June 17, 2025

Curriculum Vitae

Daniel E. Weeks
Professor of Human Genetics
Professor of Biostatistics and Health Data Science

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Mastodon: https://fediscience.org/@StatGenDan
Twitter: @StatGenDan

Academic Interests

- Statistical human genetics in the area of mapping susceptibility loci involved in complex diseases.
- Developing algorithms and statistics, implementing them in computer programs, and testing them on real and simulated data.
- Genetic influences on obesity, lipids, and body composition.
- The effects of methylation on patient recovery outcomes after traumatic brain injury, and on cognitive function within the context of treatment for breast cancer.

Citizenship: United States of America

Education and Training:

Undergraduate

1983	B.A., summa cum laude, Biology and Mathematics	Colby College, Waterville, ME

Graduate

1983-84	Graduate studies in Applied Mathematics	Rutgers University, New Brunswick, NJ
1985	M.S., Biomathematics	University of California, Los Angeles
1988	Ph.D., Biomathematics (Kenneth Lange, mentor)	University of California, Los Angeles

Post-Graduate

1989-90	Postdoctoral training (Jurg Ott, mentor)	Columbia University, New York, NY

Fellowships:

1982 Research Training Program, The Jackson Laboratory, Bar Harbor, ME (David E. Harrison, mentor)
1983 Summer Student Fellow, Woods Hole Oceanographic Institution, MA (Hal Caswell, mentor)
1986-87 Genetic Mechanisms Training Program, UCLA
1987-88 Systems and Integrative Biology Training Program, UCLA
1989-90 Postdoctoral Fellow with Jurg Ott, Ph.D., Columbia University

Academic Appointments:

1989-90 Research Scientist, New York State Psychiatric Institute
1990-96 Assistant Professor of Human Genetics (tenure-track), University of Pittsburgh
1992-00 Member, W. M. Keck Center for Advanced Training in Computational Biology
1994-95 Executive Committee, W. M. Keck Center for Advanced Training in Computational Biology
1994-98 Head of Statistical Genetics - Methods, Wellcome Trust Centre for Human Genetics, University of Oxford
1996-02 Associate Professor of Human Genetics (tenured), University of Pittsburgh
2002-03 Associate Professor of Biostatistics (joint appointment), University of Pittsburgh
2004 Acting Chair, Department of Human Genetics
2005 Acting Vice Chair, Department of Human Genetics
2002- Professor of Human Genetics (tenured), University of Pittsburgh
2003- Professor of Biostatistics (joint appointment), University of Pittsburgh
2021-22 Acting Chair, Department of Human Genetics

Professional Organizations:

American Society of Human Genetics
International Genetic Epidemiology Society
American Statistical Association (Life member since 2011)

Honors and Awards:

1982 Phi Beta Kappa, elected Junior year
1983 Graduated second in class from Colby College
1984-85 University Fellow, UCLA
1986-87 Dr. Ursula Mandel Scholarship, UCLA
1986-87 National Research Service Award, Genetic Mechanisms Training Program, UCLA
1987-88 National Research Service Award, Systems and Integrative Biology Training Program, UCLA
1987-88 Distinguished Scholar Award, UCLA
2001 The Mortimer Spiegelman Award, awarded by the American Public Health Association, for outstanding contributions in health statistics.
2003 Delta Omega, National Honor Society for Schools of Public Health
2007 Pitt Innovator Award, University of Pittsburgh
2008 Pitt Innovator Award, University of Pittsburgh
2010 Pitt Innovator Award, University of Pittsburgh

Teaching and Training:

Training Programs:

2000-06 Program Director, post-doctoral training program in statistical genetics: "Discovering Genes for Mental Health"
2002-10 Program Director, international training program in genetic epidemiology: "India-US Research Training Program in Genetics"

Helped mentor the following post-doctoral trainees who were supported by one of our Training Programs:

2000-02 Dr. Karen T.Cuenco
2001-03 Dr. Bobby L. Jones
2002-04 Dr. Sarah Buxbaum
2003-05 Dr. Brian H. Reck
2003-05 Dr. Guy Brock
2004-05 Dr. Jin P. Szatkiewicz
2004-07 Dr. Anbupalam Thalamuthu
2005-06 Dr. Abigail Matthews
2003-09 Dr. Indranil Mukhopadhyay

Courses:

Spring 1991	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 25 enrolled)
Fall 1991	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics and Evolution (HUGEN 2023, 3 hrs/week, 3 credits, 4 enrolled)
Spring 1992	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 25 enrolled)
Fall 1992	Assistant Professor, University of Pittsburgh, co-taught Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 enrolled)
Spring 1993	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 15 enrolled)
Fall 1993	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics and Evolution (HUGEN 2023, 3 hrs/week, 3 credits, 5 enrolled)
Spring 1994	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 26 enrolled)
Fall 1994	Assistant Professor, University of Pittsburgh, co-taught Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 4 enrolled)
Spring 1995	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 24 enrolled)
Fall 1995	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics and Evolution (HUGEN 2023, 3 hrs/week, 3 credits, 7 enrolled)
Spring 1996	Assistant Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 27 enrolled)
Fall 1996	Assistant Professor, University of Pittsburgh, co-taught Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 10 enrolled)
Spring 1997	Associate Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 21 enrolled)
Fall 1997	Associate Professor, University of Pittsburgh, organized and co-taught Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 3 enrolled)
Spring 1998	Associate Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 15 enrolled)
Fall 1998	Associate Professor, University of Pittsburgh, co-taught Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered)
Fall 1999	Associate Professor, University of Pittsburgh, co-taught Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 8 registered)
Fall 2000	Associate Professor, University of Pittsburgh, co-taught Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered)
Spring 2001	Associate Professor, University of Pittsburgh, co-taught Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 18 registered)
Fall 2001	Associate Professor, University of Pittsburgh, co-taught half Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 13 registered)
Fall 2002	Professor, University of Pittsburgh, co-taught half Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 10 registered)
Fall 2003	Professor, University of Pittsburgh, co-taught more than half Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 12 registered)
Fall 2004	Professor, University of Pittsburgh, co-taught half Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 9 registered)
Fall 2005	Professor, University of Pittsburgh, co-taught half Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 9 registered)
Summer 2006	Professor, University of Pittsburgh, co-led a break-out discussion section Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2006)
Fall 2006	Professor, University of Pittsburgh, co-taught half Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered)
Summer 2007	Professor, University of Pittsburgh, co-led two break-out discussion sections

	Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2007)
Fall 2007	Professor, University of Pittsburgh, taught the majority of Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 5 registered)
Summer 2008	Professor, University of Pittsburgh, led a break-out discussion section Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2008)
Fall 2008	Professor, University of Pittsburgh, co-taught half Quantitative Genetics (HUGEN 2033, 3 hrs/week, 3 credits, 6 registered)
Summer 2009	Professor, University of Pittsburgh, led two break-out discussion sections Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, June 1, 2009 and June 8, 2009)
Fall 2009	Professor, University of Pittsburgh, co-taught half Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 6 registered)
Fall 2010	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 10 registered)
Spring 2012	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 10 registered)
Fall 2012	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 14 registered, 1 auditor)
Spring 2014	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 5 registered, 1 auditor)
Fall 2014	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 1 auditor)
November 2015	Professor, University of Pittsburgh, taught three lectures on sequencing in Introduction to Gene Mapping (HUGEN 2029, 3 hrs/week, 3 credits, 11 registered).
Spring 2016	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 4 registered, 2 auditors)
Fall 2016	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 3 auditors)
Spring 2018	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 10 registered, 8 auditors)
Fall 2018	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 16 registered, 4 auditors)
Fall 2019	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 10 registered, 1 auditor)
Spring 2020	Professor, University of Pittsburgh, co-taught ~80% Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 8 registered, 2 auditors)
Fall 2020	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 19 registered, 1 auditor)
Fall 2021	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 9 registered, 1 auditor)
Spring 2022	Professor, University of Pittsburgh, co-taught ~70% Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 14 registered, 1 auditor)
Fall 2022	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 14 registered, 1 auditor)
Spring 2023	Professor, University of Pittsburgh, co-led Human Genetics Seminar (HUGEN 2025, 1 hr/week, 1 credit, 68 registered)

Fall 2023	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 19 registered, 1 auditor)
Fall 2023	Professor, University of Pittsburgh, co-led Human Genetics Seminar (HUGEN 2025, 1 hr/week, 1 credit, 55 registered)
Spring 2024	Professor, University of Pittsburgh, co-taught ~70% Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 13 registered)
Fall 2024	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 15 registered)
Spring 2025	Professor, University of Pittsburgh, co-led Human Genetics Seminar (HUGEN 2025, 1 hr/week, 1 credit, 52 registered)

Other teaching:

1983-84	Teaching Assistant, Rutgers University, New Brunswick, NJ Taught three recitation sections of Precalculus each semester.
1984-85	Mathematics Tutor, University of California, Los Angeles Assisted students in Precalculus, Calculus, Linear Algebra, and Differential Equations.
1985-86	Teaching Associate, Department of Biomathematics, UCLA Assisted Medical students in Biomathematics.
March 1989	Instructor, Columbia University, New York, NY, Course in Linkage Analysis
March 1990	Instructor, Columbia University, New York, NY, Course in Linkage Analysis
Nov. 1990	Instructor, Columbia University, New York, NY, Advanced Course in Linkage Analysis
May 1991	Instructor, Columbia University, New York, NY, Course in Linkage Analysis
May 1991	University of Pittsburgh Medical School Genetics Course, 2 hour lecture on Population Genetics, Segregation and Linkage Analysis.
Oct. 1991	Instructor, Columbia University, New York, NY, Advanced Course in Linkage Analysis
Dec. 1992	University of Pittsburgh Medical School Genetics Course, 3 hour lecture on Population Genetics, Segregation and Linkage Analysis.
Dec. 1992	Advanced Molecular Genetics, Department of Molecular Genetics and Biochemistry, University of Pittsburgh Medical School, 2.5 hour lecture on Linkage Analysis.
Jan. 1993	Instructor, Columbia University, New York, NY, Advanced Course in Linkage Analysis
April 1993	University of Pittsburgh Medical School Genetics Course, 3 hour lecture on Population Genetics, Segregation and Linkage Analysis.
May 1993	University of Pittsburgh Medical Genetics Board Review Course, 4 hour lecture on Population Genetics and Linkage Analysis.
Dec. 1993	University of Pittsburgh Medical School Genetics Course, 4 hour lecture on Population Genetics, Segregation and Linkage Analysis.
July 1995	Wellcome Trust Summer School Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases.
July 1996	Wellcome Trust Summer School Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
May 1997	Duke University Course: Genetic Analysis Methods for Medical Researchers, lectures on statistical methods of linkage analysis.
July 1997	Wellcome Trust Summer School Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
April 1998	Duke University Course: Genetic Analysis Methods for Medical Researchers, lectures on statistical methods of linkage analysis.
July 1998	Wellcome Trust Summer School Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Nov. 1998	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
March 1999	Duke University Course: Genetic Analysis Methods for Medical Researchers, lectures on statistical methods of linkage analysis.

July 1999	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Nov. 1999	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
April 2000	Duke University Course: Genetic Analysis Methods for Medical Researchers, lectures on statistical methods of linkage analysis.
July 2000	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Jan. 2001	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
May 2001	Duke University Course: Genetic Analysis of Human Complex Diseases, lectures on statistical methods of linkage analysis.
July 2001	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Oct. 2001	Short Course on Mathematical Approaches to the Analysis of Complex Phenotypes, The Jackson Laboratory, lectures on non-parametric linkage analysis.
Dec. 2001	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
April 2002	Abstract Writing Session, Graduate School of Public Health, University of Pittsburgh, PA, discussed how to write abstracts.
May 2002	INSERM Ateliers de formation / Workshop 136 – Methods for the elucidation of genomic variation, La Roche-Posay and Paris, France, lectures on linkage analysis (Co-organizer).
July 2002	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Dec. 2002	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
June 2003	Co-director, Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India.
July 2003	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Dec. 2003	Advanced Course in Linkage Analysis at Rockefeller University, New York, NY, lectures on statistical methods of linkage analysis.
July 2004	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Dec. 2004	Co-director, Second Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India.
May 2005	Co-organizer, Paris Workshop on Molecular and Statistical Genomic Epidemiology, Paris, France.
July 2005	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
July 2006	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Jan. 2007	Co-director, Third Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India.
May 2007	Co-organizer, Second Paris Workshop on Molecular and Statistical Genomic Epidemiology, Paris, France.
July 2007	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
July 2008	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
Feb. 2009	Co-director, Fourth Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India.
March 2009	Co-organizer, Third Paris Workshop on Genetic Epidemiology, Paris, France.
July 2009	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).

Feb. 2010	Co-director, Fifth Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India.
June 2010	Led a discussion session on case studies in scientific ethics for the SIBS (Summer Institute for Training in Biostatistics) program, June 22, 2010.
July 2010	Participated in a "Brown bag lunch panel discussion: Interdisciplinary training" for the SIBS (Summer Institute for Training in Biostatistics) program, July 1, 2010.
July 2010	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
May 2011	Co-organizer, Fourth Paris Workshop on Genetic Epidemiology, Paris, France.
June 2011	Guest lecture on "Scientific Ethics" for the SIBS (Summer Institute for Training in Biostatistics) program, June 22, 2011.
June 2011	Led a discussion session on case studies in scientific ethics for the SIBS (Summer Institute for Training in Biostatistics) program, June 22, 2011.
July 2011	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
July 2011	Guest lecture on "Genetic variants and personalized medicine" for the SIBS (Summer Institute for Training in Biostatistics) program, July 15, 2011.
August 2011	Plunge into Public Health: Human Subjects Ethics lecture, August 26, 2011.
August 2011	Co-led Plunge into Public Health: Human Subjects Ethics discussion group, August 26, 2011.
July 2012	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
August 2012	Co-led Plunge into Public Health: Human Subjects Ethics discussion group, August 23, 2012.
January 2013	Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, taught about rare variants association analyses. January 15-19, 2013.
May 2013	Co-organizer, Fifth Paris Workshop on Genetic Epidemiology, Paris, France.
June 2013	Co-led a discussion session on case studies in scientific ethics for the SIBS (Summer Institute for Training in Biostatistics) program, June 19, 2013.
July 2013	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
March 2014	The Second Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, taught about association analyses. March 10-14, 2014.
July 2014	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
October 2014	Freshman Seminar: Genomics in the Era of Personalized Medicine, at Carnegie Mellon University. Guest lecture on "Genetic Variants and Personalized Medicine". October 9, 2014.
March 2015	The Third Kyoto Course and Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, taught about rare variants association analyses. March 16-20, 2015.
May 2015	Co-organizer, Sixth International Workshop on Genetic Epidemiology, May 14-16, 2015, London, United Kingdom.
July 2015	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
July 2016	Wellcome Trust Advanced Course on Human Genome Analysis: Genetic Analysis of Multifactorial Diseases (Course leader).
February 2017	Co-led a Human Genetics Journal Club session, February 3, 2017.
July 2017	Wellcome Genome Campus Advanced Course on Genetic Analysis of Mendelian and Complex Disorders (Course leader).
September 2017	Co-organizer, Seventh International Workshop on Genomic Epidemiology, September 20-22, 2017, Barcelona, Spain (missed due to illness).
July 2018	Wellcome Genome Campus Advanced Course on Genetic Analysis of Mendelian and Complex Disorders (Course leader).
July 2019	Wellcome Genome Campus Advanced Course on Genetic Analysis of Mendelian and Complex Disorders (Course leader).

February 2021	Guest lecture on 'Imputation' in HuGen 2072, Genomic Data Pipelines and Tools, on February 17, 2021.
July 2021	Wellcome Genome Campus Advanced Course (virtual) on Genetic Analysis of Mendelian and Complex Disorders (Course leader).
July 2022	Wellcome Genome Campus Advanced Course (virtual) on Genetic Analysis of Mendelian and Complex Disorders (Course leader).

Service on Masters and Doctoral Committees

1991	Laura Lasher, M.S. "The estimation of genome length from genetic linkage data"
1992	Carmella A. Sarneso, M.S. "Analysis of computer simulated family data using the affected pedigree member method of linkage analysis"
1992	Tara K. Cox, Ph.D. "Automated genetic linkage mapping: development and performance assessment of an expert computer program"
1993	Lisa D. Harby, M.S. "A teratogen information service: profile of the patient caller and development of a pregnancy outcome questionnaire"
1993	D. Andrew Merriwether, Ph.D. "Mitochrondrial DNA variation in South American Indians"
1994	Pamela L. St. Jean, Ph.D. "The genetic etiology of abdominal aortic aneurysms"
1994	Deborah L. Brown, M.S. "Strategies for genomic searching using the affected pedigree member method of linkage analysis" (Chair of Committee)
1994	Kelly E. Jackson, M.S. "An exon-2 peripherin/RDS mutation causes macular and peripheral retinal degeneration"
1994	Sang Ahnn, Ph.D. "Sample size determination in clinical trials"
1997	Sean Davis, Ph.D., Human Genetics, "Nonparametric Statistics in Linkage Analysis" (Chair of Committee)
1997	Robert W. Kramer, Ph.D., Computer Science, "An incremental algorithm for finding maximum likelihood in genetic linkage analysis"
1999	Michael Barmada, Ph.D., Human Genetics, "Genetic epidemiology of type 2 (non-insulin dependent) diabetes mellitus"
2000	Kai Yu, Ph.D., Biostatistics, "Statistical methods for analyzing tetrad crossover probabilities"
2000	Brion Maher, Ph.D. "Genetic analyses of attention deficit hyperactivity disorder and its underlying dimensions"
2001-2002	Jacqueline Wicks, The Australian National University, "On modeling and testing for linkage in nuclear families" (External examiner for her PhD examination).
2004	Hui-Ju Tsai, Ph.D., Human Genetics, "Comparison of methods incorporating covariates into affected sib pair linkage analysis" (Chair of Committee).
2004	Feng Dai, M.S., Biostatistics, "Imprinting in variance components-based linkage analysis" (Chair of Committee).
2004	Jin P. Szatkiewicz, Ph.D., Biostatistics, "Mapping genes for quantitative traits using selected samples of sibling pairs".
2007	Yan Lin, Ph.D., Biostatistics, "Statistical Issues in Family-Based Genetic Association Studies with Application to Congenital Heart Defects in Down Syndrome".
2007	Amrita Ray, Ph.D., Human Genetics, "Affected relative pair linkage statistics that model relationship uncertainty" (Chair of Committee).
2007	Feng Dai, Ph.D., Biostatistics, "Variance components models in statistical genetics: extensions and applications" (Chair of Committee).
2008	John Shaffer, Ph.D., Human Genetics, "Genetic Epidemiology of Five-Year Change in Bone Mineral Density in Mexican Americans".
2008	Ankur Mukherjee, Ph.D., Human Genetics, "Candidate gene association study of baseline and longitudinal bone-quality traits in a healthy older population".
2008	Samsiddhi Bhattacharjee, Ph.D., Human Genetics, "Variance component score statistics for QTL mapping".
2009	Johanna Jakobsdottir, Ph.D. Biostatistics, "Genetics of age-related maculopathy & score statistics for X-linked quantitative trait loci" (Chair of Committee).
2010	Chia-Ling Kuo, Ph.D., Biostatistics, "Topics in statistical methods for human gene mapping".

2011	Ryan Minster, Ph.D., Human Genetics, "Pleiotropic relationships among measures of bone mineral density, bone geometry, lean muscle mass and fat mass".
2010-2011	Ross Curtis, Ph.D., Computational Biology, Carnegie Mellon University, "Using visualization and automation to accelerate genetics discovery".
2011-2012	Yerkebulan Talzhanov, M.S., Human Genetics, "Computational modeling of the pancreas: lifelong simulations of pancreatitis".
2012	Tero Hiekkalinna, Ph.D., Statistical Genetics, University of Helsinki, "On the superior power of likelihood-based linkage disequilibrium mapping in large multiplex families compared to population based case-control designs". Served as an external examiner.
2012-13	Umut Ozbek, Ph.D., Biostatistics, "Statistical Methods for Recovering GWAS Data".
2012-14	Chi-Ting Su, Ph.D., Human Genetics, "Molecular Mechanisms of LTBP4-related Cutis Laxa."
2013-14	Shaowu Tang, Ph.D., Biostatistics, "Investigations on Genomic Meta-Analysis: Imputation for Incomplete Data and Properties of Adaptively Weighted Fisher's Method".
2013-14	Ying Ding, Ph.D., Computational Biology, "Prognostic biomarker detection, machine learning bias correction, and differential coexpression module detection".
2013-14	Lun-Ching Chang, Ph.D., Biostatistics, "Candidate Marker and Module Detection and Genotype Calling Incorporating Family Information".
2013-14	Olive D. Buhule, Ph.D., Biostatistics, "Bayesian Hierarchical Joint Modeling of Repeatedly Measured Mixed Biomarkers of Disease Severity and Time-To-Event".
2013-16	Nandita Mukhopadhyay, Ph.D., Human Genetics, "Computational methods for calculating meiotic recombination from nuclear pedigrees".
2014	Philip Robinson, Ph.D., "The genetics of ankylosing spondylitis and anterior uveitis", The University of Queensland Diamantina Institute. Served as an external thesis examiner.
2014-15	Hui-Min Lin, Ph.D., Biostatistics, "Behavior Of Statistics for Genetic Association in Genome-Wide Scan Context".
2014-15	Zhen Zhen, Ph.D., Biostatistics, "A pipeline for classifying close family relationships with dense SNP data and putative pedigree information".
2014-15	SungHwan Kim, Ph.D., Biostatistics, "Statistical learning methods for multi-omics data integration in dimension reduction, supervised and unsupervised machine learning".
2015	Randy Beadling, M.S. in Genetic Counseling, Human Genetics, "Restoring spermatogenesis: Lentiviral gene therapy for male infertility in mice".
2015	Jia Jia, Ph.D., Biostatistics, "Association analysis between binary traits and common or rare genetic variants on family-based data" (Chair of Committee).
2015	Yingda Jiang, Ph.D., Biostatistics, "Gene-based association testing of dichotomous traits using generalized functional linear mixed models for family data" (Chair of Committee).
2015	MyoungKeun Lee, Ph.D., Biostatistics, "The effect of error models on analysis pipelines in sequencing data".
2016	Ying Shan, Ph.D., Biostatistics, "Statistical methods for genetic risk confidence intervals, Bayesian disease risk prediction, and estimating mutation screening saturation" (Chair of Committee).
2016	Steven Troung, M.Phil., "Determinants of radiographic severity in ankylosing spondylitis", The University of Queensland Diamantina Institute. Served as an external thesis examiner.
2017	Chien-Wei Lin, Ph.D., Biostatistics, "Power calculation and study design in RNA-seq and methyl-seq".
2017	Yi Liu, Ph.D., Biostatistics, "Novel single and gene-based test procedures for large-scale bivariate time-to-event data, with application to a genetic study of AMD progression"
2017	Kevin K. McDade, Ph.D., Biomedical Informatics, "Enabling data-guided evaluation of bioinformatics workflow quality".
2018	Yunqi Li, M.S., Human Genetics, "Epigenome-wide association study of recovery outcomes of traumatic brain injury patients" (Co-chair of Committee).
2018	Richard J. Biedrzycki, M.S., Human Genetics, "Genome-wide association studies, false positives, and how we interpret them" (Chair of Committee).
2018	Winston W. H. Eng, M.S., Biostatistics, "Exploring the genetic characteristics underlying a multidimensional latent chemotherapy symptom burden" (Chair of Committee).

2018-19	Li Zhu, Ph.D., Biostatistics, "Bayesian variable selection model and differential co-expression network analysis for multi-omics data integration".
2015-19	Annie Arockiaraj, M.S., Human Genetics, "Epigenome-wide association studies in aneurysmal subarachnoid hemorrhage patients".
2016-19	Emily Russell, Ph.D., Human Genetics, "Discrepant effects of CREBRF on obesity and metabolic phenotypes and signals of selection in Samoans".
2019-20	Lacey Heinsberg, Ph.D., Nursing, "Multi-omics of the iron homeostasis pathway in patient outcomes after aneurysmal subarachnoid hemorrhage".
2019-24	Qianqian Liang, Ph.D. Human Genetics, “Computational approaches for characterization and prioritization of human genetic variants”
2020	Dongjing Liu, Ph.D., Human Genetics, "Integrated genome-wide analysis of human facial morphology".
2020	Chen’Ao Qian, M.S. Biostatistics, "Genome-wide association studies in Samoans give insight into obesity by investigating skinfold thickness" (Chair of Committee).
2020	Tao Sun, Ph.D. Biostatistics, "New Statistical Methods for Complex Survival Data with High-Dimensional Covariates".
2020-22	Frances M. Peterson-Burch, Ph.D., School of Nursing, "miRNAs Related to Age-Related Macular Degeneration, Given Genetic Susceptibility".
2020-22	Zeynep Erdogan-Yildirim, Ph.D., Human Genetics, "Identification of genetic factors involved in the etiology of polycystic ovary syndrome in Samoan women".
2020-	Shuwei Liu, Ph.D., Human Genetics
2021-22	Ellyn Dunbar, Ph.D., Human Genetics, "Psychiatric and Pain Risk Genes that may Worsen Quality of Life in Chronic Pancreatitis Patients".
2021	Peng Liu, Ph.D., Biostatistics, "Outcome-Guided Disease Subtyping and Power Calculation for High-Dimensional Omics Studies".
2021-22	Laura Stackhouse, M.S., Human Genetics, "*CREBRF* Missense Variant rs373863828 and Relative Grip Strength".
2022	Devin Dikec, M.S. Human Genetics – Genome Bioinformatics, "Inclusion of custom markers does not improve genotype imputation accuracy in a population isolate".
2022	Elizabeth A. Chiyka, M.S. Human Genetics – Genome Bioinformatics, "Evidence of genotype imputation differences when phasing population isolate participants with a cosmopolitan haplotype reference panel".
2022	Kevin Anderson, M.S. Human Genetics – Genome Bioinformatics, "Inclusion of 48 Pacific Islanders within a cosmopolitan reference panel is sufficient for high accuracy genotype imputation of Samoans".
2021-22	Kaitlin Kirkpatrick Heimke, M.P.H. Public Health Genetics, "Association Between BDNF DNA Methylation and Depression and Anxiety in Postmenopausal Individuals with Breast Cancer".
2022	Jordan A. Driscoll, M.S. Human Genetics – Genome Bioinformatics, "Comparison of Genome-Wide Association Study Approaches: Meta-Analysis vs Mega-Analysis".
2022	Kaylea M. Flick, M.P.H. Public Health Genetics, "Conjunctival Melanoma from an Epigenetic Perspective".
2022-23	Amanda Koloskee, M.S. Human Genetics, "Effect of Exercise on DNA Methylation Age Acceleration in Breast Cancer Patients Undergoing Aromatase Inhibitor Therapy".
2023	Jaime Wehr, M.S. Human Genetics – Genome Bioinformatics, "Genome-wide Association Studies of Type 2 Diabetes in Samoan Adults".
2023	Joshua Witten, M.S. Human Genetics – Genome Bioinformatics, "Comparison of genotype imputation on chromosome 5 in a population isolate using haplotypes phased with and without TOPMed genotypes".
2023-24	Yidi Qin, Ph.D. Human Genetics, “Deriving Biological Meaning and Clinical Application for Pediatric Sepsis with Data-driven Analysis”
2024-25	Wenjia Wang, Ph.D. Biostatistics and Health Data Science, “Computing and Modeling Issues in Omics Data Analysis”.

Graduate students

1994	Deborah L. Brown, M.S., Human Genetics, "Strategies for genomic searching using the affected pedigree member method of linkage analysis".
1997	Sean Davis, Ph.D., Human Genetics, "Nonparametric Statistics in Linkage Analysis".
2004	Hui-Ju Tsai, Ph.D., Human Genetics, "Comparison of methods incorporating covariates into affected sib pair linkage analysis".
2004	Feng Dai, M.S., Biostatistics, "Imprinting in variance components-based linkage analysis".
2007	Amrita Ray, Ph.D., Human Genetics, "Affected relative pair linkage statistics that model relationship uncertainty"
2007	Feng Dai, Ph.D., Biostatistics, "Variance components models in statistical genetics: extensions and applications".
2009	Johanna Jakobsdottir, Ph.D., Biostatistics, "Genetics of age-related maculopathy & score statistics for X-linked quantitative trait loci".
2015	Jia Jia, Ph.D., Biostatistics, "Association analysis between binary traits and common or rare genetic variants on family-based data".
2015	Yingda Jiang, Ph.D., Biostatistics, "Gene-based association testing of dichotomous traits using generalized functional linear mixed models for family data".
2016	Ying Shan, Ph.D., Biostatistics, "Statistical methods for genetic risk confidence intervals, Bayesian disease risk prediction, and estimating mutation screening saturation".
2018	Yunqi Li, M.S., Human Genetics, "Epigenome-wide association study of recovery outcomes of traumatic brain injury patients", co-supervised with Dr. John R. Shaffer.
2018	Richard J. Biedrzycki, M.S., Human Genetics, "Genome-wide association studies, false positives, and how we interpret them".
2018	Winston W. H. Eng, M.S., Biostatistics, "Exploring the genetic characteristics underlying a multidimensional latent chemotherapy symptom burden".
2019	Annie Arockiaraj, M.S., Human Genetics, "Epigenome-wide association studies in aneurysmal subarachnoid hemorrhage patients", co-supervised with Dr. John R. Shaffer.
2020	Chen'Ao Qian, M.S., Biostatistics, "Genome-wide association studies in Samoans give insight into obesity by investigating skinfold thickness".
2020-	Shuwei Liu, Ph.D., Human Genetics
2021-22	Laura Stackhouse, M.S. Human Genetics, "*CREBRF* Missense Variant rs373863828 and Relative Grip Strength".
2021-22	Kaitlin Kirkpatrick Heimke, M.P.H. Public Health Genetics, "Association Between BDNF DNA Methylation and Depression and Anxiety in Postmenopausal Individuals with Breast Cancer", co-mentored with Dr. Lacey W. Heinsberg.
2022-23	Amanda Koloskee, M.S. Human Genetics, "Effect of Exercise on DNA Methylation Age Acceleration in Breast Cancer Patients Undergoing Aromatase Inhibitor Therapy".

Post-doctoral Fellows

1992-1994	Dr. Tara Cox Matise
1994-1995	Dr. Alan Young
1995	Dr. William Shannon
1999-2003	Dr. Kyunghee Song
1999-2004	Dr. Haydar Sengul
2004-2006	Dr. Jeesun Jung
2006-2008	Dr. Karolina Åberg
2010-2012	Dr. Ryan Minster
2017-2018	Dr. Jenna C. Carlson, co-supervised with Dr. Ryan Minster.
2019-2022	Dr. Mohanraj Krishnan, co-supervised with Dr. Ryan Minster.

2020-2024	Dr. Lacey W. Heinsberg
2025-	Dr. Amit K. Srivastava, co-supervised with Dr. Jenna Carlson.

Mentoring

Summer 2000	Co-mentored a summer medical student, Kristen DiGirolamo, with Dr. David Finegold. She worked on the genetics of normal height.
1996-2000	Mentored Jeffrey O'Connell, who obtained his D.Phil. from the University of Oxford in July 2000.
2000-2006	Co-mentored Krina Zondervan, an MRC Training Fellow in Bioinformatics at the University of Oxford.
2001	Co-mentored Lai Sze Lee, a Biostatistics Ph.D. student from Carnegie Mellon University who did her applied data analysis project on Dr. Gorin's age-related macular degeneration data.
2002-2007	Feng Dai, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2003-2007	Amrita Ray, a Human Genetics Ph.D. student from the University of Pittsburgh.
2004-2009	Johanna Jakobsdottir, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2007-2008	Sajjad Ahmad Khan, a pre-doctoral visiting student from the University of Peshawar, Pakistan, supported by a scholarship from the Higher Education Commission of Pakistan.
2007-2008	Ferdouse Begum, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2007-2009	Xinyu Tang, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2009-2010	Chia-Ling Kuo, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2010-2011	Umut Ozbek, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision. Helped co-mentor through 2013.
2011-2015	Jia Jia, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2011-2015	Yingda Jiang, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2012-2014	Olive Buhule, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2012-2016	Ying Shan, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2014-2015	Jerome Lin, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher half-time under my supervision.
2015-2019	Annie Arockiaraj, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my co-supervision.
2016-2018	Co-supervised Yunqi Li, a Human Genetics M.S. student from the University of Pittsburgh.
2016-2018	Winston Eng, a Biostatistics M.S student from the University of Pittsburgh, worked as an hourly researcher under my supervision.
2016-2019	Secondary mentor for Emily Russell, a Human Genetics Ph.D. student from the University of Pittsburgh.
2017-2018	Supervised Rich Biedrzycki, a Human Genetics M.S. student from the University of Pittsburgh.
Fall 2018	Adam Kruchten, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2018-2020	Haoyi Fu, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2018-2020	Jerry Zhang, a Biostatistics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2018-2020	Dongjing Liu, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my co-supervision.
2018-2022	Co-mentor of Qi Yan on his K01 research project "Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma".

2020	Supervised Chen'Ao Qian, a Biostatistics M.S. student from the University of Pittsburgh.
2020-	Shuwei Liu, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2021-2022	Mentored Laura Stackhouse, a Human Genetics M.S. student from the University of Pittsburgh on her thesis project.
2021-2022	Co-mentored Kaitlin Kirkpatrick Heimke, an M.P.H. Public Health Genetics student from the University of Pittsburgh on her M.P.H. essay project.
2021-2022	Mentored Joshua Witten, a Human Genetics M.S. in Genome Bioinformatics from the University of Pittsburgh.
2022-2023	Mentored Amanda Koloskee, a Human Genetics M.S. student from the University of Pittsburgh on her thesis project.
2022-2023	Mentored Dylan Maher, a Human Genetics Ph.D. student from the University of Pittsburgh on two research projects.
2025-	Mentored Ishta Madan, a Biostatistics and Health Data Sciences M.S. student from the University of Pittsburgh.

Scientific Writing (HUGEN 2011) mentoring

Fall 2020	Ellyn Dunbar
Fall 2021	Kaitlin Kirkpatrick Heimke
Fall 2021	Laura Stackhouse
Fall 2022	Amanda Koloskee
Fall 2022	Shuwei Liu
Fall 2022	Elynna Youm

Scholarly Oversight Committee Service

2016-2018	Dr. Erick Forno
2019-2020	Dr. Erica Stevens
2019-2021	Dr. Soyeon Kim
2023	Dr. Soyeon Kim

K99/R00 Postdoctoral Scholar/Early Faculty mentoring

2022-	Dr. Mitali Ray
2024-	Dr. Carolyn Harris
2024-	Dr. Lacey Heinsberg

Service on Faculty Mentoring Committee

2023-	Dr. Jenna C. Carlson

Presentations:

Effect of family size on power of linkage analysis, at the Ataxia-Telangiectasia Workshop. February 1987.

The affected-pedigree-member method of linkage analysis, at the 38th Annual Meeting of the American Society of Human Genetics. October 1987.

The Affected-Pedigree-Member Method of Linkage Analysis, at:

Columbia University.	June 1988.	Medical College of Virginia.	December 1987.
Duke University.	March 1989.	Collaborative Research, MA.	March 1988.
CEPH, Paris	June 1989.	Johns Hopkins.	May 1988.
University of Michigan	November 1992.	Boston University.	June 1988.

Heterozygote identification in an Amish pedigree with ataxia-telangiectasia, at the Ataxia-Telangiectasia Workshop. May 1989.

Preliminary ranking procedures for multilocus ordering based on radiation hybrid data, at the Genetic Analysis Workshop, October 1990.

A multilocus extension of the affected-pedigree-member method of linkage analysis, invited speaker at the Interface '91 conference, April 1991.

Using the affected pedigree member method of linkage analysis, invited speaker at the INSERM Atelier 44, Le Vesinet, France, March 1992.

Genomic searching using the affected pedigree member method of linkage analysis, invited speaker at the Biometric Society ENAR spring meeting, March 1993.

Mapping complex traits with the affected pedigree member method, invited speaker at the Joint Statistical Meetings of the American Statistical Association, the Biometric Society, and the Institute of Mathematical Statistics, August 1993.

Strategies for mapping complex traits with the affected pedigree member method, Rockefeller University, January 1995.

Haplotyping algorithms, invited speaker at a meeting entitled "Mathematical foundations and practical solutions in human linkage analysis", Galton Laboratory, University College London, March 1995.

Computer programs for multilocus haplotyping of general pedigrees, invited speaker at Guy's Hospital, London, November 1995.

Nonparametric simulation-based statistics for detecting linkage in general pedigrees, invited speaker at the European Union meeting on Genetic Mapping of Disease Genes, University of Oxford, December 1995.

Nonparametric simulation-based statistics for detecting linkage in general pedigrees, invited speaker at the 5th Rheumatoid Arthritis Genetics Workshop, University of Manchester, United Kingdom, March 1996.

Advances in statistical methods for linkage analysis, invited speaker at the International Symposium on Theoretical and Computational Genome Research, Heidelberg, Germany, March 1996.

From genetic linkage to gene identification, MRC Workshop on Behavioral Genetics, London, November 1996.

Nonparametric statistics for detecting linkage in general pedigrees, invited speaker at the Departement de Genetique et Microbiologies, Geneva, Switzerland, March 1998.

Nonparametric simulation-based statistics for detecting linkage in general pedigrees, invited speaker, The Jackson Laboratory, January 1997.

Parametric vs. non-parametric methods for linkage analysis, invited speaker, National Cancer Institute Gene Discovery Workshop, Fred Hutchinson Cancer Research Center, Seattle, Washington, May 1998.

Nonparametric simulation-based statistics for detecting linkage in general pedigrees, invited speaker, Fred Hutchinson Cancer Research Center, Seattle, Washington, May 1998.

Mapping complex traits with non-parametric linkage analysis, invited speaker, Memorial Sloan-Kettering Cancer Center, New York, November 1998.

Linkage analysis of complex traits, invited speaker, University of Michigan, Ann Arbor, Michigan, November 1998.

"Monte Carlo Markov Chain Linkage Analysis" and "Simulation-based allele-sharing methods for general pedigrees", invited speaker. Boden Conference, Thredbo, Australia, February 1999.

Linkage analysis of complex traits, invited speaker, Department of Biological Sciences, Binghamton University, Binghamton, New York, May 1999.

The Morton Number, invited speaker, Genetic dissection of complex traits: challenges for the next millennium, a symposium in honor of Newton E. Morton, St. Louis, Missouri, September 1999.

A robust integrated system for mapping complex diseases, invited speaker, Statistical Genetics Initiative Workshop, sponsored by the National Institutes of Health. Half Moon Bay, California, October 1999.

The complexity of linkage analysis with neural networks, invited speaker, Department of Biostatistics, University of Pittsburgh, February 2000.

Linkage analysis in human genetics, invited speaker, Bioinformatics@Pitt, Distinguished Lecture Series in Bioinformatics, University of Pittsburgh, January 2001.

Genome-wide scan for loci affecting adult height in the Framingham Study, Departmental Seminar, Department of Human Genetics, November 2001.

Linkage mapping of complex human disease, invited speaker, Spotlight Session on Genetic Linkage and Genomic Evolution, Science2002 conference, University of Pittsburgh, September 2002.

Comparison of methods incorporating covariates into affected sib pair linkage analysis, invited speaker, Human Genetics Department, Emory University School of Medicine, March 2004.

Statistical challenges in genetics and genomics, Paris Workshop on Molecular and Statistical Genomic Epidemiology, Paris, France, May 2005.

Statistical challenges: covariates, heterogeneity, and affected sib pair linkage analysis, invited speaker, Computational Genetics: a perspective - Celebrating the scientific contributions of Kenneth Lange, UCLA, Los Angeles, February 2007.
Survey of statistical issues – Is linkage dead?, Second Paris Workshop on Molecular and Statistical Genomic Epidemiology, Paris, France, May 2007.
Linkage statistics that model relationship uncertainty, invited speaker, 'Statistical methods for High-throughput Genetic Data' Workshop at The Banff International Research Station for Mathematical Innovation and Discovery, June 24 – 29, 2007.
Associated genetic variants and personalized medicine, invited speaker, 'Illuminating the Genetic Architecture of Common Eye Disease' Conference, Avalon, CA, February 3-7, 2009.
Associated genetic variants and personalized medicine, invited speaker, The Third Paris Workshop on Genomic Epidemiology, Paris, France, March 25-27, 2009.
Associated genetic variants and personalized medicine, invited speaker, 'Analysis of human genetic data: A celebration of Jurg Ott's work in honor of his 70th birthday', Rockefeller University, New York, NY, June 4, 2009.
Interpretation of genetic association studies: markers with replicated highly significant odds ratios may be poor classifiers, invited speaker, International Genetic Epidemiology Society: 'The next frontier: advancing from genetic risk to functionality and testing', 59th Annual Meeting of the American Society of Human Genetics, Honolulu, HI, October 22, 2009 (Johanna Jakobsdottir and I both spoke).
Genetic variants and personalized medicine, invited speaker, Vanderbilt University, Nashville, TN, January 28, 2010.
Genetic variants and personalized medicine, invited speaker, Yale University, New Haven, CT, April 13, 2010.
Genetic variants and personalized medicine, Brown University, April 14, 2010.
Genetic variants and personalized medicine, invited speaker, The Seventh Annual C.C. Li Memorial Lecture, University of Pittsburgh, Pittsburgh, PA, April 23, 2010.
Genetic variants and personalized medicine, invited speaker, The Fourth Paris Workshop on Genetic Epidemiology, Paris, France, June 1, 2011.
Genetic variants and personalized medicine, invited speaker, Kyoto Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, January 19, 2013.
Genetic variants and personalized medicine, invited speaker, National Yang-Ming University, Taipei, Taiwan, January 24, 2013.
Genetic variants and personalized medicine, invited speaker, National Health Research Institutes, Zhunan, Taiwan, January 25, 2013.
Personalized genetic risks: Confidence is key, invited speaker, The Second Kyoto Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, Kyoto, Japan, March 13, 2014.
Gene-based association testing using functional linear models, invited speaker, The Third Kyoto Symposium on Bioinformatics for Next Generation Sequencing with Applications in Human Genetics, Kyoto, Japan, March 19, 2015.
A thrifty variant in *CREBRF* strongly influences body mass index in Samoans, trainee-selected invited speaker, The Cleveland Clinic, January 23, 2017.
Spinning Convincing Stories for Association Signals - All That Glitters is Not Gold, Human Genetics Seminar, University of Pittsburgh, November 22, 2019.
Spinning Convincing Stories for Association Signals - All That Glitters is Not Gold, Invited Seminar (virtual), Genetics & Epidemiology Seminar Series 2022, Division of Genetics and Epidemiology, The Institute of Cancer Research, London, United Kingdom, March 10, 2022.

Teaching and Mentoring Professional Development

2017 Attended the Detecting Plagiarism Workshop, part of the Professional Development Workshop series, February 2, 2017.
2018 Attended the Encouraging Student Participation Workshop, led by the University of Pittsburgh Center for Teaching and Learning, June 8, 2018.
2018 Attended a Faculty Mentor Training Workshop, August 7, 2018.
2019 Attended the Evidence-Based Teaching Practices Workshop on "What factors motivate students to learn?", March 13, 2019.

2019 Attended the Evidence-Based Teaching Practices Workshop on "What kinds of practice and feedback enhance learning", April 10, 2019.
2019 Attended the Evidence-Based Teaching Practices Workshop on "Applying principles of learning to ourselves", May 22, 2019.
2020 Attended the Better Grading and Feedback with Gradescope Workshop, Feb 11, 2020.
2021 Attended four Institute for Clinical Research Education Mentor Training Workshops, October 15, 2020; October 29, 2020; November 12, 2020; December 10, 2020
2022 Attended lecture about Specification Grading at the Spring 2022 Pitt Public Health meeting, June 21, 2022.
2023 Attended The Top Five Canvas Integrations for Course Innovation Teaching Workshop, January 3, 2023.
2023 Attended an Anti-Racist Pedagogy Workshop, February 22, 2023.
2024 Attended the Planning Effective and Inclusive Class Discussions Workshop, April 4, 2024

Advancement of Diversity, Equity, and Inclusion
2020 Attended the school-wide Social Justice Action Committee Town Hall meeting, October 8, 2020.
2021 Participated in three journal club discussions of the book 'Reproductive Injustice. Racism, Pregnancy, and Premature Birth' by Dána-Ain Davis (2019) New York University Press.
2021 Attended workshop on "Preventing Sexual Misconduct: Understanding Your Responsibility", offered by the University of Pittsburgh's Faculty & Staff Development Program, November 4, 2021.
2021 Attended a workshop on "Intercultural Competency", offered by the University of Pittsburgh's Faculty & Staff Development Program, December 9, 2021.
2022 Attended a workshop on "Individuals with Disabilities: Creating an Accommodating and Inclusive Environment", offered by the University of Pittsburgh's Faculty & Staff Development Program, June 8, 2022.
2022 Attended a workshop on "Workplace Bullying: Understanding a Barrier to Equal Opportunity", offered by the University of Pittsburgh's Faculty & Staff Development Program, June 9, 2022.
2022 Attended a workshop on "Creating Equal Access: Getting Started with Digital Accessibility", offered by the University of Pittsburgh's Faculty & Staff Development Program, October 26, 2022.
2023 Attended a workshop on "Fostering a Diverse and Inclusive Workplace", offered by the University of Pittsburgh's Faculty & Staff Development Program, May 10, 2022.
2023 Attended the "Diversity & Inclusion Certificate Program Capstone"", offered by the University of Pittsburgh's Faculty & Staff Development Program, June 27, 2023.
2023 Completed the Diversity and Inclusion Certificate Program organized by the Office of Equity, Diversity, and Inclusion, June 27, 2023.

Publications
†*Graduate student*; ‡*Post-doctoral trainee*.

Refereed Articles:
1. Caswell H, DE Weeks (1986) Two-sex models: chaos, extinction, and other dynamic consequences of sex. The American Naturalist **128**:707-735

2. Gatti RA, RC Davis, DE Weeks, NJG Jaspers, RS Sparkes, K Lange (1987) Genetic linkage studies of ataxia-telangiectasia: Phenotypic blood markers. Disease Markers **5**:207-213

3. Weeks DE, K Lange (1987) Preliminary ranking procedures for multilocus ordering. Genomics **1**:236-242

4. Gatti RA, I Berkel, E Boder, G Braedt, P Charmley, P Concannon, F Ersoy, T Foroud, N Jaspers, K Lange, G Lathrop, M Leppert, Y Nakamura, P O'Connell, M Paterson, W Salser, O Sanal, J Silver, R Sparkes, E Susi, D Weeks, S Wei, R White, F Yoder (1988) Localization of an ataxia-telangiectasia gene to chromosome 11q22-23. Nature **336**:577-580

5. Weeks DE, K Lange (1988) The affected-pedigree-member method of linkage analysis. Am J Hum Genet **42**:315-326

6. Goldstein AM, DE Weeks, V Cortessis, RW Haile (1989) Comparison of the affected-pedigree-member and lod score methods. In: Multipoint Mapping and Linkage Based Upon Affected Pedigree Members: Genetic Analysis Workshop 6 (Elston RC et al., Eds). New York: Alan R. Liss, pp. 135-140

7. Lange K, DE Weeks (1989) Efficient computation of lod scores: Genotype elimination, genotype redefinition, and hybrid maximum likelihood algorithms. Ann Human Genet **53**:67-83

8. Weeks DE, K Lange (1989) Trials, tribulations, and triumphs of the EM algorithm in pedigree analysis. IMA J Math Appl Med Biol **6**:209-232

9. Charmley P, T Foroud, S Wei, P Concannon, DE Weeks, K Lange, RA Gatti (1990) A primary linkage map of the human chromosome 11q22-23 region. Genomics **6:**316-323

10. Haile RW, AM Goldstein, DE Weeks, RS Sparkes, A Paganini-Hill (1990) Genetic epidemiology of bilateral breast cancer: A linkage analysis using the affected-pedigree-member method. Genet Epidemiol **7:**47-55

11. Lange K, DE Weeks (1990) Linkage methods for identifying genetic risk factors. World Rev Nutr Diet **63**:236-249

12. Smith M, S Smalley, R Cantor, M Pandolfo, MI Gomez, R Baumann, P Flodman, K Yoshiyama, Y Nakamura, C Julier, K Dumars, J Haines, J Trofatter, MA Spence, D Weeks, M Conneally (1990) Mapping of a gene determining tuberous sclerosis to human chromosome 11q14-11q23. Genomics **6:**105-114

13. Weeks DE, L Brzustowicz, E Squires-Wheeler, B Cornblatt, T Lehner, M Stefanovich, TC Gilliam, J Ott, L Erlenmeyer-Kimling (1990) Report of a workshop on genetic linkage studies in schizophrenia. Schiz Bull **16**:673-686

14. Weeks DE, T Lehner, E Squires-Wheeler, C Kaufmann, J Ott (1990) Measuring the inflation of the lod score due to its maximization over model parameter values in human linkage analysis. Genet Epidemiol **7**:237-243

15. Wilhelmsen KC, DE Weeks, TG Nygaard, CB Moskowitz, RL Rosales, DC dela Paz, EE Sobrevega, S Fahn, TC Gilliam (1991) Genetic mapping of "Lubag" (X-linked dystonia-parkinsonism) in a Filipino kindred to the pericentromeric region of the X chromosome. Ann Neurol **29**:124-131

16. Weeks DE, Paterson MC, Lange K, Andrais B, Davis RC, Yoder F, Gatti RA (1991) Assessment of chronic γ radiosensitivity as an *in vitro* assay for heterozygote identification of ataxia-telangiectasia. Radiat Res **128**:90-99

17. Weeks DE, Lange K (1992) A multilocus extension of the affected-pedigree-member method of linkage analysis. Am J Hum Genet **50**:859-868

18. Weeks DE, Lehner T, Ott J (1992) Preliminary ranking procedures for multilocus ordering based on radiation hybrid data. Cytogenet Cell Genet **59**:125-127

19. Angrist M, Kauffman E, Slaugenhaupt SA, Matise TC‡, Puffenberger EG, Washington SS, Lipson A, Cass DT, Reyna T, Weeks DE, Sieber W, Chakravarti A (1993) A gene for Hirschsprung disease (megacolon) in the pericentromeric region of human chromosome 10. Nature Genetics **4**:351-356

20. Goldin LR, Weeks DE (1993) Two-locus models of disease: comparison of likelihood and non-parametric linkage methods. Am J Hum Genet **53**:908-915.

21. Li CC, Weeks DE, Chakravarti A (1993) Similarity of DNA fingerprints due to chance and relatedness. Hum Hered **43**:45-52

22. Matise TC‡, Weeks DE (1993) Detecting heterogeneity with the affected-pedigree-member (APM) method. Genet Epidemiol **10**:401-406

23. Nygaard TG, Wilhelmsen KC, Risch NJ, Brown DL†, Trugman JM, Gilliam TC, Fahn S, Weeks DE (1993) Linkage mapping of dopa-responsive dystonia (DRD) to chromosome 14q. Nature Genetics **5**:386-391

24. Weeks DE, Lathrop GM, Ott J (1993) Multipoint mapping under genetic interference. Hum Hered **43**:86-97

25. Berrettini WH, Ferraro TN, Goldin LR, Weeks DE, Detera-Wadleigh S, Nurnberger JI, Gershon ES (1994) Chromosome 18 DNA markers and manic-depressive illness: evidence for a susceptibility gene. Proc Natl Acad Sci USA **91:**5918-5921

26. Brown DL†, Gorin MB, Weeks DE (1994) Efficient strategies for genomic searching using the affected-pedigree-member method of linkage analysis. Am J Hum Genet **54**:544-552

27. Matise TC‡, Chakravarti A, Patel PI, Lupski JR, Nelis E, Timmerman V, Van Broeckhoven C, Weeks DE (1994) Detection of tandem duplications and implications for linkage analysis. Am J Hum Genet **54**:1110-1121

28. Schroeder M, Brown DL†, Weeks DE (1994) Improved programs for the affected-pedigree-member method of linkage analysis. Genet Epidemiol **11**:69-74

29. Weeks DE, Ott J, Lathrop GM (1994) Detection of genetic interference: simulation studies and mouse data. Genetics **136**:1217-1226

30. Kramer RW, Weeks DE, Chiarulli DM (1995) An incremental algorithm for efficient multipoint linkage analysis. Hum Hered **45**:323-336

31. Matise TC‡, Schroeder MD, Chiarulli DM, Weeks DE (1995) Parallel computation of genetic likelihoods using CRI-MAP, PVM, and a network of distributed workstations. Hum Hered **45**:103-116

32. O'Connell JR, Weeks DE (1995) The VITESSE algorithm for rapid exact multilocus linkage analysis via genotype set-recoding and fuzzy inheritance. Nat Genet **11**:402-408

33. Tanaka H, Endo K, Tsuji S, Nygaard TG, Weeks DE, Nomura Y, Segawa M (1995) The gene for hereditary progressive dystonia with marked diurnal fluctuation (HPD) maps to chromosome 14q. Ann Neurol **37**:405-408

34. Weeks DE, Harby LD† (1995) The affected-pedigree-member method: power to detect linkage. Hum Hered **45**:13-24

35. Weeks DE, Lathrop GM (1995) Polygenic disease: Methods for mapping complex disease traits. Trends Genet **11**:513-519

36. Weeks DE, Nygaard TG, Neystat M, Harby LD, Wilhelmsen KC (1995) A high resolution genetic linkage map of the pericentromeric region of the human X chromosome. Genomics **26**:39-46

37. Weeks DE, Valappil TI, Schroeder M, Brown DL† (1995) An X-linked version of the affected-pedigree-member method of linkage analysis. Hum Hered **45**:25-33

38. Weeks DE, Young A‡, Li CC (1995) DNA profile match probabilities in a subdivided population: When can subdivision be ignored? Proc Natl Acad Sci USA **92**:12031-12035

39. Davis S†, Schroeder M, Goldin LR, Weeks DE (1996) Nonparametric simulation-based statistics for detecting linkage in general pedigrees. Am J Hum Genet **58**:867-880

40. Hall FC, Weeks DE, Camilleri J, Williams LA, Amos N, Darke C, Gibson K, Pile K, Wordsworth BP, Jessop JD (1996) The influence of the HLA-DRB1 locus on susceptibility and severity in rheumatoid arthritis. QJM - Monthly J Assoc Phys **89**:821-829

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1. Heath SC, Weeks DE (2016) Lack of convincing statistical evidence of the involvement of Nuclear Receptor NR1H3 in Familial Multiple Sclerosis. https://www.cell.com/neuron/comments/S0896-6273(16)30126-X

Software:
†*Graduate student*; ‡*Post-doctoral trainee*.

I have written or helped develop many software packages during my career. Several of these (SLINK, Mega2, VITESSE, PedCheck, SimWalk2) were widely used by the international research community. Biotech companies have, in the past, purchased commercial licenses to use PedCheck and Mega2.

dGene: A dBASE database for storing and managing linkage analysis data. Programmed by Daniel Weeks.
Lange K, Weeks D, Boehnke M (1988) Programs for pedigree analysis: MENDEL, FISHER, and dGENE. Genet Epidemiol **5**:471-472

APM: Implements the non-parametric affected pedigree member method of linkage analysis. Programmed by Daniel Weeks.
Weeks DE, Lange K (1988) The affected-pedigree-member method of linkage analysis. Am J Hum Genet **42**:315-326

recode: Conversion utility for recoding marker data recorded in base-pair sizes into LINKAGE format data. Programmed by Daniel Weeks.

pedprep: Converts MENDEL-format files into PedDraw format, for drawing pedigrees using PedDraw. Programmed by Daniel Weeks.

map: Converts multipoint linkage output from the LINKAGE programs into proper multipoint lod score curves. Programmed by Daniel Weeks.

LinkMend: Converts LINKAGE-format files into MENDEL-format files. Programmed by Daniel Weeks.

SLINK, FastSLINK: Simulates linkage data conditional on specified phenotypes. Primary programmer of SLINK: Daniel Weeks.
Weeks DE, Ott J, Lathrop GM (1990) SLINK: a general simulation program for linkage analysis. Am J Hum Genet **47**:A204

cintmax: A program for computing multipoint likelihoods under various models of interference. Programmed by Daniel Weeks.
Weeks DE, Lathrop GM, Ott J (1993) Multipoint mapping under genetic interference. Hum Hered **43**:86-97

pedi: Efficient incremental multipoint lod score computations.
Kramer RW, Weeks DE, Chiarulli DM (1995) An incremental algorithm for efficient multipoint linkage analysis. Hum Hered **45**:323-336

haplo, simcross: Programs for haplotyping marker data on pedigrees. Programmed by Daniel Weeks.
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crimap-pvm: Allows for parallel computation of likelihoods on pedigrees for rapid map construction.
Matise TC‡, Schroeder MD, Chiarulli DM, Weeks DE (1995) Parallel computation of genetic likelihoods using CRI-MAP, PVM, and a network of distributed workstations. Human Hered **45**:103-116

VITESSE: A program for rapid likelihood computations on general pedigrees.
O'Connell JR, Weeks DE (1995) The VITESSE algorithm for rapid exact multilocus linkage analysis via genotype set-recoding and fuzzy inheritance. Nat Genet **11**:402-408

SimWalk2: Carries out haplotype, parametric linkage, non-parametric linkage, identity by descent and mistyping analyses on any size of pedigree using Markov chain Monte Carlo (MCMC) and simulated annealing algorithms.
Sobel E, Lange K, O'Connell JR, Weeks DE (1995) Haplotyping algorithms. In: Speed TP, Waterman MS (eds) Genetic mapping and DNA sequencing: IMA Volumes in Mathematics and its Applications. Springer-Verlag, New York

SimIBD: Implements our simulation-based affected relative pair method of linkage analysis for general pedigrees.
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PedCheck: Detects Mendelian inconsistencies in marker data on pedigrees.
O'Connell JR, Weeks DE (1998) PedCheck: A program for identifying genotype incompatibilities in linkage analysis. Am J Hum Genet **63**:259-66

Mega2: A data-handling program for facilitating genetic linkage and association analyses.
Mukhopadhyay N, Almasy L, Schroeder M, Mulvihill WP, Weeks DE (2005) Mega2: data-handling for facilitating genetic linkage and association analyses. Bioinformatics **21**:2556-2557
Baron RV, Kollar C, Mukhopadhyay N, Weeks DE (2014) Mega2: validated data-reformatting for linkage and association analyses. Source Code Biol Med **9**:26. PMC4269913

nplplot: Plotting Linkage and Association Results. DOI: https://doi.org/10.32614/CRAN.package.nplplot
Authors: Robert V. Baron, Nandita Mukhopadhyay, Xinyu Tang†, Daniel E. Weeks

QTL-ALL: software for QTL linkage analysis using score statistics.
Bhattacharjee S, Kuo CL, Mukhopadhyay N, Brock GN, Weeks DE, Feingold E (2008) Robust score statistics for QTL linkage analysis. Am J Hum Genet **82**:567-582.

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Genetic ME: a visualization application for merging and editing pedigrees.
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powerpkg: Power Analyses for the Affected Sib Pair and the TDT Design. DOI:
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Mega2R: an R package for loading and manipulating data frames containing genotype, phenotype, and family information from an SQLite database created by Mega2. DOI: https://doi.org/10.32614/CRAN.package.Mega2R
Baron RV, Stickel JR, Weeks DE (2018) The Mega2R package: R tools for accessing and processing genetic data in common formats. F1000Res **7**:1352. PMCID: PMC6137409.2

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dbGaPCheckup: an R package which implements a series of check, awareness, reporting, and utility functions to support data integrity and proper formatting of the subject phenotype data set and data dictionary prior to dbGaP submission. DOI: https://doi.org/10.32614/CRAN.package.dbGaPCheckup

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81. Mukhopadhyay N, Reck BH, Weeks DE (2005) Simulation study of empirical NULL distribution of LODPAL's LOD scores. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah

82. Ray A†, Weeks DE (2005) A linkage analysis test statistic which models relationship uncertainty. Genet Epidemiol **29**:275

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84. Sanghera DK, Bhatti JS, Bhatti GK, Ralhan SK, Wander GS, Singh JR, Bunker CH, Weeks DE, Kamboh MI, Ferrell RE (2005) The Khatri Sikh Diabetes Study (SDS): Study Design, Methodology, Sample Collection and Initial Results. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah

85. Zondervan KT, Lin J, Dawson G, Zabaneh D, Smith V, Bennett S, Lambert A, Carey A, Weeks DE, Treloar SA, Montgomery GW, Nyholt DR, Martin NG, Cardon LR, MacKay I, Mangion J, Kennedy SH (2005) First evidence that one or more rare genetic polymorphisms with high penetrance may be involved in the aetiology of endometriosis. Genet Epidemiol **29**:292

86. Zondervan KT, Lin J, Dawson G, Zabaneh D, Smith V, Bennett ST, Lambert A, Carey A, Weeks DE, Treloar SA, Montgomery GW, Nyholt DR, Martin NG, Cardon LR, Mackay IJ, Mangion J, Kennedy SH (2005) First evidence that one or more rare genetic polymorphisms with high penetrance may be involved in the etiology of endometriosis. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah

87. Gorin MB, Jakobsdottir J†, Conley YP, Weeks DE, Mah TS, Ferrell RE (2006) Replication of association of CFH, PLEKHA1/LOC387715 and ELOVL4 genes with ARM in the AREDS cohort. Paper presented at the annual meeting of the Association for Research in Vision and Ophthalmology (ARVO). Fort Lauderdale, Florida

88. Åberg K‡, Dai F†, Keighley ED, Sun G, Smelser D, Viali S, Tuitele J, Indugula SR, Zhang Q, Deka R, Weeks DE, McGarvey ST (2006) Promising susceptibility loci for lipid levels in blood serum detected in extended pedigrees from Samoa. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

89. Bhattacharjee S, Kuo C, Mukhopadhyay N, Weeks DE, Feingold E (2006) A comparison of robust methods for QTL mapping in nuclear families. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

90. Conley Y, Jakobsdottir J†, Mah T, Weeks D, Ferrell R, Gorin M (2006) CFH and LOC387715 genes and susceptibility to Age-Related Maculopathay: AREDS cohort and a meta-analysis. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

91. He C, Kong X, Buyske S, Weeks DE, Matise TC (2006) Enhanced linkage maps from family-based genetics studies. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

92. Mukhopadhyay N, Bhattacharjee S, Kuo C-L, Weeks DE, Feingold E (2006) QTL-ALL: software for QTL linkage analysis using score statistics and other new approaches. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

93. Smelser DT, Sun G, Kaushal R, Pal P, Viali S, Tufa J, Chakraborty R, Weeks DE, McGarvey ST, Deka R (2006) Association testing of candidate genes in the anabolic neuropeptide pathway with obesity among the Samoans of Polynesia. Paper presented at the annual meeting of The American Society of Human Genetics. New Orleans, Louisiana

94. Åberg K‡, Sun G, Indugula SR, Smelser D, Zhang Q, Deka R, Weeks DE, McGarvey ST (2007) Susceptibility loci for blood pressure detected in adults from the Samoan islands. Paper presented at the annual meeting of The American Society of Human Genetics. San Diego, California.

95. Bhattacharjee S, Kuo C, Mukhopadhyay N, Brock GN, Weeks DE, Feingold E (2007) Robust methods for QTL linkage analysis in nuclear families. Paper presented at the annual meeting of The American Society of Human Genetics. San Diego, California.

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100. Ray A†, Weeks DE (2007) Further exploration of linkage statistics that model relationship uncertainty. Genet Epidemiol **31**:495. Presented at the 2006 annual meeting of the International Genetic Epidemiology Society. St. Petersburg, Florida.

101. Mukhopadhyay I‡, Feingold E, Weeks DE (2007) Estimation of trait parameters in human QTL mapping under different ascertainment schemes. Genet Epidemiol **31**:639. Presented at the 2007 annual meeting of the International Genetic Epidemiology Society. York, England.

102. Thalamuthu A‡, Weeks DE (2007) Gene based association tests using inferred haplotypes for case-control samples. Genet Epidemiol **31**:646-647. Presented at the 2007 annual meeting of the International Genetic Epidemiology Society. York, England.

103. Åberg K‡, Dai F†, Sun G, Keighley ED, Indugula SR, Roberts ST, Zhang Q, Smelser D, Viali S, Tuitele J, Jin L, Deka R, Weeks DE, McGarvey ST (2008) Susceptibility loci for adiposity-related phenotypes in a combined adult study sample from American Samoa and Samoa. Paper presented at the Society for the Study of Human Biology 50th Anniversary Symposium. Oxford, England, April 2008.

104. Jakobsdottir J†, Gorin MB, Conley YP, Ferrell RE, Weeks DE (2008) Interpretation of genetic association studies: markers with replicated highly significant odds ratios may be poor classifiers. Paper presented at 2008 annual meeting of The American Society of Human Genetics. Philadelphia, Pennsylvania, November 12, 2008.

105. Mukhopadhyay N, Bhattacharjee S, Kuo CL, Weeks DE, Feingold E (2008) QTL-ALL: software for QTL linkage analysis. Genet Epidemiol **32**:708-708. Presented at the 2008 annual meeting of the International Genetic Epidemiology Society. St. Louis, Missouri.

106. Weeks DE, Jakobsdottir J†, Conley YP, Ferrell RE, Gorin MB (2008) Further explorations in the genetics of age-related maculopathy (ARM). Paper presented at 2008 annual meeting of The American Society of Human Genetics. Philadelphia, Pennsylvania, November 13, 2008.

107. Casselbrant M, Mandel E, Ferrell R, Jung J‡, Tekely K, Ray A†, Szatkiewicz J, Weeks D (2009) Genetic epidemiology of Otitis Media. Paper presented at The 6th Extraordinary International Symposium on Recent Advances in Otitis Media. Seoul, Korea, May, 2009.

108. Sanghera DK, Begum MF, Mukerjee A, Ralhan S, Wander GS, Mehra NK, Singh JR, Ferrell RE, Kamboh MI, Weeks DE (2009) A genome-wide linkage scan for blood lipid phenotypes in the Khatri Sikh Diabetes Study (SDS). Paper presented at the 59th Annual Meeting of the American Society of Human Genetics. Honolulu, Hawaii

109. Kuo C, Weeks D, Mukhopadhyay N, Bhattacharjee S, Feingold E (2009) Robust Score Statistics for QTL Linkage Analysis Using Extended Pedigrees. Paper presented at the 59th Annual Meeting of the American Society of Human Genetics. Honolulu, Hawaii

110. Chen W, Stambolian D, Edwards AO, Branham KE, Othman M, Jakobsdottir J†, Tosakulwong N, Pericak-Vance MA, Campochiaro PA, Klein ML, Weeks DE, Zack D, Chew EY, Heckenlively JR, Francis PJ, Katsanis N, Haines JL, Gorin MB, Abecasis GR, Swaroop A, CAPT Research Group, AMD GWAS Consortium (2009) Genome Wide Association Study of Age-Related Macular Degeneration Identifies TIMP3 and HDL-associated alleles as new susceptibility loci. Paper presented at the 59th Annual Meeting of the American Society of Human Genetics. Honolulu, Hawaii

111. Bui DK, Ortube MC, Weeks DE, Martinez A, Conley Y, Gorin MB (2010) Genetic ME - A visualization application for merging and editing pedigrees for genetic studies. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

112. Feenstra B, Geller F, Zhang H, Boyd HA, Ryckman KK, Shaffer JR, Dagle JM, Weeks DE, Marazita ML, Feingold E, Murray JC, Melbye M (2010) Assessing the Combined Significance of SNPs in Candidate Genes for Preterm Birth. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

113. Feingold E, Shaffer JR, Wang XJ, Lee MK, Begum F, Weeks DE, Barmada M, T.Cuenco K, Wendell S, Crosslin D, Laurie C, Doheny K, Pugh E, Geller F, Feenstra B, Zhang H, Boyd H, Melbye M, Weyant RJ, Crout R, McNeil D, Levy SM, Slayton RL, Willing M, Broffitt B, Marazita ML (2010) Whole genome-scan of genetic determinants for dental caries in the primary dentition. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

114. Geller F, Feenstra B, Zhang H, Boyd HA, Ryckman KK, Shaffer JR, Dagle J, Weeks DE, Marazita M, Feingold E, Murray JC, Melbye M (2010) Set Level Association Testing in a GWA Study on Preterm Birth. Genet Epidemiol **34**:974. Presented at the Nineteenth Annual Meeting of the International Genetic Epidemiology Society

115. Lee M, Cuenco KT, Wang X, Shaffer JR, Begum F, Feingold E, Weeks DE, Barmada MM, Wendell S, Crosslin D, Laurie C, Weir B, Doheny KF, Pugh E, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2010) Genome-Wide Association Study of Saliva Flow Rates from the COHRA-GENEVA Study. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

116. Marazita ML, Shaffer JR, Wang XJ, Lee MK, Begum F, Feingold E, Weeks DE, Barmada MM, Cuenco KT, Wendell S, Crosslin D, Laurie C, Weir B, Doheny K, Pugh E, Weyant RJ, Crout R, Mcneil D, Levy SM, Slayton RL, Willing M, Broffitt B, Vieira AR (2010) Genome-wide Association Study of Caries in the Primary Dentition. Paper presented at the American Association for Dental Research Annual Meeting. Washington, DC

117. Mukhopadhyay N, Tang X, Weeks DE (2010) Genetic Map Interpolator. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington D.C.

118. Schaffer AA, Lemire M, Ott J, Lathrop GM, Weeks DE (2010) Coordinated New Versions of the Pedigree Simulation Packages SLINK and SUP. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

119. Shaffer JR, Feingold E, Ryckman K, Begum F, Feenstra B, Geller F, Boyd HA, Weeks DE, Barmada MM, Laurie C, Zhang Q, Doheny K, Pugh E, Marazita ML, Melbye M, Murray JC (2010) Intergenerational allelic interaction: Excess maternal-fetal allele sharing in the HLA genomic region is

associated with preterm birth. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

120. Wang X, Shaffer JR, Feingold E, Lee M, Cuenco KT, Begum F, Weeks DE, Barmada MM, Wendell S, Crosslin D, Laurie C, Doheny K, Pugh E, Weyant RJ, Vieira AR, Crout RJ, McNeil DW, Marazita ML (2010) Whole genome-scan of genetic determinants for dental caries in the permanent dentition. Paper presented at the 60th Annual Meeting of the American Society of Human Genetics. Washington, DC

121. Lee M, Cuenco KT, Wang X, Shaffer JR, Begum F, Feingold E, Weeks DE, Barmada MM, Wendell S, Crosslin D, Laurie C, Doheny KF, Pugh E, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2011) Genome-wide association study of saliva flow rate and integration of protein-gene networks. Paper presented at European Human Genetics Conference 2011. Amsterdam, The Netherlands

122. Lee M, T.Cuenco K, Zhen Z, Shaffer JR, Wang X, Barmada MM, Weyant RJ, Crout RJ, McNeil DW, Weeks DE, Feingold E, Marazita ML (2011) Identification of gene networks for caries of pit and fissure vs. smooth tooth surfaces through GWAS and protein network integration. Paper presented at the 12th International Congress of Human Genetics. Montreal, Canada

123. Menard HL, Kelsey KT, Weeks DE, Deka R, Laumoli TS, Viali S, McGarvey ST (2011) DNA global methylation in American Samoa and Samoa. Paper presented at the 36th Annual Meeting of the Human Biology Association. Minneapolis, Minnesota, (American Journal of Human Biology **23**(2):266-267)

124. Sale M, Chen W-M, Weeks D, Chen F, Hou X, Allen EK, Mattos J, Mychaleckyj J, Segade F, Casselbrant M, Mandel E, Ferrell R, Rich S, Daly K (2011) A Genome-Wide Association Study of Chronic Otitis Media with Effusion and Recurrent Otitis Media Identifies a Novel Susceptibility Locus on Chromosome 2. Paper presented at the 10th International Symposium on Recent Advances in Otitis Media. New Orleans, Louisiana

125. Shaffer JR, Zeng Z†, Wang X, Lee M, T.Cuenco K, Barmada MM, Polk DE, Weyant RJ, Crout R, McNeil DW, Weeks DE, Feingold E, Marazita ML (2011) In silico candidate gene study for childhood tooth decay. Paper presented at the 12th International Congress of Human Genetics. Montreal, Canada

126. Wang X, Vieira AR, Shaffer JR, Begum F, Lee M, T.Cuenco K, Zheng Z, Polk DE, Barmada MM, Noel J, Anjomshoaa I, Weeks DE, Feingold E, Marazita ML (2011) Follow-up GWAS analysis and in silico candidate gene study for dental caries in permanent teeth. Paper presented at the 12th International Congress of Human Genetics. Montreal, Canada

127. Zeng Z†, Shaffer JR, Wang X, Lee M, T.Cuenco K, Barmada MM, Polk DE, Weyant RJ, Crout R, McNeil DW, Weeks DE, Feingold E, Marazita ML (2011) GWAS for childhood tooth decay implicates novel genes for pit and fissure and smooth surfaces. Paper presented at the 12th International Congress of Human Genetics. Montreal, Canada

128. McGarvey ST, Baylin A, Quested C, Tuitele J, Weeks DE, Deka R (2012) INSIG2 variants rs9308762 and rs7566605 modify the association of dietary patterns with serum triglycerides in Samoans. American Journal of Human Biology 24:234-234

129. Conley YP, Jiang Y†, Kenney MC, Udar N, Ferrell RE, Weeks DE, Gorin MB (2012) Mitochondrial haplogroups and age-related maculopathy. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

130. Cuenco K, Lee MK, Zeng Z†, Shaffer JR, Wang X, Feingold E, Weeks DE, Levy SM, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2012) Overlapping G x G interactions associated with caries in permanent and primary dentition. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

131. Lee M, T.Cuenco K, Zeng Z†, Wang X, Shaffer JR, Feingold E, Weeks DE, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2012) Identification of host gene-gene interaction in saliva flow and Streptococcus mutans using MDR. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

132. Minster RL‡, Sun G, Indugula SR, Cheng H, Hawley NL, Viali S, Deka R, Weeks DE, McGarvey ST (2012) Genomewide Association Study of Body Mass Index in Samoans. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

133. Mukhopadhyay N, Govil M, Zheng Z, Feingold E, Weeks DE, Shaffer JR, Wang X, Weyant RJ, Crout R, McNeil DW, Marazita ML (2012) Whole genome linkage analysis to identify genes for childhood dental caries. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

134. Ozbek U†, Weeks DE, Chen W, Shaffer J, Purcell SM, Feingold E (2012) Statistics for X-chromosome association. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA (Platform presentation).

135. Shaffer JR, Feingold E, Wang X, Lee M, T.Cuenco K, Weeks DE, Weyant RJ, Crout R, McNeil DW, Marazita ML (2012) GWAS needs a good phenotype: clustering tooth surfaces into biologically-informative dental caries outcomes. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

136. Wang X, Zeng Z†, Shaffer JR, Feingold E, Weeks DE, Lee M, T.Cuenco K, Weyant RJ, Crout R, McNeil DW, Marazita ML (2012) OFCD syndrome gene BCOR is associated with dental caries. Paper presented at the 62nd Annual Meeting of the American Society of Human Genetics. San Francisco, CA

137. Brehm JM, Chen W, Boutaoui N, Han Y-Y, Schmitz C, Acosta-Perez E, Alvarez M, Colon-Semidey A, Baccarelli A, Weeks DE, Kolls JK, Canino G, Celedon JC (2013) Methylation of ADCYAP1R1 and asthma In Puerto Rican children. Paper presented at the American Thoracic Society 2013 International Conference. Philadelphia, PA. Am J Respir Crit Care Med **187**:A2131.

138. Lam V, Ortube MC, Conley Y, Weeks DE, Martinez A, Aguilar NJ, Andon V, Machuca O, Su A, Gorin M (2013) The Genetics of Age-Related Maculopathy II (GARM II) study: an interim analysis. Paper presented at The Association for Research in Vision and Ophthalmology (ARVO) annual meeting. Seattle, WA

139. Cuenco KT, Lee M, Zheng X, Feingold E, Weeks DE, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2013) Genome-wide CNV association study of primary caries. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

140. Lee M, T.Cuenco K, Zheng X, Feingold E, Weeks DE, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2013) Identification of CNVs association in saliva flow using PennCNV. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

141. Minster RL, Hawley NL, Sun G, Cheng H, Viali S, Deka R, Weeks DE, McGarvey ST (2013) Genomewide association studies of lipids in Samoans. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

142. Baron RV, Conley YP, Gorin MB, Weeks DE (2013) dbVÖR: An open source database system for managing phenotype and genotype information for complex trait studies. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

143. Buhule OD†, Hawley NL, Medvedovic M, Minster RL, Sun G, Cheng H, Viali S, Deka R, Weeks DE, McGarvey ST (2013) A pilot study testing DNA methylation profiles in Samoan obese and lean young adult males. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

144. Fung C, Trent K, Joyce S, Zhou P, Nukui T, Weeks DE, Diergaarde B, Ye YQ, Wu XF, Yuan JM, Grandis J, Weissfeld JL, Romkes M, Egloff AM (2013) Identification of epidermal growth factor receptor (EGFR) polymorphisms that modify risk for squamous cell carcinoma of the head and neck (HNSCC). Proceedings of the 104th Annual Meeting of the American Association for Cancer Research. Cancer Research **73** (8 Suppl), Abstract 1340.

145. Kollar CP, Baron RV, Mukhopadhyay N, Weeks DE (2013) Mega2: enhanced data-handling for facilitating genetic linkage and association analyses. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

146. Shan Y†, Smelser DT, Tromp G, Kuivaniemi H, Weeks DE (2013) Genetic risk models: model size and confidence intervals of the risk estimates. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA

147. Chang L, Li B, Vrieze S, McGue M, Lacono W, Weeks D, Abecasis G, Tseng G, Chen W (2014) Genotype calling and phasing in sequence data from complex families. Paper presented at the 64th Annual Meeting of The American Society of Human Genetics. San Diego, CA

148. Conley YP, Ren D, Beers S, Puccio A, Okonkwo D, Weeks DE (2014) Novel locus in 15q23 implicated in recovery after severe traumatic brain injury. Paper presented at the 64th Annual Meeting of The American Society of Human Genetics. San Diego, CA

149. Minster RL, Buhule OD†, Hawley NL, Sun G, Viali S, Deka R, Weeks DE, McGarvey ST (2014) Comparison of GWAS results from imputed SNPs and multiple anchor and partner genotyped SNPs in an isolated population, Samoa. Paper presented at the 64th Annual Meeting of The American Society of Human Genetics. San Diego, CA

150. Weeks DE, Baron RV, Kollar C, Mukhopadhyay N (2014) Mega2: data reformatting for facilitating genetic linkage and association analyses. Paper presented at the 64th Annual Meeting of The American Society of Human Genetics. San Diego, CA

151. Zeng Z†, Weeks DE, Chen W, Mukhopadhyay N, Feingold E (2014) Identifying relative pairs within large datasets. Paper presented at the 64th Annual Meeting of The American Society of Human Genetics. San Diego, CA

152. Chiu C, Jung J, Weeks D, Wilson A, Bailey-Wilson J, Amos C, Xiong M, Fan R (2015) A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. Paper presented at Presented at the 65th Annual Meeting of The American Society of Human Genetics. Baltimore, MD

153. Ding Y, Yan Q‡, Liu Y, Fritsche LG, Abecasis GR, Swaroop A, Chew EY, Weeks DE, Chen W (2015) Bivariate Analysis and Prediction of AMD progression Using Genetic Scores. Paper presented at Presented at the 65th Annual Meeting of The American Society of Human Genetics. Baltimore, MD

154. Fan R, Chiu C, Wang Y, Jung J, Jiang Y†, Chen W, Weeks D, Ren H, Amos C, Wilson A, Bailey-Wilson J, Xiong M (2015) Functional Regression Models for Gene-based Association Studies of Complex Traits. Paper presented at Presented at the 65th Annual Meeting of The American Society of Human Genetics. Baltimore, MD

155. McGarvey ST, Lambert-Messerlian G, Minster RL, Buhle O†, Lin J†, Maredia H, Viali S, Hawley NL, Sun G, Cheng H, Deka R, Weeks DE (2015) Genome-wide association study of Samoan women's reproductive biomarkers. American Journal of Human Biology **27**:276-277. Paper presented at the 40th Annual Meeting of the Human Biology Association, St. Louis, MO

156. Yan Q‡, Fan R, Weeks D, Boutaoui N, Canino G, Celedon J, Chen W (2015) Set-based methods for DNA methylation analysis. Paper presented at Presented at the 65th Annual Meeting of The American Society of Human Genetics. Baltimore, MD

157. Wang Y, Chen W, Weeks DE, Ren H, Li Y, Lobach I, Amos CI, Moore JH, Boehnke M, Xiong M, Fan R (2015) Meta-analysis of Complex Diseases at Gene Level by Functional Regression. Paper presented at Presented at the 65th Annual Meeting of The American Society of Human Genetics. Baltimore, MD

158. Arockiaraj A†, Koleck TA, Shaffer JR, Sherwood PR, Crago EA, Poloyac SM, Weeks DE, Conley YP (2016) Epigenome-wide association study of delayed cerebral ischemia in stroke patients. Paper presented at the 66th Annual Meeting of The American Society of Human Genetics. Vancouver, Canada

159. Blackwell T, Abecasis G, Barnes K, Blangero J, Burchard E, Correa A, Cupples LA, Curran JE, Ellinor PT, Gabriel S, Germer S, Hernandez R, Jaquish C, Kang HM, Kathiresan S, Laurie CC, Lin X, Mathias RA, McGarvey ST, Mitchell BD, Nickerson D, O'Connell JE, Papanicolaou G, Ramachandran V, Redline S, Rice K, Silverman E, Weeks DE, Weiss ST, Wilson JG, on behalf of the NHLBI TOPMed Program (2016) Sequence data processing and analysis of 18,000 human genomes in the NHLBI TOPMed sequencing program. Paper presented at the 66th Annual Meeting of The American Society of Human Genetics. Vancouver, Canada

160. Fan R, Chiu C, Mills JL, Jung JS, Wang YF, Wilson AF, Bailey-Wilson JE, Weeks DE, Amos CI, Boehnke M, Xiong MM (2016) A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for next-generation sequencing. Paper presented at the 66th Annual Meeting of The American Society of Human Genetics. Vancouver, Canada

161. Minster RL, Hawley NL, Su C-T, Sun G, Kershaw EE, Cheng H, Buhule OD, Lin J, Reupena MS, Viali S, Tuitele J, Naseri T, Urban Z, Deka R, Weeks DE, McGarvey ST (2016) A thrifty variant in CREBRF strongly influences body mass index in Samoans. Paper presented at the 66th Annual Meeting of The American Society of Human Genetics. Vancouver, Canada

162. Su CT, Minster RL, Hawley NL, Kershaw EE, Deka R, Weeks DE, McGarvey ST, Urban Z (2016) Thrifty functional characteristics of the major variant in CREBRF associated with body mass index in Samoans. Paper presented at the 66th Annual Meeting of The American Society of Human Genetics. Vancouver, Canada

163. Rosenthal SL‡, Minster RL, Hawley NL, Sun G, Buhule OD, Cheng H, Naseri T, Reupena MS, Deka R, Weeks DE, McGarvey ST (2017) A CREBRF missense mutation substantially affects height in Samoans. Paper presented at the 67th Annual Meeting of the American Society of Human Genetics. Orlando, FL

164. Russell EM†, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Miljkovic I, Deka R, Weeks DE, McGarvey ST, Minster RL (2017) Effects of the interaction between a CREBRF missense variant and body mass index on type 2 diabetes risk in Samoans. Paper presented at the 67th Annual Meeting of the American Society of Human Genetics. Orlando, FL

165. Shur A, McGarvey ST, Hawley NL, Minster R, Weeks DE, Naseri T. (2017). Associations of thrifty CREBRF variant with body fat distribution in Samoans. Paper presented at the 42nd Annual Human Biology Association meeting, New Orleans, LA.

166. Weeks DE, Baron RV, Stickel JR (2017) The Mega2R suite of R packages: Tools for accessing and processing common genetic data formats in R. Paper presented at the 67th Annual Meeting of The American Society of Human Genetics. Orlando, Florida

167. Carlson JC‡, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Deka R, McGarvey ST, Minster RL, Weeks DE, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium (2018) Creating population-specific reference panels for improved genotype imputation. Paper presented at the 68th meeting of the American Society of Human Genetics. San Diego, California

168. Forno E, Wang T, Qi C, Yan Q, Xu C, Boutaoui N, Han Y, Weeks D, Jiang Y, Rosser F, Vonk J, Brouwer S, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Koppelman GH, Chen W, Celedon JC (2019) Nasal Methylation Panel Accurately Classifies Children by Atopy or Atopic Asthma. American

Journal of Respiratory and Critical Care Medicine **199**:A1060. Paper presented at the International Conference of the American Thoracic Society, Dallas, Texas

169. Krishnan M‡, Phipps-Green A, Altaf S, Major TJ, Cadzow M, Stamp L, Dalbeth N, Russell EM, Minster RL, Hawley NL, Naseri T, Reupena MS, Deka R, Weeks DE, McGarvey ST, Merriman TR, Murphy R (2018) FTO in the Polynesians: Association of FTO-rs9939609 with body mass index in a fixed-effect meta-analysis in people of Polynesian ancestry living in Aotearoa/New Zealand and other Pacific nations. Paper presented at the 68th meeting of the American Society of Human Genetics. San Diego, California

170. Minster RL, Russell EM†, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Deka R, Weeks DE, McGarvey ST, TOPMed Diabetes Working Group (2018) Rare variation in and near CREBRF and association with fasting glucose in non-Polynesian participants in the TOPMed Program. Paper presented at the 68th meeting of the American Society of Human Genetics. San Diego, California

171. McGarvey ST, Minster RL, Weeks DE, Naseri T (2018) Longitudinal adiposity change and CREBRF p.Arg457Gln genotype among Samoans. American Journal of Human Biology **30**(2):P:80. Paper presented at the 43rd annual meeting of the Human Biology Association, Austin, Texas

172. Russell EM†, Carlson JC‡, Hawley NL, Sun G, Naseri HCT, Reupena MS, Deka R, Weeks DE, McGarvey ST, Minster RL, TOPMed Diabetes Working Group (2018) Genome-wide association study of type 2 diabetes phenotypes in Sāmoans. Paper presented at the 68th meeting of the American Society of Human Genetics. San Diego, California

173. Carlson JC, Russell EM†, Zhang JZ†, Hawley NL, Moors J, Cheng H, Dalbeth N, de Zoysa J, Hindmarsh JH, Murphy R, Naseri T, Reupena MS, Stamp L, Tuitele J, Deka R, McGarvey ST, Merriman TR, Weeks DE, Minster RL, TOPMed Lipids Working Group (2019) A large effect, Polynesian-specific, stop-gained variant in BTNL9 is associated with atherogenic lipid profiles. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

174. Erdogan-Yildirim Z†, Carlson JC, Pomer A, Hawley NL, Cheng H, Naseri T, Reupena SM, Deka R, Lambert-Messerlian G, McGarvey ST, Weeks DE, Minster RL, TOPMed Reproductive Health Working Group (2019) Identification of susceptibility loci for reproductive traits in Samoan women. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

175. Forno E, Wang T, Qi C, Yan Q, Xu C, Boutaoui N, Han Y, Weeks D, Jiang Y, Rosser F, Vonk J, Brouwer S, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Koppelman GH, Chen W, Celedon JC (2019) Nasal Methylation Panel Accurately Classifies Children by Atopy or Atopic Asthma. American Journal of Respiratory and Critical Care Medicine **199**:A1060

176. Harris DN, Kessler MD, Shetty AC, Weeks DE, Minster RL, Browning S, Cochrane EE, Deka R, Hawley NL, Reupena MS, Naseri T, TOPMed Population Genetics Working Group, McGarvey ST, O'Connor TD. (2019). Recent Samoan Population History Suggests Dynamic Population Size Changes and Migrations. Paper presented at the 2019 Society for Molecular Biology & Evolution. Manchester, UK.

177. Heinsberg L†, Weeks D, Poloyac S, Conley Y (2019) Dna Methylation Trajectories in the Amyloid Precursor Protein Gene and Patient Outcomes after Subarachnoid Hemorrhage. Journal of Neurotrauma **36**:A59-A59

178. Krishnan M‡, Leask M, Major TJ, Carlson JC, Zhang JZ, Russell EM, Minster RL, Weeks DE, Hawley NL, Naseri T, Reupena MS, Deka R, Cheng H, McGarvey ST, Dalbeth N, Zoysa J, Murphy R, Stamp L, Hindmarsh JH, Merriman TR, Moors J, TOPMed Lipids Working Group (2019) A novel variant in CETP is associated with higher HDL-cholesterol in people of Polynesian ancestry. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

179. McGarvey ST, Hawley NL, Duckham RL, Pomer A, Wetzel AI, Minster R, Weeks DE, Naseri T, Reupena MS (2019) CREBRF p.Arg457Gln genotype, type 2 diabetes and body composition among adult

Samoans. American Journal of Human Biology **31**(2):P:52. Paper presented at the 44th annual meeting of the Human Biology Association, Cleveland, Ohio

180. Russell EM†, Harris DN, Carlson JC, Zhang JZ, Hawley NL, Cheng H, Naseri T, Reupena MS, Chen IY, Rao DC, Hsiung AC, Chuang L-M, Sheu W, Darbar D, Deka R, O'Connor TD, McGarvey ST, Weeks DE, Minster RL, TOPMed Population Genetics Working Group (2019) Evidence of natural selection in Samoans is associated with BMI and the immune system. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

181. Tiner J†, Hawley NL, Weeks DE, Minster RL, Sun G, Cheng H, Deka R, Naseri T, Reupena SM, Pomer A, McGarvey ST (2019) The utility of combining CREBRF genotype with BMI to screen Samoans for type 2 diabetes. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

182. Yan Q, Weeks DE, Xin H, Huang H, Swaroop A, Chew EY, Chen W, Ding Y (2019) Deep-learning-based prediction of late age-related macular degeneration progression. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

183. Zhang JZ†, Carlson JC, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Deka R, McGarvey ST, Minster RL, Weeks DE (2019) A multivariate Bayesian genetic association analysis of a CREBRF variant and adiposity-related phenotypes. Paper presented at the 69th Annual Meeting of The American Society of Human Genetics. Houston, Texas

184. Carlson JC, Zhang JZ†, Hawley NL, Blobner BM, Cheng H, Naseri T, Reupena M, Viali S, Tuitele J, Deka R, McGarvey ST, Minster RL, Weeks DE, TOPMed Blood Pressure Working Group (2020) Samoan genome-wide association studies identify novel associations with blood pressure phenotypes. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

185. Erdogan-Yildirim Z†, Carlson JC, Zhang JZ†, Pomer A, Hawley NL, Cheng H, Naseri T, Reupena MS, Deka R, Lambert-Messerlian G, McGarvey ST, Weeks DE, Minster RL, TOPMed Reproductive Health Working Group (2020) Genome-wide association study of high vs low risk of polycystic ovarian syndrome in Samoan women. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

186. Fu H†, Hawley NL, Carlson JC, Russell EM, Cheng H, Naseri T, Reupena MS, Deka R, Choy CC, McGarvey ST, Minster RL, Weeks DE (2020) The missense variant, rs373863828, in CREBRF plays a role in longitudinal changes in BMI across adulthood. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

187. Heinsberg LW‡, Weeks DE, Alexander SA, Crago EA, Minster RL, Poloyac SM, Conley YP (2020) Associations Between DNA Methylation Trajectories for Genes Regulating Iron Homeostasis and Patient Outcomes Up to One Year After Subarachnoid Hemorrhage. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

188. Heinsberg LW‡, Weeks DE, Shaffer JR, Conley YP (2020) Characterization of DNA methylation age in cerebrospinal fluid following subarachnoid hemorrhage. Podium presentation at the International Society of Nurses in Genetics, November 2020, Virtual.

189. Krishnan M‡, Taub MA, Carlson JC, Cheng H, Naseri T, Reupena M, Deka R, Hawley NL, McGarvey ST, Weeks DE, Mathias RA, Minster RL, TOPMed Hematology & Hemostasis and Structural Variation Working Groups (2020) Genome-wide association study of telomere length in individuals of Samoan ancestry. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

190. Minster RL, Carlson J, Zhang JZ†, Hawley NL, Rosenthal SL, Cheng H, Naseri T, Reupena MS, Viali S, Tuitele J, Deka R, McGarvey ST, Weeks DE (2020) Genome-wide association study of height in Samoan

individuals. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

191. Ray M, Heinsberg LW‡, Conley YP, Weeks DE, Schmella MJ (2020) Utilization of Epigenome-wide DNA Methylation for Longitudinal Comparison of Leukocyte Proportions Across Preeclamptic and Normotensive Pregnancy. Podium presentation at the International Society of Nurses in Genetics, November 2020, Virtual.

192. Russell E‡, Rivara AC, Fu H†, Cheng H, Naseri T, Reupena M, Kershaw EE, Deka R, Weeks DE, McGarvey ST, Minster RL, Hawley NL (2020) Association of a missense variant in CREBRF with type 2 diabetes and fasting glucose in a longitudinal Samoan cohort. Paper presented at the 70th Annual Meeting of The American Society of Human Genetics (virtual)

193. Schmella MJ, Fu HY†, Conley YP, Weeks DE (2020) DNA Methylomic Profiling of Preeclampsia Across the Three Trimesters of Pregnancy. Reproductive Sciences **27**:265A-266A

194. Carlson JC, Hawley NL, Cheng H, Naseri T, Reupena MS, Deka R, McGarvey ST, Minster RL, Weeks DE (2021) The role of population-specific genotype reference panels in genetic association studies. American Journal of Physical Anthropology **174**:15-15

195. Heinsberg LW‡, Arslanian KJ, Mullett SJ, Kershaw EE, Fidow UT, Naseri T, Conley YP, Weeks DE, Wendell SG, Hawley NL (2021) Exploration of the *CREBRF* obesity-risk variant in Samoan infants using untargeted metabolomic analysis and pathway discovery. Podium presentation at the International Society of Nurses in Genetics, November 2021, Virtual.

196. Liu S†, Fu H†, Hawley NL, Carlson JC, Pomer A, Russell EM, Cheng H, Naseri T, Reupena MS, Deka R, Choy CC, Kershaw EE, McGarvey ST, Minster RL, Weeks DE (2021) Genetic variation in/near *LIPC*, *MGAT1*, and *APOA1* is associated with longitudinal change in serum lipid levels in Samoan adults. Paper presented at the 71st meeting of the American Society of Human Genetics (virtual)

197. Ray M, Heinsberg LW‡, Wallace MK, Conley YP, Weeks DE, Schmella MJ (2021) Longitudinal DNA methylation of Chromosome 19 microRNA Cluster Across Preeclamptic and Normotensive Pregnancy. Podium presentation at the International Society of Nurses in Genetics, November 2021, Virtual.

198. Rivara AC, Russell EM‡, Viali S, Reupena MS, Naseri TK, Pomer A, Minster RL, Weeks DE, McGarvey ST, Hawley N (2021) 1108-P: Care Cascade Engagement and Characteristics of Diabetes Awareness in Adult Samoans in 2010 and 2018. Diabetes **70**:1108-P

199. Treble-Barna A, Heinsberg L‡, Puccio A, Shaffer J, Okonkwo D, Beers S, Weeks D, Conley Y (2021) Acute *Brain-Derived Neurotrophic Factor* DNA Methylation Trajectories in CSF and Associations with Outcomes Following Severe Trauma. Journal of Neurotrauma **38**:A22-A22. Poster presented at the National Neurotrauma Society meeting, July 2021, Virtual.

200. Wallace M, Heinsberg LW‡, Ray M, Conley YP, Weeks DE, Schmella MJ (2021) Identifying Alterations in the Inflammatory Milieu of Preeclamptic Pregnancies. Podium presentation at the International Society of Nurses in Genetics, November 2021, Virtual.

201. Ray M, Heinsberg LW‡, Chen NX, Conley YP, Weeks DE, Schmella MJ (2022) MicroRNA-associated DNA Methylation in a Longitudinal, Exploratory Study of Preeclamptic and Normotensive Pregnancy. Am J Obstet Gynecol **226**:S202-S203. Poster presented at the Society for Maternal-Fetal Medicine, February 2022, Virtual.

202. Wallace MK, Heinsberg LW‡, Ray M, Conley YP, Weeks DE, Schmella MJ (2022) Suggestive Differences of DNA Methylation at *ICAM1* between Preeclamptic and Normotensive Pregnancies. Reproductive Sciences **29** (Suppl 1):254A-255A. Poster presented at the Society for Reproductive Investigation, March 2022, Denver, Colorado

203. Liu S†, Liu D, Bender CM, Erickson KI, Sereika SM, Conley YP, Shaffer JR, Weeks DE (2022) Variation in DNA methylation is associated with cognitive function in post-surgery breast cancer patients prior to adjuvant therapy. Paper presented at the Annual Meeting of The American Society of Human Genetics. Los Angeles, California

204. Carlson J, Krishnan M‡, Liu S†, Rosenthal S, Hawley N, Cheng H, Naseri T, Reupena M, Viali S, Deka R, McGarvey S, Minster R, Weeks D (2022) Portability of a multiethnic polygenic risk score for low-density lipoprotein cholesterol in a Samoan population. Paper presented at the Annual Meeting of The American Society of Human Genetics. Los Angeles, California

205. Wehr J, Carlson JC, Russell EM, Krishnan M‡, Liu S†, Cheng H, Naseri T, Reupena MS, Vialia S, Tuitele J, Kershaw E, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2022) Genome-wide association studies of metabolic traits in Samoans. Paper presented at the Annual Meeting of The American Society of Human Genetics. Los Angeles, California

206. Carlson J, Krishnan M‡, Liu S†, Anderson K, Zhang J, Cheng H, Naseri T, Reupena M, Viali S, Deka R, Hawley N, McGarvey S, Weeks DE, Minster RL (2023) The extent to which augmenting extant reference panels with population-specific sequences improves imputation quality. Paper presented at the Annual Meeting of The American Society of Human Genetics. Washington, D.C.

207. Yapp T-A, Zhang JZ†, Krishnan M‡, Liu S†, Blobner BM, Cheng H, Naseri T, Reupena MS, Viali S, Tuitele J, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL, Carlson JC (2023) Genome-wide association studies of blood pressure phenotypes in 4,819 participants from Samoa and American Samoa. Paper presented at the Annual Meeting of The American Society of Human Genetics. Washington, D.C.

208. Liu S†, Liu D, Bender CM, Erickson KI, Sereika SM, Conley YP, Shaffer JR, Weeks DE (2023) Associations between DNA methylation and cognitive function in early-stage breast cancer patients. Paper presented at the Annual Meeting of The American Society of Human Genetics. Washington, D.C.

209. Shan Y†, Weeks D (2023) BayesRB: a Markov Chain Monte Carlo-based polygenic genetic risk score algorithm for dichotomous traits. European Journal of Human Genetics (2024) **32**:659. Paper presented at 56th Annual Conference of the European Society of Human Genetics (ESHG), Glasgow, Scotland.

210. Dinh B, Wang X, Tian H, Tang J, Sheng X, Carlson JC, Weeks DE, Wilkens LR, Le Marchand L, Haiman CA, Chiang CWK (2024) Statistical and population genetic approaches to enhance the discovery of trait-associated loci in understudied populations with small sample size. Paper presented at the Annual Meeting of The American Society of Human Genetics. Denver, Colorado, November 2024

211. Spor L, Carlson JC, Wehr J, Russell EM, Krishnan M, Liu S†, Cheng H, Naseri T, Reupena M, Viali S, Tuitele J, Kershaw EE, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2024) GWAS meta-analyses of fasting glucose, fasting insulin, and HOMA-IR in Samoans. Paper presented at the Annual Meeting of The American Society of Human Genetics. Denver, Colorado, November 2024

212. Wang X, Dinh B, Sheng X, Young E, Leask M, Taparra K, Stamp LK, Dalbeth N, Murphy R, Zoysa Jd, Naseri T, Reupena M, Viali S, Castel SE, Merriman TR, Carlson J, Weeks DE, Wilkens L, Le Marchand L, Hall I, Haiman CA, Stitziel N, Chiang CWK (2024) A multi-ancestry reference panel from 10,721 individuals to improve the genotype imputation for individuals of East Asian- and Polynesian-Ancestry. Paper presented at the Annual Meeting of The American Society of Human Genetics. Denver, Colorado, November 2024

213. Yapp T-A, Krishnan M, Liu S†, Manna S, Cheng H, Naseri T, Reupena M, Viali S, Tuitele J, Deka R, Hawley N, McGarvey ST, Weeks D, Minster RL, Carlson J (2024) Validation of Multi-ancestry Polygenic Scores for Lipid Levels in 3,119 Participants from Samoa and American Samoa. Paper presented at the Annual Meeting of The American Society of Human Genetics. Denver, Colorado, November 2024

214. Yapp TJ, Krishnan M, Liu S†, Manna SL, Cheng H, Naseri T, Reupena MS, Viali S, Tuitele J, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL, Carlson JC (2024) Validation of Multi-ancestry

Polygenic Scores for Lipid Levels in 3,119 Participants from Samoa and American Samoa. Paper presented at the 33rd Annual Meeting of the International Genetic Epidemiology Society (IGES). Genet Epidemiol **48**:394 Denver, Colorado, November 2024.

215. Conley Y, Liu S, Weeks D, Shaffer J, Erickson K, Bender C (2025) Data-Driven Epigenomic Analyses Reveal Different Signaling Pathways for Subjective and Objective Cognitive Function in Early-Stage Breast Cancer. Paper presented at at the 50th Annual Oncology Nursing Society (ONS) Congress. Oncology Nursing Forum **52**(2):60-61. Denver, Colorado, April 2025.

216. Miller S, Tejada-Martinez D, Liu C, Reilly P, Weeks D, Naseri T, Viali S, Minster R, McGarvey S, Tucci S (2025) The contribution of archaic introgression to local adaptation in Oceania. American Journal of Biological Anthropology (2025) **186** (Suppl 79):113. Paper presented at the 94th Annual Meeting of the American Association of Biological Anthropologists. Baltimore, Maryland.

Patents

Gorin MB, Jakobsdottir J, Conley YP, Weeks DE, Mah-Fraser TS, Ferrell RE. Susceptibility genes for age-related maculopathy (ARM) on chromosome 10q26. US Patent Number: US 7,695,909 B2; awarded April 13, 2010.

Gorin MB, Jakobsdottir J, Conley YP, Weeks DE, Mah-Fraser TS, Ferrell RE. Susceptibility genes for age-related maculopathy (ARM) on chromosome 10q26. US Patent Number: US 8,053,190; awarded November 8, 2011.

Other research-related activities

Attended a one-week course entitled "Supercomputing Techniques: Connection Machine" at the Pittsburgh Supercomputing Center, June 1991.

Invited attendee, 2nd International inflammatory bowel disease genetics workshop, Denver, Colorado, October 1998.

Invited attendee, conference on "Genetics and Molecular Biology of Glaucoma", sponsored by the Glaucoma Research Foundation. San Juan, Puerto Rico, December 1998.

Invited attendee, Statistical Genetics Initiative Workshop, sponsored by the National Institutes of Health. Half Moon Bay, California, October 1999.

Attended a Clinical Research Workshop on the Fundamentals of Human Subject Research, University of Pittsburgh, June 2000.

Invited attendee, "Gene discovery in complex disorders – How to proceed?", sponsored by the National Institute of Mental Health. Laguna Beach, California, March 2004.

Invited attendee, "Gene-environment interactions and epigenesis in mental disorders", sponsored by the National Institute of Mental Health, Rockville, Maryland, November 15, 2004.

Invited attendee, NIGMS Workshop on Systems Genetics and Complex Phenotypes, sponsored by the National Institute of General Medical Sciences, Bethesda, MD, September 7-8, 2006.

Invited attendee, First Meeting of the International AMD Genetics Consortium for Meta-Analysis, sponsored by the National Eye Institute, Bethesda, MD, June 15, 2010

Invited attendee, "Next Generation Analytic Tools for Large Scale Genetic Epidemiology Studies of Complex Diseases", sponsored by the National Cancer Institute, Bethesda, MD, September 15-16, 2010

Invited attendee, Consortium of Food Allergy Research (CoFAR) Investigator/Steering Committee Meeting, Bethesda, MD, January 10, 2011

Service

Departmental (at the University of Pittsburgh)

1992	Chair of the computer committee, Summer 1992
1992-93	Co-supervisor of Tricia Graham, the departmental computer specialist
1997-98	Member of the Search Committee for a new chair of the Department of Human Genetics
2000-01	Chair, Search Committee for a new faculty member
2002-03	Member, Curriculum Committee
2002-15	Chair, M.S. and Ph.D. Admissions Committee
2003-05	Head, Faculty Search Committee, Department of Human Genetics
2004	Member, Faculty Search Committee, Department of Biostatistics
2004	Acting Chair, Department of Human Genetics
2005	Acting Vice Chair, Department of Human Genetics
2006-08	Member, Search Committee for a new chair of the Department of Human Genetics

2007 Chair, Department of Human Genetics Strategic Planning Committee
2008 Organizer, Fall 2008 Department of Human Genetics Seminar Series
2010-21 Member, Department of Human Genetics Curriculum Committee
2011 Organizer, Spring 2011 Department of Human Genetics Seminar Series
2012 Chair, Department of Human Genetics Strategic Planning Committee
2014 Member, Strategic Planning Committee for the University of Pittsburgh Genetic Counseling Program
2015-18 Member, M.S. and Ph.D. Admissions Committee
2017 Chair, Department of Human Genetics Faculty Search Committee
2017 Member, Faculty Search Committee, Department of Biostatistics
2018-21 Chair, Strategic Planning Committee
2018-21 Chair, Computing Committee
2018-21 Member, Communications Committee (Chair, Development Subcommittee)
2019-20 Chair, Department of Human Genetics Faculty Search Committees for three faculty positions.
2021 Co-leader of the Departmental Gaps and Assets review process, April 2021.
2021-22 Acting Chair, Department of Human Genetics
2021- Chair, M.S. and Ph.D. Admissions Committee
2021 Judge, Department of Biostatistics Research Day Poster Session, March 4, 2021.
2022 Judge for the Biostatistics Research Day, Department of Biostatistics, March 3, 2022.
2023 Judge, Department of Biostatistics Research Day Poster Session, March 3, 2023.
2023- Member, Department of Human Genetics Curriculum Committee

<u>School-wide (at the University of Pittsburgh)</u>
1992 Member of the GSPH Convocation Committee, Spring 1992
1997 Member of the Ad hoc Committee on Long-Range Planning
1997-98 Member of the Faculty Senate Executive Committee
1997-98 Member of the Long-Range Planning Committee
2001 Member of the Informal Working Group on the GSPH Standardized CV
2003 Dean's Day Juror, evaluating posters and spoken presentations of students
2001-04 Member of the Health Science Faculty Advisory Committee
2001-06 Member of the Faculty Appointment, Promotion, and Tenure Committee (FAPTC)
2004 Member of the Graduate School of Public Health Council
2005 Moderator, Ethics over Lunch, Survival Skills & Ethics Program, University of Pittsburgh, April 9, 2005.
2005 Moderator, Ethics over Lunch, Survival Skills & Ethics Program, University of Pittsburgh, September 17, 2005.
2007 Moderator, Ethics over Lunch, Survival Skills & Ethics Program, University of Pittsburgh, October 20, 2007.
2010 Trained to qualify to serve on the University of Pittsburgh Institutional Review Board (IRB).
2011 Dean's Day Juror, evaluating students' posters.
2012 Reviewed two grants for the Clinical and Translational Science Institute (CTSI), February 2012.
2012 Dean's Day Juror, evaluating students' posters, April 13, 2012.
2012-18 Member of the Faculty Appointment, Promotion, and Tenure Committee (FAPTC)
2013 Dean's Day Juror, evaluating students' posters, April 1, 2013.
2014 Dean's Day Juror, evaluating students' posters, April 8, 2014.
2014 Presentation about the Faculty Appointment, Promotion, and Tenure Committee at the New Faculty Orientation, October 30, 2014.
2014 Presentation about the Faculty Appointment, Promotion, and Tenure Committee at the Pitt Public Health Promotion Packets Workshop, December 17, 2014.
2014-15 Chair, Faculty Appointment, Promotion, and Tenure Committee (FAPTC)
2015 Dean's Day Juror, evaluating students' posters, April 1, 2015.
2016 Dean's Day Juror, evaluating students' posters, April 4, 2016.
2017 Dean's Day Juror, evaluating students' posters, April 6, 2017.
2017 Member, Department of Epidemiology Faculty Search Committee.
2019 Dean's Day Juror, evaluating students' posters, April 4, 2019.
2020-22 Faculty Mentoring Steering Committee
2021 Service on an *ad hoc* Faculty Appointment, Promotion, and Tenure Committee (FAPTC) committee, January 8, 2021.
2021 Dean's Day Juror, evaluating students' posters, April 6, 2021.

2022 Dean's Day Juror, evaluating students' posters, April 5, 2022.
2022- Member, School of Public Health Faculty Mentoring Executive Committee.
2023 Dean's Day Juror, evaluating students' posters, April 3, 2023.
2024 Dean's Day Juror, evaluating students' posters, April 3, 2024.
2025 Dean's Day Juror, evaluating students' posters, April 2, 2025.

University-wide (at the University of Pittsburgh)

2016 Served on an *ad hoc* School of Dental Medicine Promotion Committee.
2016 Science 2016 moderator of the Spotlight Session on Personalized and Precision Medicine, October 20, 2016.
2019 Reviewed a KL2 application for the Multidisciplinary Clinical Research Scholars Program (CRSP) of the University of Pittsburgh, March 2019.
2019 Participated in a mock study section, reviewing an R01 application for the Mellon Institute at the Children's Hospital of Pittsburgh, May 2019.
2020 Reviewed two KL2 applications for the Multidisciplinary Clinical Research Scholars Program (CRSP) of the University of Pittsburgh, May 2020.
2021 Reviewed a grant proposal for the Department of Psychiatry Research Review Committee, December 2021.
2022 Served on an *ad hoc* promotion committee for the Department of Oral and Craniofacial Sciences, University of Pittsburgh School of Dental Medicine, August 1, 2022.
2023-24 School of Public Health representative, Provost's Advisory Council on Tenure and Promotion (PACTP), Pittsburgh Campus Subcommittee.

National/International

Manuscript Review

Refereed articles for many journals, including Science, Nature, the American Journal of Human Genetics, Nature Genetics, PLOS Genetics, Human Molecular Genetics, Genomics, Genetic Epidemiology, Diabetes, Human Heredity, Bioinformatics, IMA Journal of Mathematics Applied in Medicine and Biology, Theoretical and Applied Genetics, Theoretical Population Biology, Human Genetics, Proceedings of the National Academy of Sciences U.S.A, Neurogenetics, CABIOS, Journal of the American Medical Association, Journal of Mathematical Biology, and several Genetic Analysis Workshops.
Verified Peer Review Record: https://www.webofscience.com/wos/author/record/769878

2001-11 Member, Faculty of 1000 (online literature awareness tool).

Editorial Boards and Editorships

1996-98 Associate Editor, American Journal of Human Genetics
1999 Editor, proceedings of the Genetic Analysis Workshop 11.
1999-00 Editorial Board, Human Molecular Genetics
2004-07 Associate Editor, Biometrics
2001-11 Editorial Board, Genetic Epidemiology
2004-13 Associate Editor, Statistical Applications in Genetics and Molecular Biology

Study Sections and Advisory Boards

Served on a site visit team for a Genome Center Grant and a RO1 application.
1993 Served on an *ad hoc* Study Section for the National Cancer Institute.
1994 Served on the Genome Research Review Committee to review a P41 application.
1998 Served on an *ad hoc* Study Section for the National Cancer Institute reviewing a program project.
1998 Served on an *ad hoc* Study Section for the National Institute of Mental Health.
1995-99 Member of the Review Committee for the NHLBI Mammalian Genotyping Service (James Weber, PI).
1998 Advisory meeting regarding future genetic studies in the Framingham Study, Boston University School of Medicine.
1998-00 Scientific Advisory Board, Center for Genomic Sciences, University of Pittsburgh
1999 Served on an *ad hoc* Study Section for the National Institute of Mental Health.
2000 Served on a Site Visit Team for the National Heart, Lung, and Blood Institute.
2000 Served on an *ad hoc* Study Section for the National Institute of Mental Health reviewing a program project.

2000 Served on an *ad hoc* Study Section for the National Heart, Lung, and Blood Institute.
2001 Served on an *ad hoc* Study Section for the National Institute on Alcohol Abuse and Alcoholism
2001 Served on an *ad hoc* Study Section for the National Institutes of Health.
2002 Served on an *ad hoc* Study Section for the National Heart, Lung, and Blood Institute reviewing a program project.
2003 Served on an *ad hoc* Study Section for a National Institutes of Health Special Emphasis Panel in Psychiatric Genetics.
2004 Served on an *ad hoc* NIH Study Section reviewing several Morris K. Udall Centers of Excellence for Parkinson's Disease Research, March 16-17, 2004.
2007 External member, Statistical Genetics Graduate Certificate Program Review Committee, University of Washington, Seattle, Washington, April 2-3, 2007.
2007 Member, National Eye Institute (NEI) Ocular Epidemiology Planning Panel, an NIH Strategic Planning Committee, May 24-25, 2007.
2007- External advisory board, Training Program on Genetic Variation and Human Phenotypes, Vanderbilt University Medical Center, Jonathan L. Haines, Program Director.
2005-08 Regular member, Genomics, Computational Biology and Technology (GCAT) NIH Study Section.
2010 Site visit, External advisory board, Training Program on Genetic Variation and Human Phenotypes, Vanderbilt University, Nashville, TN, January 28, 2010.
2012 Served on an *ad hoc* Study Section for the United States Department of Veterans Affairs, June 1, 2012.
2012 Reviewed a Center of Excellence in Genome Health Research proposal for the Academy of Finland, August 2012.
2016 Reviewed a research grant proposal for the Medical Research Council, United Kingdom, August 2016.
2017 Served as an ad hoc reviewer of an NIH T32 training grant proposal on the "Training and Workforce Development Subcommittee – A" study section, March 20, 2017.

Meeting Organization

1995 Co-organizer of the Map Integration Workshop, Pittsburgh Supercomputing Center, December 1995.
1996 Co-organizer of the 5th Rheumatoid Arthritis Genetics Workshop, University of Manchester, March 1996.
2002 Co-organizer of the INSERM Ateliers de formation / Workshop 136 – Methods for the elucidation of genomic variation, La Roche-Posay and Paris, France, May 2002.
2002 Co-organizer of an invited session on "Statistical Genetics and Complex Disease" at the Joint Statistical Meetings, New York City, August 2002.
2003 Co-organizer, Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India, June 2003.
2004 Co-organizer, Second Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India, December 2004.
2005 Co-organizer, *Paris Workshop on Molecular and Statistical Genomic Epidemiology*, Paris, France, May 2005.
2007 Co-organizer, Third Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India, January 2007.
2007 Co-organizer, *Second Paris Workshop on Molecular and Statistical Genomic Epidemiology*, Paris, France, May 2007.
2009 Co-organizer, Fourth Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India, February 2009.
2009 Co-organizer, *Third Paris Workshop on Genetic Epidemiology*, Paris, France, March 2009.
2010 Co-organizer, Fifth Workshop on *Genetic Epidemiological Methods for Dissection of Complex Human Traits*, Kolkata, India, February 2010.
2011 Co-organizer, *Fourth Paris Workshop on Genetic Epidemiology*, Paris, France, May 2011.
2013 Co-organizer, *Fifth Paris Workshop on Genetic Epidemiology*, Paris, France, May 2013.
2015 Co-organizer, *The 6th International Workshop on Genetic Epidemiology*, London, United Kingdom, May 2015.
2017 Co-organizer, *The 7th International Workshop on Genomic Epidemiology*, Barcelona, Spain, September 2017 (missed due to illness).

Meeting Workshops

2017 Participant, Mock NIH Study Section Workshop, the 67th Annual Meeting of The American Society of Human Genetics. Orlando, Florida, October 20, 2017.

Collaborative Research Service

2007-2009 Co-chair of the Analysis Subcommittee of the NIH Genes Environment Association Studies (GENEVA) consortium of genome-wide association studies.

Consultantships

1996-1997 Consultant in statistical genetics, Columbia University, New York, USA.
1997-2000 Consultant in statistical genetics, and member of the Population Genetics Advisory Committee, Glaxo Wellcome Inc., North Carolina, USA.
1997-2004 Consultant in statistical genetics, Oxagen Limited, Abingdon, England.
2001-2004 Consultant in statistical genetics, Triaj, Inc.
2005 Consultant in statistical genetics, OptiGen, LCC.
2006-2008 Consultant in statistical genetics, Rutgers University, New Jersey, USA (Derek Gordon).
June 9-10, 2009 Consultant in statistical genetics for a pharmacogenetics study, Eli Lilly and Company, Indianapolis, Indiana, USA.
2009-2011 Consultant in statistical genetics for a genome-wide association study of pre-term birth, Children's Memorial Hospital, Chicago, Illinois, USA (Xiaobin Wang).
2011-2012 Consultant in statistical genetics for a law firm.

Research and Training
Grants and Contracts Received:

"Epigenetic Age and Patient Outcomes after Severe Traumatic Brain Injury"
Principal Investigator: Conley, Yvette — Annual Direct Costs: $472,708
Agency: NIH/NIA — R01 AG082734 — Period: 8/24-4/29
The major goals of this project are to use omics-based approaches to identify biological underpinnings influencing patient outcomes post-TBI and to use this information to proceed towards evidence-based interventions to improve patient outcomes.

"Epigenetic Aging Cognitive Function and Exercise in Older Adults"
Principal Investigator: Conley, Yvette; Erickson, Kirk — Total Direct Costs: $1,557,590
Agency: NIH/NIA — RF1 AG084554 — Period: 9/24-8/27
The major goals of this project are to determine the effect of epigenetic age acceleration on cognitive function, brain health, biomarkers of Alzheimer disease, and response to exercise in older adults.

"CREBRF Genomics, Gestational Diabetes, and Early Life Body Size in American Samoa"
Principal Investigator: Heinsberg, Lacey — Annual Direct Costs: $156,601
Agency: NIH/NICHD — R00 HD107030 — Period: 8/24-7/27
The major goals of this project are to investigate how maternal/fetal *CREBRF* rs373863828 genotype combination is associated with (1) gestational diabetes mellitus in pregnancy, (2) early life body size/composition during infancy, and (3) cord blood DNA methylation at birth.

"Allostatic Load and Race: Implications for Cardiovascular Health in Pregnancy and Beyond"
Principal Investigator: Ray, Mitali — Annual Direct Costs: $159,941
Agency: NIH/NINR — R00 NR020215 — Period: 9/24-8/27
Focusing on cardiovascular health at two timepoints, 2-7 and 7-12 years, following pregnancy in the Nulliparous Pregnancy Outcomes Study: Monitoring Mothers-to- be Heart Health Study, we aim (1) to evaluate the effect of Allostatic Load index trajectories on the relationship between self-identified race and post-pregnancy cardiovascular health and (2) to evaluate the association between DNA methylation trajectory and post-pregnancy cardiovascular health.

"Methylomics of pediatric traumatic brain injury and neurobehavioral recovery"
Principal Investigator: Treble-Barna, Amery — Annual Direct Costs: $117,669
Agency: NIH/NICHD — R01 NS135492 — Period: 5/24 - 4/29

The major goals of this project are to investigate DNA methylation (DNAm), a major epigenetic regulator of gene expression, as an untapped source of biologic complexity underlying recovery from pediatric traumatic brain injury (TBI). We will generate methylome-wide DNAm data from an ongoing longitudinal study of children aged 3-18 years with complicated mild to severe TBI or orthopedic injury (OI; comparison group). We will then use these data to (1) Determine the association of pediatric TBI with acute DNAm; (2) Identify associations between acute DNAm and long-term neurobehavioral outcomes; (3) Identify associations between acute DNAm and disparities in neurobehavioral outcomes as a function of psychosocial adversity; and (4) Explore associations between longitudinal DNAm and neurobehavioral recovery.

"Lipidomics and structural genomics of cardiometabolic health in Samoan adults"
Principal Investigator: Minster, Ryan Annual Direct Costs: $1,098,836
Agency: NIH/NHLBI R01 HL133040 Period: 4/24 - 3/28
The major goals of this project are to determine associations between comprehensive serum lipid profiles and both simple nucleotide variation and cardiometabolic traits in 4,300 Samoan adults from Samoa and American Samoa; (2) evaluate associations between structural genetic variation and both comprehensive lipid profiles and cardiometabolic phenotypes; (3) conduct exploratory integrative analyses to identify systems-level patterns among the layers of information available; and (4) propose and lead collaborative investigations of our findings with collaborators among the TOPMed Program.

"Leveraging the Evolutionary History to Improve Identification of Trait-Associated Alleles and Risk Stratification Models in Native Hawaiians"
Principal Investigator: Chiang, Charleston Annual Direct Costs: $248,352
Agency: NIH/NHGRI R01 HG011646 Period: 9/22 - 6/27
The major goals of this project are to develop a Polynesian-specific imputation reference panel that will accelerate future large-scale genetic studies in Polynesian populations; (2) to leverage the unique evolutionary history to elucidate population-enriched genetic risk factors to obesity and T2D and improve risk stratification models using polygenic risk scores; and (3) to understand any causes for community concerns of research participations.

"Epigenomics of orofacial clefts"
Principal Investigator: Shaffer, John
Agency: NIH X01 HD114124 Period: 7/23 - 6/24
The major goals of this project are to expand the Gabriella Miller Kids First resource by collecting genome-wide DNA methylation assays in a large cohort of affected children as well as DNA methylation and transcriptomics assays in a subset of children with available discarded surgical tissue. The resulting data should help expand and deepen our understanding of the genetic architecture and regulatory landscape of orofacial clefts including identifying new risk loci and determining the mechanisms through which known risk loci influence the development of orofacial clefts.

"Epigenomics of Neurocognitive Function in Breast Cancer" Annual Direct Costs: $428,428
Principal Investigator: Conley, Yvette P.
Agency: NIH/NCI R01 CA221882 Period: 6/18 - 5/24
The main goal of this project is to use methylation data to identify genes and pathways involved with cognitive function and brain health within the context of breast cancer, initiation of treatment, and an exercise intervention.

"Impact of the obesity-risk variant CREBRF p.Arg457Gln on energy expenditure, intake, and substrate utilization in Samoans" Annual Direct Costs: $719,935
Principal Investigator: McGarvey, Stephen T. and Delaney, James P.
Agency: NIH/NHLBI R01 HL140570 Period: 2/18 - 1/24
The main goal of this project is to measure the impact of the CREBRF missense variant on measures of energy expenditure, energy intake, and longitudinal relationships between these energy metabolism parameters and adiposity phenotypes.

"Next Generation Association Studies of Adiposity in Samoans Enhanced by a Samoan-Specific Whole Genome Sequence Reference Panel" Annual Direct Costs: $494,807
Principal Investigator: Minster, Ryan
Agency: NIH/NHLBI R01 HL133040 Period: 4/17 - 3/23
The main goal of this project is to use a whole genome sequenced Samoan reference panel to impute into a sample of Samoan adults so as to carry out comprehensive association analyses of adiposity-related traits.

"Integrated cellular, mouse and human research on a novel missense variant influencing adiposity in Samoans"
Principal Investigator: McGarvey, Stephen T Annual Direct Costs: $735,219
Agency: NIH/NHLBI R01 HL093093 Period: 9/09 - 4/21
The main goal of this project is to characterize a missense variant influencing adiposity in Samoans in cultured cell models, mouse models, and in Samoan adipose tissue, and to characterize the impact of the variant on metabolic and behavioral traits that impact energy homeostasis in deeply phenotyped Samoans selected based on genotype.

"DNA methylomic profiling of preeclampsia across pregnancy" Annual Direct Costs: $150,000
Principal Investigator: Schmella, Mandy
Agency: NIH/NICHD R21 HD092770 Period: 7/17 – 8/20
The main goal of this project is to longitudinally characterize DNA methylation profiles across the three trimesters of pregnancy in the maternal blood at time points before and after clinically overt preeclampsia.

"Statistical methods for population and family-based whole-genome sequence data" Annual Direct Costs: $241,427
Principal Investigator: Chen, Wei
Agency: NIH R01 HG007358 Period: 4/14 - 7/19
The main goal of this project is to develop methods and software for family-based whole-genome sequencing association studies.

"Mega2: Manipulation Environment for Genetic Analysis" Annual Direct Costs: $207,633
Principal Investigator: Weeks
Agency: NIH/NIGMS R01 GM076667 Period: 3/06 – 6/19
The main goal of this project is to improve and extend our Mega2 program for transforming genetic data into proper files for statistical analyses.

"Mapping Disease pathways in Biliary Atresia" Annual Direct Costs: $424,458
Principal Investigator: Rakesh, Sindhi
Agency: NIH/NIDDK R01 DK109365 Period: 4/17 - 3/19
The main goal of this project is to carry out association tests to identify genes associated with biliary atresia, to evaluate the function of these genes using zebrafish models and liver tissue, and to examine pathways that these genes are involved in.

"Symptom Clusters in Oncology Patients Receiving Chemotherapy" Annual Direct Costs: $54,717
Principal Investigator: Miaskowski, Christine
Agency: The Sharon Lamb Period: 1/17 – 12/17
Endowed Chair Fund
The main goal of this project is to carry out genome-wide association analyses testing for association with clusters of symptom trajectories in oncology patients during the 4 weeks post-treatment.

"AMD genetics: methods and analysis for progression, prediction, and association" Annual Direct Costs: $31,369 (subcontract)
Principal Investigator: Chen, Wei
Agency: NIH/NEI R01 EY024226 Period: 4/14 - 3/18
The main goal of this project is to develop and apply novel statistical methods for the study of progression, association, and prediction of age-related macular degeneration (AMD), using existing data from our collaborators and public databases.

"Epigenomics of Patient Outcomes after Traumatic Brain Injury" Annual Direct Costs: $32,640 (subcontract)
Principal Investigator: Conley, Yvette P
Agency: NIH/NR R21 NR015142 Period: 8/14 - 7/17
The major goals of this project are to characterize the DNA methylome from samples representing the central nervous system environment post-traumatic brain injury and to use these methylation data to differentiate patient outcomes.

"Epigenetic Variation and Childhood Asthma in Puerto Ricans" Annual Direct Costs: $21,065 (subcontract)
Principal Investigator: Celedon, Juan Carlos
Agency: NIH R01 HL117191 Period: 7/13 - 6/18

The main goal of this project is to study the influence of methylation on risk for childhood asthma in Puerto Ricans.

"Post Genome-Wide Association Study of Food Allergy" Annual Direct Costs: $13,387 (subcontract)
Principal Investigator: Wang
Agency: NIH/NIAID U01 AI090727 Period: 7/10 – 6/15
The central focus of this study is to further replicate promising genetic variants identified by the ongoing GWAS and to conduct fine mapping to search for potential causative genes of food allergy.

"Epigenomics of Patient Outcomes after Aneurysmal SAH" Annual Direct Costs: $251,780
Principal Investigator: Conley, Yvette P
Agency: NIH/NR R01 NR013610 Period: 9/12 - 6/18
The main goal of this project is to study how methylation of the genome after aneurysmal subarachnoid hemorrhage (aSAH) impacts symptoms and complications in the aSAH survivor.

"Improving Vision and Preventing Visual Impairment in rural Amish and urban African Americans"
Principal Investigator: Stambolian, Dwight Annual Direct Costs: $69,411 (subcontract)
Agency: Pennsylvania Department of Health State funding Period: 6/10 - 5/14
The main goal of this project is to carry out gene and gene-environment studies, combined with modern imaging technology, in age-related macular degeneration in African Americans and Amish.

"Genome-Wide Association Studies of Adiposity in Samoans" Annual Direct Costs: $127,898 (subcontract)
Principal Investigator: McGarvey Total Direct Costs (TDC): $1,161,658
Agency: NIH/NHLBI R01 HL093093 Period: 9/09 - 12/15
The main goal of this project is to carry out a genome-wide association study of obesity and obesity-related phenotypes in adult Samoans.

"Genetics of age-related maculopathy" Annual Direct Costs: $99,737 (subcontract)
Principal Investigator: Gorin
Agency: NIH/NEI R01 EY009859 Period: 9/93 - 3/14
The main goal of this project is to map genes involved in age-related maculopathy via linkage and association analysis of marker data collected on disease families by my collaborators.

"Genetics of age-related maculopathy" Annual Direct Costs: $80,207 (subcontract)
Principal Investigator: Gorin
Agency: NIH/NEI R01 EY009859 Administrative Supplement Period: 9/09 - 9/12
The major goals of this project are to map genes involved in age-related maculopathy via linkage and association analyses of marker data collected on disease families. Our efforts under this Supplement will be aimed at improving our databases that store and manage our genetic data.

"Utility of Genomic Data in Population Screening for Abdominal Aortic Aneurysm"
Principal Investigator: Carey, David J Annual Direct Costs: $13,870 (subcontract)
Agency: Pennsylvania Department of Health PA CURE Period: 6/12 - 6/16
The main goal of this project is to create a risk stratification tool for abdominal aortic aneurysm screening that combines clinical and genetic risk factor data and to test the tool in a real-world clinical setting.

"Genomic variability and symptomatology after traumatic brain injury" Annual Direct Costs: $281,851
Principal Investigator: Conley, Yvette P
Agency: NIH R01 NR013342 Period: 9/11 - 7/15
The main goal of this project is to determine the extent that variability in genes involved in the mitochondrial oxidative phosphorylation (OXPHOS) pathway, responsible for cellular energy production, is responsible for variability in symptoms related to cognition, behavior, and emotion after traumatic brain injury.

"Genetics of Emphysema: Extracellular Matrix and Growth Factor Signaling" Annual Direct Costs: $25,000
Principal Investigator: Urban, Zsolt
Agency: University of Pittsburgh BaCCoR Period: 7/11 - 6/12
The main goal of this project is to investigate genetic risk factors of pulmonary emphysema using a candidate gene approach.

"Genome-Wide Association Study of Food Allergy" Annual Direct Costs: $20,461 (subcontract)
Principal Investigator: Wang, Xiaobin
Agency: NIH/NIAID R56 AI080627 Period: 8/10 – 7/11
The major goals of this project are to carry out a genome-wide association study to identify susceptibility genes for food allergy.

"Genomic and Proteomic Biomarkers for Head and Neck Cancer Risk and Prognosis "
Principal Investigator: Egloff, Ann Marie
Agency: NIH/NCI K07 CA137140 Period: 9/09 - 8/14
The main goal of this project is to evaluate the effect of Epidermal growth factor receptor (EGFR) and gastrin-releasing peptide receptor (GRPR) on head and neck squamous cell carcinoma development/progression.

"Dental caries: whole genome association and gene x environment studies" Annual Direct Costs: $323,836
Principal Investigator: Marazita
Agency: NIH/NIDCR 5U01DE018903 Period: 8/07 - 5/10
The main goal of this project is to carry out genome-wide association and gene x environment studies of dental caries.

"Genome-wide association studies of prematurity and its complications"
Principal Investigator: Murray
Agency: NIH/NHGRI U01 HG004423 Period: 8/07 - 5/09
The main goal of this project is to carry out genome-wide association studies of preterm birth.

"Autism Genome Project" Annual Direct Costs: $178,580
Principal Investigator: Devlin
Agency: Autism Speaks/Medical Research Council No number Period: 3/07-3/10
The main goal of this project is to fine-map genes for autism and to carry out a genome-wide association study of autism.

"Statistical Genetic Analysis of Orofacial Cleft Families" Annual Direct Costs: $100,000
Principal Investigator: Maher
Agency: NIH/NIDCR R03DE016632 Period: 8/07 - 7/09
The main goal of this project is to study the genetics of nonsyndromic cleft lip with or without cleft palate, testing for gene x gene interaction, association, and to model diagnostic uncertainity.

"Predictors for drug selection and minimization in pediatric liver transplantation"
Principal Investigator: Sindhi Annual Direct Costs: $10,000 (subcontract)
Agency: NIH/NIAID R01AI073895 Period: 9/06-8/10
The main goal of this project is to minimize organ rejection and immunosuppressant toxicity, in each child with liver transplantation (LTx), by searching for genes influencing rejector/non-rejector status.

"Alcoholism Susceptibility Genes in High Density Families" Annual Direct Costs: $495,266
Principal Investigator: Hill
Agency: NIH/NIAAA R01AA015168 Period: 6/05 – 5/11 (no cost extension)
The main goal of this project is to localize alcoholism susceptibility genes using a genetically informative set of pedigrees.

"Human QTL Mapping with Selected Samples" Annual Direct Costs: $125,000
Principal Investigator: Feingold
Agency: NIH R01HG002374 Period: 07/00 - 07/08

The main goal of this project is to develop powerful statistics for QTL mapping in humans with selected samples, and powerful designs for selecting such samples. (NOTE: My support on this grant started 7/1/05).

"Indo-US Collaboration in Genomic Studies on Diabetes"
Principal Investigator: Sanghera
Agency: NIH/Fogarty 5K01TW006087 Period: 9/02 - 8/08
The main goal of this project is to carry out a genome-wide scan for Type 2 Diabetes susceptibility genes in an endogamous community from North India.

"The Genetic Basis of a Disease Free Model of Aging" Annual Direct Costs: $175,000
Principal Investigator: Conley
Agency: NIH/NIA R21AG024177 Period: 6/05 – 3/07
The main goal of this project is to evaluate the feasibility of using the normal decline in human lens transparency with age as a biomarker of the aging process. The long term goals of this project are to utilize these lens measurements to conduct a genome wide scan for gene involved with the normal aging process using genetic epidemiologic analyses.

"India-US Research Training Program in Genetics" Total Direct Costs (TDC): $1,771,498
Principal Investigator: Daniel E. Weeks
Agency: NIH/Fogarty 5D43TW006180 Period: 9/02 - 8/10 (no cost extension)
The main goal of this project is to enhance genetic-epidemiological capacity in India via a pre- and post-doctoral training program.

"Enhanced linkage maps from family-based genetics studies" Total Direct Costs (TDC): $200,000
Principal Investigator: Matise; Co-Investigator: Daniel E. Weeks
Agency: NIH 1R01HL071029 Period: 9/02 – 8/05
The main goal of this project is to build highly-precise sex-specific linkage maps utilizing thousands of individuals who have already been genotyped.

"Genetic epidemiology of otitis media" Annual Direct Costs: 308,793
Principal Investigator: Casselbrant; Co-Investigator: Daniel E. Weeks
Agency: NIH/NIDCD 1 R01 DC005630 Period: 8/02 – 7/07
The main goal of this project is to carry out a genome-wide screen for genes influencing otitis media in a sample of 500 affected sib pairs.

"Robust integrated system for mapping complex diseases" TDC: $2,009,755
Principal Investigator: Daniel E. Weeks
Agency: NIH/NIA 9R01MH064205 Period: 9/98 – 6/06
The main goal of this project is to develop robust allele-sharing statistics and to implement them in a program that uses Markov chain Monte Carlo methods to compute approximate likelihoods on large pedigrees.

"Discovering Genes for Mental Health" (NRSA Institutional Training Grant) TDC: $501,000
Principal Investigator and Program Director: Daniel E. Weeks
Agency: NIH/NIMH T32 MH20053 Period: 7/00 – 6/06
The Training Program in Statistical Genetics provides support for post-doctoral training at the interface of human genetics, statistics, and psychiatry.

"Genome scan for obesity susceptibility loci among Samoans" Total Direct Costs (TDC): $124,170
Co-Investigator: Daniel E. Weeks (McGarvey/subcontract to Weeks)
Agency: NIH/NIDDK 1 R01 DK59642 Period: 9/00 – 7/06
The major goal of this project is to carry out a genome-wide scan for obesity susceptibility loci among the Samoans.

"Genome scan for NIDDM susceptibility genes among Samoans" TDC: $102,616
Co-Investigator: Daniel E. Weeks (Deka/subcontract to Weeks)
Agency: NIH 5 R01 DK55406 Period: 6/98 – 4/03
The major goal of this project is to carry out a genome-wide scan for NIDDM susceptibility genes among the Samoans.

"Rapid multipoint methods for mapping complex diseases" TDC: $401,020
Co-Investigator: Daniel E. Weeks, Ph.D (O'Connell)
Agency: NIH/NIA 5 R01 AG16992 Period: 9/98 – 8/01
The major goal of this project is to develop a faster engine for computing likelihoods on general pedigrees.

"Novel algorithms for genetic mapping" TDC: $488,270
Principal Investigator: Daniel E. Weeks
Agency: NIH/NCHGR 5 R01 HG00932 Period: 9/93 – 8/00
The major goals of this project are to improve and extend the capabilities of our memory-efficient computer program, VITESSE, for extremely rapid computation of exact multipoint likelihoods.

"Statistical methods and software tools for the genetic analysis of monogenic and multifactorial diseases"
Principal Investigator: Daniel E. Weeks
Agency: European Community BIOMED EC PL 96 2532 Period: 7/97 – 6/00
The major goals of this project are to develop and improve theoretical models and software tools for analysis of the genetics of monogenic and multifactorial diseases. In particular, we will integrate VITESSE with the REGRESS program.

"Collaborative molecular genetic study of autism"
Co-Investigator: Daniel E. Weeks (Rutter and Monaco)
Agency: MRC Period: 5/95 - 11/98
To undertake a genomic scan for autism-susceptibility genes using an affected-sibling approach.

"Isolation of the gene causing dopa-responsive dystonia" TDC: $22,386
Co-Investigator: Daniel E. Weeks (Nygaard)
Agency: NIH/NINDS 5 R29 NS32035 Period: 7/93 – 6/98
The major goal of this project is to fine-map the dopa-responsive dystonia locus via linkage analysis of marker data collected on disease families by my collaborators at Columbia University.

"Linkage analysis of complex human traits using affected pedigree members" TDC: $496,915
Principal Investigator: Daniel E. Weeks
Agency: NIH/NCHGR 5 R29 HG00719 Period: 7/92 – 12/97
The major goals of this project are to evaluate by computer simulation, improve, and extend the Affected Pedigree Member (APM) method of linkage analysis.

"Linkage studies of candidate genes for growth and adult height"
Co-Investigator: Daniel E. Weeks (Finegold)
Agency: Genetech Foundation Period: 11/94 - 10/96
This grant supports linkage analysis of candidate genes for growth and adult height, using a sib-pair approach for mapping quantitative trait loci (QTLs).

"Multilocus models of genetic interference"
Principal Investigator: Daniel E. Weeks
Agency: NATO Collaborative Research Grant CRG 910950 Period: 1/92 - 12/94
This grant supported travel and living costs for collaborative research with Dr. Mark Lathrop. We explored genetic chiasma interference using human and mouse marker data, using a specialized linkage program that models interference in a more general way than was previously possible.

"Genetic linkage study of essential myoclonus"
Principal Investigator: Daniel E. Weeks (on subcontract; PI: Wilhelmsen)
Agency: Myoclonus Foundation Period: 3/91 - 3/93
This grant supported linkage analysis of marker data collected on disease families by my collaborators at Columbia University.

"Genetic linkage study of dopa-responsive dystonia"
Principal Investigator: Daniel E. Weeks (on subcontract; PI: Wilhelmsen)
Agency: Dystonia Medical Research Foundation Period: 3/91-3/92
This grant supported linkage analysis of marker data collected on the appropriate disease families by my collaborators at Columbia University.

"Linkage analysis methods for human gene mapping"
Co-Investigator: Daniel E. Weeks (Ott)
Agency: National Center for Human Genome Research R01HG00008 Period: 4/90 - 12/91
This grant supported the development of computer simulation methods in the area of human gene mapping. These simulation methods were used to investigate empirical significance levels of lod scores, interval estimation, the effects of unequal marker heterozygosity, and tests for heterogeneity of recombination fractions.