of unknown significance (VUS) in BRCA1 and BRCA2 as well as in other known breast cancer susceptibility genes.

Completed

HHS0100201000001C Nelson Chao (PI) 12/16/2009 – 06/30/2019
HHS/BARDA/DxTerity Diagnostics
Point of Care or High–Throughput Biological Assays For Determining Absorbed Ionizing Radiation Dose (Biodosimetry) After Radiological and Nuclear Events (BAA BARDA 09-36)
The primary objectives of this proposal are to: 1) Develop and refine a peripheral blood gene expression signature of radiation injury using the research CLPA assay, 2) Develop the single cartridge prototype biodosimetry instrument, 3) Optimize and verify the performance characteristics of the cartridge-based CLPA-RET (radiation exposure test) in a high throughput system, 4) Develop the manufacturing and quality control procedures for the instrument, 5) Manufacture and quality control release of the CLPA- RET kits and high-throughput instruments, 6) Clinical testing and external validation studies of the CLPA-RET against human PB samples, 7) FDA submission for product review.

2U01-CA116167-06A1 Couch (PI) 04/01/13 – 03/31/18
Mayo Clinic/NIH Iversen (PI of Duke subcontract)
BRCA1 and BRCA2 Missense Mutations and Breast Cancer Risk
The goal of the proposed research is to expand and adapt existing statistical models for the classification of variants of unknown significance (VUS) in BRCA1 and BRCA2 to (1) incorporate functional assay data, sequence conservation data and genetic/family history data and (2) to utilize additional data from the ENIGMA (Evidence-based Network for the Interpretation of Germline Mutant Alleles) Consortium to inform the new, more comprehensive models.

1R01-CA168758-01A1 Doherty/Rossing (Co-PIs) 04/01/13 – 03/31/17
FHCRC/NIH Iversen (PI of Duke subcontract)
Epidemiologic Factors and Survival by Molecular Subtypes of Ovarian Cancer
Epithelial ovarian cancer is now considered not as a single disease, but rather as a diverse group of tumors with subtypes that can best be classified based on molecular genetic features. In this project, we will assess the association of these subtypes with known or suspected ovarian cancer risk and preventive factors and with disease outcome using data from two population–based studies comprising 2,240 invasive ovarian cancer cases and 2,900 controls with detailed information on reproductive, lifestyle and medical histories, and on germline genetic variation. This study has the potential to influence the development of more effective strategies for disease prevention and treatment.

1R01-DK094841-01A1 Neelon (PI) 08/01/12 – 06/30/17
NIH
Early Child Care and Risk of Obesity
This study examines factors contributing to the development of obesity that may be influenced by the child care setting, including dietary behaviors, physical activity and inactivity, stress, and sleep duration and quality. To accomplish these aims, the study follows a diverse southern cohort of 800 predominately black and white infants in various child care arrangements, from birth to 12 months of age. Results of this study will provide new information on the relationship between child care attendance and obesity and may help determine causality in instances where the associations between these variables have been unclear. Findings will inform state and federal policy governing child care settings and will also guide intervention efforts to help prevent obesity in young children in child care.

1R21-ES020796-01 Iversen/Clyde (Co–PIs) 09/15/12 – 08/31/15
NIEHS/NIH r
Models for consortium level analysis of G×E interaction in complex disease
Association studies in the 'Post–GWAS' era achieve the sample sizes necessary to mount adequately powered studies of gene-environment association by being based in consortia that draw on data from many studies of similar design, however they raise new analytical challenges. Chief amongst these is maintaining power to reliably detect and localize gene by environment (G×E) interactions given the expanded scope these studies embrace while allowing for the (very real) possibility for study–to–study heterogeneity in effects. The program of research that we propose addresses these analytic challenges, challenges that need to be met before the full potential of Post–GWAS studies and their public health benefits are realized.
Role: Co–PI

1R01-CA-142081-01A1 Schildkraut (PI) 06/01/10 – 04/30/15
NIH
Epidemiology of Ovarian Cancer in African–American Women
The purpose of this project is to establish a multi–center case–control study involving nine geographic regions within the US to study the etiology of ovarian cancer among African Americans. The study will explore risk factors that have been established as important in white women and investigate associations with factors that may be specific to African Americans. Its large sample size and the diverse populations it includes will provide critical insight into the similarities and differences in ovarian cancer risk factors between African American and white women and may contribute to a better understanding of the poorer survival experience by African Americans.

2U01-CA084955-11 Marks (PI) 09/01/10 – 06/30/15
NIH
Atlantic Breast and Gynecologic Clinical Validation Center
The purpose of this study is to use a carefully collected and annotated bank of specimens to evaluate and compare a series of assays and lead markers to determine whether a clinically useful tool can be developed to augment mammography and ultrasound for the detection of breast cancer.

1R01-CA142983-01 Hoyo (PI) 06/01/10 – 04/30/14
NIH
Disparities in cervical cancer precursors and deregulation of imprinted genes
The purpose of this study is to determine the extent to which disregulation of imprint regulatory elements of known imprinted genes is associated with increased risk of progression of intraepithelial lesions to cervical cancer and to determine if patterns of deregulation of known imprinted genes in cervical cells can be used to identify women likely to progress among those classified as ASCUS.

1R01-DK085173-01A1 Hoyo (PI) 07/27/10 – 04/30/14
NIH
Obesity and deregulation of imprinted genes in early life
The purpose of this project is to determine whether early exposures increase the risk of epigenetic deregulation of imprinted gene regulatory elements, resulting in altered expression of growth regulatory genes and subsequent rapid weight gain in the offspring, fueling the childhood obesity epidemic. To this end, the project will: (1) Determine if altered methylation of imprinted gene regulatory regions controlling selected imprinted genes at birth is associated with increased risk of rapid weight gain and obesity in children; (2) Determine if in utero exposures to a maternal methyl group donor-rich diet and/or cigarette smoke is associated with increased risk of aberrant DNA methylation at imprinted gene regulatory regions and risk of obesity in children; and (3) Determine if the child's diet is associated with alterations in methylation profiles at these imprint regulatory elements. Genome–wide methylation profiles will also be assessed for their association with rapid growth and obesity.

1U19-CA148112-01 Sellers (PI) 07/02/10 – 06/30/14
10-15915-01-05-G1 Iversen (Duke Subaward PI)
Moffit Comprehensive Cancer Center/NIH
Follow–up to Ovarian Cancer Genetic Association and Interaction Studies (FOCI)

This study is part of the NCI's Cancer Post Genome–Wide Association Initiative and comprises three separate projects. Projects 1 and 2 focus on identifying new risk loci by combining data from four genome–wide association studies and functionally evaluating these loci, respectively. Our focus is Project 3. The goal of this project is to investigate both genetic and environmental modifiers of genetic association with ovarian cancer using the combined data from the four genome-wide association studies, each of which utilizes samples drawn from case–control studies participating in the international Ovarian Cancer Association Consortium (OCAC), in addition to extensive second phase follow–up data, and to develop a comprehensive risk model for ovarian cancer that encompasses existing and newly discovered epidemiologic and genetic risk factors.
Role: Co-PI of Duke Subcontract/Project 3.

1R21-CA155965-01A1 Fuemmeler (PI) 07/01/11 – 06/30/13
NIH
FitFab 4 Survivors
The objective of this proposal is to develop an innovative and unique intervention that supports healthy dietary intake, physical activity and healthy weight maintenance among adolescent cancer survivors who are at least 2 years off treatment. The 16 week intervention will include the use a specialized smartphone application (app) and weekly supportive counseling. The app will include tools for self–monitoring of diet and physical activity, the use of rewards, and will incorporate social–networking features which will allow participants to connect with and support one another through the intervention period.

5R01-CA-076016-12 Schildkraut (PI) 08/05/09 – 06/30/12
NIH
The Molecular Epidemiology of Ovarian Cancer
The purpose of this study is to identify molecular and genetic signatures of ovarian cancer risk. The primary aim is to identify ovarian cancer susceptibility polymorphisms using both a candidate gene and a high–throughput SNP search, with the former focusing on DNA damage response pathways. The pathway analysis involves genotypes at 3,700 SNPs tagging to a high R2 about 170 genes representing the pathway for approximately 40,000 subjects drawn from the almost 40 studies that make up the Ovarian Cancer Association Consortium (OCAC). These data will be augmented by the OCAC core data set of epidemiologic and phenotype variables. The combined data set will form the basis of a comprehensive pathway wide investigation of the combined role of polymorphic variation in the pathway and environmental exposures play in the etiology of ovarian cancer.
Role: Co-Investigator

HHSN261201000389P Iversen (PI) 04/01/11 – 03/30/12
NIH
Analysis of Glutathione S–transferase polymorphism, Lifestyle & Cancer Risk
The goal of this project is to examine the associations and interactions of GST deletion polymorphisms with lifetime physical activity and cruciferous vegetable intake on risk for early onset breast cancer. This study seeks to measure evidence in favor of the hypothesis that healthy lifestyle behaviors are protective for premenopausal breast cancer in women with at risk GST genotypes.
Role: PI

10-14922-99-03-G1 Sellers (PI) 03/15/07 – 02/28/12
NIH/Moffit Cancer Center
Haplotype–based Genome Screen for Novel Ovarian Cancer Loci
The goal of this project is to conduct an unbiased search for novel ovarian cancer susceptibility loci using a modern high–throughput genome–wide SNP scan and a two–phased study design. Phase I of the study is a genome–wide scan of more than 500,000 tagging polymorphisms conducted in approximately 3,800 subjects (1,800 cases, 2,000 controls). The second phase involves genotyping 15,000 SNPs in approximately 40,000 subjects drawn from the nearly 40 studies that comprise the Ovarian Cancer Association Consortium (OCAC). The second stage analysis plan will involve scans for main, epistatic and gene-environment effects. The latter will be facilitated by OCAC's core database of known ovarian cancer risk factors.
Role: Co-Investigator

5R01-CA-116167 Couch (PI) 03/15/07 – 02/28/12

Mayo Clinic/NIH
BRCA2 Missense Mutations and Cancer
The goal of the study is to improve risk assessment and counseling for carriers of BRCA1 and BRCA2 missense mutations and to establish a protocol for evaluation of the disease relatedness of other missense mutations in these and other tumor suppressor genes. To achieve this, we propose to develop a statistical model to determine whether missense mutations in BRCA1 or BRCA2 are associated with increased susceptibility to cancer or are neutral sequence alterations utilizing a variety of data types.
Role: PI of Duke Subcontract.

1 R01 HL090559-03 09/21/07 – 07/31/11
NHLBI/NIH
Bayesian Modeling and Optimal Design for Studies of Gene–Environment Association
The goal of this project is to utilize Bayesian statistical approaches to identify optimal experimental designs, develop methodological approaches to the analysis of data generated by both hypothesis driven gene/pathway and genome-wide gene-environment association studies and develop efficient, portable and open source software implementations of these approaches.
Role: PI

1 R01 HL090559 (S) 07/15/09 – 07/31/11
NHLBI/NIH
Bayesian Modeling and Optimal Design for Studies of Gene–Environment Association
This is an administrative supplement to HL090559 to increase the scope of software development (Aim 3) in the parent R01 by adding a full time programmer to the research team. This purpose of this project is to improve the speed and efficiency of software developed in context of the parent grant and coded in the R statistical language by re–coding it in the C programming language and by making use of cluster computing extensions and the multi-threading capabilities of the current generation of workstations.
Role: PI

PI: Moorman, P. 09/30/03 – 08/31/08
NIH/NIA
Ovarian Failure Among Hysterectomized Women
Role: Statistician
This study will investigate whether hysterectomized women who retain at least one ovary are more likely to experience ovarian failure than women of similar age who have an intact uterus and ovaries and will evaluate associations between medical,reproductive and lifestyle characteristics and early ovarian failure.

PI: Ingle 9/01/05 – 8/31/09
Mayo Clinic/NIH
BRCA2 Missense Mutations and Breast Cancer
Role: P.I. of Duke Subcontract
Develop and implement a statistical model to assess the association to cancer of a set of BRCA2 missense mutations.

PI: Parmigiani 9/30/03 – 6/30/08
Johns Hopkins University/NIH
Statistical Methods for Cancer Susceptibility Genes
Role: P.I. of Duke Subcontract
Develop and refine statistical models for probabilistic inference of cancer gene carrier status.

PI: Murphy, S. 11/15/04 – 12/14/07
DOD
Epigenetic Characterization of Ovarian Cancer
Role: Statistician
This proposal will elucidate the role of epigenetic gene silencing in the etiology of ovarian cancer. Its goal is to identify epigenetic patterns associated with histologic subtypes of ovarian cancer and evidence of age-related accumulation of epigenetic alterations.

Duke PI: Schildkraut, J 10/01/05 – 05/30/08
NIH/RTI
Cancer Family Registries Informatics Center
Role: Statistician
To provide genetic epidemiology and statistics domain support to the NCI Breast and Colon Cancer Family Registries. Duke's role in this grant is to provide consultative expertise on the design and analysis of family and individual–based studies of cancer using the registry's population–based and high–risk datasets.

PI: Ellis 08/01/03 – 07/31/07
Washington University/NIH
Novel Biomarkers for Aromatase Inhibitor Therapy
Role: P.I. of Duke Subcontract
The goal of this project will be to identify gene expression biomarkers for response to aromatase inhibitor therapy in postmenopausal breast cancer patients with ER+ tumors.

PI: Schildkraut 05/01/01 – 04/30/06
NIH/NCI
Validation of BRCA 1 & 2 Carrier Probability Models
Role: Co-Investigator
Compared and validated the major BRCA1/2 mutation carrier probability models on an independent sample of high-risk pedigrees.

PI: Marcom, PK 05/01/05 – 04/30/06
The Susan G. Komen Breast Cancer Foundation
A Tumor-Based Analysis of Uncharacterized Variants in BRCA1/2 Focusing On Under-tested Populations
Role: Statistician
The goal of this project is to identify tumor characteristics that can be used to improve our ability to classify BRCA1/2 variants of unknown significance as disease associated or not. This will be accomplished through a comparative analysis of patterns in tumor LOH, promoter methylation, FISH aberration and extent of family history among carriers of known deleterious mutations, non-carriers and carriers of UVs at BRCA1 and BRCA2.

PI: Berchuck, A 09/30/04 – 09/29/05
University of Alabama/NIH
Expression Array Analysis of Outcome in Advanced Serous Ovarian Cancers
Role: Statistician
This project will identify gene expression profiles predictive of survival outcome in advanced stage ovarian cancer.

PI: Schildkraut, J 08/01/03 – 07/30/04
NIH/NCI
Carolina and Georgia Cancer Genetics Network Center
Role: Statistician
The aim of this project is to provide collaborative statistical support to Cancer Genetics Network projects and personnel.

PI: Goldschmidt, P. 09/30/03 – 04/31/04
NIH/NHLBI
AGENDA Study of Atherosclerosis
Role: Research Scientist
Statistical research and development for large genomic datasets derived from molecular and genetic studies of atherosclerosis.

PI: Colvin, M. 07/01/01 – 06/03/04
W.M. Keck Foundation
The W.M. Keck Center for Neurooncogenomics
Role: Research Scientist

Develop and apply computational and statistical methods for analysis of genomic and proteomic data with emphasis on applications to the study molecular characteristics of brain cancers.

PI: Schildkraut, J 05/01/01 – 04/30/04
NIH/NCI
Modifiers of BRCA1 and BRCA2 Penetrance
Role: Co-Investigator
Evaluated candidate genetic and environmental exposures for synergistic or antagonistic interaction with BRCA1 or BRCA2.

Computer Skills

Statistical Packages
R, S-Plus, SAS, Matlab, GLIM, SCA, and Minitab.

Languages
C, Fortran, Perl.

Operating Systems
UNIX System Administrator, DOS, VMS, TSO.