

Contact Information

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Research interests

Dr. Santorico's research interests are in the area of statistical genetics, specifically in the development of statistical methods and study designs for gene discovery through the use of pedigree and population-based data. Her methodological work initially centered on the use of linkage disequilibrium between alleles at two loci in order to localize susceptibility genes for both disease and quantitative traits. Through the use of complementary information gained by applying statistical genetics principles to gene expression studies, Dr. Santorico's current research is aimed at enhancing the ability to dissect complex interacting pathways that lead to disease susceptibility. Dr. Santorico has developed algorithms, software and advanced experimental designs that incorporate genetic variation, patterns of genetic inheritance, measures of relevant environmental influences and gene expression components, all facilitated by the latest in microarray technology. Her ongoing research investigates refinement of multiple-testing correction, combining genetic data across multiple ethnic groups, and modeling epistasis and pleiotropy for multivariate traits in an association testing framework. She has a track record of conducting research in a collaborative setting among federal, state, private and corporate institutions.

Key interests: Statistical genetics, genetic epidemiology, genetics of gene expression, variance components methods, multivariate linkage, linkage disequilibrium, family-based association tests, meta-analysis

Education

North Carolina State University, Raleigh, NC: Ph.D. in Statistics, 1999
North Carolina State University, Raleigh, NC: M.Stat., 1996
Northeastern State University, Tahlequah, OK: B.S. in Mathematics with minors in Computer Science and Physics, *summa cum laude*, 1993

Professional Positions

Associate Professor, Department of Mathematical and Statistical Sciences, University of Colorado Denver, 2008-
Associate Professor, Department of Statistics, Oklahoma State University, 2006-2008
Undergraduate Advisor, Department of Statistics, Oklahoma State University, 2006-2008
Affiliate Assistant Professor, Department of Biostatistics, University of Washington, 2004-2008

CURRICULUM VITAE

Stephanie A. Santorico, Ph.D.
(formerly Stephanie A. Monks)

Assistant Professor, Department of Statistics, Oklahoma State University, 2004-2006
Consultant, Rosetta Inpharmatics Inc., 2003-2005
Senior Statistician, Rosetta Inpharmatics Inc., 2001-2003
Assistant Professor, Institute for Public Health Genetics, 1999-2004
Assistant Professor, University of Washington, Department of Biostatistics, 1999-2004
Fellow, Biostatistics Branch, National Institute of Environmental Health Sciences, 1997-1999
Staff Scientist, NeuralMed, Inc., 1996-1997
Statistical Intern, GlaxoWellcome, Inc., Summer 1996
Instructor, North Carolina State University, 1995-1996

Honors

Sigma Xi, The Scientific Research Society, 1999
Gertrude M. Cox Outstanding Academic Achievement Award Fellow/Outstanding Masters Candidate, NCSU
Department of Statistics, 1996
Mu Sigma Rho, Statistical Honor Society, 1996
Recipient of a National Science Foundation Graduate Fellowship, 1995-1997
Recipient of a Patricia Roberts Harris Graduate Fellowship, 1994-1995
Invited delegate to the NSF Summer Mathematics Institute at the University of California at Berkeley, 1993
Twice selected Northeastern State University Mathematics Student of the Year, 1992, 1993
Kappa Mu Epsilon, Mathematical Honor Society, 1991

Bibliography

Manuscripts in Preparation

Guo Q, K. Hanford, M Allan, D Pomp, **Santorico SA**. Dimension Reduction Methods in the study of Genetics of Gene Expression. Paper won Women's Faculty Council's 2008 Dean's Award
Morris TL, Payton ME, **Santorico SA**. A Permutation Test for Compound Symmetry
Shi L, **Santorico SA**. Homozygosity Mapping when the Common Ancestor is Unknown
Razzaghi H, **Santorico SA**, Kamboh I. Re-sequencing of LIPG and ZNF202 Genes in Population-based Subjects with Extreme Ends of HDL Distribution
Edwards KL, Wan JY, Hutter CM, Fong PY, **Santorico SA**. Evidence for pleiotropic effects on features of the Metabolic Syndrome in white families with Type 2 Diabetes

Submitted Manuscripts

Wan JW, **Santorico SA** (submitted) Bivariate linkage analysis of quantitative traits under incomplete pleiotropy

Refereed Research Articles

Edwards KL, Hutter CM, Wan JY, Kim H, **Monks SA** (2008) Genome-wide linkage scan for the metabolic syndrome: the GENNID study. *Obesity* 16(7):1596-601 – *Article has been highlighted by Nature Publishing for research on the Metabolic Syndrome*
Bis JC, Heckbert SR, Smith NL, Reiner AP, Rice K, Lumley T, Hindorff LA, Marcianti KD, Enquobahrie DA, **Monks SA**, Psaty BM (2008) Variation in inflammation-related genes and risk of incident nonfatal myocardial infarction or ischemic stroke. *Atherosclerosis* 198(1):166-73.

- Marcianti KD, Bis JC, Rieder MJ, Reiner AP, Lumley T, **Monks SA**, Kooperberg C, Carlson C, Nickerson DA, Heckbert SR, Psaty BM (2007) Renin-angiotensin system haplotypes and the risk of myocardial infarction and stroke in pharmacologically treated hypertensive patients. *Am J Epidemiol.* 166(1):19-27
- French B, Lumley T, **Monks SA**, Rice KM, Hindorff LA, Reiner AP, Psaty BM (2006) Simple estimates of haplotype relative risks in case-control data. *Genet Epidemiol* 30(6):485-494
- Hing AV, Leblond C, Sze RW, Starr JR, **Monks S**, Parisi MA (2006) A novel oculo-oto-facial dysplasia in a Native Alaskan community with autosomal recessive inheritance. *Am J Med Genet A.* 140(8):804-12
- Sieh W, Edwards KL, Fitzpatrick AL, Srinouanprachanh SL, Farin FM, **Monks SA**, Kronmal RA, Eaton DL (2006) Genetic susceptibility to prostate cancer: prostate-specific antigen and its interaction with the androgen receptor. *Cancer Causes and Control.* 17:187-197
- Simon JS, Karnoub MC, Devlin DJ, Arreaza MG, Qiu P, **Monks SA**, Severino ME, Deutsch P, Palmisano J, Sachs AB, Bayne ML, Plump AS, Schadt EE (2005) Sequence variation in NPC1L1 and association with improved LDL-Cholesterol lowering in response to ezetimibe treatment. *Genomics* 86(6):648-56
- Kim H, Hutter CM, **Monks SA**, Edwards KL (2005) Comparison of SNPs and microsatellites in detecting quantitative trait loci for alcoholism: The Collaborative Study on the Genetics of Alcoholism. *BMC Genetics* 6 (Suppl 1):S5
- Schadt EE, Lamb J, Yang X, Zhu J, Edwards S, Guhathakurta D, Sieberts SK, **Monks S**, Reitman M, Zhang C, Lum PY, Leonardson A, Thieringer R, Metzger JM, Yang L, Castle J, Zhu H, Kash SF, Drake TA, Sachs A, Lusis AJ (2005) An integrative genomics approach to infer causal associations between gene expression and disease. *Nat Genet* 37(7):710-7
- Monks SA**, Leonardson A, Zhu H, Cundiff P, Pietrusiak P, Edwards S, Phillips J, Sachs A, Schadt EE (2004) Genetic Inheritance of Gene Expression in Human Cell Lines. *Am J Hum Genet* 75(6):1094-105
- Austin MA, Edwards KL, **Monks SA**, Koprowicz KM, Brunzell JD, Motulsky AG, Mahaney MC, Hixson JE (2003) Genomewide scan for quantitative trait loci influencing low-density lipoprotein size and plasma triglyceride in familial hypertriglyceridemia. *J Lipid Res.* 44(11):2161-8
- Schadt EE, **Monks SA**, Friend SH (2003) A new paradigm for drug discovery: integrating clinical, genetic, genomic and molecular phenotype data to identify drug targets. *Biochem Soc Trans.* 31(2):437-43
- Schadt EE*, **Monks SA** * et al (2003) The genetics of gene expression: a survey across man, mouse and maize. *Nature.* 422:297-302 *Equal contributions by marked authors
- LaGasse JM, Brantley MS, Leech NJ, Rowe RE, **Monks SA**, Palmer JP, Nepom GT, McCulloch DK, Hagopian WA (2002). Successful prospective prediction of Type 1 diabetes in school children through multiple defined autoantibodies: An eight year follow-up of the Washington State Diabetes Prediction Study. *Diabetes Care.* 25(3):505-511
- Mberu EK, Nzila AM, Nduati E, Kokwaro GO, Watkins WM, **Monks SA**, Sibley CH (2002) Plasmodium falciparum: In vitro activity of sulfadoxine and dapson in field isolates from Kenya: point mutations in dihydropteroate synthase are not the whole story in sulfa resistance. *Exp Parasitol.* 101(2-3): 90-96
- Hastings MD, Bates SJ, Blackstone EA, **Monks SA**, Mutabingwa TK, Sibley CH (2002) Highly pyrimethamine-resistant alleles of dihydrofolate reductase in isolates of Plasmodium falciparum from Tanzania *Trans. Trans R Soc Trop Med Hyg.* 96(6):674-6
- Monks SA**, Kaplan NL (2000) Removing the sampling restrictions from family-based tests of association for a quantitative-trait locus. *Am J Hum Genet* 66:576-592
- Martin ER, **Monks SA**, Warren LL, Kaplan NL (2000) A test for linkage and association in general pedigrees: the pedigree disequilibrium test (PDT). *Am J Hum Genet* 67: 146-154
- Nzila AM, Nduati E, Mberu EK, Sibley CH, **Monks SA**, Winstanley PA, Watkins WM (2000) Molecular evidence of greater selective pressure for drug resistance exerted by the long acting antifolate pyrimethamine/sulfadoxine compared with the shorter acting chlorproguanil/dapsone on Kenyan Plasmodium falciparum. *J Infect Dis* 181:2023-2028

- Monks SA**, Martin ER, Umbach DM, Kaplan NL (1999) Two tests of association for a susceptibility locus for families of variable size: an example using two sampling strategies. *GENETIC EPIDEMIOLOGY* 17: S655-S660
- Anderson JL, Hauser ER, Martin ER, Scott WK, Ashley-Koch A, Kim KJ, **Monks SA**, Haynes CS, Speer MC, Pericak-Vance MA (1999) Complete genomic screen for disease susceptibility loci in nuclear families. *GENETIC EPIDEMIOLOGY* 17: S473-S478
- Monks SA**, Kaplan NL, Weir BS (1998) A comparative study of sibship tests of linkage and/or association. *Am J Hum Genet*: 63:1507-1516

Meeting Abstracts

- Guo Q, Hanford K, **Monks SA** (2008) Dimension Reduction in the Study of the Genetics of Gene Expression. Oklahoma State University Research Day
- Kippola TA, Edwards KL, **Santorico SA** (2008) A Variance Components Method to Test for QTL Heterogeneity among Multiple Ethnic Groups. *Am J of Human Genetics*
- Kippola TA, Edwards KL, **Santorico SA** (2008) A Variance Components Method to Test for QTL Heterogeneity among Multiple Ethnic Groups. Joint Statistical Meetings
- Kippola TA, Edwards KL, **Santorico SA** (2008) A Variance Components Method to Test for QTL Heterogeneity among Multiple Ethnic Groups . Oklahoma State University Research Day
- Shi L, Hing AV, **Monks SA** (2008) Homozygosity Mapping with Unknown Common Ancestors. Oklahoma State University Research Day
- Guo Q, Hanford K, **Monks SA** (2007) Dimension Reduction in the Study of the Genetics of Gene Expression. Oklahoma Research Day
- Kippola TA, Edwards KL, **Santorico SA** (2007) A Variance Components Method to Test for QTL Heterogeneity among Multiple Ethnic Groups. Oklahoma Research Day
- Mccann MH, **Monks SA** (2007) Simultaneous Confidence Intervals for Odds Ratios in Candidate Gene Studies. ENAR Spring Meetings.
- Shi L, Hing AV, **Monks SA** (2007) Homozygosity Mapping with Unknown Common Ancestors. Oklahoma Research Day
- French B, Lumley T, **Monks SA**, Reiner AP, Hindorff LA, Psaty BM (2005) Simple estimates of relative risks of common haplotypes in case-control studies. *Circulation* 111 (14): P179
- Bis JC, Marcianti, KL, Psaty BM, Heckbert SR, Lumley T, Reiner AP, Kooperberg CL, Nickerson DA, Rieder MJ, **Monks SA** (2005) Genetic variation in the angiotensin-converting enzyme and angiotensinogen genes, antihypertensive therapy, and risk of incident nonfatal myocardial infarction among hypertensive patients. *Circulation* 111 (14): P197
- Marcianti KD, Bis JC, Rieder MJ, Reiner AP, Lumley T, **Monks SA**, Heckbert SR, Kooperberg C, Nickerson DA, Psaty BM (2005) Renin-angiotensin system gene haplotypes and the risk of myocardial infarction or stroke in pharmacologically treated hypertensive patients. *Circulation* 111 (14): P199
- Kim H, Edwards KL, **Monks SA**, Longstreth WT, Carlson CS, Siscovick DS, Schwartz SM (2004) Genetic variation in matrix metalloproteinase-3 and risk of subarachnoid hemorrhage. *Am J of Epidemiology* 159 (11): S24-S24
- Edwards KL, Hutter CM, Kim H, McNeely MJ, **Monks SA**, Fujimoto WY (2004) Differences in risk factor clustering in Japanese American families with coronary heart disease and diabetes. *Circulation* 109 (7): P262
- Monks SA**, Schadt EE (2002) Unraveling complex traits through the genetics of gene expression. *Am J of Human Genetics* 71 (4): 2381

- Pfeiffer EM, Kukull WA, Larson EB, **Monks SA**, McCormick WC, Bowen JB (2002) Exploring the relationship between microtubule-associated protein tau (MAPT) gene variation and Alzheimer's disease. *Neurobiology of Aging* 23 (1): 1201
- Pfeiffer EM, Larson EB, **Monks SA**, Edwards KL, McCormick WC, Bowen JD, Schellenberg GD, Kukull WA (2002) Genetic influences of the microtubule-associated protein tau gene on rate of cognitive decline in Alzheimer's disease. *Neurology* 58 (7): A42-A42
- Edwards KL, **Monks SA**, LeBoeuf R, Leonetti D, Talmud PJ, Humphries S, Austin MA, Fujimoto WY (2001) Common genetic influences on fasting insulin and waist circumference: The Japanese American Family Study. *Circulation* 103 (9): P13
- Monks SA**, Kaplan NL (1999) Extensions of transmission/disequilibrium tests for correlated data or how to use your entire dataset for a test of linkage and association. *Am J of Human Genetics* 65 (4): 449
- Martin ER, **Monks SA**, Kaplan NL (1999) A weighted sibship disequilibrium test for linkage and association in discordant sibships. *Am J of Human Genetics* 65 (4): 2462
- Monks SA**, Martin ER, Weir BS, Kaplan NL (1997) A sibship test of linkage in the absence of parental information. *Am J of Human Genetics* 61 (4): 1669

Other Scholarly Publications

- Kippola TA, **Santorico SA** (in press) Methods for combining information across multiple genome-wide studies. In *Statistical Methods in Molecular Biology: a Beginner's Guide* by H Bang, XK Zhou, HL VanEpps and M Mazumdar. Humana Press
- Santorico SA** (2008) Data made available for data mining at The GeneNetwork (<http://www.genenetwork.org/>) for my paper: Genetic Inheritance of Gene Expression in Human Cell Lines. *Am J Hum Genet* 75(6):1094-105
- Monks SA** (2006) Statistical Issues in Ecogenetic Studies. In *Fundamentals of Ecogenetics*, edited by LG Costa and DL Eaton. Wiley
- Monks SA** (2003) The genetics of gene expression: a new tool for hunting the elusive disease gene. University of Washington, School of Public Health and Community Medicine, Spotlight on Research. Issue 11: Winter 2003, p. 3

Conferences, Symposiums and Invited Talks

- "Dimension Reduction Techniques for Genetic Studies of Gene Expression," Department of Biology, University of Colorado Denver, 2009
- "Dimension Reduction Techniques for Genetic Studies of Gene Expression," Department of Mathematical and Statistical Sciences, University of Colorado Denver, 2008
- "Dimension Reduction Techniques for Genetic Studies of Gene Expression," Department of Anatomy and Neurobiology, University of Tennessee, Memphis, 2008
- "To combine or not to combine..." COPD Gene Investigators Meeting, 2008
- "Hunting for disease genes using multi-ethnic samples," Department of Mathematical and Statistical Sciences, University of Colorado Denver, 2008
- "I have to take what? (How to get thru your enrollment period)", OSU Faculty Fellows, 2007
- "Dimension Reduction Methods in the Study of the Genetics of Gene Expression," ENAR 2007
- "Genetic Inheritance of Gene Expression in Humans", Department of Statistics, University of Nebraska-Lincoln, 2006
- "Genetic inheritance of gene expression in humans", The Third Seattle Symposium in Biostatistics - Statistical Genetics and Genomics, 2005

- “Genetics of expression by use of dimension reduction techniques”, NSF Research Coordination Network Retreat: Development, Evaluation, & Dissemination of Methods for the Analysis of Gene Expression, 2005
- “Genetic influences on gene expression in humans”, University of Michigan, Department of Biostatistics, 2005
- “Expression QTLs”, Oklahoma Medical Research Foundation, 2005
- “What do you need to know to do quantitative research in genetics or genomics?”, Department of Statistics, Oklahoma State University, 2004
- “RAS genes, antihypertensive drugs, and the risk of MI or stroke: methods and preliminary results”, NHLBI Ancillary Pharmacogenetics Investigators Meeting, 2004
- “Genetic influences on gene expression in humans”, Department of Biostatistics, University of Washington, 2004
- “The use of genetics, genomics and statistics to unravel complex traits”, Women in Rheumatology Meeting, 2004
- “An innovative approach that synthesizes expression profiles, genotypes and phenotypes”, Meeting of the Eastern North American Region of the International Biometric Society, 2004
- “The Genetics of Gene Expression in Mice”, Keystone Symposia: Human genome sequence variation and the inherited basis of common disease, 2004
- “Integrating clinical, genetic, genomic, and molecular phenotype data to dissect a complex trait”, Department of Statistics, North Carolina State University, 2003
- “Integrating clinical, genetic, genomic, and molecular phenotype data to dissect a complex trait”, University of Washington Cardiovascular Health Research Unit, 2003
- “Integrating clinical, genetic, genomic, and molecular phenotype data to dissect a complex trait”, University of Alabama Section on Statistical Genetics, 2003
- “Genetics of gene expression surveyed in maize, mouse and man”, Wellcome Trust Advanced Course in Human Genome Analysis: Genetic Analysis of Multifactorial Diseases, 2003
- “The genetics of gene expression: a survey of maize, mouse and man”, Centre National de Genotypage, Evry, France, 2002
- “Studying the genetics of gene expression in humans”, Puget Sound Chapter of the ASA, 2002
- “The genetics of gene expression: a survey of maize, mouse and man”, Department of Biostatistics, University of Washington, 2002
- “Hunting the elusive disease gene”, Careers in Statistics Seminar, Shorewood High School 2002
- “Exploring the Genetics of Gene Expression in Humans”, Rosetta Inpharmatics, 2002
- “Fine mapping of quantitative trait loci using gametic phase disequilibrium within general pedigrees”, Gordon Research Conference in Quantitative Genetics and Genomics, 2001
- “What can I do with a degree in statistics?” Local meeting of the American Statistical Association, 2001
- “Studying the genetics of gene expression”, Workshop in Statistical Genetics and Computational Molecular Biology, 2001
- “Linkage disequilibrium studies: the what, why, when and how”, Interactive Seminar in Public Health Genetics, University of Washington, 2000
- “Removing the Size Restrictions from Family-based Tests of Association for a Quantitative Trait Locus”, Department of Biostatistics, University of North Carolina, 1999
- “Removing the Size Restrictions from Family-based Tests of Association for a Quantitative Trait Locus”, Department of Mathematical Sciences, University of Arkansas, 1999
- “Removing the Size Restrictions from Family-based Tests of Association for a Quantitative Trait Locus”, Department of Biostatistics, University of Michigan, 1999
- “Removing the Size Restrictions from Family-based Tests of Association for a Quantitative Trait Locus”, Department of Biostatistics, University of Washington, 1999

“Family-based association testing: a review of days gone by and greater things to come”, Department of Genetics, University of Washington, 1999

Funding History*Pending Grants*

Santorico Submitted Feb 2009

NIH

Subcontract with KL Edwards at the University of Washington

“Targeted Sequencing in a Multiethnic Sample for CVD Risk Factors”

Dr. Santorico is a statistical geneticist with a background in family and population based association testing. She will provide statistical genetics expertise for all analyses over the full time period of the grant, including the sequencing stage which includes SNP selection and the association testing stage.

Santorico Submitted Feb 2009

DTI-CFD Teaching Enhancement Grants

“Creation of an Online Tutorial for R Statistical Software”

We are adrift in a vast sea of data and information. IBM estimates that data volume doubles every two years worldwide. Our statistics courses focus on the methods needed to deal with this wealth of information. Beyond an understanding of statistical methods, there is an urgent need to be able to use statistical software to carry out the analyses on large data sets. Gone are the days when analysis could be carried out with a calculator or with an Excel worksheet. Working with a graduate student, I will develop a tutorial for R statistical software to be made freely available online. This will include video paralleling a program demonstration, PowerPoint slides and an accompanying “Guide to R” manual that can be printed and used as a reference. This tool will be piloted in MATH4830/5830, Applied Statistics, in the Fall of 2009.

Spritz Submitted Feb 2009

NIH

“Functional Genomics of Craniofacial Development and Disease”

Dr. Santorico will provide expertise for the human phase of this grant. This will include selection and application of statistical methods for association of mouse midfacial genes in human midfacial morphology.

Santorico Submitted Dec 2008

University of Colorado Denver, College of Liberal Arts and Sciences, Research Dissemination Grant

Grant funds will be used to cover publications costs of: Wan JW, Santorico SA (submitted) Bivariate linkage analysis of quantitative traits under incomplete pleiotropy

Budoff Submitted Nov 2008

NIH

“Thoracic Aorta Calcification and Coronary Artery Calcification in the COPD Gene Study”

Chronic obstructive pulmonary disease (COPD) is the 4th leading cause of death in the United States and will be the third leading cause of death worldwide by 2020. Cardiovascular disease is an important cause of death and hospitalization among patients with COPD (Curkendall S, Ann Epidemiol 2006). Recent data indicates that, among COPD patients, the rate of hospitalization for cardiovascular disease (CVD) is higher than that for COPD itself (Huart L, Chest 2005). Morbidity and mortality from CVD are nearly twice as high in COPD patients compared to the general population. This proposed study will investigate thoracic aortic calcification (TAC) and coronary artery calcification (CAC) among subjects enrolled in the COPD Gene Study,

a large prospective epidemiologic study in individuals with COPD investigating phenotypic characterization using CT as well as genome-wide association studies to identify genetic determinants for COPD susceptibility. We have requested 15% FTE for Dr. Santorico to oversee all statistical aspects of the study, particularly those related to genome-wide association tests.

Heyn P
NIH

Submitted Nov 2008

“Interventions to Remediate Age-related Cognitive Decline”

We request support for 10% effort for Dr. Santorico as Co-Investigator and biostatistician for this proposal. Dr. Santorico will have overall responsibility for the statistical plan and design of this study. She will be responsible for: 1) development of statistical methodology as needed to address study demands; 2) analysis of the data and interpretation of the results; 3) assistance with the construction of charts, tables, and figures for presentation, and publication of the results; and 4) assistance with the preparation of manuscripts. She will participate in all meetings of the research team, assist the PI with the preparation of annual renewal applications and progress reports, and assist with the publication of the research findings.

Razzaghi
NIH/NHLBI HL090949

Submitted Nov 2008

“Role of Transcriptional Factor ZNF202 in Regulation of HDL Metabolism”

Almost half of the one million deaths attributed to cardiovascular diseases annually in the United States are due to coronary heart disease (CHD). Furthermore, one third of early familial CHD is primary due to low levels of high-density lipoprotein cholesterol (HDL-C), called hypoalphalipoproteinemia (Williams et al. 1990). Zinc Finger Protein 202 (ZNF202) is a new candidate gene (Monaco et al. 1998) that genetically linked to hypoalphalipoproteinemia (low HDL-C) in a large Utah pedigree (Kort et al. 2000). Using sequencing data, we have identified 20 significant sequence variants associated with HDL-C levels that will be screened for in the two population-based samples of Hispanics (n= 458) and Whites (n= 674) using high-throughput Pyrosequencing. We have requested 20% FTE for Dr. Santorico to oversee all statistical aspects of this study.

Reagon
NIH

Submitted June 2008

“Genetic Associations with Bone Density and Muscle Mass in COPD”

Chronic Obstructive Pulmonary Disease (COPD) is a multisystem, inflammatory disease characterized by airflow limitations and losses of lung parenchyma. It is a smoking related illness that affects approximately 12 million Americans, and is the fourth leading cause of death in the US. Two extrapulmonary effects of COPD, low bone mineral density (osteoporosis) and low muscle mass (cachexia) are related to poorer outcomes: greater morbidity and mortality, and reduced health-related quality of life in COPD. Both bone mineral density and muscle mass have significant genetic determinants. Heritability estimates are in the range of 60-80% for each. We postulate that genetic associations to low bone density and muscle mass in COPD will identify novel pathways and confirm the role of inflammatory cytokines in the disease. In addition, COPD offers a useful condition in which to identify genetic associations to low bone and muscle mass, because there is higher variability for these traits in COPD subjects than in the normal population. We propose to utilize the valuable resources of COPDGene to identify the genetic factors associated with low bone mineral density and muscle mass in COPD and to confirm the impact of these traits on severity of disease. We have requested 20% FTE for Dr. Santorico who will be responsible for the statistical genetic aspects of the study.

Edwards
NIH

Submitted July 2008

“Genome-wide Family-based Association Study of Metabolic Syndrome”

The metabolic syndrome (MetS) is an important public health problem and currently affects 20-30% of the US population. Estimates indicate an alarming and rapid increase in prevalence of MetS across all groups. The epidemic of MetS has major public health implications regarding quality of life, health care economics and societal productivity. MetS is characterized by a cluster of risk factors, including: elevated triglycerides, low levels of high density lipoprotein cholesterol, hypertension, obesity, hyperinsulinemia and hyperglycemia. MetS is associated with increased risk for cardiovascular disease, type 2 diabetes and overall mortality. Although there is solid evidence that genetic factors are involved in the pathogenesis of MetS, specific genes have not yet been identified. The overall goal of this project is to identify susceptibility loci for the MetS with three proposed aims focused on identification, data harmonization and meta-analysis. We have requested 10% FTE for Dr. Santorico in addition to a graduate research assistant.

Geraci
NIH

Submitted June 2008

“Genomic Phenotyping of Pulmonary Vasuclar Disease”

I have offered to serve as a consultant on this grant advising on design and methods for studying the genetics of gene expression.

Funded Projects

(Monks)

7/2007

OSU A&S Summer Research Grant

“Building a Toolbox for Understanding the Genetics of Complex Traits”

The metabolic syndrome is an important public health problem. I am currently working with a group of investigators at the University of Washington on the study of the genetics of the metabolic syndrome. We have existing trait and environmental data, as well as stored DNA samples for 1,949 subjects in 438 families collected as part of the Genetics of Non-Insulin Dependent Diabetes Mellitus (GENNID) study. To date our work has been geared toward the applied needs of the overall project, including determining what traits are controlled by genetic influences, what environmental variables have an effect on these traits and identifying genomic regions responsible for the mentioned effects. The A&S SRG will be used to develop methods for use in multiethnic studies for testing linkage and/or association, pleiotropy, epistasis, gene-environment interactions and for building complex models allowing for pleiotropy, epistasis and GxE in a multiethnic study.

(Monks)

1/24/2006

OSU-Big XII Faculty Fellowship Program

In recent publications, my coworkers and I have suggested a novel approach for combining many types of genomic information in order to better understand the underlying causes of disease. These papers provided the initial data needed to determine if such an approach is feasible. In particular, it provided a survey of the genetic effects on the expression of genes (how genes affect other genes) in humans, mouse and corn. The unique potential of this avenue of investigation is supported by the fact that these publications have been cited by other investigators 167 times in just the last 2 years. I recently had the pleasure of meeting Kathy Hanford from the University of Nebraska at Lincoln. Dr. Hanford has a data set that fits well with this scenario. The OSU-Big XII Faculty fellowship funds will be used to visit Dr. Hanford to: (1) to learn more about the experimental design used by Dr. Hanford, (2) better understand her data set, and (3) determine whether my statistical methods would be applicable. If I were to successfully apply my methods to her data, this would serve as an excellent illustration for use in a paper I am currently writing which details my statistical methods with accompanying simulations that access validity and power.

(Monks)

7/1/2006-7/31/2006

OSU A&S Dean's Incentive Grant

"Finding Racial Differences in the Genetic and Environmental Causes of the Metabolic Syndrome"

The metabolic syndrome affects 20-30% of the United States population and is characterized by a cluster of type 2 diabetes and cardiovascular disease risk factors, including: obesity, elevated triglycerides, low HDL-cholesterol, hypertension, and abnormal glucose metabolism. The basis for the metabolic syndrome is unknown, although it is likely that both genetic and environmental influences are involved. In addition, it is possible that different patterns of genetic and environmental correlations may result in similar multivariate outcomes. Such potential differences could have important implications for gene mapping studies and for prevention efforts in different racial/ethnic groups. Our research group hypothesizes that racial/ethnic differences in patterns of genetic and environmental correlations between metabolic syndrome features exist and that knowledge of these patterns can improve gene mapping efforts. We are currently developing a grant proposal for submission to the National Institutes of Health to explore these issues. The requested DIG funds will be used for travel to visit collaborators in order to finalize details of this NIH grant proposal.

R03 HD 50631-01 (Monks)

7/1/2005 – 6/30/2006

NIH

Subcontract with Children's Hospital and Regional Medical (Anne Hing)

"Homozygosity Mapping of Oculo-Oto-Facial Dysplasia"

The goal of this project is to determine the molecular basis of oculo-oto-facial dysplasia. We hypothesize that the affected individuals in this extended family have inherited two copies of the same gene mutation from a common ancestor and that homozygosity mapping to identify regions of identical genomic sequence in the affected individuals will determine the OOFD gene locus. My goal on this project will be to guide a research assistant in the application and development of necessary statistical methods. The work includes estimation of the inbreeding coefficient for individuals with available genotype data and using this information to test for linkage in a genome-wide scan.

5R01HL043201-13 (Monks)

9/1/2004 – 8/31/2006

NIH / PHS

Subcontract from the University of Washington, Cardiovascular Health Research Unit (Bruce Psaty)

"Anti-hypertensive Drug-Gene Interactions and CV Events"

The overall project goal is to identify interactions between the usage of anti-hypertensive drugs and genetic variation with respect to cardiovascular events. My role on this project will be to provide consultation, research and analysis relating to the use of genetic data. Potential projects include research of 1) methods for drug-gene interaction for continuous traits in the context of a case-only study design and 2) the effects on power of haplotype association tests when haplotype uncertainty is ignored. In addition, extensions of projects will be pursued, including a genome-wide association scan for drug-gene interactions and the use of gene expression from peripheral blood.

(Monks)

8/1/2005-8/31/2005

OSU A&S Summer Research Grant

"Separating the Wheat from the Chaff: Use of Dimension Reduction Methods in Large Scale Genomic Studies"

In recent publications, my coworkers and I have suggested a novel approach for combining many types of genomic information in order to better understand the underlying causes of disease. These papers provided the initial data needed to determine if such an approach is feasible. In particular, it provided a survey of the genetic effects on the expression of genes (how genes affect other genes) in humans, mouse and corn. One

of the challenges of such an approach is how to study the genetics of a vast set of highly interrelated measures which likely represent a much smaller set of truly meaningful responses. In other words, how do we separate the wheat from the chaff to find those genetic “kernels” that impact human disease. The objective of this proposal is to use currently available data to apply two traditional statistical methods of dimension reduction along with a new approach.

(Monks) 7/1/2005-7/31/2005

OSU A&S Dean’s Incentive Grant

“Using Caution in the Analysis of Multi-site Human Genetic Studies”

Recently developed technology has made it possible to measure a person’s genetic make-up at 100,000 different locations across the genome (Matsuzaki et al. 2004). One common assumption made in the statistical analysis of human genetic data is that of random assortment of alleles into genotypes. This assumption is called Hardy Weinberg Equilibrium (HWE). As an initial step in most analyses, HWE is tested for each genetic marker. If the study has been conducted across many study sites, this test is performed for each site individually as well as for the combined study. The results of the test can sometimes find a single study site that does not satisfy the HWE assumption. Given this scenario, some investigators exclude the anomalous study site from further analyses with the belief that some unknown cause must be producing the heterogeneous results. The research proposed herein will show this to be a faulty conclusion resulting in inefficient use of data and resources.

ASPH Grant No. S1946-21/23 (Monks) 8/16/2004 – 8/15/2005

CDC/HHS

Subcontract from the University of Washington (Karen Edwards)

“Centers for Genomics and Public Health”

The University of Washington Center for Genomics and Public Health (UW CGPH) aims to integrate advances in genetic technology into public health practice and offer research and educational opportunities for public health students and professionals. This includes contributing to the knowledge base on genomics and public health in asthma, diabetes, and familial hypercholesterolemia. My role for the center is to contribute to the UW CGPH goals by providing: 1) a manuscript or manuscripts pertaining to the use of ethnically diverse populations in the context of genetic studies. This is of particular importance in order to optimally power genetic studies, obtain accurate interpretations and to ensure scientific results are of interest to the larger population, 2) consultation on data analyses for ongoing projects and 3) assistance in the creation of review papers aimed at integrating advances in genetic technology into public health practice.

Sub-contract (S Monks) 8/1/2003-7/31/2004

Rosetta Inpharmatics, Inc.

"Genetics of Gene Expression for Identification of Susceptibility Genes"

Roles on project: Provide sound recommendations for research program design and novel methods of experimentation to solve problems relating to statistics, genetics, and molecular profiling (to include gene expression). Propose and develop analytical methods that integrate a diversity of data, including family or population data, clinical phenotype data, gene expression data, and genotype data. The primary aim is to elucidate complex pathways and provide solutions that lead to the discovery and development of new and/or existing drug products.

CDF (S Monks) 7/1/2003-6/30/2004

UW-Biostatistics

"Elucidating the genetic web: a theoretical framework for model-free tests of genetic interaction" Roles on project: Derive the theoretical framework for testing genetic interaction through the use of correlation

between linkage evidence for two regions and establish how this model-free test of genetic interaction corresponds to the classical model for genetic interaction.

RO1 CA97934 (D Strom) 4/1/2003-3/31/2004

NIH

"Interactions of KSHV and Endothelial Cells"

Roles on project: Advise on aspects of experimental design, conduct necessary statistical analyses and assist in manuscript preparation.

Sub-contract (S Monks) 8/1/2002-7/31/2003

Rosetta Inpharmatics, Inc.

"Genetics of Gene Expression for Identification of Susceptibility Genes"

Roles on project: Provide sound recommendations for research program design and novel methods of experimentation to solve problems relating to statistics, genetics, and molecular profiling (to include gene expression). Propose and develop analytical methods that integrate a diversity of data, including family or population data, clinical phenotype data, gene expression data, and genotype data. The primary aim is to elucidate complex pathways and provide solutions that lead to the discovery and development of new and/or existing drug products.

RO1 GM 32618 (D Strom) 7/1/2002-2/28/2004

NIH

"Molecular Basis of Crown Gall Tumorigenesis"

Roles on project: Advise on aspects of experimental design, conduct necessary statistical analyses and assist in manuscript preparation.

S1946-21/22 (K Edwards) 10/1/2001-9/30/2005

ACPH/CDC

"UW Center for Genomics and Public Health"

Roles on project: Provide biostatistics and statistical genetics technical assistance as well as provide guidance for data analyses.

5 U01 AG16976-02 (WA Kukull) 7/1/2000-6/30/2001

NIH/NIA

"Alzheimer's Disease Data Coordinating Center"

Roles on project: Provide statistical genetics expertise to participating Alzheimer's disease centers and review applications for pilot grants.

5 R01 HL50268-07 (MA Austin) 6/1/2000-5/31/2001

NIH/NHLBI

"Genetics of the Metabolic Syndrome in Japanese Americans"

Roles on project: Provide expertise in experimental design, conduct linkage and association analyses for phenotypes relevant to the Metabolic Syndrome, assist in manuscript preparation

5 R01 HL49513-07 (MA Austin) 7/1/1999-6/30/2001

NIH/NHLBI

"Genetic Epidemiology of Hypertriglyceridemia"

Roles on project: Provide expertise in experimental design, conduct linkage and association analyses for phenotypes relevant to Hypertriglyceridemia, assist in manuscript preparation and grant applications

Patents and Other Intellectual Property

United States Patent Application: 20070166707

Computer systems and methods for associating genes with traits using cross species data

Inventors: E.E. Schadt, **S.A. Monks**, J Lamb

United States Patent Application: 20060122816

Computer systems and methods for subdividing a complex disease into component diseases

Inventors: E.E. Schadt, **S.A. Monks**

United States Patent Application: 20030224394

Computer systems and methods for identifying genes and determining pathways associated with traits

Inventors: E.E. Schadt, **S.A. Monks**

Formal Teaching

MATH 6388 Advanced Statistical Methods for Research (Spring 2009) The second in a two-semester course in applied statistics. Topics include multifactor analysis of variance and covariance, categorical data, general linear models, bootstrapping, and other computationally intensive statistical methods.

MATH 7926 Readings in Applied Probability and Statistics (Spring 2009) with Melissa Santos focusing on Bayesian Statistics, includes weekly meetings to go through Bayesian Methods for Data Analysis by Bradley P. Carlin and Thomas A. Louis (3rd Edition, 2008)

MATH 4830/5830 Applied Statistics (Fall 2008) Review of estimation, confidence intervals and hypothesis testing; ANOVA; categorical data analysis; non-parametric tests; linear and logistic regression.

STAT5910/6910, Methods in Statistical Genetics (Fall 2006) Coverage focuses on the theory of statistical techniques used in human genetic studies. The course will include discussion of segregation/aggregation, linkage and association methods.

STAT5513, Multivariate Analysis (Fall 2005 and 2007) Statistical theory concerning: Multivariate normal distribution, simple, partial and multiple correlation, multivariate sampling distributions. Wishart distribution, general T-distribution, estimation of parameters and tests of hypotheses on vector means and covariance matrix. Classification problems, discriminate analysis and applications.

STAT5063, Multivariate Methods (Spring 2005-2008) Use of Hotelling's T-squared statistic, multivariate analysis of variance, canonical correlation, principal components, factor analysis and linear discriminant functions.

STAT5073, Categorical Data Analysis (Spring 2005-2008) Analysis of data involving variables of a categorical nature. Contingency tables, exact tests, binary response models, loglinear models, analyses involving ordinal variables, multinomial response models. Computer usage for analysis is discussed.

STAT5023, Statistics for Experimenters II (Autumn 2004 & 2006) Analysis of variance, covariance, use of variance components and their estimation, completely randomized, randomized block and Latin square designs, multiple comparisons.

Biostat 516, Statistical Methods in Genetic Epidemiology (Autumn 2003) Responsible for the creation, development and assessment of this course. Coverage includes theory and application of statistical techniques used in genetic epidemiology. The course will include discussion of association studies, linkage and segregation analyses. Examples stressed with reference to assumptions and limitations.

Biostat 111, Lectures in Applied Statistics (Spring 2001) Organized a series of guest lectures aimed at introducing undergraduate students to potential career areas in statistics

Biostat 551, Statistical Genetics II: Quantitative Traits (Winter 2000, 2001 and 2003) Responsible for the creation, development and assessment of this course. The course presents the statistical basis for describing genetic and environmental variation in quantitative traits, and methods of mapping and characterizing quantitative trait loci. (Note: this course draws students from biostatistics, statistics, epidemiology, medicine, computer science, ecology, applied mathematics and mathematics)

PHG 580, Seminar in Public Health Genetics (Autumn 2000-Spring 2001) Coordinated seminar series on topics related to public health genetics, including current bioethical, legal, medical, biotechnology, and public policy issues

Stat 311, Introduction to Statistics (1995-1996) Examining relationships between two variables using graphical techniques, simple linear regression and correlation methods; Producing data using experimental design and sampling.

Other Teaching

Member of the American Society of Human Genetics' NSF-funded Geneticist-Educator Network of Alliances (GENA) project, 2009-present

Instructor to be (NIMH grant under review), "Short Course on Statistical Genetics & Genomics for Mental Health Investigators", Submitted 2008

Seminar/Discussant, Broken Arrow High School Honors Statistics Class, "Careers in Statistics," 2006

Instructor, NSF Annual Plant Microarray Short Course on Design and Analysis of Plant Microarray Experimentation: "QTL Analysis of Expression" 2005 and 2006

Instructor, Seattle Epidemiology, Biostatistics & Clinical Research Methods: "Statistical Methods in Genetic Epidemiology", 2004

National Human Genome Research Institute Mentor for local high school teachers and students, 2003-present

Instructor, BioPharmaceutical Technology Center Institute, Course in Computational Approaches to Analyzing Gene Expression Data, "Treating Gene Expression Data as Quantitative Traits", 2003

Instructor: Genetics in the New Millennium: Myths, Medicine and Public Health: "Tools for gene discovery: molecular biology, genetic epidemiology and population genetics", 2000

Instructor: Summer Institute in Statistical Genetics at North Carolina State University, 1999-2001

Guest Lecture, *Epi 518, Computer Applications in Genetic Epidemiology*, Spring 2000-2003

Guest Lecture, *Epi 517, Genetic Epidemiology*, Spring 2000, 2001, 2003

Guest Lecture, *Biostat 111, Lectures in Applied Statistics*, Spring 2000, 2001, 2003

Current Advisees

Ph.D. Committee Member and Thesis Advisor

Qiang Guo (OSU Statistics): Spring 2006-present; PhD qualifying exams passed Fall 2008

Trecia Kippola (OSU Statistics): Spring 2007-present; PhD qualifying exams passed Fall 2008

M.S. Committee Member

Sarah Tocheri (UCD): Fall 2008

Sarah Schmidt (UCD): Spring 2009

Shoshana Rosskamm (UCD): Spring 2009 -present

Ph.D. Committee Member

Deb Batistas (UCD): Fall 2008; Comprehensive exam taken but not passed

Melissa Santos (UCD): Fall 2008-present; Comprehensive exam in Feb 2009

Certificate students in Statistics at UCD, 2008-present

I am currently advising all undergraduate and graduate certificate students. During Fall 2008, this has involved 5 students.

B.S. Advisor

I advised all Statistics Undergraduate majors at OSU during 2007-2008. During that year, the program grew from 11 to 19 undergraduate students.

Past Advisees

Ph.D. Committee Member and Thesis Advisor

Leon Shi (OSU Statistics): Autumn 2004-2008

Ph.D. Committee Member and Reader

Amy Wagler (OSU Statistics): Spring 2005-2007

Tracy Morris (OSU Statistics): Spring 2006-2007

Elisabeth Rosenthal (UW Biostatistics): Summer 2003-2008

Josh Bis (UW Epidemiology): Autumn 2003-2006

Shenaz Hussain (UW Epidemiology): Autumn 2003-2006

Helen Kim (UW Epidemiology): Winter 2000-Autumn 2003

M.S. Committee Member and Reader

Hui Zeng (OSU Statistics): Spring-Fall 2006

Sungmi Brown (OSU Statistics): Spring 2006-2007

Yanina Grant (OSU Statistics): Spring 2005-2006

Janae Nicholson (OSU Statistics): Spring 2005-2006

Dongmei Yu (UW Biostatistics): Autumn 2003

M.S. Committee Member and Thesis Advisor

Aiwu Zhang (OSU Statistics): Spring 2005-2007

Angel Wan (UW Biostatistics): Autumn 2002-2006

Master of Public Health in Public Health Genetics, Committee Member and Chair

Erin Pfeiffer: Winter-Spring 2001

B.S. Research Project Advisor

Dustin Weems (OSU Statistics): Autumn 2005-2007

University Service

Organizer, UCD Statistics Seminar Series, 2008-present

Member, Graduate Committee, 2008-present

Mentor, Steve Culpepper, 2008-present
Chair, Search Committee for a tenure-track assistant professor position in statistics, 2008-2009
Member, Appeal Committee for Anatolii Puhalskii's Post Tenure Review (PTR) Primary Unit Committee's Conclusion, Aug 2008
Member, Extensive Review Committee on Research for Burt Simon, Aug 2008
Organizer, "Introduction to using the HPCC at OSU" by Dana Brunson, Ph.D., Sr. Systems Engineer, High Performance Computing Center, Oklahoma State University, Feb 2008
Member, Committee for Assessment and Development Policy on Research, OSU, Department of Statistics, 2008
Mentor, Lan Zhu, OSU Department of Statistics, 2007-2008
Chair, OSU Departmental Head Search Committee, 2007-2008
OSU Faculty Associate (mentoring program for dormitory), 2007-2008
Member and Chair, OSU College of Arts and Sciences Scholarship Committee, 2006-2008
Member, OSU College of Arts and Sciences Faculty Council, 2006-2008
Member of the Personnel Committee, Department of Statistics, Oklahoma State University, 2006-2008
Member, Dispute Resolution Hearing Committee at Oklahoma State University Dec 2005-Jan 2006
Organizer of the "Student Research Symposium in Statistics" at Oklahoma State University, 2005
Co-developer of PhD level assessment plans and reports for the Office of University Assessment and Testing, Department of Statistics, Oklahoma State University, 2005
Member of the Graduate Committee, Department of Statistics, Oklahoma State University, 2004-2008
Evaluation of student teaching assistants, Department of Statistics, Oklahoma State University, 2004-2008
Grader, PhD qualifying exams, Department of Statistics, Oklahoma State University, 2004-2008
Co-organizer and co-chair of Second Workshop in Statistical Genetics and Computational Molecular Biology, 2003
Member of the University of Washington, School of Public Health and Community Medicine, Committee on Distance Learning, 2003
Member of the Admissions and Curriculum Committee, UW, M.S. Program in Genetic Epidemiology, 2002-2004
Member of the Consulting Committee, Department of Biostatistics, University of Washington, 2002-2004
Member of the Education Policy and Teaching Evaluation Committee, Department of Biostatistics, University of Washington, 2000-2004
Member of the Public Health Genetics Committee responsible for the creation of a Ph.D. in Public Health Genetics, 2000-2001
Member of the Faculty Committee for the development and creation of a certificate program and PhD pathway in Statistical Genetics, Department of Biostatistics University of Washington, 1999
Member of the Faculty Search Committee, Department of Biostatistics, University of Washington, 1999-2001
Member of the Academic Program Committee, Admissions Committee and Curriculum Committee for Public Health Genetics, 1999-2001
Member of an implementation team for the North Carolina State University Strategic Plan, 1999

Service Outside University Setting

Session proposal for American Society of Human Genetics 2009 Meeting: "Strength in Numbers: Combining Genetic Studies for Better Understanding of Complex Traits" Submitted Dec 2008
Member, NIMH grant review panel for "Limited Competition for Data Deposition and Analyses of Genome Wide Association Studies of Mental Disorders (Collaborative R01)", July 2008

Member, NHGRI grant review panel for “Epidemiological Investigation of Putative Causal Genetic Variants”, Mar 2008
Review Editor, *Frontiers in Neurogenomics*, 2008-present
Statistical Expert for *The Plant Cell* (provide reviews of statistical analyses), 2008-current
Book evaluation for CRC PRESS, 2007
Book evaluation for SAGE Publications, Inc., 2005
Associate Editor for the journal *Molecular Biology and Evolution*, 2005-current
Temporary member for grant reviews: Genes, Genomes and Genetics Integrated Review Group; NIH Genomics, Computational Biology and Technology Study Section, 2005 and 2006
Organizer and Moderator, Invited session at the Annual Meeting of the American Society for Human Genetics: “Genetics of Gene Expression: New Strategies for Studying Complex Traits”, 2003
Session Moderator, Linkage disequilibrium and haplotypes. Annual Meeting of the American Society of Human Genetics, 2003
Representative, Western North American Region of the International Biometric Society, 2003-present
Statistical Genetics Consultant for Insightful Inc., 2001-2004
Statistical Genetics Consultant for the Pacific Northwest Research Institute, 2001-2004
Grant reviewer, Center for Ecogenetics and Environmental Health, 2001
Member of the American Statistical Association
Member of the American Society for Human Genetics
Member of the International Genetic Epidemiology Society
Referee for the *American Journal of Human Genetics*, *Behavior Genetics*, *Biological Psychiatry*, *Biometrics*, *Clinical Genetics*, *Computational Statistics and Data Analysis*, *Genetic Epidemiology*, *Genetical Research*, *Genetics*, *Human Heredity*, *Journal of Statistics Education*, *Obesity*, *Nature*, *Science*, *Statistical Applications in Genetics and Molecular Biology*, *The Plant Cell*, *Trends in Genetics*, ongoing

Participant in Workshops/Symposiums

CUOnline Winter Webcamp Workshops: “Blackboard fundamentals” and “Producing and adding video to your course”, Jan 2009
UCD College of Liberal Arts and Sciences, Assessment Workshop, Jan 2009
Preparation for Proposal Writing: Strategic Elements of Success, Workshop, University of Colorado Denver, Office of Research Development and Education, Jan 2009
Attended American Society of Human Genetics Meeting, Nov 2008
Science Webinar: “Analyzing CNV Data Across Array Platforms: Hapmap Project”, Oct 2008
“Dollars and Sense: Fund Searching for Survival”, University of Colorado Denver, Office of Research Development and Education, Oct 2008
One-on-one training with Brian Yuhnke of CUOnline, “Adobe Connect for Creating Online Lectures”, Oct 2008
Science Webinar: “CNVs vs SNPs: Understanding Human Structural Variation in Disease”, July 2008
Attended Joint Statistical Meetings including a full day short course on “Bayesian Methods and Software for Data Analysis” by Bradley P. Carlin and Thomas A. Louis, Aug 2008
University of Colorado Denver, New Faculty Orientation Sessions: “Meet Our Students - Panel Discussion”, “Other Faculty Resources (GLBS, women, faculty of color)”, “New Employee Orientation with HR & Benefit Services”, “College Teaching 101”, Aug 2008
“IRB 101”, Oklahoma State University, October 2007
“A Field Guide to Genbank and NCBI Molecular Biology Resources”, September 2005
“Human Participant Protections Education for Research Teams”, May 2005
“Write Winning Grants” Seminar at Oklahoma State University, 2004

CURRICULUM VITAE

***Stephanie A. Santorico, Ph.D.
(formerly Stephanie A. Monks)***

Training course: MATLAB Fundamentals and Programming Techniques, August 2002
Certificate Program in Distance Learning Design and Development, 2000-2001
"The Ethical Conduct of Research with Humans" held at University of Washington, 2000
"Genetics and Public Health: The Future is Now", 2000
"Second Seattle Symposium in Biostatistics: Analysis of Correlated Data", 1999
Faculty Fellows Program at the University of Washington, 1999-2000
Short Course on Statistical Analysis for Genetic Epidemiology (S.A.G.E.) software, 1998
Workshop: Helping Today's Students Learn Statistics: Using Visual Statistics, 1998
Genetic Analysis Workshop 11, 1998
Workshop: An Overview of the Role of the Biopharmaceutical Statistician, 1998