

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,
Associate Research Professor, September 2007 to present.

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

Raska P, **Iversen Jr ES**, Chen A, Chen Z, Fridley BL, Permut-Wey J, Tsai Y-Y, Vierkant RA, Goode EL, Risch H, Schildkraut JM, Sellers TA, Barnholtz-Sloan J (2012) European American Stratification in Ovarian Cancer Case Control Data: The Utility of Genome-Wide Data for Inferring Ancestry. *PLoS ONE* 7(5): e35235. doi:10.1371/journal.pone.0035235.

Kelemen LE, Wang Q, Dinu I, Vierkant RA, Tsai YY, Cunningham JM, Phelan CM, Fridley BL, Amankwah E, **Iversen Jr ES**, Berchuck A, Schildkraut JM, Goode EL, Sellers TA (2012). Regular multivitamin supplement use, single nucleotide polymorphisms in ATIC, SHMT2 and SLC46A1 and risk of ovarian carcinoma. *Frontiers in Genetics*. 3(00033). doi:10.3389/fgene.2012.00033.

Hoyo C, Murtha AP, Schildkraut JM, Jirtle RL, Demark-Wahnefried W, Forman MR, **Iversen Jr ES**, Kurtzberg J, Overcash F, Huang Z, Murphy SK (2011). Methylation variation at IGF2 differentially methylated regions and maternal folic acid use before and during pregnancy. *Epigenetics*. 6(7):928–36. PMID: 21636975.

Fridley BL, **Iversen Jr ES**, Tsai Y-Y, Jenkins GD, Goode EL, et al. (2011) A Latent Model for Prioritization of SNPs for Functional Studies. *PLoS ONE*. 6(6): e20764. doi:10.1371/journal.pone.0020764

Iversen Jr ES, Couch FJ, Goldgar DE, Tavtigian SV, Monteiro ANA (2011). A computational method to classify variants of uncertain significance using functional assay data with application to BRCA1. *Cancer Epidemiology, Biomarkers & Prevention*. 20:1078–1088. doi:10.1158/1055-9965.EPI-10-1214.

Moorman PG, Myers ER, Schildkraut JM, **Iversen Jr ES**, Wang F, Warren N (2011). Effect of hysterectomy with ovarian preservation on ovarian function. *Obstetrics and Gynecology* 118(6):1271–9. PMID: 22067716.

Matsumura N, Huang Z, Mori S, Baba T, Fujii S, Konishi I, **Iversen Jr ES**, Berchuck A, Murphy SK (2011). Epigenetic suppression of the TGF- β pathway revealed by transcriptome profiling in ovarian cancer. *Genome Research*. 21(1):74–82. PMID: 21156726.

Pearce CL, Doherty JA, Van Den Berg DJ, Moysich K, Hsu C, Cushing-Haugen KL, Conti DV, Ramus SJ, Gentry-Maharaj A, Menon U, Gayther SA, Pharoah PD, Song H, Kjaer SK, Hogdall E, Hogdall C, Whittemore AS, McGuire V, Sieh W, Gronwald J, Medrek K, Jakubowska A, Lubinski J, Chenevix-Trench G; AOCs/ACS Study Group, Beesley J, Webb PM, Berchuck A, Schildkraut JM, **Iversen Jr ES**, Moorman PG, Edlund CK, Stram DO, Pike MC, Ness RB, Rossing MA, Wu AH (2011). Genetic variation in insulin-like growth factor 2 may play a role in ovarian cancer risk. *Human Molecular Genetics*. 20(11):2263–72. PMID: 21422097.

Notaridou M, Quaye L, Dafou D, Jones C, Song H, Hogdall E, Kjaer SK, Christensen L, Hogdall C, Blaakaer J, McGuire V, Wu AH, Van Den Berg DJ, Pike MC, Gentry-Maharaj A, Wozniak E, Sher T, Jacobs IJ, Tyrer J, Schildkraut JM, Moorman PG, **Iversen Jr ES**, Jakubowska A, Medrek K, Lubinski J, Ness RB, Moysich KB, Lurie G, Wilkens LR, Carney ME, Wang-Gohrke S, Doherty JA, Rossing MA, Beckmann MW, Thiel FC, Ekici AB, Chen X, Beesley J; Australian Ovarian Cancer Study Group/Australian Cancer Study (Ovarian Cancer), Gronwald J, Fasching PA, Chang-Claude J, Goodman MT, Chenevix-Trench G, Berchuck A, Pearce CL, Whittemore AS, Menon U, Pharoah PD, Gayther SA, Ramus SJ; Ovarian Cancer Association Consortium (2011). Common alleles in candidate susceptibility genes associated with risk and development of epithelial ovarian cancer. *International Journal of Cancer*. 128(9):2063–74. doi: 10.1002/ijc.25554. PMID: 20635389.

Amankwah EK, Wang Q, Schildkraut JM, Tsai YY, Ramus SJ, Fridley BL, Beesley J, Johnatty SE, Webb PM, Chenevix-Trench G; Australian Ovarian Cancer Study Group, Dale LC, Lambrechts D, Amant F, Despierre E, Vergote I, Gayther SA, Gentry-Maharaj A, Menon U, Chang-Claude J, Wang-Gohrke S, Anton-Culver H, Ziogas A, Dork T, Durst M, Antonenkova N, Bogdanova N, Brown R, Flanagan JM, Kaye SB, Paul J, Butzow R, Nevanlinna H, Campbell I, Eccles DM, Karlan BY, Gross J, Walsh C, Pharoah PD, Song H, Kruger Kjaer S, Hogdall E, Hogdall C, Lundvall L, Nedergaard L, Kiemeny LA, Massuger LF, van Altena AM, Vermeulen SH, Le ND, Brooks-Wilson A, Cook LS, Phelan CM, Cunningham JM, Vachon CM, Vierkant RA, **Iversen Jr ES**, Berchuck A, Goode EL, Sellers TA, Kelemen LE (2011). Polymorphisms in stromal genes and susceptibility to serous epithelial ovarian cancer: a report from the Ovarian Cancer Association Consortium. *PLoS One*. 6(5):e19642. PMID: 21637745.

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Chanock SJ, Pharoah PD, Song H, Whitmore AS, Pearce CL, Stram DO, Wu AH, Pike MC, Gayther SA, Ramus SJ, Menon U, Gentry–Maharaj A, Anton–Culver H, Ziogas A, Hogdall E, Kjaer SK, Hogdall C, Berchuck A, Schildkraut JM, **Iversen Jr ES**, Moorman PG, Phelan CM, Sellers TA, Cunningham JM, Vierkant RA, Rider DN, Goode EL, Haviv I, Chenevix–Trench G, Ovarian Cancer Association Consortium (2010). Evaluation of Candidate Stromal Epithelial Cross–Talk Genes Identifies Association between Risk of Serous Ovarian Cancer and TERT, a Cancer Susceptibility “Hot-Spot”. *PLoS Genet* 6(7):e1001016. doi:10.1371/journal.pgen.1001016

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White KL, Sellers TA, Fridley BL, Vierkant RA, Phelan CM, Tsai YY, Kalli KR, Berchuck A, **Iversen Jr ES**, Hartmann LC, Liebow M, Armasu S, Fredericksen Z, Larson MC, Duggan D, Couch FJ, Schildkraut JM, Cunningham JM and Goode EL (2010). Variation at 8q24 and 9p24 and risk of epithelial ovarian cancer. *Twin Research and Human Genetics*. 13(1):43–56.

Peedicayil A, Vierkant RA, Hartmann LC, Fridley BL, Fredericksen ZS, White KL, Elliott EA, Phelan CM, Tsai YY, Berchuck A, **Iversen Jr ES**, Couch FJ, Peethamabaran P, Larson MC, Kalli KR, Kosel ML, Shridhar V, Rider DN, Liebow M, Cunningham JM, Schildkraut JM, Sellers TA and Goode EL (2010). Risk of ovarian cancer and inherited variants in relapse-associated genes. *PLoS One*. 5(1):e8884. doi:10.1371/journal.pone.0008884.

Moorman, PG, **Iversen Jr ES**, Marcom, PK, Marks, JR, Wang, F, Kathleen Cunningham Consortium for Research into Familial Breast Cancer (kConFab), Lee, E, Ursin, G, Rebbeck, TR, Domchek, SM, Arun, B, Susswein, L, Isaacs, C, Garber, JE, Visvanathan, K, Griffin, CA, Sutphen, R, Brzosowicz, J, Gruber, S, Finkelstein, DM, Schildkraut, JM (2010). Evaluation of Established Breast Cancer Risk Factors as Modifiers of BRCA1 or BRCA2: A Multi–Center Case–Only Analysis. *Breast Cancer Research and Treatment*. DOI:10.1007/s10549-010-0842-y.

Schildkraut, JM, **Iversen Jr ES**, Wilson, MA, Clyde, MA, Moorman, PG, Palmieri, RT, Whitaker, R, Bently, RC, Marks, JR, Berchuck, A (2010). Association Between DNA Damage Response and Repair Genes and Risk of Invasive Serous Ovarian Cancer. *PLoS One*. 5(4):e10061. DOI:10.1371/journal.pone.0010061.

Wilson, MA, **Iversen Jr ES**, Clyde, MA, Schmidler, SC, Schildkraut, JM (2010). Bayesian Model Search and Multilevel Inference for SNP Association Studies. *Annals of Applied Statistics*. 4(3):1342–1364. DOI:10.1214 / 09-AOAS322.

Orlando, DA, **Iversen Jr ES**, Hartemink, AJ, Haase, SB (2009). A Branching Process Model for Flow Cytometry and Budding Index Measurements in Cell Synchrony Experiments. *Annals of Applied Statistics*. 3(4):1521-1541.

Schildkraut, JM, Goode, EL, Clyde, MA, **Iversen Jr ES**, Moorman, P, Berchuck, A, Marks, J, *et al.* (2009). Single Nucleotide Polymorphisms in TP53 and susceptibility to invasive epithelial ovarian cancer. *Cancer Research*. 69(6): 2349–2357.

Berchuck, A, **Iversen Jr ES**, Luo, J, Clarke, JP, Horne, H, Levine, DA, Boyd, J, Alonso, MA, Secord, AA, Bernardini, MQ, Barnett, JC, Boren, T, Murphy, SK, Dressman, HK, Marks, JR, Lancaster, JM (2009). Microarray analysis of early stage serous ovarian cancers shows profiles predictive of favorable outcome. *Clinical Cancer Research*. 15(7):2448–2455.

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- 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). 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.

Work in Progress

Bayesian models, model selection and prior specification for pathway wide and genome wide gene and environment association studies. With M Clyde and M Wilson.

Model selection and high dimensional retrospective models for outcome classification using gene expression data. With J Luo and M Clyde.

Modeling multiple sources of evidence for the disease association status of BRCA1 and BRCA2 variants of unknown significance. With F Couch, D Goldgar, A Montiero, and S Tavgian.

Analysis of high-risk pedigree data for purposes of gene characterization; to detect genetic and environmental modifiers of cancer penetrance among carriers of BRCA1 and BRCA2 mutations and to account for genetic heterogeneity in penetrance. With G Parmigiani, YC Tai, and J Schildkraut.

Invited Talks

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 Initiative 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. 13th 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 Prediction 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

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

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

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 – Present.

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 Epidemiology 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:

'Tumor Microenvironment Network,' June 2011.

'SPOR 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:

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

1U19-CA148112-01	Sellers (PI)	07/02/10 – 06/30/14	1.35 academic
10-15915-01-05-G1	Schildkraut/Iversen (Duke Co-PIs)	\$313,608	0.45 summer

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.

10-14922-99-03-G1	Sellers (PI)	03/15/07 – 02/28/12	1.80 academic
NIH/Moffit Cancer Center		\$80,996	0.60 summer

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	1.20 calendar
Mayo Clinic/NIH		\$20,606	

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.

5R01-CA-076016-12	Schildkraut (PI)	08/05/09 – 06/30/12	0.67 academic
NIH		\$461,561	0.23 summer

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

1R01-CA-142081-01A1	Schildkraut (PI)	06/01/10 – 05/31/15	0.75 academic
NIH		\$1,764,416	0.08 summer

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.

1R01-CA142983-01	Hoyo (PI)	06/01/10 – 05/31/14	0.80 academic
NIH		\$411,625	0.30 summer

Disparities in cervical cancer precursors and deregulation of imprinted genes

The purpose of this study is to determine the extent to which dysregulation 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.

2U01-CA084955-11	Marks (PI)	09/01/10 – 06/30/15	0.60 academic
NIH		\$329,280	

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-DK085173-01A1	Hoyo (PI)	07/27/10 – 04/30/14	0.80 academic
NIH		\$454,308	0.12 summer

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.

HHSN261201000389P	Iversen (PI)	04/01/11 – 03/30/12	0.65 academic
NIH		\$15,657	0.22 summer

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

1R21-CA155965-01A1	Fuemmeler (PI)	07/01/11 – 06/30/13	0.00 academic
NIH		\$153,000	0.00 summer

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.

Pending

1R21-ES020796-01	Iversen/Clyde (Co-PIs)	01/01/12 – 12/31/14	0.56 academic
NIEHS/NIH			1.00 summer

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-HD069668-01	Fuemmeler (PI)	07/01/11 – 03/31/12	0.45 academic
NIH		\$496,408	0.15 summer

Epigenetic influence on behavioral phenotypes and obesity in preschoolers

This longitudinal epidemiology study, combining biological and behavioral data, will clarify the effect of children's eating behaviors and their ability to control their impulses on the development of obesity. Further, it will assess the extent to which potentially reversible epigenetic factors contributes to these behaviors and subsequent obesity. Results from this study will lead to new methods for preventing obesity in children.

Role: Co-Investigator

	Fuemmeler (PI)	09/30/11 – 09/29/13	0.45 academic
NIH		\$150,000	

Epigenetic influence on early childhood self-regulation capacities and obesity

Self-regulation failures, such as impulsivity, could make some children vulnerable to obesity. A better understanding of the types of self-regulation failures relevant to childhood obesity, as well as the underlying basic mechanism leading to these self-regulation failures could enhance prevention and treatment efforts. This study will clarify the association that self-regulation capacities have with childhood obesity as well as determine the degree to which epigenetic changes acquired prenatally are associated with the development of these self-regulatory capabilities. Knowledge generated from this study will contribute to our understanding of basic mechanisms of self-regulation and its influence on early childhood obesity.

Role: Co-Investigator

1R01CA141154-01	Schildkraut (PI)	07/01/10 – 06/30/13	0.23 academic
NIH/University of Southern California		\$14,167	0.08 summer

Identifying Ovarian Cancer Susceptibility Alleles using Genome-Wide Scan Data

This project proposes the use of Frequentist generalizations of case-only methods for detecting gene by environment interactions with main-effects evident from genome-wide scans in ovarian cancer.

Completed

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.