

Curriculum Vitae

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

Address:

Department of Human Genetics
University of Pittsburgh
Crabtree Hall, Room A303
130 DeSoto Street
Pittsburgh, PA 15261
USA

1 412 624 5388
FAX: 1 412 624 3020
weeks@pitt.edu

Website: <https://sites.pitt.edu/~weeks/>

ORCID: <https://orcid.org/0000-0001-9410-7228>

Web of Science Researcher ID: B-2995-2012

GitHub: <https://github.com/DanielEWeeks>

BlueSky: @statgendan.bsky.social

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

Fall 2007	Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2007) Professor, University of Pittsburgh, taught the majority of
Summer 2008	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 5 registered) Professor, University of Pittsburgh, led a break-out discussion section
Fall 2008	Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2008) Professor, University of Pittsburgh, co-taught half
Summer 2009	Quantitative Genetics (HUGEN 2033, 3 hrs/week, 3 credits, 6 registered) Professor, University of Pittsburgh, led two break-out discussion sections
Fall 2009	Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, June 1, 2009 and June 8, 2009) Professor, University of Pittsburgh, co-taught half
Fall 2010	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 6 registered) Professor, University of Pittsburgh, co-taught half
Spring 2012	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 10 registered) Professor, University of Pittsburgh, co-taught half
Fall 2012	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 10 registered) Professor, University of Pittsburgh, co-taught half
Spring 2014	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 14 registered, 1 auditor) Professor, University of Pittsburgh, co-taught half
Fall 2014	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 5 registered, 1 auditor) Professor, University of Pittsburgh, co-taught half
November 2015	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 1 auditor) 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
Fall 2016	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 4 registered, 2 auditors) Professor, University of Pittsburgh, co-taught half
Spring 2018	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 3 auditors) Professor, University of Pittsburgh, co-taught half
Fall 2018	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 10 registered, 8 auditors) Professor, University of Pittsburgh, co-taught half
Fall 2019	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 16 registered, 4 auditors) Professor, University of Pittsburgh, co-taught half
Spring 2020	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 10 registered, 1 auditor) Professor, University of Pittsburgh, co-taught ~80%
Fall 2020	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 8 registered, 2 auditors) Professor, University of Pittsburgh, co-taught half
Fall 2021	Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 19 registered, 1 auditor) Professor, University of Pittsburgh, co-taught half
Spring 2022	Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 9 registered, 1 auditor) Professor, University of Pittsburgh, co-taught ~70%
Fall 2022	Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 14 registered, 1 auditor) Professor, University of Pittsburgh, co-taught half
Spring 2023	Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 14 registered, 1 auditor) 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)
Fall 2025	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 16 registered)
Spring 2026	Professor, University of Pittsburgh, co-led Human Genetics Seminar (HUGEN 2025, 1 hr/week, 1 credit, 40 registered)
Spring 2026	Professor, University of Pittsburgh, taught Special Studies in Human Genetics – Statistical Genetics (HUGEN 2058, 1 hr/week, 1 credit, 2 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 <i>Genetic Epidemiological Methods for Dissection of Complex Human Traits</i> , 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 <i>Genetic Epidemiological Methods for Dissection of Complex Human Traits</i> , 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 <i>Genetic Epidemiological Methods for Dissection of Complex Human Traits</i> , 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. "Mitochondrial 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".
- 2020-25 Shuwei Liu, Ph.D., Human Genetics, "Deciphering Cognitive Function through DNA Methylation: Insights from the Exercise Program in Cancer and Cognition Study"
- 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".
2025-26	Ishta Madan, M.S. Biostatistics, "Acute and Longitudinal Overview of Traumatic Brain Injury Severity and Epigenetic Age Acceleration in Children"
2025-	Leah Fenimore, M.P.H. Public Health Genetics.
2025-	Lauren Spor, Ph.D. Human Genetics

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".
2020-25	Shuwei Liu, Ph.D., Human Genetics, "Deciphering Cognitive Function through DNA Methylation: Insights from the Exercise Program in Cancer and Cognition Study"
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".

2025-26	Ishta Madan, M.S. Biostatistics, "Acute and Longitudinal Overview of Traumatic Brain Injury Severity and Epigenetic Age Acceleration in Children"
2025-	Leah Fenimore, M.P.H. Public Health Genetics.
2025-	Nure Sharaf Nower Samia, Ph.D. Human Genetics.

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. Jeusun 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.
2020-2025	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.
2025-2026	Mentored Ishta Madan, a Biostatistics and Health Data Sciences M.S. student from the University of Pittsburgh on her thesis project.
2025-	Mentored Leah Fenimore, an M.P.H. Public Health Genetics student from the University of Pittsburgh on her M.P.H. thesis project.
2025-	Nure Sharaf Nower Samia, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my co-supervision.

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	Elynn Youm
Fall 2025	Leah Fenimore

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
 2024-2025 Dr. Carolyn Harris
 2024- Dr. Lacey Heinsberg

Service on Faculty Mentoring Committee

2023-2025 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
- 2025 Attended the Teaching Effectively with PowerPoint Teaching Workshop, June 26, 2025

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
41. Maestrini E, Monaco AP, McGrath JA, Ishida-Yamamoto A, Camisa C, Hovnanian A, Weeks DE, Lathrop M, Uitto J, Christiano AM (1996) A molecular defect in lorcin, the major component of the cornified cell envelope, underlies Vohwinkel's syndrome. Nature Genet **13**:70-77
42. Davis S[†], Sobel E, Marinov M, Weeks DE (1997) Analysis of bipolar disorder using affected relatives. Genetic Epidemiol **14**:605-610
43. Davis S[†], Weeks DE (1997) Comparison of nonparametric statistics for detection of linkage in nuclear families: Single-marker evaluation. Am J Hum Genet **61**:1431-1444
44. Hall FC, Brown MA, Weeks DE, Walsh S, Nicod A, Butcher S, Andrews LJ, Wordsworth BP (1997) A linkage study across the T cell receptor A and T cell receptor B loci in families with rheumatoid arthritis. Arthritis Rheum **40**:1798-1802
45. Julier C, Delépine M, Keavney B, Terwilliger J, Davis S[†], Weeks DE, Bui T, Jeunemaître X, Velho G, Froguel P, Ratcliffe P, Corvol P, Soubrier F, Lathrop GM (1997) Genetic susceptibility for human familial essential hypertension in a region of homology with blood pressure linkage on rat chromosome 10. Hum Mol Genet **6**:2077-2086
46. Kennedy S, Hadfield R, Barlow D, Weeks DE, Laird E, Golding S (1997) Use of MRI in genetic studies of endometriosis. Am J Med Genet **71**:371-372
47. O'Connell JR, Davis S[†], Weeks DE (1997) Analysis of a complex oligogenic disease. Genetic Epidemiol **14**:861-866

48. Terwilliger JD, Shannon WD[‡], Lathrop GM, Nolan JP, Goldin LR, Chase GA, Weeks DE (1997) True and false positive peaks in genome-wide scans: applications of length-biased sampling to linkage mapping. Am J Hum Genet **61**:430-438
49. Brown MA, Pile KD, Kennedy LG, Campbell D, Andrew L, March R, Shatford JL, Weeks DE, Calin A, Wordsworth BP (1998) A genome-wide screen for susceptibility loci in ankylosing spondylitis. Arthritis Rheum **41**:588-95
50. Duerr RH, Barmada MM, Zhang L, Davis S[†], Preston RA, Chensny LJ, Brown JL, Ehrlich GD, Weeks DE, Aston CE (1998) Linkage and association between inflammatory bowel disease and a locus on chromosome 12. Am J Hum Genet **63**:95-100
51. Hirano M, Garcia-de-Yebenes J, Jones AC, Nishino I, DiMauro S, Carlo JR, Bender AN, Hahn AF, Salberg LM, Weeks DE et al (1998) Mitochondrial neurogastrointestinal encephalomyopathy syndrome Maps to Chromosome 22q13.32-qter. Am J Hum Genet **63**:526-533
52. International Molecular Genetic Study of Autism Consortium [including Weeks DE] (1998) A full genome screen for autism with evidence for linkage to a region on chromosome 7q. Hum Mol Genet **7**:571-578
53. Jones AC, Yamamura Y, Almasy L, Bohlega S, Elibol B, Hubble J, Kuzuhara S, Uchida M, Yanagi T, Weeks DE et al (1998) Autosomal recessive juvenile parkinsonism maps to 6q25.2-q27 in four ethnic groups: detailed genetic mapping of the linked region. Am J Hum Genet **63**:80-87
54. Maestrini E, Marlow AJ, Weeks DE, Monaco AP (1998) Molecular genetic investigations of autism. J Autism Dev Disord **28**:427-37
55. O'Connell JR, Weeks DE (1998) PedCheck: A program for identifying genotype incompatibilities in linkage analysis. Am J Hum Genet **63**:259-66
56. Fisher SE, Marlow AJ, Lamb J, Maestrini E, Williams DF, Richardson AJ, Weeks DE, Stein JF, Monaco AP (1999) A quantitative trait locus on chromosome 6p influences different aspects of developmental dyslexia. Am J Hum Genet **64**:146-156
57. Hadfield RM, Manek S, Nakago S, Mukherjee S, Weeks DE, Mardon HJ, Barlow DH, et al (1999) Absence of a relationship between endometriosis and the N314D polymorphism of galactose-1-phosphate uridyl transferase in a UK population. Mol Hum Reprod **5**:990-993
58. Maestrini E, Lai C, Marlow A, Matthews N, Wallace S, Bailey A, Cook EH, Weeks DE, Monaco AP (1999) Serotonin transporter (5-HTT) and gamma-aminobutyric acid receptor subunit beta3 (GABRB3) gene polymorphisms are not associated with autism in the IMGSA families. Am J Med Genet **88**:492-496
59. Marinov M, Matise TC, Lathrop GM, Weeks DE (1999) A comparison of two algorithms, MultiMap and gene mapping system, for automated construction of genetic linkage maps. Genet Epidemiol **17**:S649-54
60. O'Connell JR, Weeks DE (1999) An optimal algorithm for automatic genotype elimination. Am J Hum Genet **65**:1733-40
61. Schaid DJ, Buetow K, Weeks DE, Wijsman E, Guo S-W, Ott J, Dahl C (1999) Discovery of cancer susceptibility genes: study designs, analytic approaches, and trends in technology. J Nat Cancer Inst Monographs **26**:1-16
62. Brown MA, Edwards S, Hoyle E, Campbell S, Laval S, Daly AK, Pile KD, Calin A, Ebringer A, Weeks DE, Wordsworth BP (2000) Polymorphisms of the CYP2D6 gene increase susceptibility to ankylosing spondylitis. Hum Mol Genet **9**:1563-1566

63. Conley YP, Erturk D, Keverline A, Mah TS, Keravala A, Barnes LR, Bruchis A, Hess JF, FitzGerald PG, Weeks DE, Ferrell RE, Gorin MB (2000) A juvenile-onset, progressive cataract locus on chromosome 3q21-q22 is associated with a missense mutation in the beaded filament structural protein-2. Am J Hum Genet **66**:1426-1431
64. Duerr RH, Barmada MM, Zhang L, Pfutzer R, Weeks DE (2000) High-density genome scan in Crohn disease shows confirmed linkage to chromosome 14q11-12. Am J Hum Genet **66**:1857-1862
65. Feingold E, Song KK[‡], Weeks DE (2000) Comparison of allele-sharing statistics for general pedigrees. Genet Epidemiol **19** (Suppl 1):S92-S98
66. Parkes M, Barmada MM, Satsangi J, Weeks DE, Jewell DP, Duerr RH (2000) The IBD2 locus shows linkage heterogeneity between ulcerative colitis and Crohn disease. Am J Hum Genet **67**:1605-10
67. Weeks DE, Conley YP, Mah TS, Paul TO, Morse L, Ngo-Chang J, Dailey JP, Ferrell RE, Gorin MB (2000) A full genome scan for age-related maculopathy. Hum Mol Genet **9**:1329-49
68. Hadfield RM, Manek S, Weeks DE, Mardon HJ, Barlow DH, Kennedy SH (2001) Linkage and association studies of the relationship between endometriosis and genes encoding the detoxification enzymes GSTM1, GSTT1 and CYP1A1. Mol Hum Reprod **7**:1073-1078
69. Hadfield RM, Pullen JG, Davies KF, Wolfensohn SE, Kemnitz JW, Weeks DE, Bennett ST, Kennedy SH (2001) Towards developing a genome-wide microsatellite marker set for linkage analysis in the rhesus macaque (*Macaca mulatta*): identification of 76 polymorphic markers. Am J Primatology **54**:223-31
70. International Molecular Genetic Study of Autism Consortium (including Weeks DE) (2001) Further characterization of the autism susceptibility locus AUTS1 on chromosome 7q. Hum Mol Genet **10**:973-982
71. International Molecular Genetic Study of Autism Consortium (including Weeks DE) (2001) A genomewide screen for autism: Strong evidence for linkage to chromosomes 2q, 7q, and 16p. Am J Hum Genet **69**:570-581. PMC1235486
72. Kennedy S, Bennett S, Weeks DE (2001) Genetics and infertility II: Affected sib-pair analysis in endometriosis. Hum Reprod Update **7**:411-418
73. Laval SH, Timms A, Edwards S, Bradbury L, Brophy S, Milicic A, Rubin L, Siminovitch KA, Weeks DE, Calin A, Wordsworth BP, Brown MA (2001) Whole-genome screening in ankylosing spondylitis: evidence of non-mhc genetic-susceptibility loci. Am J Hum Genet **68**:918-26
74. Marinov M, Weeks DE (2001) The complexity of linkage analysis with neural networks. Hum Hered **51**:169-76
75. Nakago S, Hadfield RM, Zondervan KT, Mardon H, Manek S, Weeks DE, Barlow D, Kennedy S (2001) Association between endometriosis and N-acetyl transferase 2 polymorphisms in a UK population. Mol Hum Reprod **7**:1079-1083
76. Sengul H[‡], Weeks DE, Feingold E (2001) A survey of affected-sibship statistics for nonparametric linkage analysis. Am J Hum Genet **69**:179-90
77. Sobel E, Sengul H[‡], Weeks DE (2001) Multipoint estimation of IBD probabilities at arbitrary positions among marker loci on general pedigrees. Hum Hered **52**:121-131

78. Tsai H-J[†], Sun G, Weeks DE, Kaushal R, Wolujewicz M, McGarvey ST, Tufa J, Viali S, Deka R (2001) Type 2 diabetes and three calpain-10 gene polymorphisms in Samoans: no evidence of association. Am J Hum Genet **69**:1236-44
79. Weeks DE, Conley YP, Tsai H-J[†], Mah TS, Rosenfeld PJ, Paul TO, Eller AW, Morse LS, Dailey JP, Ferrell RE, Gorin MB (2001) Age-related maculopathy: An expanded genome-wide scan with evidence of susceptibility loci within the 1q31 and 17q25 regions. Am J Ophthal **132**:682-692
80. Duerr RH, Barmada MM, Zhang L, Achkar JP, Cho JH, Hanauer SB, Brant SR, Bayless TM, Baldassano RN, Weeks DE (2002) Evidence for an inflammatory bowel disease locus on chromosome 3p26: linkage, transmission/disequilibrium and partitioning of linkage. Hum Mol Genet **11**:2599-2606
81. McGarvey ST, Forrest W, Weeks DE, Sun G, Smelser D, Tufa J, Viali S, Deka R (2002) Human leptin locus (LEP) alleles and BMI in Samoans. Int J Obes Relat Metab Disord **26**:783-8
82. Schmidt S, Klaver C, Saunders A, Postel E, De La Paz M, Agarwal A, Small K, Udari N, Ong J, Chalukya M, Nesburn A, Kenney C, Domurath R, Hogan M, Mah T, Conley Y, Ferrell R, Weeks D, de Jong P, van Duijn C, Haines J, Pericak-Vance M, Gorin M (2002) A pooled case-control study of the apolipoprotein E (APOE) gene in age-related maculopathy. Ophthalmic Genet **23**:209-23
83. Song KK[‡], Feingold E, Weeks DE (2002) Statistics for nonparametric linkage analysis of X-linked traits in general pedigrees. Am J Hum Genet **70**:181-91
84. Weeks DE, Conley YP, Ferrell RE, Mah TS, Gorin MB (2002) A tale of two genotypes: consistency between two high-throughput genotyping centers. Genome Res **12**:430-5
85. Zondervan K, Cardon L, Desrosiers R, Hyde D, Kemnitz J, Mansfield K, Roberts J, Scheffler J, Weeks DE, Kennedy S (2002) The genetic epidemiology of spontaneous endometriosis in the rhesus monkey. Ann N Y Acad Sci **955**:233-8
86. Goedecke V, Crane AM, Jaakkola E, Kaluza W, Laiho K, Weeks DE, Wilson J, Kauppi M, Kaarela K, Tuomilehto J, Wordsworth BP, Brown MA (2003) Interleukin 10 polymorphisms in ankylosing spondylitis. Genes Immun **4**:74-6
87. Mukhopadhyay N, Finegold DN, Larson MG, Cupples LA, Myers RH, Weeks DE (2003) A genome-wide scan for loci affecting normal adult height in the Framingham Heart Study. Hum Hered **55**:191-201
88. Mukhopadhyay N, Weeks DE (2003) Linkage analysis of adult height with parent-of origin effects in the Framingham Heart Study. BMC Genet **4(Suppl 1)**:S76
89. Mukhopadhyay N, Buxbaum SG, Weeks DE (2004) Comparative study of multipoint methods for genotype error detection. Hum Hered **58**:175-89
90. Schmidt S, Scott WK, Postel EA, Agarwal A, Hauser ER, De La Paz MA, Gilbert JR, Weeks DE, Gorin MB, Haines JL, Pericak-Vance MA (2004) Ordered subset linkage analysis supports a susceptibility locus for age-related macular degeneration on chromosome 16p12. BMC Genet **5**:18
91. Song KK[‡], Weeks DE, Sobel E, Feingold E (2004) Efficient simulation of p values for linkage analysis. Genet Epidemiol **26**:88-96
92. Tsai H-J[†], Sun G, Smelser D, Viali S, Tufa J, Jin L, Weeks DE, McGarvey ST, Deka R (2004) Distribution of genome-wide linkage disequilibrium based on microsatellite loci in the Samoan population. Human Genomics **1**:327-334

93. Weeks DE, Conley YP, Tsai H-J[†], Mah TS, Schmidt S, Postel EA, Agarwal A, Haines JL, Pericak-Vance MA, Rosenfeld PJ, Paul TO, Eller AW, Morse LS, Dailey JP, Ferrell RE, Gorin MB (2004) Age-related maculopathy: A genomewide scan with continued evidence of susceptibility loci within the 1q31, 10q26, and 17q25 regions. Am J Hum Genet **75**:174-89
94. Zondervan KT, Weeks DE, Colman R, Cardon LR, Hadfield R, Schleffler J, Trainor AG, Coe CL, Kemnitz JW, Kennedy SH (2004) Familial aggregation of endometriosis in a large pedigree of rhesus macaques. Hum Reprod **19**:448-455
95. Barnby G, Abbott A, Sykes N, Morris A, Weeks DE, Mott R, Lamb J, Bailey AJ, Monaco AP, the International Molecular Genetics Study of Autism Consortium (IMGSAC) (2005) Candidate gene screening and association analysis at the autism susceptibility locus on chromosome 16p; evidence for association at GRIN2A and ABAT. Am J Hum Genet **76**:950-966
96. Conley YP, Thalamuthu A[‡], Jakobsdottir J[†], Weeks DE, Mah T, Ferrell RE, Gorin MB (2005) Candidate gene analysis suggests a role for fatty acid biosynthesis and regulation of the complement system in the etiology of age-related maculopathy. Hum Mol Genet **14**:1991-2002
97. Fisher SA, Abecasis GR, Yashar BM, Zarepari S, Swaroop A, Iyengar SK, Klein BE, Klein R, Lee KE, Majewski J, Schultz DW, Klein ML, Seddon JM, Santangelo SL, Weeks DE, Conley YP, Mah TS, Schmidt S, Haines JL, Pericak-Vance MA, Gorin MB, Schultz HL, Pardi F, Lewis CM, Weber BHF (2005) Meta-analysis of genome scans of age-related macular degeneration. Hum Mol Genet **14**:2257-2264
98. Jakobsdottir J[†], Conley YP, Weeks DE, Mah TS, Ferrell RE, Gorin MB (2005) Susceptibility genes for age-related maculopathy on chromosome 10q26. Am J Hum Genet **77**:389-407
99. Lamb JA, Barnby G, Bonora E, Sykes N, Bacchelli E, Blasi F, Maestrini E, Broxholme J, Tzenova J, Weeks D, Bailey AJ, Monaco AP (2005) Analysis of IMGSAC autism susceptibility loci: evidence for sex limited and parent of origin specific effects. J Med Genet **42**:132-7
100. 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
101. Reck BH[‡], Mukhopadhyay N, Tsai H-J[†], Weeks DE (2005) Analysis of alcohol dependence phenotype on the COGA families using covariates to detect linkage. BMC Genet **6 Suppl 1**:S143
102. Thalamuthu A[‡], Mukhopadhyay I[‡], Ray A[†], Weeks DE (2005) A comparison between microsatellite and single-nucleotide polymorphism markers with respect to two measures of information content. BMC Genet **6 Suppl 1**:S27
103. Treloar SA, Wicks J, Nyholt DR, Montgomery GW, Bahlo M, Smith V, Dawson G, Mackay IJ, Weeks DE, Bennett ST, Carey A, Ewen-White KR, Duffy DL, O'Connor D T, Barlow DH, Martin NG, Kennedy SH (2005) Genomewide linkage study in 1,176 affected sister pair families identifies a significant susceptibility locus for endometriosis on chromosome 10q26. Am J Hum Genet **77**:365-376
104. Conley YP, Jakobsdottir J[†], Mah T, Weeks DE, Klein R, Kuller L, Ferrell RE, Gorin MB (2006) CFH, ELOVL4, PLEKHA1 and LOC387715 genes and susceptibility to age-related maculopathy: AREDS and CHS cohorts and meta-analyses. Hum Mol Genet **15**:3206-3218
105. Dai F[†], Weeks DE (2006) Ordered genotypes: an extended ITO method and a general formula for genetic covariance. Am J Hum Genet **78**:1035-1045
106. Jung J[‡], Weeks DE, Feingold E (2006) Gene-dropping vs. empirical variance estimation for allele-sharing linkage statistics. Genet Epidemiol **30**:652-665

107. Mukhopadhyay I[‡], Feingold E, Wang T, Elston RC, Weeks DE (2006) Treatment of uninformative families in mean allele sharing tests for linkage. Statistical Applications in Genetics and Molecular Biology **5**:Article 13
108. Sanghera DK, Bhatti JS, Bhatti GK, Ralhan SK, Wander GS, Singh JR, Bunker CH, Weeks DE, Kamboh MI, Ferrell RE (2006) The Khatri Sikh diabetes study (SDS): study design, methodology, sample collection, and initial results. Human Biology **78**:43-63
109. Tsai H-J[†], Weeks DE (2006) Comparison of methods incorporating quantitative covariates into affected sib pair linkage analysis. Genet Epidemiol **30**:77-93
110. Brock GN[‡], Weeks DE, Sobel E, Feingold E (2007) A hierarchical model for estimating significance levels of non-parametric linkage statistics for large pedigrees. Genet Epidemiol **31**:417-430
111. Dai F[†], Keighley ED, Sun G, Indugula SR, Roberts ST, Åberg K[‡], Smelser D, Tuitele J, Jin L, Deka R, Weeks DE, McGarvey ST (2007) Genome-wide scan for adiposity-related phenotypes in adults from American Samoa. Int J Obes (Lond) **31**:1832-1842
112. Mukhopadhyay N, Halder I, Bhattacharjee S, Weeks DE (2007) Two-dimensional linkage analyses of rheumatoid arthritis. BMC Proceedings **1**:(Suppl 1):S68. PMC2367460
113. Sengul H[‡], Bhattacharjee S, Feingold E, Weeks DE (2007) The elusive goal of pedigree weights. Genet Epidemiol **31**:51-65
114. Szatmari P, Paterson AD, Zwaigenbaum L, Roberts W, Brian J, Liu XQ, Vincent JB, et al. (including Weeks DE) (2007) Mapping autism risk loci using genetic linkage and chromosomal rearrangements. Nat Genet **39**:319-328
115. Zondervan KT, Treloar SA, Lin J, Weeks DE, Nyholt DR, Mangion J, MacKay IJ, Cardon LR, Martin NG, Kennedy SH, Montgomery GW (2007) Significant evidence of one or more susceptibility loci for endometriosis with near-Mendelian inheritance on chromosome 7p13-15. Hum Reprod **22**:717-728
116. Åberg K[‡], Dai F[†], Sun G, Keighley E, Indugula SR, Bausserman L, Viali S, Tuitele J, Deka R, Weeks DE, McGarvey ST (2008) A genome-wide linkage scan identifies multiple chromosomal regions influencing serum lipid levels in the population on the Samoan islands. J Lipid Res **49**:2169-2178. PMC2533415
117. Åberg K[‡], Sun G, Smelser D, Indugula SR, Tsai H-J[†], Steele MS, Tuitele J, Deka R, McGarvey ST, Weeks DE (2008) Applying novel genome-wide linkage strategies to search for loci influencing Type 2 Diabetes and adult height in American Samoa. Hum Biol **80**:99-123
118. 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. PMC2427220
119. Dai F[†], Sun G, Åberg K[‡], Keighley ED, Indugula SR, Roberts ST, Smelser D, Viali S, Jin L, Deka R, Weeks DE, McGarvey ST (2008) A whole genome linkage scan identifies multiple chromosomal regions influencing adiposity-related traits among Samoans. Ann Hum Genet **72**:780-792. PMC2574874
120. Hill SY, Hoffman EK, Zezza N, Thalamuthu A[‡], Weeks DE, Matthews AG[‡], Mukhopadhyay I[‡] (2008) Dopaminergic mutations: within-family association and linkage in multiplex alcohol dependence families. Am J Med Genet B Neuropsychiatr Genet **147B**:517-526
121. Jakobsdottir J[†], Conley YP, Weeks DE, Ferrell RE, Gorin MB (2008) C2 and CFB genes in age-related maculopathy and joint action with CFH and LOC387715 genes. PLoS ONE **3**:e2199. PMC2374901

122. Presson AP, Sobel EM, Pajukanta P, Plaisier C, Weeks DE, Åberg K[‡], Papp JC (2008) Merging microsatellite data: enhanced methodology and software to combine genotype data for linkage and association analysis. BMC Bioinformatics **9**:317. PMC2515855
123. Ray A[†], Weeks DE (2008) Relationship uncertainty linkage statistics (RULS): affected relative pair statistics that model relationship uncertainty. Genet Epidemiol **32**:313-324
124. Sindhi R, Higgs BW, Weeks DE, Ashokkumar C, Jaffe R, Kim C, Wilson P, Chien N, Glessner J, Talukdar A, Mazariegos G, Barmada MM, Frackelton E, Petro N, Eckert A, Hakonarson H, Ferrell R (2008) Genetic variants in major histocompatibility complex-linked genes associate with pediatric liver transplant rejection. Gastroenterology **135**:830-839. PMC2956436
125. 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 (2009) Susceptibility loci for adiposity phenotypes on 8p, 9p, and 16q in American Samoa and Samoa. Obesity (Silver Spring) **17**:518-524. PMC2879592
126. Åberg K[‡], Dai F[†], Viali S, Tuitele J, Sun G, Indugula SR, Deka R, Weeks DE, McGarvey ST (2009) Suggestive linkage detected for blood pressure related traits on 2q and 22q in the population on the Samoan islands. BMC Med Genet **10**:107. PMC2770055
127. Casselbrant ML, Mandel EM, Jung J[‡], Ferrell RE, Tekely K, Szatkiewicz JP, Ray A[†], Weeks DE (2009) Otitis media: a genome-wide linkage scan with evidence of susceptibility loci within the 17q12 and 10q22.3 regions. BMC Med Genet **10**:85. PMC2751750
128. Deka R, Xu L, Pal P, Toelupe PT, Laumoli TS, Xi H, Zhang G, Weeks DE, McGarvey ST (2009) A tagging SNP in *INSIG2* is associated with obesity-related phenotypes among Samoans. BMC Med Genet **10**:143. PMC2804583
129. Jakobsdottir J[†], Gorin MB, Conley YP, Ferrell RE, Weeks DE (2009) Interpretation of genetic association studies: markers with replicated highly significant odds ratios may be poor classifiers. PLoS Genet **5**:e1000337. PMC2629574
130. Weeks DE, Tang X, Kwon AM (2009) Casares' map function: No need for a 'corrected' Haldane's map function. Genetica **135**:305-307. PMC2704907
131. Chen W, Stambolian D, Edwards AO, Branham KE, Othman M, Jakobsdottir J[†], Tosakulwong N, Pericak-Vance MA, Campochiaro PA, Klein ML, Tan PL, Conley YP, Kanda A, Kopplin L, Li Y, Augustaitis KJ, Karoukis AJ, Scott WK, Agarwal A, Kovach JL, Schwartz SG, Postel EA, Brooks M, Baratz KH, Brown WL, Brucker AJ, Orlin A, Brown G, Ho A, Regillo C, Donoso L, Tian L, Kaderli B, Hadley D, Hagstrom SA, Peachey NS, Klein R, Klein BE, Gotoh N, Yamashiro K, Ferris Iii F, Fagerness JA, Reynolds R, Farrer LA, Kim IK, Miller JW, Corton M, Carracedo A, Sanchez-Salorio M, Pugh EW, Doheny KF, Brion M, Deangelis MM, Weeks DE, Zack DJ, Chew EY, Heckenlively JR, Yoshimura N, Iyengar SK, Francis PJ, Katsanis N, Seddon JM, Haines JL, Gorin MB, Abecasis GR, Swaroop A (2010) Genetic variants near *TIMP3* and high-density lipoprotein-associated loci influence susceptibility to age-related macular degeneration. Proc Natl Acad Sci U S A **107**:7401-7406. PMC2867722
132. Mukhopadhyay I[‡], Feingold E, Weeks DE, Thalamuthu A[‡] (2010) Association tests using kernel-based measures of multi-locus genotype similarity between individuals. Genet Epidemiol **34**:213-221. PMC3272581
133. He C, Weeks DE, Buyske S, Abecasis GR, Stewart WC, Matise TC (2011) Enhanced genetic maps from family-based disease studies: population-specific comparisons. BMC Med Genet **12**:15. PMC3037840

134. McKay GJ, Patterson CC, Chakravarthy U, Dasari S, Klaver CC, Vingerling JR, Ho L, de Jong PT, Fletcher AE, Young IS, Seland JH, Rahu M, Soubrane G, Tomazzoli L, Topouzis F, Vioque J, Hingorani AD, Sofat R, Dean M, Sawitzke J, Seddon JM, Peter I, Webster AR, Moore AT, Yates JR, Cipriani V, Fritsche LG, Weber BH, Keilhauer CN, Lotery AJ, Ennis S, Klein ML, Francis PJ, Stambolian D, Orlin A, Gorin MB, Weeks DE, Kuo CL, Swaroop A, Othman M, Kanda A, Chen W, Abecasis GR, Wright AF, Hayward C, Baird PN, Guymer RH, Attia J, Thakkinstian A, Silvestri G (2011) Evidence of association of APOE with age-related macular degeneration - a pooled analysis of 15 studies. Hum Mutat **32**:1407-1416. PMC3217135
135. McKay GJ, Silvestri G, Chakravarthy U, Dasari S, Fritsche LG, Weber BH, Keilhauer CN, Klein ML, Francis PJ, Klaver CC, Vingerling JR, Ho L, De Jong PT, Dean M, Sawitzke J, Baird PN, Guymer RH, Stambolian D, Orlin A, Seddon JM, Peter I, Wright AF, Hayward C, Lotery AJ, Ennis S, Gorin MB, Weeks DE, Kuo CL, Hingorani AD, Sofat R, Cipriani V, Swaroop A, Othman M, Kanda A, Chen W, Abecasis GR, Yates JR, Webster AR, Moore AT, Seland JH, Rahu M, Soubrane G, Tomazzoli L, Topouzis F, Vioque J, Young IS, Fletcher AE, Patterson CC (2011) Variations in apolipoprotein E frequency with age in a pooled analysis of a large group of older people. Am J Epidemiol **173**:1357-1364. PMC3145394
136. Ningappa M, Higgs BW, Weeks DE, Ashokkumar C, Duerr RH, Sun Q, Soltys KA, Bond GJ, Abu-Elmagd K, Mazariegos GV, Alissa F, Rivera M, Rudolph J, Squires R, Hakonarson H, Sindhi R (2011) NOD2 gene polymorphism rs2066844 associates with need for combined liver-intestine transplantation in children with short-gut syndrome. Am J Gastroenterol **106**:157-165
137. Sale MM, Chen WM, Weeks DE, Mychaleckyj JC, Hou X, Marion M, Segade F, Casselbrant ML, Mandel EM, Ferrell RE, Rich SS, Daly KA (2011) Evaluation of 15 functional candidate genes for association with chronic otitis media with effusion and/or recurrent otitis Media (COME/ROM). PLoS ONE **6**:e22297. PMC3156706
138. Schäffer AA, Lemire M, Ott J, Lathrop GM, Weeks DE (2011) Coordinated conditional simulation with SLINK and SUP of many markers linked or associated to a trait in large pedigrees. Hum Hered **71**:126-134. PMC3136384
139. Shaffer JR, Wang X, Feingold E, Lee M, Begum F, Weeks DE, Cuenco KT, Barmada MM, Wendell SK, Crosslin DR, Laurie CC, Doheny KF, Pugh EW, Zhang Q, Feenstra B, Geller F, Boyd HA, Zhang H, Melbye M, Murray JC, Weyant RJ, Crout R, McNeil DW, Levy SM, Slayton RL, Willing MC, Broffitt B, Vieira AR, Marazita ML (2011) Genome-wide association scan for childhood caries implicates novel genes. J Dent Res **90**:1457-1462. PMC3215757
140. Spencer KL, Olson LM, Schnetz-Boutaud N, Gallins P, Wang G, Scott WK, Agarwal A, Jakobsdottir J†, Conley Y, Weeks DE, Gorin MB, Pericak-Vance MA, Haines JL (2011) Dissection of chromosome 16p12 linkage peak suggests a possible role for CACNG3 variants in age-related macular degeneration susceptibility. Investigative Ophthalmology & Visual Science **52**:1748-1754. PMC3101690
141. Tsai H-J†, Hong X, Chen J, Liu X, Pearson C, Ortiz K, Hirsch E, Heffner L, Weeks DE, Zuckerman B, Wang X (2011) Role of African ancestry and gene-environment interactions in predicting preterm birth. Obstet Gynecol **118**:1081-1089. PMC3218119
142. Hill SY, Weeks DE, Jones BL, Zezza N, Stiffler S (2012) ASTN1 and alcohol dependence: Family-based association analysis in multiplex alcohol dependence families. Am J Med Genet B Neuropsychiatr Genet **159B**:445-455. PMC3623684
143. Karns R, Viali S, Tuitele J, Sun G, Cheng H, Weeks DE, McGarvey ST, Deka R (2012) Common variants in FTO are not significantly associated with obesity-related phenotypes among Samoans of Polynesia. Ann Hum Genet **76**:17-24. PMC3272784

144. Polk DE, Wang X, Feingold E, Shaffer JR, Weeks DE, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2012) Effects of smoking and genotype on the PSR index of periodontal disease in adults aged 18-49. *Int J Environ Res Public Health* **9**:2839-2850. PMC3447590
145. Ryckman KK, Feenstra B, Shaffer JR, Bream EN, Geller F, Feingold E, Weeks DE, Gadow E, Cosentino V, Saleme C, Simhan HN, Merrill D, Fong CT, Busch T, Berends SK, Comas B, Camelo JL, Boyd H, Laurie CC, Crosslin D, Zhang Q, Doheny KF, Pugh E, Melbye M, Marazita ML, Dagle JM, Murray JC (2012) Replication of a genome-wide association study of birth weight in preterm neonates. *J Pediatr* **160**:19-24. PMC3237813
146. Shaffer JR, Feingold E, Wang X, TCuenco K, Weeks DE, Desensi RS, Polk DE, Wendell S, Weyant RJ, Crout R, McNeil DW, Marazita ML (2012) Heritable patterns of tooth decay in the permanent dentition: principal components and factor analyses. *BMC Oral Health* **12**:7. PMC3328249
147. Shaffer JR, Polk DE, Feingold E, Wang X, Cuenco KT, Weeks DE, Desensi RS, Weyant RJ, Crout R, McNeil DW, Marazita ML (2012) Demographic, socioeconomic, and behavioral factors affecting patterns of tooth decay in the permanent dentition: principal components and factor analyses. *Community Dent Oral Epidemiol*. PMC3568445
148. Sofat R, Casas JP, Webster AR, Bird AC, Mann SS, Yates JR, Moore AT, Sepp T, Cipriani V, Bunce C, Khan JC, Shahid H, Swaroop A, Abecasis G, Branham KE, Zareparsy S, Bergen AA, Klaver CC, Baas DC, Zhang K, Chen Y, Gibbs D, Weber BH, Keilhauer CN, Fritsche LG, Lotery A, Cree AJ, Griffiths HL, Bhattacharya SS, Chen LL, Jenkins SA, Peto T, Lathrop M, Leveillard T, Gorin MB, Weeks DE, Ortube MC, Ferrell RE, Jakobsdottir J[†], Conley YP, Rahu M, Seland JH, Soubrane G, Topouzis F, Vioque J, Tomazzoli L, Young I, Whittaker J, Chakravarthy U, de Jong PT, Smeeth L, Fletcher A, Hingorani AD (2012) Complement factor H genetic variant and age-related macular degeneration: effect size, modifiers and relationship to disease subtype. *Int J Epidemiol* **41**:250-262. PMC3304526
149. Wang X, Shaffer JR, Zeng Z[†], Begum F[†], Vieira AR, Noel J, Anjomshoaa I, Cuenco KT, Lee MK, Beck J, Boerwinkle E, Cornelis MC, Hu FB, Crosslin DR, Laurie CC, Nelson SC, Doheny KF, Pugh EW, Polk DE, Weyant RJ, Crout R, McNeil DW, Weeks DE, Feingold E, Marazita ML (2012) Genome-wide association scan of dental caries in the permanent dentition. *BMC Oral Health* **12**:57. PMC3574042
150. Allen EK, Chen WM, Weeks DE, Chen F, Hou X, Mattos JL, Mychaleckyj JC, Segade F, Casselbrant ML, Mandel EM, Ferrell RE, Rich SS, Daly KA, Sale MM (2013) A genome-wide association study of chronic otitis media with effusion and recurrent otitis media identifies a novel susceptibility locus on chromosome 2. *J Assoc Res Otolaryngol* **14**:791-800. PMC3825021
151. Baylin A, Deka R, Tuitele J, Viali S, Weeks DE, McGarvey ST (2013) INSIG2 variants, dietary patterns and metabolic risk in Samoa. *Eur J Clin Nutr* **67**:101-107. PMC3634362
152. Chen W, Boutaoui N, Brehm JM, Han YY, Schmitz C, Cressley A, Acosta-Perez E, Alvarez M, Colon-Semidey A, Baccarelli AA, Weeks DE, Kolls JK, Canino G, Celedon JC (2013) ADCYAP1R1 and Asthma in Puerto Rican Children. *Am J Respir Crit Care Med* **187**:584-588. PMC3733434
153. Shaffer JR, Feingold E, Wang X, Lee M, TCuenco K, Weeks DE, Weyant RJ, Crout R, McNeil DW, Marazita ML (2013) GWAS of dental caries patterns in the permanent dentition. *J Dent Res* **92**:38-44. PMC3521449
154. Shaffer JR, Feingold E, Wang X, Weeks DE, Weyant RJ, Crout R, McNeil DW, Marazita ML (2013) Clustering tooth surfaces into biologically informative caries outcomes. *J Dent Res* **92**:32-37. PMC3521447

155. The AMD Gene Consortium, Fritsche LG, Chen W, Schu M, Yaspan BL, Yu Y, Thorleifsson G, Zack DJ, Arakawa S, Cipriani V, Ripke S, Igo RP, Jr., Buitendijk GH, Sim X, Weeks DE, Guymer RH, Merriam JE, Francis PJ, Hannum G, Agarwal A, Armbrecht AM, Audo I, Aung T, Barile GR, Benchaboune M, Bird AC, Bishop PN, Branham KE, Brooks M, Brucker AJ, Cade WH, Cain MS, Campochiaro PA, Chan CC, Cheng CY, Chew EY, Chin KA, Chowers I, Clayton DG, Cojocaru R, Conley YP, Cornes BK, Daly MJ, Dhillon B, Edwards AO, Evangelou E, Fagerness J, Ferreyra HA, Friedman JS, Geirsdottir A, George RJ, Gieger C, Gupta N, Hagstrom SA, Harding SP, Haritoglou C, Heckenlively JR, Holz FG, Hughes G, Ioannidis JP, Ishibashi T, Joseph P, Jun G, Kamatani Y, Katsanis N, C NK, Khan JC, Kim IK, Kiyohara Y, Klein BE, Klein R, Kovach JL, Kozak I, Lee CJ, Lee KE, Lichtner P, Lotery AJ, Meitinger T, Mitchell P, Mohand-Said S, Moore AT, Morgan DJ, Morrison MA, Myers CE, Naj AC, Nakamura Y, Okada Y, Orlin A, Ortube MC, Othman MI, Pappas C, Park KH, Pauer GJ, Peachey NS, Poch O, Priya RR, Reynolds R, Richardson AJ, Ripp R, Rudolph G, Ryu E, Sahel JA, Schaumberg DA, Scholl HP, Schwartz SG, Scott WK, Shahid H, Sigurdsson H, Silvestri G, Sivakumaran TA, Smith RT, Sobrin L, Souied EH, Stambolian DE, Stefansson H, Sturgill-Short GM, Takahashi A, Tosakulwong N, Truitt BJ, Tsironi EE, Uitterlinden AG, van Duijn CM, Vijaya L, Vingerling JR, Vithana EN, Webster AR, Wichmann HE, Winkler TW, Wong TY, Wright AF, Zelenika D, Zhang M, Zhao L, Zhang K, Klein ML, Hageman GS, Lathrop GM, Stefansson K, Allikmets R, Baird PN, Gorin MB, Wang JJ, Klaver CC, Seddon JM, Pericak-Vance MA, Iyengar SK, Yates JR, Swaroop A, Weber BH, Kubo M, Deangelis MM, Leveillard T, Thorsteinsdottir U, Haines JL, Farrer LA, Heid IM, Abecasis GR (2013) Seven new loci associated with age-related macular degeneration. *Nat Genet* **45**:433-439, 439e431-432. PMC3739472
156. Zeng Z[†], Shaffer JR, Wang X, Feingold E, Weeks DE, Lee M, Cuenco KT, Wendell SK, Weyant RJ, Crout R, McNeil DW, Marazita ML (2013) Genome-wide Association Studies of Pit-and-Fissure- and Smooth-surface Caries in Permanent Dentition. *J Dent Res* **92**:432-437. PMC3627505
157. Zhan X, Larson DE, Wang C, Koboldt DC, Sergeev YV, Fulton RS, Fulton LL, Fronick CC, Branham KE, Bragg-Gresham J, Jun G, Hu Y, Kang HM, Liu D, Othman M, Brooks M, Ratnapriya R, Boleda A, Grassmann F, von Strachwitz C, Olson LM, Buitendijk GH, Hofman A, van Duijn CM, Cipriani V, Moore AT, Shahid H, Jiang Y[†], Conley YP, Morgan DJ, Kim IK, Johnson MP, Cantsilieris S, Richardson AJ, Guymer RH, Luo H, Ouyang H, Licht C, Pluthero FG, Zhang MM, Zhang K, Baird PN, Blangero J, Klein ML, Farrer LA, DeAngelis MM, Weeks DE, Gorin MB, Yates JR, Klaver CC, Pericak-Vance MA, Haines JL, Weber BH, Wilson RK, Heckenlively JR, Chew EY, Stambolian D, Mardis ER, Swaroop A, Abecasis GR (2013) Identification of a rare coding variant in complement 3 associated with age-related macular degeneration. *Nat Genet* **45**:1375-1379. PMC3812337
158. Fan R, Wang Y, Mills JL, Carter TC, Lobach I, Wilson AF, Bailey-Wilson JE, Weeks DE, Xiong M (2014) Generalized functional linear models for gene-based case-control association studies. *Genet Epidemiol* **38**:622-637. PMC4189986
159. Hawley NL, Minster RL, Weeks DE, Viali S, Reupena MS, Sun G, Cheng H, Deka R, McGarvey ST (2014) Prevalence of adiposity and associated cardiometabolic risk factors in the Samoan genome-wide association study. *Am J Hum Biol* **26**:491-501. PMC4292846
160. Ratnapriya R, Zhan X, Fariss RN, Branham KE, Zipprer D, Chakarova CF, Sergeev YV, Campos MM, Othman M, Friedman JS, Maminishkis A, Waseem NH, Brooks M, Rajasimha HK, Edwards AO, Lotery A, Klein BE, Truitt BJ, Li B, Schaumberg DA, Morgan DJ, Morrison MA, Souied E, Tsironi EE, Grassmann F, Fishman GA, Silvestri G, Scholl HP, Kim IK, Ramke J, Tuo J, Merriam JE, Merriam JC, Park KH, Olson LM, Farrer LA, Johnson MP, Peachey NS, Lathrop M, Baron RV, Igo RP, Jr., Klein R, Hagstrom SA, Kamatani Y, Martin TM, Jiang Y[†], Conley Y, Sahel JA, Zack DJ, Chan CC, Pericak-Vance MA, Jacobson SG, Gorin MB, Klein ML, Allikmets R, Iyengar SK, Weber BH, Haines JL, Leveillard T, Deangelis MM, Stambolian D, Weeks DE, Bhattacharya SS, Chew EY, Heckenlively JR, Abecasis GR, Swaroop A (2014) Rare and common variants in extracellular matrix gene Fibrillin 2 (FBN2) are associated with macular degeneration. *Hum Mol Genet* **23**:5827-5837. PMC4189898

161. Schrodi SJ, Mukherjee S, Shan Y[†], Tromp G, Sninsky JJ, Callear AP, Carter TC, Ye Z, Haines JL, Brilliant MH, Crane PK, Smelser DT, Elston RC, Weeks DE (2014) Genetic-based prediction of disease traits: Prediction is very difficult, especially about the future. *Frontiers in Genetics* **5**:162 DOI: 10.3389/fgene.2014.00162. PMC4040440
162. Shaffer JR, Polk DE, Wang X, Feingold E, Weeks DE, Lee MK, Cuenco KT, Weyant RJ, Crout RJ, McNeil DW, Marazita ML (2014) Genome-wide association study of periodontal health measured by probing depth in adults ages 18-49 years. *G3 (Bethesda)* **4**:307-314. PMC3931564
163. Zeng Z[†], Feingold E, Wang X, Weeks DE, Lee M, Cuenco DT, Broffitt B, Weyant RJ, Crout R, McNeil DW, Levy SM, Marazita ML, Shaffer JR (2014) Genome-wide association study of primary dentition pit-and-fissure and smooth surface caries. *Caries Res* **48**:330-338. PMC4043868
164. Buhule OD[†], Minster RL, Hawley NL, Medvedovic M, Sun G, Viali S, Deka R, McGarvey ST, Weeks DE (2014) Stratified randomization controls better for batch effects in 450K methylation analysis: a cautionary tale. *Front Genet* **5**:354. PMC4195366
165. 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
166. Gorin MB, Weeks DE, Baron RV, Conley YP, Ortube MC, Nusinowitz S (2014) Endophenotypes for age-related macular degeneration: extending our reach into the preclinical stages of disease. *J Clin Med* **3**:1335-1356. PMC4284143
167. Baron RV, Conley YP, Gorin MB, Weeks DE (2015) dbVOR: a database system for importing pedigree, phenotype and genotype data and exporting selected subsets. *BMC Bioinformatics* **16**:91. PMC4407391
168. Bui DK, Jiang Y[†], Wei X, Ortube MC, Weeks DE, Conley YP, Gorin MB (2015) Genetic ME-a visualization application for merging and editing pedigrees for genetic studies. *BMC Res Notes* **8**:241. PMC4478623
169. Fung C, Zhou P, Joyce S, Trent K, Yuan JM, Grandis JR, Weissfeld JL, Romkes M, Weeks DE, Egloff AM (2015) Identification of epidermal growth factor receptor (EGFR) genetic variants that modify risk for head and neck squamous cell carcinoma. *Cancer Lett* **357**:549-556. PMC4295492
170. Hafren L, Einarsdottir E, Kentala E, Hammaren-Malmi S, Bhutta MF, MacArthur CJ, Wilmot B, Casselbrant M, Conley YP, Weeks DE, Mandel EM, Vaarala O, Kallio A, Melin M, Nieminen JK, Leinonen E, Kere J, Mattila PS (2015) Predisposition to childhood otitis media and genetic polymorphisms within the Toll-Like Receptor 4 (TLR4) locus. *PLoS One* **10**:e0132551. PMC4503307
171. Hong X, Hao K, Ladd-Acosta C, Hansen KD, Tsai HJ, Liu X, Xu X, Thornton TA, Caruso D, Keet CA, Sun Y, Wang G, Luo W, Kumar R, Fuleihan R, Singh AM, Kim JS, Story RE, Gupta RS, Gao P, Chen Z, Walker SO, Bartell TR, Beaty TH, Fallin MD, Schleimer R, Holt PG, Nadeau KC, Wood RA, Pongratic JA, Weeks DE, Wang X (2015) Genome-wide association study identifies peanut allergy-specific loci and evidence of epigenetic mediation in US children. *Nat Commun* **6**:6304. PMC4340086
172. Ozbek U[†], Feingold E, Weeks DE (2015) Efficient identification of null-allele single nucleotide polymorphism markers. *Hum Hered* **80**:79-89
173. Yan Q[‡], Weeks DE, Celedon JC, Tiwari HK, Li B, Wang X, Lin WY, Lou XY, Gao G, Chen W, Liu N (2015) Associating multivariate quantitative phenotypes with genetic variants in family samples with a novel kernel machine regression method. *Genetics* **201**:1329-1339. PMC4676518
174. Fan R, Chiu CY, Jung J, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Chen Z, Mills JL, Xiong M (2016) A Comparison Study of Fixed and Mixed Effect Models for Gene Level Association Studies of Complex Traits. *Genet Epidemiol* **40**:702-721. NIHMS817749

175. Fan R, Wang Y, Yan Q[‡], Ding Y, Weeks DE, Lu Z, Ren H, Cook RJ, Xiong M, Swaroop A, Chew EY, Chen W (2016) Gene-based association analysis for censored traits via fixed effect functional regressions. *Genet Epidemiol* **40**:133-143. PMC4724326
176. Fritsche LG, Igl W, Bailey JN, Grassmann F, Sengupta S, Bragg-Gresham JL, Burdon KP, Hebring SJ, Wen C, Gorski M, Kim IK, Cho D, Zack D, Souied E, Scholl HP, Bala E, Lee KE, Hunter DJ, Sardell RJ, Mitchell P, Merriam JE, Cipriani V, Hoffman JD, Schick T, Lechanteur YT, Guymer RH, Johnson MP, Jiang Y[†], Stanton CM, Buitendijk GH, Zhan X, Kwong AM, Boleda A, Brooks M, Gieser L, Ratnapriya R, Branham KE, Foerster JR, Heckenlively JR, Othman MI, Vote BJ, Liang HH, Souzeau E, McAllister IL, Isaacs T, Hall J, Lake S, Mackey DA, Constable IJ, Craig JE, Kitchner TE, Yang Z, Su Z, Luo H, Chen D, Ouyang H, Flagg K, Lin D, Mao G, Ferreyra H, Stark K, von Strachwitz CN, Wolf A, Brandl C, Rudolph G, Olden M, Morrison MA, Morgan DJ, Schu M, Ahn J, Silvestri G, Tsironi EE, Park KH, Farrer LA, Orlin A, Brucker A, Li M, C AC, Mohand-Said S, Sahel JA, Audo I, Benchaboune M, Cree AJ, Rennie CA, Goverdhan SV, Grunin M, Hagbi-Levi S, Campochiaro P, Katsanis N, Holz FG, Blond F, Blanche H, Deleuze JF, Igo RP, Jr., Truitt B, Peachey NS, Meuer SM, Myers CE, Moore EL, Klein R, Hauser MA, Postel EA, Courtenay MD, Schwartz SG, Kovach JL, Scott WK, Liew G, Tan AG, Gopinath B, Merriam JC, Smith RT, Khan JC, Shahid H, Moore AT, McGrath JA, Laux R, Brantley MA, Jr., Agarwal A, Ersoy L, Caramoy A, Langmann T, Saksens NT, de Jong EK, Hoyng CB, Cain MS, Richardson AJ, Martin TM, Blangero J, Weeks DE, Dhillon B, van Duijn CM, Doheny KF, Romm J, Klaver CC, Hayward C, Gorin MB, Klein ML, Baird PN, den Hollander AI, Fauser S, Yates JR, Allikmets R, Wang JJ, Schaumberg DA, Klein BE, Hagstrom SA, Chowers I, Lotery AJ, Leveillard T, Zhang K, Brilliant MH, Hewitt AW, Swaroop A, Chew EY, Pericak-Vance MA, DeAngelis M, Stambolian D, Haines JL, Iyengar SK, Weber BH, Abecasis GR, Heid IM (2016) A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. *Nat Genet* **48**:134-143. PMC4745342
177. Minster RL, Hawley NL, Su C-T, Sun G, Kershaw EE, Cheng H, Buhule OD[†], Lin J[†], Reupena MaS, Viali Si, 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. *Nat Genet* **48**:1049-1054. PMC5069069
178. Ningappa M, Ashokkumar C, Higgs BW, Sun Q, Jaffe R, Mazariegos G, Li D, Weeks DE, Subramaniam S, Ferrell R, Hakonarson H, Sindhi R (2016) Enhanced B cell alloantigen presentation and its epigenetic dysregulation in liver transplant rejection. *Am J Transplant* **16**:497-508. PMC5082419.
179. Yan Q[‡], Weeks DE, Tiwari HK, Yi N, Zhang K, Gao G, Lin WY, Lou XY, Chen W, Liu N (2016) Rare-variant kernel machine test for longitudinal data from population and family samples. *Hum Hered* **80**:126-138. PMC4916415
180. Yan Q[‡], Chen R, Sutcliffe JS, Cook EH, Weeks DE, Li B, Chen W (2016) The impact of genotype calling errors on family-based studies. *Sci Rep* **6**:28323. PMC4916415
181. Zeng Z[†], Weeks DE, Chen W, Mukhopadhyay N, Feingold E (2016) A pipeline for classifying relationships using dense SNP/SNV data and putative pedigree information. *Genet Epidemiol* **40**:161-171. PMC514699
182. Chen W, Wang T, Pino-Yanes M, Forno E, Liang L, Yan Q, Hu D, Weeks DE, Baccarelli A, Acosta-Perez E, Eng C, Han Y-Y, Boutaoui N, Laprise C, Davies GA, Hopkin JM, Moffatt MF, Cookson WOCM, Canino G, Burchard EG, Celedón JC (2017) An epigenome-wide association study of total serum immunoglobulin E in Hispanic children. *The Journal of Allergy and Clinical Immunology* **140**:571-577. PMID: PMC5500449
183. Chiu CY, Jung J, Chen W, Weeks DE, Ren H, Boehnke M, Amos CI, Liu A, Mills JL, Ting Lee ML, Xiong M, Fan R (2017) Meta-analysis of quantitative pleiotropic traits for next-generation sequencing with multivariate functional linear models. *Eur J Hum Genet* **25**:350-359. PMC5315507
184. Chiu CY, Jung J, Wang Y, Weeks DE, Wilson AF, Bailey-Wilson JE, Amos CI, Mills JL, Boehnke M, Xiong M, Fan R (2017) A comparison study of multivariate fixed models and Gene Association with Multiple Traits (GAMuT) for next-generation sequencing. *Genet Epidemiol* **41**:18-34. PMC5154843
185. Ding Y, Liu Y, Yan Q, Fritsche LG, Cook RJ, Clemons T, Ratnapriya R, Klein ML, Abecasis GR, Swaroop A, Chew EY, Weeks DE, Chen W (2017) Bivariate Analysis of Age-Related Macular Degeneration Progression Using Genetic Risk Scores. *Genetics* **206**:119-133. PMC5419464

186. Grassmann F, Kiel C, Zimmermann ME, Gorski M, Grassmann V, Stark K, International AMD Genomics Consortium (including Weeks DE), Heid IM, Weber BH (2017) Genetic pleiotropy between age-related macular degeneration and 16 complex diseases and traits. Genome Med **9**:29. PMC5368911
187. Hong X, Hao K, Ji H, Peng S, Sherwood B, Di Narzo A, Tsai HJ, Liu X, Burd I, Wang G, Ji Y, Caruso D, Mao G, Bartell TR, Zhang Z, Pearson C, Heffner L, Cerda S, Beaty TH, Fallin MD, Lee-Parritz A, Zuckerman B, Weeks DE, Wang X (2017) Genome-wide approach identifies a novel gene-maternal pre-pregnancy BMI interaction on preterm birth. Nat Commun **8**:15608. PMC5472707
188. Persad PJ, Heid IM, Weeks DE, Baird PN, de Jong EK, Haines JL, Pericak-Vance MA, Scott WK, International Age-Related Macular Degeneration Genomics Consortium (2017) Joint Analysis of Nuclear and Mitochondrial Variants in Age-Related Macular Degeneration Identifies Novel Loci TRPM1 and ABHD2/RLBP1. Invest Ophthalmol Vis Sci **58**:4027-4038. PMC5559178
189. Shan Y[†], Tromp G, Kuivaniemi H, Smelser DT, Verma SS, Ritchie MD, Elmore JR, Carey DJ, Conley YP, Gorin MB, Weeks DE (2017) Genetic risk models: Influence of model size on risk estimates and precision. Genet Epidemiol **41**:282-296. PMC5628612
190. 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
191. Govil M, Mukhopadhyay N, Weeks DE, Feingold E, Shaffer JR, Levy SM, Vieira AR, Slayton RL, McNeil DW, Weyant RJ, Crout RJ, Marazita ML (2018) Novel caries loci in children and adults implicated by genome-wide analysis of families. BMC Oral Health **18**:98. PMCID: PMC5984765
192. Krishnan M, Major TJ, Topless RK, Dewes O, Yu L, Thompson JMD, McCowan L, de Zoysa J, Stamp LK, Dalbeth N, Harre Hindmarsh J, Rapana N, Deka R, Eng WWH, Weeks DE, Minster RL, McGarvey ST, Viali S, Naseri T, Sefuiva Reupena M, Wilcox P, Grattan D, Shepherd PR, Shelling AN, Murphy R, Merriman TR (2018) Discordant association of the CREBRF rs373863828 A allele with increased BMI and protection from type 2 diabetes in Maori and Pacific (Polynesian) people living in Aotearoa/New Zealand. Diabetologia **61**:1603-1613. PMCID: PMC6434933
193. Liu X, Hong X, Tsai HJ, Mestan KK, Shi M, Kefi A, Hao K, Chen Q, Wang G, Caruso D, Geng H, Gao Y, He J, Kumar R, Wang H, Yu Y, Bartell T, Tan XD, Schleimer RP, Weeks DE, Pongracic JA, Wang X (2018) Genome-wide association study of maternal genetic effects and parent-of-origin effects on food allergy. Medicine (Baltimore) **97**:e0043. PMCID: PMC5851764
194. Ozbek U[†], Lin HM, Lin Y, Weeks DE, Chen W, Shaffer JR, Purcell SM, Feingold E (2018) Statistics for X-chromosome associations. Genet Epidemiol **42**:539-550. PMCID: PMC6394852
195. Yan Q, Ding Y, Liu Y, Sun T, Fritsche LG, Clemons T, Ratnapriya R, Klein ML, Cook RJ, Liu Y, Fan R, Wei L, Abecasis GR, Swaroop A, Chew EY, Group AR, Weeks DE, Chen W (2018) Genome-wide analysis of disease progression in age-related macular degeneration. Hum Mol Genet **27**:929-940. PMCID: PMC6059197
196. Biedrzycki RJ[†], Sier AE[†], Liu D[†], Dreikorn EN[†], Weeks DE (2019) Spinning convincing stories for both true and false association signals. Genet Epidemiol **43**:356-364.
197. Chiu CY, Yuan F, Zhang BS, Yuan A, Li X, Fang HB, Lange K, Weeks DE, Wilson AF, Bailey-Wilson JE, Musolf AM, Stambolian D, Lakhali-Chaieb ML, Cook RJ, McMahon FJ, Amos CI, Xiong M, Fan R (2019) Linear mixed models for association analysis of quantitative traits with next-generation sequencing data. Genet Epidemiol **43**:189-206. PMCID: PMC6375753
198. Forno E, Wang T, Qi C, Yan Q, Xu CJ, Boutaoui N, Han YY, Weeks DE, Jiang Y, Rosser F, Vonk JM, Brouwer S, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Koppelman GH, Chen W, Celedon JC (2019) DNA methylation in nasal epithelium, atopy, and atopic asthma in children: a genome-wide study. Lancet Respir Med **7**:336-346. PMCID: PMC6441380

199. Grassmann F, Kiel C, den Hollander AI, Weeks DE, Lotery A, Cipriani V, Weber BHF, International Age-related Macular Degeneration Genomics C (2019) Y chromosome mosaicism is associated with age-related macular degeneration. *Eur J Hum Genet* **27**:36-41. PMID: PMC6303255
200. Carlson JC, Rosenthal SL[‡], Russell EM[†], Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Tuitele J, Deka R, McGarvey ST, Weeks DE, Minster RL (2020) A missense variant in CREBRF is associated with taller stature in Samoans. *Am J Hum Biol*:e23414
201. Forno E, Zhang R, Jiang Y, Kim S, Yan Q, Ren Z, Han YY, Boutaoui N, Rosser F, Weeks DE, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Chen W, Celedon JC (2020) Transcriptome-wide and differential expression network analyses of childhood asthma in nasal epithelium. *J Allergy Clin Immunol* **146**:671-675. PMID: PMC7438239
202. Arockiaraj AI[†], Liu D[†], Shaffer JR, Koleck TA, Crago EA, Weeks DE, Conley YP (2020) Methylation Data Processing Protocol and Comparison of Blood and Cerebral Spinal Fluid Following Aneurysmal Subarachnoid Hemorrhage. *Front Genet* **11**:671. PMID: PMC7332758
203. Harris DN, Kessler MD, Shetty AC, Weeks DE, Minster RL, Browning S, Cochrane EE, Deka R, Hawley NL, Reupena MS, Naseri T, Trans-Omics for Precision Medicine Consortium, TOPMed Population Genetics Working Group, McGarvey ST, O'Connor TD (2020) Evolutionary history of modern Samoans. *Proc Natl Acad Sci U S A* **117**:9458-9465 PMID: PMC7196816
204. Hawley NL, Pomer A, Rivara AC, Rosenthal SL[‡], Duckham RL, Carlson JC, Naseri T, Reupena MS, Selu M, Lupematisila V, Unasa F, Vesi L, Fatu T, Unasa S, Faasalele-Savusa K, Wetzel AI, Soti-Ulberg C, Prescott AT, Siufaga G, Penaia C, To SB, LaMonica LC, Lameko V, Choy CC, Crouter SE, Redline S, Deka R, Kershaw EE, Urban Z, Minster RL, Weeks DE, McGarvey ST (2020) Exploring the paradoxical relationship of a Creb 3 Regulatory Factor missense variant with body mass index and diabetes among Samoans: study protocol for the Soifua Manuia ('Good Health') observational cohort study. *JMIR Research Protocols* **9**:e17329. PMID: PMC7413272
205. Heinsberg LW[†], Arockiaraj AI[†], Crago EA, Ren D, Shaffer JR, Sherwood PR, Sereika SM, Weeks DE, Conley YP (2020) Genetic Variability and Trajectories of DNA Methylation May Support a Role for *HAMP* in Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. *Neurocrit Care* **32**:550-563. PMID: PMC6981002
206. Heinsberg LW[†], Alexander SA, Crago EA, Minster RL, Poloyac SM, Weeks DE, Conley YP (2020) Genetic Variability in the Iron Homeostasis Pathway and Patient Outcomes After Aneurysmal Subarachnoid Hemorrhage. *Neurocrit Care* **33**:749-758. PMID: PMC7541432
207. Yan Q, Weeks DE, Xin H, Swaroop A, Chew EY, Huang H, Ding Y, Chen W (2020) Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. *Nat Mach Intell* **2**:141-150. PMID: PMC7153739
208. Arslanian KJ, Fidow UT, Atanoa T, Unasa-Apelu F, Naseri T, Wetzel AI, Pomer A, Duckham RL, McGarvey ST, Strayer JA, Kershaw EE, Weeks DE, Hawley NL (2021) A missense variant in CREBRF, rs373863828, is associated with fat-free mass, not fat mass in Samoan infants. *Int J Obes (Lond)* **45**:45-55
209. Carlson JC, Weeks DE, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Tuitele J, Deka R, McGarvey ST, Minster RL (2021) Genome-wide association studies in Samoans give insight into the genetic architecture of fasting serum lipid levels. *J Hum Genet* **66**:111-121. PMID: PMC7785639
210. Heinsberg LW[‡], Ray M, Conley YP, Roberts JM, Jeyabalan A, Hubel CA, Weeks DE, Schmella MJ (2021) An Exploratory Study of Epigenetic Age in Preeclamptic and Normotensive Pregnancy Reveals Differences by Self-Reported Race but Not Pregnancy Outcome. *Reprod Sci* **28**:3519-3528. PMID: PMC8526649
211. Heinsberg LW[‡], Weeks DE, Alexander SA, Minster RL, Sherwood PR, Poloyac SM, Deslouches S, Crago EA, Conley YP (2021) Iron homeostasis pathway DNA methylation trajectories reveal a role for STEAP3 metalloreductase in patient outcomes after aneurysmal subarachnoid hemorrhage. *Epigenetics Commun* **1**. PMID: PMC8788201

212. Heinsberg LW[‡], Liu D, Shaffer JR, Weeks DE, Conley YP (2021) Characterization of cerebrospinal fluid DNA methylation age during the acute recovery period following aneurysmal subarachnoid hemorrhage. *Epigenetics Commun* **1**. PMID: PMC8787331
213. Jiang Y[†], Chiu CY, Yan Q, Chen W, Gorin MB, Conley YP, Lakhal-Chaieb ML, Cook RJ, Amos CI, Wilson AF, Bailey-Wilson JE, McMahon FJ, Vazquez AI, Yuan A, Zhong X, Xiong M, Weeks DE, Fan R (2021) Gene-Based Association Testing of Dichotomous Traits with Generalized Functional Linear Mixed Models Using Extended Pedigrees: Applications to Age-Related Macular Degeneration. *J Am Stat Assoc* **116**:531-545. PMID: PMC8315575
214. Kanshana JS, Mattila PE, Ewing MC, Wood AN, Schoiswohl G, Meyer AC, Kowalski A, Rosenthal SL, Gingras S, Kaufman BA, Lu R, Weeks DE, McGarvey ST, Minster RL, Hawley NL, Kershaw EE (2021) A murine model of the human CREBRF^{R457Q} obesity-risk variant does not influence energy or glucose homeostasis in response to nutritional stress. *PLoS One* **16**:e0251895. PMID: PMC8439463
215. Ray M, Heinsberg LW[‡], Conley YP, Roberts JM, Jeyabalan A, Hubel CA, Weeks DE, Schmella MJ (2021) An exploratory study of white blood cell proportions across preeclamptic and normotensive pregnancy by self-identified race in individuals with overweight or obesity. *Hypertens Pregnancy* **40**:312-321. PMID: PMC8740522
216. Simon MT, Eftekharian SS, Ferdinandusse S, Tang S, Naseri T, Reupena MS, McGarvey ST, Minster RL, Weeks DE, Samoan Obesity, Lifestyle Genetic Adaptations Study Group, Nguyen DD, Lee S, Ellsworth KA, Vaz FM, Dimmock D, Pitt J, Abdenur JE (2021) ECHS1 disease in two unrelated families of Samoan descent: Common variant - rare disorder. *Am J Med Genet A* **185**:157-167. PMID: PMC7746601
217. Yan Q, Jiang Y, Huang H, Swaroop A, Chew EY, Weeks DE, Chen W, Ding Y (2021) Genome-Wide Association Studies-Based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. *Transl Vis Sci Technol* **10**:29. PMID: PMC7900884
218. Yan Q, Forno E, Celedon JC, Chen W, Weeks DE (2021) CHIT: an allele-specific method for testing the association between molecular quantitative traits and phenotype-genotype interaction. *Bioinformatics* **37**:4764-4770. PMID: PMC8711119
219. Treble-Barna A, Heinsberg LW[‡], Puccio AM, Shaffer JR, Okonkwo DO, Beers SR, Weeks DE, Conley YP (2021) Acute Brain-Derived Neurotrophic Factor DNA Methylation Trajectories in Cerebrospinal Fluid and Associations With Outcomes Following Severe Traumatic Brain Injury in Adults. *Neurorehabil Neural Repair* **35**:790-800. PMID: PMC8546867
220. Bastard P, Hsiao KC, Zhang Q, Choin J, Best E, Chen J, Gervais A, Bizien L, Materna M, Harmant C, Roux M, Hawley NL, Weeks DE, McGarvey ST, Sandoval K, Barberena-Jonas C, Quinto-Cortes CD, Hagelberg E, Mentzer AJ, Robson K, Coulibaly B, Seeleuthner Y, Bigio B, Li Z, Uze G, Pellegrini S, Lorenzo L, Sbihi Z, Latour S, Besnard M, Adam de Beaumais T, Jacqz Aigrain E, Beziat V, Deka R, Esera Tulifau L, Viali S, Reupena MS, Naseri T, McNaughton P, Sarkozy V, Peake J, Blincoe A, Primhak S, Stables S, Gibson K, Woon ST, Drake KM, Hill AVS, Chan CY, King R, Ameratunga R, Teiti I, Aubry M, Cao-Lormeau VM, Tangye SG, Zhang SY, Jouanguy E, Gray P, Abel L, Moreno-Estrada A, Minster RL, Quintana-Murci L, Wood AC, Casanova JL (2022) A loss-of-function IFNAR1 allele in Polynesia underlies severe viral diseases in homozygotes. *J Exp Med* **219**. PMID: PMC9026234
221. Blobner BM, Kirabo A, Kashlan OB, Sheng S, Arnett DK, Becker LC, Boerwinkle E, Carlson JC, Gao Y, Gibbs RA, He J, Irvin MR, Kardina SLR, Kelly TN, Kooperberg C, McGarvey ST, Menon VK, Montasser ME, Naseri T, Redline S, Reiner AP, Reupena MS, Smith JA, Sun X, Vaidya D, Viaud-Martinez KA, Weeks DE, Yanek LR, Zhu X, NHLBI Trans-Omics for Precision Medicine Consortium, Minster RL, Kleyman TR (2022) Rare variants in genes encoding subunits of the epithelial Na⁽⁺⁾ channel are associated with blood pressure and kidney function. *Hypertension* **79**:2573-2582. PMID: PMC9669116
222. Fu H[†], Hawley NL, Carlson JC, Russell EM[‡], Pomer A, Cheng H, Naseri T, Reupena MS, Deka R, Choy CC, McGarvey ST, Minster RL, Weeks DE (2022) The missense variant, rs373863828, in CREBRF plays a role in longitudinal changes in body mass index in Samoans. *Obes Res Clin Pract* **16**:220-227. PMID: PMC9373717

223. Heinsberg LW[‡], Carlson JC, Pomer A, Cade BE, Naseri T, Reupena MS, Weeks DE, McGarvey ST, Redline S, Hawley NL (2022) Correlates of daytime sleepiness and insomnia among adults in Samoa. *Sleep Epidemiol* **2**. PMID: PMC9635619
224. Heinsberg LW[‡], Weeks DE (2022) Post hoc power is not informative. *Genet Epidemiol* **46**:390-394. PMID: PMC9452450
225. Liu D, Zusman BE, Shaffer JR, Li Y, Arockiaraj AI[†], Liu S[†], Weeks DE, Desai SM, Kochanek PM, Puccio AM, Okonkwo DO, Conley YP, Jha RM (2022) Decreased DNA Methylation of RGMA is Associated with Intracranial Hypertension After Severe Traumatic Brain Injury: An Exploratory Epigenome-Wide Association Study. *Neurocrit Care* **37**:26-37. PMID: PMC9287123
226. Russell EM[‡], Carlson JC, Krishnan M[‡], Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Viali S, Tuitele J, Major TJ, Miljkovic I, Merriman TR, Deka R, Weeks DE, McGarvey ST, Minster RL (2022) CREBRF missense variant rs373863828 has both direct and indirect effects on type 2 diabetes and fasting glucose in Polynesian peoples living in Samoa and Aotearoa New Zealand. *BMJ Open Diabetes Res Care* **10**. PMID: PMC8845200
227. Carlson JC, Krishnan M[‡], Rosenthal SL, Russell EM[‡], Zhang JZ[†], Hawley NL, Moors J, Cheng H, Dalbeth N, de Zoysa JR, Watson H, Qasim M, Murphy R, Naseri T, Reupena MS, Viali S, Stamp LK, Tuitele J, Kershaw EE, Deka R, McGarvey ST, Merriman TR, Weeks DE, Minster RL (2023) A stop-gain variant in BTNL9 is associated with atherogenic lipid profiles. *HGG Adv* **4**:100155. PMID: PMC9630829
228. Heinsberg LW[‡], Hawley NL, Duckham RL, Pomer A, Rivara AC, Naseri T, Reupena MS, Weeks DE, McGarvey ST, Minster RL (2023) Validity of anthropometric equation-based estimators of fat mass in Samoan adults. *Am J Hum Biol* **35**:e23838. PMID: PMC10023273
229. Heinsberg LW[‡], Koleck TA, Ray M[‡], Weeks DE, Conley YP (2023) Advancing nursing research through interactive data visualization with R shiny. *Biol Res Nurs* **25**:107-116. PMID: PMC9900251
230. Heinsberg LW[‡], Weeks DE (2023) dbGaPCheckup: pre-submission checks of dbGaP-formatted subject phenotype files. *BMC Bioinformatics* **24**:77. PMID: PMC9985192
231. Krishnan M[‡], Phipps-Green A, Russell EM, Major TJ, Cadzow M, Stamp LK, Dalbeth N, Hindmarsh JH, Qasim M, Watson H, Liu S, Carlson JC, Minster RL, Hawley NL, Naseri T, Reupena MS, Deka R, McGarvey ST, Merriman TR, Murphy R, Weeks DE (2023) Association of rs9939609 in FTO with BMI among Polynesian peoples living in Aotearoa New Zealand and other Pacific nations. *Journal of Human Genetics* **68**:463-468. PMID: PMC10313811
232. Liu S[†], Fu H[†], Ray M[‡], Heinsberg LW[‡], Conley YP, Anderson CM, Hubel CA, Roberts JM, Jeyabalan A, Weeks DE, Schmella MJ (2023) A longitudinal epigenome-wide association study of preeclamptic and normotensive pregnancy. *Epigenetics Commun* **3**. PMID: PMC10101051
233. Moors J, Krishnan M[‡], Sumpter N, Takei R, Bixley M, Cadzow M, Major TJ, Phipps-Green A, Topless R, Merriman M, Rutledge M, Morgan B, Carlson JC, Zhang JZ, Russell EM, Sun G, Cheng H, Weeks DE, Naseri T, Reupena MS, Viali S, Tuitele J, Hawley NL, Deka R, McGarvey ST, de Zoysa J, Murphy R, Dalbeth N, Stamp L, Taumoepeau M, King F, Wilcox P, Rapana N, McCormick S, Minster RL, Merriman TR, Leask M (2023) A Polynesian-specific missense CETP variant alters the lipid profile. *HGG Adv* **4**:100204. PMID: PMC10209881
234. Treble-Barna A, Heinsberg LW[‡], Stec Z, Breazeale S, Davis TS, Kesbhat AA, Chattopadhyay A, VonVille HM, Ketchum AM, Yeates KO, Kochanek PM, Weeks DE, Conley YP (2023) Brain-derived neurotrophic factor (BDNF) epigenomic modifications and brain-related phenotypes in humans: A systematic review. *Neurosci Biobehav Rev* **147**:105078. PMID: PMC10164361
235. Zhang JZ[†], Heinsberg LW[‡], Krishnan M[‡], Hawley NL, Major TJ, Carlson JC, Harre Hindmarsh J, Watson H, Qasim M, Stamp LK, Dalbeth N, Murphy R, Sun G, Cheng H, Naseri T, Reupena MS, Kershaw EE, Deka R, McGarvey ST, Minster RL, Merriman TR, Weeks DE (2023) Multivariate analysis of a missense variant in CREBRF reveals associations with measures of adiposity in people of Polynesian ancestries. *Genet Epidemiol* **47**:105-118. PMID: PMC9892232

236. Heinsberg LW[‡], Niu S, Arslanian KJ, Chen R, Bedi M, Unasa-Apelu F, Fidow UT, Soti-Ulberg C, Conley YP, Weeks DE, Ng CA, Hawley NL (2024) Characterization of per- and polyfluoroalkyl substances (PFAS) concentrations in a community-based sample of infants from Samoa. *Chemosphere* **353**:141527. PMID: PMC10997188
237. Heinsberg LW[‡], Pomer A, Cade BE, Carlson JC, Naseri T, Reupena MS, Viali S, Weeks DE, McGarvey ST, Redline S, Hawley NL (2024) Characterization of sleep apnea among a sample of adults from Samoa. *Sleep Epidemiol* **4**. PMID: PMC11694763
238. Rivara AC, Russell EM[‡], Carlson JC, Pomer A, Naseri T, Reupena MS, Manna SL, Viali S, Minster RL, Weeks DE, DeLany JP, Kershaw EE, McGarvey ST, Hawley NL (2024) Associations between fasting glucose rate-of-change and the missense variant, rs373863828, in an adult Samoan cohort. *PLoS One* **19**:e0302643. PMID: PMC11146712
239. Erdogan-Yildirim Z, Carlson JC, Krishnan M[‡], Zhang JZ[†], Lambert-Messerlian G, Naseri T, Viali S, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2025) A Genome-Wide Association Study of Anti-Mullerian Hormone (AMH) Levels in Samoan Women. *Genes (Basel)* **16**. PMID: PMC12294779
240. Heinsberg LW, Davis TS, Maher D, Bender CM, Conley YP, Weeks DE (2025) Multivariate Bayesian Analyses in Nursing Research: An Introductory Guide. *Biol Res Nurs* **27**:316-325. PMID: PMC12289463
241. Heinsberg LW, Loia M, Tasele S, Faasalele-Savusa K, Carlson JC, Anesi S, Desobry K, Yuchongco E, Guevara BF, Sesaga A, Iloilo A, Tofaeono V, Bryan K, Tauasosi-Posiulai T, Kershaw EE, Conley YP, Weeks DE, Hawley NL, Muasau-Howard BT (2025) Study protocol for the Health Outcomes in Pregnancy and Early Childhood (HOPE) Study: A mother-infant study in American Samoa. *PLoS One* **20**:e0326644. PMID: PMC12435730
242. Liu S[†], Liu D, Bender CM, Erickson KI, Sereika SM, Shaffer JR, Weeks DE, Conley YP (2025) DNA methylation associations with cognitive function in early-stage hormone receptor-positive breast cancer patients. *Epigenomics* **17**:879-889. PMID: PMC12369613
243. Heinsberg LW, Kesbhat A, Petersen B, Kaseman L, Stec Z, Anton N, Kochanek PM, Yeates KO, Weeks DE, Conley YP, Treble-Barna A (2026) Differential DNA Methylation of the Brain-Derived Neurotrophic Factor Gene is Observed after Pediatric Traumatic Brain Injury Compared with Orthopedic Injury. *J Neurotrauma* **43**:575-584. PMID: PMC12990021
244. Ray M, Heinsberg LW, McNeil RB, Grobman WA, Lueth A, Silver RM, Bairey Merz CN, Levine LD, Yee LM, Weeks DE, Conley YP, Catov JM (2026) Allostatic Load Mediates Associations between Race and Ethnicity and Hypertensive Disorders of Pregnancy. *Obstet Gynecol* **147**:242-254. PMID: PMC12412905

Trans-Omics for Precision Medicine (TOPMed) peer-reviewed manuscripts:

245. Bick AG, Weinstock JS, Nandakumar SK, Fulco CP, Bao EL, Zekavat SM, Szeto MD, Liao X, Leventhal MJ, Nasser J, Chang K, Laurie C, Burugula BB, Gibson CJ, Lin AE, Taub MA, Aguet F, Ardlie K, Mitchell BD, Barnes KC, Moscati A, Fornage M, Redline S, Psaty BM, Silverman EK, Weiss ST, Palmer ND, Vasani RS, Burchard EG, Kardina SLR, He J, Kaplan RC, Smith NL, Arnett DK, Schwartz DA, Correa A, de Andrade M, Guo X, Konkole BA, Custer B, Peralta JM, Gui H, Meyers DA, McGarvey ST, Chen IY, Shoemaker MB, Peyser PA, Broome JG, Gogarten SM, Wang FF, Wong Q, Montasser ME, Daya M, Kenny EE, North KE, Launer LJ, Cade BE, Bis JC, Cho MH, Lasky-Su J, Bowden DW, Cupples LA, Mak ACY, Becker LC, Smith JA, Kelly TN, Aslibekyan S, Heckbert SR, Tiwari HK, Yang IV, Heit JA, Lubitz SA, Johnsen JM, Curran JE, Wenzel SE, Weeks DE, Rao DC, Darbar D, Moon JY, Tracy RP, Buth EJ, Rafaels N, Loos RJF, Durda P, Liu Y, Hou L, Lee J, Kachroo P, Freedman BI, Levy D, Bielak LF, Hixson JE, Floyd JS, Whitsel EA, Ellinor PT, Irvin MR, Fingerlin TE, Raffield LM, Armasu SM, Wheeler MM, Sabino EC, Blangero J, Williams LK, Levy BD, Sheu WH, Roden DM, Boerwinkle E, Manson JE, Mathias RA, Desai P, Taylor KD, Johnson AD, NHLBI Trans-Omics for Precision Medicine Consortium, Auer PL, Kooperberg C, Laurie CC, Blackwell TW, Smith AV, Zhao H, Lange E, Lange L, Rich SS, Rotter JI, Wilson JG, Scheet P, Kitzman JO, Lander ES, Engreitz JM, Ebert BL, Reiner AP, Jaiswal S, Abecasis G, Sankaran VG, Kathiresan S, Natarajan P (2020) Inherited causes of clonal haematopoiesis in 97,691 whole genomes. *Nature* **586**:763-768. PMID: PMC7944936

246. Li X, Li Z, Zhou H, Gaynor SM, Liu Y, Chen H, Sun R, Dey R, Arnett DK, Aslibekyan S, Ballantyne CM, Bielak LF, Blangero J, Boerwinkle E, Bowden DW, Broome JG, Conomos MP, Correa A, Cupples LA, Curran JE, Freedman BI, Guo X, Hindy G, Irvin MR, Kardina SLR, Kathiresan S, Khan AT, Kooperberg CL, Laurie CC, Liu XS, Mahaney MC, Manichaikul AW, Martin LW, Mathias RA, McGarvey ST, Mitchell BD, Montasser ME, Moore JE, Morrison AC, O'Connell JR, Palmer ND, Pampana A, Peralta JM, Peyser PA, Psaty BM, Redline S, Rice KM, Rich SS, Smith JA, Tiwari HK, Tsai MY, Vasani RS, Wang FF, Weeks DE, Weng Z, Wilson JG, Yanek LR, NHLBI Trans-Omics for Precision Medicine Consortium, TOPMed Lipids Working Group, Neale BM, Sunyaev SR, Abecasis GR, Rotter JI, Willer CJ, Peloso GM, Natarajan P, Lin X (2020) Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. *Nat Genet* **52**:969-983. PMID: PMC7483769
247. Kwong AM, Blackwell TW, LeFaive J, de Andrade M, Barnard J, Barnes KC, Blangero J, Boerwinkle E, Burchard EG, Cade BE, Chasman DI, Chen H, Conomos MP, Cupples LA, Ellinor PT, Eng C, Gao Y, Guo X, Irvin MR, Kelly TN, Kim W, Kooperberg C, Lubitz SA, Mak ACY, Manichaikul AW, Mathias RA, Montasser ME, Montgomery CG, Musani S, Palmer ND, Peloso GM, Qiao D, Reiner AP, Roden DM, Shoemaker MB, Smith JA, Smith NL, Su JL, Tiwari HK, Weeks DE, Weiss ST, NHLBI Trans-Omics for Precision Medicine Consortium, TOPMed Analysis Working Group, Scott LJ, Smith AV, Abecasis GR, Boehnke M, Kang HM (2021) Robust, flexible, and scalable tests for Hardy-Weinberg equilibrium across diverse ancestries. *Genetics* **218**. PMID: PMC8128395
248. Natarajan P, Pampana A, Graham SE, Ruotsalainen SE, Perry JA, de Vries PS, Broome JG, Pirruccello JP, Honigberg MC, Aragam K, Wolford B, Brody JA, Antonacci-Fulton L, Arden M, Aslibekyan S, Assimes TL, Ballantyne CM, Bielak LF, Bis JC, Cade BE, Do R, Doddapaneni H, Emery LS, Hung YJ, Irvin MR, Khan AT, Lange L, Lee J, Lemaitre RN, Martin LW, Metcalf G, Montasser ME, Moon JY, Muzny D, O'Connell JR, Palmer ND, Peralta JM, Peyser PA, Stilp AM, Tsai M, Wang FF, Weeks DE, Yanek LR, Wilson JG, Abecasis G, Arnett DK, Becker LC, Blangero J, Boerwinkle E, Bowden DW, Chang YC, Chen YI, Choi WJ, Correa A, Curran JE, Daly MJ, Dutcher SK, Ellinor PT, Fornage M, Freedman BI, Gabriel S, Germer S, Gibbs RA, He J, Hveem K, Jarvik GP, Kaplan RC, Kardina SLR, Kenny E, Kim RW, Kooperberg C, Laurie CC, Lee S, Lloyd-Jones DM, Loos RJF, Lubitz SA, Mathias RA, Martinez KAV, McGarvey ST, Mitchell BD, Nickerson DA, North KE, Palotie A, Park CJ, Psaty BM, Rao DC, Redline S, Reiner AP, Seo D, Seo JS, Smith AV, Tracy RP, Vasani RS, Kathiresan S, Cupples LA, Rotter JI, Morrison AC, Rich SS, Ripatti S, Willer C, NHLBI Trans-Omics for Precision Medicine Consortium, FinnGen, Peloso GM (2021) Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. *Nat Commun* **12**:2182. PMID: PMC8042019
249. Stilp AM, Emery LS, Broome JG, Buth EJ, Khan AT, Laurie CA, Wang FF, Wong Q, Chen D, D'Augustine CM, Heard-Costa NL, Hohensee CR, Johnson WC, Juarez LD, Liu J, Mutalik KM, Raffield LM, Wiggins KL, de Vries PS, Kelly TN, Kooperberg C, Natarajan P, Peloso GM, Peyser PA, Reiner AP, Arnett DK, Aslibekyan S, Barnes KC, Bielak LF, Bis JC, Cade BE, Chen MH, Correa A, Cupples LA, de Andrade M, Ellinor PT, Fornage M, Franceschini N, Gan W, Ganesh SK, Graffelman J, Grove ML, Guo X, Hawley NL, Hsu WL, Jackson RD, Jaquish CE, Johnson AD, Kardina SLR, Kelly S, Lee J, Mathias RA, McGarvey ST, Mitchell BD, Montasser ME, Morrison AC, North KE, Nouraei SM, Oelsner EC, Pankratz N, Rich SS, Rotter JI, Smith JA, Taylor KD, Vasani RS, Weeks DE, Weiss ST, Wilson CG, Yanek LR, Psaty BM, Heckbert SR, Laurie CC (2021) A System for Phenotype Harmonization in the National Heart, Lung, and Blood Institute Trans-Omics for Precision Medicine (TOPMed) Program. *Am J Epidemiol* **190**:1977-1992. PMID: PMC8485147

250. Taliun D, Harris DN, Kessler MD, Carlson J, Szpiech ZA, Torres R, Taliun SAG, Corvelo A, Gogarten SM, Kang HM, Pitsillides AN, LeFaive J, Lee SB, Tian X, Browning BL, Das S, Emde AK, Clarke WE, Loesch DP, Shetty AC, Blackwell TW, Smith AV, Wong Q, Liu X, Conomos MP, Bobo DM, Aguet F, Albert C, Alonso A, Ardlie KG, Arking DE, Aslibekyan S, Auer PL, Barnard J, Barr RG, Barwick L, Becker LC, Beer RL, Benjamin EJ, Bielak LF, Blangero J, Boehnke M, Bowden DW, Brody JA, Burchard EG, Cade BE, Casella JF, Chalazan B, Chasman DI, Chen YI, Cho MH, Choi SH, Chung MK, Clish CB, Correa A, Curran JE, Custer B, Darbar D, Daya M, de Andrade M, DeMeo DL, Dutcher SK, Ellinor PT, Emery LS, Eng C, Fatkin D, Fingerlin T, Forer L, Fornage M, Franceschini N, Fuchsberger C, Fullerton SM, Germer S, Gladwin MT, Gottlieb DJ, Guo X, Hall ME, He J, Heard-Costa NL, Heckbert SR, Irvin MR, Johnsen JM, Johnson AD, Kaplan R, Kardia SLR, Kelly T, Kelly S, Kenny EE, Kiel DP, Klemmer R, Konkle BA, Kooperberg C, Kottgen A, Lange LA, Lasky-Su J, Levy D, Lin X, Lin KH, Liu C, Loos R, Garman L, Gerszten R, Lubitz SA, Lunetta KL, Mak ACY, Manichaikul A, Manning AK, Mathias RA, McManus DD, McGarvey ST, Meigs JB, Meyers DA, Mikulla JL, Minear MA, Mitchell BD, Mohanty S, Montasser ME, Montgomery C, Morrison AC, Murabito JM, Natale A, Natarajan P, Nelson SC, North KE, O'Connell JR, Palmer ND, Pankratz N, Peloso GM, Peyser PA, Pleiness J, Post WS, Psaty BM, Rao DC, Redline S, Reiner AP, Roden D, Rotter JI, Ruczinski I, Sarnowski C, Schoenherr S, Schwartz DA, Seo JS, Seshadri S, Sheehan VA, Sheu WH, Shoemaker MB, Smith NL, Smith JA, Sotoodehnia N, Stilp AM, Tang W, Taylor KD, Telen M, Thornton TA, Tracy RP, Van Den Berg DJ, Vasani RS, Viaud-Martinez KA, Vrieze S, Weeks DE, Weir BS, Weiss ST, Weng LC, Willer CJ, Zhang Y, Zhao X, Arnett DK, Ashley-Koch AE, Barnes KC, Boerwinkle E, Gabriel S, Gibbs R, Rice KM, Rich SS, Silverman EK, Qasba P, Gan W, NHLBI Trans-Omics for Precision Medicine Consortium, Papanicolaou GJ, Nickerson DA, Browning SR, Zody MC, Zollner S, Wilson JG, Cupples LA, Laurie CC, Jaquish CE, Hernandez RD, O'Connor TD, Abecasis GR (2021) Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *Nature* **590**:290-299. PMID: 33568819 PMCID: PMC7875770
251. Taub MA, Conomos MP, Keener R, Iyer KR, Weinstock JS, Yanek LR, Lane J, Miller-Fleming TW, Brody JA, Raffield LM, McHugh CP, Jain D, Gogarten SM, Laurie CA, Keramati A, Arvanitis M, Smith AV, Heavner B, Barwick L, Becker LC, Bis JC, Blangero J, Bleecker ER, Burchard EG, Celedon JC, Chang YPC, Custer B, Darbar D, de Las Fuentes L, DeMeo DL, Freedman BI, Garrett ME, Gladwin MT, Heckbert SR, Hidalgo BA, Irvin MR, Islam T, Johnson WC, Kaab S, Launer L, Lee J, Liu S, Moscati A, North KE, Peyser PA, Rafaels N, Seidman C, Weeks DE, Wen F, Wheeler MM, Williams LK, Yang IV, Zhao W, Aslibekyan S, Auer PL, Bowden DW, Cade BE, Chen Z, Cho MH, Cupples LA, Curran JE, Daya M, Deka R, Eng C, Fingerlin TE, Guo X, Hou L, Hwang SJ, Johnsen JM, Kenny EE, Levin AM, Liu C, Minster RL, Naseri T, Nouraei M, Reupena MS, Sabino EC, Smith JA, Smith NL, Su JL, Taylor JG, Telen MJ, Tiwari HK, Tracy RP, White MJ, Zhang Y, Wiggins KL, Weiss ST, Vasani RS, Taylor KD, Sinner MF, Silverman EK, Shoemaker MB, Sheu WH, Sciruba F, Schwartz DA, Rotter JI, Roden D, Redline S, Raby BA, Psaty BM, Peralta JM, Palmer ND, Nekhai S, Montgomery CG, Mitchell BD, Meyers DA, McGarvey ST, Network NC, Mak AC, Loos RJ, Kumar R, Kooperberg C, Konkle BA, Kelly S, Kardia SLR, Kaplan R, He J, Gui H, Gilliland FD, Gelb BD, Fornage M, Ellinor PT, de Andrade M, Correa A, Chen YI, Boerwinkle E, Barnes KC, Ashley-Koch AE, Arnett DK, NHLBI Trans-Omics for Precision Medicine Consortium, TOPMed Hematology/Hemostasis Working Group, TOPMed Structural Variation Working Group, Laurie CC, Abecasis G, Nickerson DA, Wilson JG, Rich SS, Levy D, Ruczinski I, Aviv A, Blackwell TW, Thornton T, O'Connell J, Cox NJ, Perry JA, Armanios M, Battle A, Pankratz N, Reiner AP, Mathias RA (2022) Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. *Cell Genom* **2**. PMCID: PMC9075703
252. Nakao T, Bick AG, Taub MA, Zekavat SM, Uddin MM, Niroula A, Carty CL, Lane J, Honigberg MC, Weinstock JS, Pampana A, Gibson CJ, Griffin GK, Clarke SL, Bhattacharya R, Assimes TL, Emery LS, Stilp AM, Wong Q, Broome J, Laurie CA, Khan AT, Smith AV, Blackwell TW, Codd V, Nelson CP, Yoneda ZT, Peralta JM, Bowden DW, Irvin MR, Boorgula M, Zhao W, Yanek LR, Wiggins KL, Hixson JE, Gu CC, Peloso GM, Roden DM, Reupena MS, Hwu CM, DeMeo DL, North KE, Kelly S, Musani SK, Bis JC, Lloyd-Jones DM, Johnsen JM, Preuss M, Tracy RP, Peyser PA, Qiao D, Desai P, Curran JE, Freedman BI, Tiwari HK, Chavan S, Smith JA, Smith NL, Kelly TN, Hidalgo B, Cupples LA, Weeks DE, Hawley NL, Minster RL, Samoan Obesity, Lifestyle and Genetic Adaptations Study (OLaGA) Group, Deka R, Naseri TT, de Las Fuentes L, Raffield LM, Morrison AC, Vries PS, Ballantyne CM, Kenny EE, Rich SS, Whitsel EA, Cho MH, Shoemaker MB, Pace BS, Blangero J, Palmer ND, Mitchell BD, Shuldiner AR, Barnes KC, Redline S, Kardia SLR, Abecasis GR, Becker LC, Heckbert SR, He J, Post W, Arnett DK, Vasani RS, Darbar D, Weiss ST, McGarvey ST, de Andrade M, Chen YI, Kaplan RC, Meyers DA, Custer BS, Correa A, Psaty BM, Fornage M, Manson JE, Boerwinkle E, Konkle BA, Loos R, Rotter JI, Silverman EK, Kooperberg C, Danesh J, Samani NJ, Jaiswal S, Libby P, Ellinor PT, Pankratz N, Ebert BL, Reiner AP, Mathias RA, Do R, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, Natarajan P (2022) Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. *Sci Adv* **8**:eabl6579. PMCID: PMC8986098

253. Kelly TN, Sun X, He KY, Brown MR, Taliun SAG, Hellwege JN, Irvin MR, Mi X, Brody JA, Franceschini N, Guo X, Hwang SJ, de Vries PS, Gao Y, Moscati A, Nadkarni GN, Yanek LR, Elfassy T, Smith JA, Chung RH, Beitelshes AL, Patki A, Aslibekyan S, Blobner BM, Peralta JM, Assimes TL, Palmas WR, Liu C, Bress AP, Huang Z, Becker LC, Hwa CM, O'Connell JR, Carlson JC, Warren HR, Das S, Giri A, Martin LW, Craig Johnson W, Fox ER, Bottinger EP, Razavi AC, Vaidya D, Chuang LM, Chang YC, Naseri T, Jain D, Kang HM, Hung AM, Srinivasasainagendra V, Snively BM, Gu D, Montasser ME, Reupena MS, Heavner BD, LeFaive J, Hixson JE, Rice KM, Wang FF, Nielsen JB, Huang J, Khan AT, Zhou W, Nierenberg JL, Laurie CC, Armstrong ND, Shi M, Pan Y, Stilp AM, Emery L, Wong Q, Hawley NL, Minster RL, Curran JE, Munroe PB, Weeks DE, North KE, Tracy RP, Kenny EE, Shimbo D, Chakravarti A, Rich SS, Reiner AP, Blangero J, Redline S, Mitchell BD, Rao DC, Ida Chen YD, Kardia SLR, Kaplan RC, Mathias RA, He J, Psaty BM, Fornage M, Loos RJF, Correa A, Boerwinkle E, Rotter JI, Kooperberg C, Edwards TL, Abecasis GR, Zhu X, Levy D, Arnett DK, Morrison AC, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, The Samoan Obesity, Lifestyle and Genetic Adaptations Study (OLaGA) Group (2022) Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. *Hypertension* 2022 Aug;79(8):1656–1667. PMID: 35652341 PMCID: PMC9593435
254. Hindy G, Dornbos P, Chaffin MD, Liu DJ, Wang M, Selvaraj MS, Zhang D, Park J, Aguilar-Salinas CA, Antonacci-Fulton L, Ardissino D, Arnett DK, Aslibekyan S, Atzmon G, Ballantyne CM, Barajas-Olmos F, Barzilai N, Becker LC, Bielak LF, Bis JC, Blangero J, Boerwinkle E, Bonnycastle LL, Bottinger E, Bowden DW, Bown MJ, Brody JA, Broome JG, Burt NP, Cade BE, Centeno-Cruz F, Chan E, Chang YC, Chen YI, Cheng CY, Choi WJ, Chowdhury R, Contreras-Cubas C, Cordova EJ, Correa A, Cupples LA, Curran JE, Danesh J, de Vries PS, DeFronzo RA, Doddapaneni H, Duggirala R, Dutcher SK, Ellinor PT, Emery LS, Florez JC, Fornage M, Freedman BI, Fuster V, Garay-Sevilla ME, Garcia-Ortiz H, Germer S, Gibbs RA, Gieger C, Glaser B, Gonzalez C, Gonzalez-Villalpando ME, Graff M, Graham SE, Grarup N, Groop LC, Guo X, Gupta N, Han S, Hanis CL, Hansen T, He J, Heard-Costa NL, Hung YJ, Hwang MY, Irvin MR, Islas-Andrade S, Jarvik GP, Kang HM, Kardia SLR, Kelly T, Kenny EE, Khan AT, Kim BJ, Kim RW, Kim YJ, Koistinen HA, Kooperberg C, Kuusisto J, Kwak SH, Laakso M, Lange LA, Lee J, Lee J, Lee S, Lehman DM, Lemaitre RN, Linneberg A, Liu J, Loos RJF, Lubitz SA, Lyssenko V, Ma RCW, Martin LW, Martinez-Hernandez A, Mathias RA, McGarvey ST, McPherson R, Meigs JB, Meitinger T, Melander O, Mendoza-Caamal E, Metcalf GA, Mi X, Mohlke KL, Montasser ME, Moon JY, Moreno-Macias H, Morrison AC, Muzny DM, Nelson SC, Nilsson PM, O'Connell JR, Orho-Melander M, Orozco L, Palmer CNA, Palmer ND, Park CJ, Park KS, Pedersen O, Peralta JM, Peyser PA, Post WS, Preuss M, Psaty BM, Qi Q, Rao DC, Redline S, Reiner AP, Revilla-Monsalve C, Rich SS, Samani N, Schunkert H, Schurmann C, Seo D, Seo JS, Sim X, Sladek R, Small KS, So WY, Stilp AM, Tai ES, Tam CHT, Taylor KD, Teo YY, Thameem F, Tomlinson B, Tsai MY, Tuomi T, Tuomilehto J, Tusie-Luna T, Udler MS, van Dam RM, Vasani RS, Viaud-Martinez KA, Wang FF, Wang X, Watkins H, Weeks DE, Wilson JG, Witte DR, Wong TY, Yanek LR, Amp-T2D-Genes, Myocardial Infarction Genetics Consortium, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, NHLBI TOPMed Lipids Working Group, Kathiresan S, Rader DJ, Rotter JI, Boehnke M, McCarthy MI, Willer CJ, Natarajan P, Flannick JA, Khera AV, Peloso GM (2022) Rare coding variants in 35 genes associate with circulating lipid levels-A multi-ancestry analysis of 170,000 exomes. *Am J Hum Genet* 109:81-96. PMCID: PMC8764201
255. DiCorpo D, Gaynor SM, Russell EM[‡], Westerman KE, Raffield LM, Majarian TD, Wu P, Sarnowski C, Highland HM, Jackson A, Hasbani NR, de Vries PS, Brody JA, Hidalgo B, Guo X, Perry JA, O'Connell JR, Lent S, Montasser ME, Cade BE, Jain D, Wang H, D'Oliveira Albanus R, Varshney A, Yanek LR, Lange L, Palmer ND, Almeida M, Peralta JM, Aslibekyan S, Baldrige AS, Bertoni AG, Bielak LF, Chen C-S, Chen Y-DI, Choi WJ, Goodarzi MO, Floyd JS, Irvin MR, Kalyani RR, Kelly TN, Lee S, Liu C-T, Loesch D, Manson JE, Minster RL, Naseri T, Pankow JS, Rasmussen-Torvik LJ, Reiner AP, Reupena MS, Selvin E, Smith JA, Weeks DE, Xu H, Yao J, Zhao W, Parker S, Alonso A, Arnett DK, Blangero J, Boerwinkle E, Correa A, Cupples LA, Curran JE, Duggirala R, He J, Heckbert SR, Kardia SLR, Kim RW, Kooperberg C, Liu S, Mathias RA, McGarvey ST, Mitchell BD, Morrison AC, Peyser PA, Psaty BM, Redline S, Shuldiner AR, Taylor KD, Vasani RS, Viaud-Martinez KA, Florez JC, Wilson JG, Sladek R, Rich SS, Rotter JI, Lin X, Dupuis J, Meigs JB, Wessel J, Manning AK. Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program. *Commun Biol.* 2022 Jul 28;5(1):756. PMID: 35902682 PMCID: PMC9334637

256. Li Z, Li X, Zhou H, Gaynor SM, Selvaraj MS, Arapoglou T, Quick C, Liu Y, Chen H, Sun R, Dey R, Arnett DK, Auer PL, Bielak LF, Bis JC, Blackwell TW, Blangero J, Boerwinkle E, Bowden DW, Brody JA, Cade BE, Conomos MP, Correa A, Cupples LA, Curran JE, de Vries PS, Duggirala R, Franceschini N, Freedman BI, Göring HHH, Guo X, Kalyani RR, Kooperberg C, Kral BG, Lange LA, Lin BM, Manichaikul A, Manning AK, Martin LW, Mathias RA, Meigs JB, Mitchell BD, Montasser ME, Morrison AC, Naseri T, O'Connell JR, Palmer ND, Peyser PA, Psaty BM, Raffield LM, Redline S, Reiner AP, Reupena MS, Rice KM, Rich SS, Smith JA, Taylor KD, Taub MA, Vasani RS, Weeks DE, Wilson JG, Yanek LR, Zhao W, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Rotter JI, Willer CJ, Natarajan P, Peloso GM, Lin X. A framework for detecting noncoding rare-variant associations of large-scale whole-genome sequencing studies. *Nat Methods*. 2022 Dec;19(12):1599–1611. PMID: 36303018 PMCID: PMC10008172
257. Chen F, Wang X, Jang SK, Quach BC, Weissenkampen JD, Khunsriraksakul C, Yang L, Sauteraud R, Albert CM, Allred NDD, Arnett DK, Ashley-Koch AE, Barnes KC, Barr RG, Becker DM, Bielak LF, Bis JC, Blangero J, Boorgula MP, Chasman DI, Chavan S, Chen YI, Chuang LM, Correa A, Curran JE, David SP, Fuentes LL, Deka R, Duggirala R, Faul JD, Garrett ME, Gharib SA, Guo X, Hall ME, Hawley NL, He J, Hobbs BD, Hokanson JE, Hsiung CA, Hwang SJ, Hyde TM, Irvin MR, Jaffe AE, Johnson EO, Kaplan R, Kardia SLR, Kaufman JD, Kelly TN, Kleinman JE, Kooperberg C, Lee IT, Levy D, Lutz SM, Manichaikul AW, Martin LW, Marx O, McGarvey ST, Minster RL, Moll M, Moussa KA, Naseri T, North KE, Oelsner EC, Peralta JM, Peyser PA, Psaty BM, Rafaels N, Raffield LM, Reupena MS, Rich SS, Rotter JI, Schwartz DA, Shadyab AH, Sheu WH, Sims M, Smith JA, Sun X, Taylor KD, Telen MJ, Watson H, Weeks DE, Weir DR, Yanek LR, Young KA, Young KL, Zhao W, Hancock DB, Jiang B, Vrieze S, Liu DJ (2023) Multi-ancestry transcriptome-wide association analyses yield insights into tobacco use biology and drug repurposing. *Nat Genet* 55:291-300. PMCID: PMC9925385
258. Zhang X, Brody JA, Graff M, Highland HM, Chami N, Xu H, Wang Z, Ferrier KR, Chittoor G, Josyula NS, Meyer M, Gupta S, Li X, Li Z, Allison MA, Becker DM, Bielak LF, Bis JC, Boorgula MP, Bowden DW, Broome JG, Buth EJ, Carlson CS, Chang KM, Chavan S, Chiu YF, Chuang LM, Conomos MP, DeMeo DL, Du M, Duggirala R, Eng C, Fohner AE, Freedman BI, Garrett ME, Guo X, Haiman C, Heavner BD, Hidalgo B, Hixson JE, Ho YL, Hobbs BD, Hu D, Hui Q, Hwu CM, Jackson RD, Jain D, Kalyani RR, Kardia SLR, Kelly TN, Lange EM, LeNoir M, Li C, Le Marchand L, McDonald MN, McHugh CP, Morrison AC, Naseri T, NHLBI Trans-Omics for Precision Medicine Consortium, O'Connell J, O'Donnell CJ, Palmer ND, Pankow JS, Perry JA, Peters U, Preuss MH, Rao DC, Regan EA, Reupena SM, Roden DM, Rodriguez-Santana J, Sitlani CM, Smith JA, Tiwari HK, Vasani RS, Wang Z, Weeks DE, Wessel J, Wiggins KL, Wilkens LR, Wilson PWF, Yanek LR, Yoneda ZT, Zhao W, Zollner S, Arnett DK, Ashley-Koch AE, Barnes KC, Blangero J, Boerwinkle E, Burchard EG, Carson AP, Chasman DI, Ida Chen YD, Curran JE, Fornage M, Gordeuk VR, He J, Heckbert SR, Hou L, Irvin MR, Kooperberg C, Minster RL, Mitchell BD, Nouraei M, Psaty BM, Raffield LM, Reiner AP, Rich SS, Rotter JI, Benjamin Shoemaker M, Smith NL, Taylor KD, Telen MJ, Weiss ST, Zhang Y, Heard-Costa N, Sun YV, Lin X, Cupples LA, Lange LA, Liu CT, Loos RJJ, North KE, Justice AE (2025) Whole genome sequencing analysis of body mass index identifies novel African ancestry-specific risk allele. *Nat Commun* 16:3470. PMCID: PMC11992084

Non-reviewed manuscripts:

1. Gatti RA, DE Weeks, M Paterson (1988) Genetic models for linkage analysis of ataxia-telangiectasia. In: Unusual Occurrences as Clues to Cancer Etiology, (RW Miller et al., Eds.), Japan Sci. Soc. Press, Tokyo/Taylor & Francis, LTD., pp. 261-273
2. Weeks DE, Lange K (1991) An overview of the affected-pedigree-member method of linkage analysis. Proceedings of the 23rd symposium on the interface, Seattle, Interface Foundation of North America, pp. 386-391
3. Weeks DE, Harby LD[†], Sarneso CA, Gorin MB (1992) Using the affected pedigree member method of linkage analysis. INSERM Atelier 44: Linkage analysis of single gene and polygenic traits, Le Vesinet, France
4. Weeks DE, Davis S[†], Schroeder M, Goldin LR (1997) Nonparametric simulation-based linkage statistics for general pedigrees. *J Rheum* 24:206-207

Book Chapters:

1. Weeks DE (1991) Human linkage analysis: Strategies for locus ordering. In: Advanced Techniques in Chromosome Research (KW Adolph, Ed) New York: Marcel Dekker, pp 297-330
2. Gorin MB, Sarneso C, Paul TO, Ngo J, Weeks DE (1993) The genetics of age-related maculopathy. In: Retinal Degeneration: Clinical and Laboratory Applications (Hollyfield JG, Anderson RE, LaVail MM, Eds) Plenum Press, New York, pp 35-47
3. Weeks DE (1994) Pedigree selection and information content. In: Current Protocols in Human Genetics (N. Dracopoli et al., Eds) New York: Current Protocols
4. Sobel E, Lange K, O'Connell JR, Weeks DE (1995) Haplotyping algorithms. In: Speed TP, Waterman MS (eds) Genetic mapping and DNA sequencing. Springer-Verlag, New York
5. Davis S[†], Goldin LR, Weeks DE (1997) SimIBD: a powerful robust nonparametric method for detecting linkage in general pedigrees. In: Pawlowitzki IH, Edwards JH, Thompson EA (eds) Genetic mapping of disease genes. Academic Press, London, pp 189-204
6. Lathrop GM, Terwilliger JD, Weeks DE (1997) Multifactorial inheritance and genetic analysis of multifactorial disease. In: Rimoin DL, Connor JM, Pyeritz RE (eds) Principles and practice of medical genetics. Churchill Livingstone, New York, pp 333-346
7. O'Connell JR, Weeks DE (1997) Advances in statistical methods for linkage analysis. International symposium on theoretical and computational genome research, Heidelberg, Germany, Plenum, pp. 153-160
8. Sobel E, Weeks DE (1998) Haplotype analysis. In: Elston RC (ed) Encyclopedia of biostatistics. Vol. 3. John Wiley and Sons Ltd, London, pp 1804-1812
9. Wilhelmsen KC, Moskowitz CB, Weeks DE, Neystat M, Nygaard TG, Clark L, Dancoup M, Sobrevega EE, Rosales R, Gamez GL et al (1998) Molecular genetic analysis of lubag. Adv Neurol **78**:341-8
10. Lathrop GM, Weeks DE (2000) Methods for mapping complex disease traits. In: Bishop T, Sham P (eds) Analysis of Multifactorial Disease. BIOS Scientific Publishers Ltd., Oxford, pp 15-35
11. Hauser ER, Weeks DE (2001) Pedigree selection and information content. Curr Protoc Hum Genet **Chapter 1**: Unit 1.2
12. Weeks DE (2001) Newton Morton's influence on genetics: the Morton Number. Adv Genet **42**:7-10
13. Yan Q, Ding Y, Weeks DE, Chen W (2021) AMD Genetics: Methods and Analyses for Association, Progression, and Prediction. Adv Exp Med Biol **1256**:191-200

Letters to the Editor:

1. Lange K, D Weeks, M Boehnke (1988) Programs for pedigree analysis: MENDEL, FISHER, and dGENE. Genet Epidemiol **5**:471-472
2. Weeks DE, J Ott (1989) Risk calculations under heterogeneity. Am J Hum Genet **45**:819-821
3. Weeks DE, J Ott (1990) Reply to Dr. Carothers: Support intervals for genetic risks. Am J Hum Genet **47**:166
4. Weeks DE (1990) A likelihood-based analysis of consistent linkage of a disease locus to two nonsyntenic marker loci: Osteogenesis imperfecta versus COL1A1 and COL1A2. Am J Hum Genet **47**:592-594
5. Weeks DE (1993) Further concerns about the genetics of pre-eclampsia. Am J Hum Genet **53**:963-964
6. Weeks DE (1994) Invalidity of the Rao map function for three loci. Hum Hered **44**:178-180

7. Weeks DE, Sobel E, O'Connell JR, Lange K (1995) Computer programs for multilocus haplotyping of general pedigrees. Am J Hum Genet **56**:1506-1507
8. Farrall M, Weeks DE (1998) Mutational mechanisms for generating microsatellite allele-frequency distributions: an analysis of 4,558 markers. Am J Hum Genet **62**:1260-2
9. Kennedy S, Hadfield R, Westbrook C, Weeks DE, Barlow D, Golding S (1998) Magnetic resonance imaging to assess familial risk in relatives of women with endometriosis. Lancet **352**:1440-1
10. Weeks DE, O'Connell JR, Schmidtova Z (1998) Nomenclature regulation and linguistic diversity. Nature **391**:118
11. Weeks DE, Sinsheimer JS (1998) Consanguinity and relative pair methods for linkage analysis. Am J Hum Genet **62**:728-731
12. Parkes M, Satsngi J, Jewell DP, Weeks DE, Barmada MM, Duerr RH (2001) Ulcerative colitis is more strongly linked to chromosome 12 than Crohn's disease. Gut **49**:311
13. Mukhopadhyay I[‡], Feingold E, Weeks DE (2004) No "bias" toward the null hypothesis in most conventional multipoint nonparametric linkage analyses. Am J Hum Genet **75**:716-8
14. Ray A[†], Weeks DE (2005) No convincing evidence of linkage for restless legs syndrome on chromosome 9p. Am J Hum Genet **76**:705-7
15. Jakobsdottir J[†], Weeks DE (2007) Estimating prevalence, false-positive rate, and false-negative rate with use of repeated testing when true responses are unknown. Am J Hum Genet **81**:1111-3. PMC2265647
16. Hong X, Ladd-Acosta C, Hao K, Sherwood B, Ji H, Keet CA, Kumar R, Caruso D, Liu X, Wang G, Chen Z, Ji Y, Mao G, Walker SO, Bartell TR, Ji Z, Sun Y, Tsai HJ, Pongratic JA, Weeks DE, Wang X (2016) Epigenome-wide association study links site-specific DNA methylation changes with cow's milk allergy. J Allergy Clin Immunol **138**:908-911.e909. PMC5392112
17. Major TJ, Krishnan M, Topless RK, Dewes O, Thompson J, Zoysa J, Stamp LK, Dalbeth N, Deka R, Weeks DE, Minster RL, Wilcox P, Grattan D, Shepherd PR, Shelling AN, Murphy R, Merriman TR (2018) Re: "Widespread prevalence of a CREBRF variant amongst Māori and Pacific children is associated with weight and height in early childhood". Int J Obes (Lond) **42**:1389-1391. PMID: PMC6054808

Preprints:

1. Forno E, Wang T, Qi C, Yan Q, Xu C-J, Boutaoui N, Han Y-Y, Weeks D, Jiang Y, Rosser F, Vonk J, Brouwer S, Acosta-Perez E, Colon-Semidey A, Alvarez M, Canino G, Koppelman G, Chen W, Celedón J (2018) A Genome-wide Study of DNA Methylation in Nasal Epithelium and Atopy and Atopic Asthma in Children. SSRN: <https://ssrn.com/abstract=3276045>
2. Krishnan M, Major TJ, Topless RK, Dewes O, Yu L, Thompson JM, McCowan L, Zoysa Jd, Stamp LK, Dalbeth N, Hindmarsh JH, Rapana N, Deka R, Eng WWH, Weeks DE, Minster RL, McGarvey ST, Viali Si, Naseri T, Reupena Ma, Wilcox P, Grattan D, Shepherd PR, Shelling AN, Murphy R, Merriman TR (2018) Discordant association of the CREBRF rs373863828 minor allele with increased body mass index and protection from type 2 diabetes in Māori and Pacific (Polynesian) people living in Aotearoa New Zealand. bioRxiv: <https://doi.org/10.1101/188110>
3. Harris DN, Kessler MD, Shetty AC, Weeks DE, Minster RL, Browning S, Cochrane EE, Deka R, Hawley NL, Reupena MaS, Naseri T, Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Population Genetics Working Group, McGarvey ST, O'Connor TD (2019) Evolutionary Genomics of Samoans. SSRN: <http://dx.doi.org/10.2139/ssrn.3329885>

4. Carlson JC, Weeks DE, Hawley NL, Gao G, Cheng H, Naseri T, Reupena MS, Deka R, McGarvey ST, Minster RL (2019) Genome-wide association studies in Samoans give insight into the genetic architecture of fasting serum lipid levels. *bioRxiv*: <https://doi.org/10.1101/411546>
5. Carlson JC, Rosenthal SL, Russell EM, Hawley NL, Sun G, Cheng H, Naseri T, Reupena MS, Tuitele J, Deka R, McGarvey ST, Weeks DE, Minster RL (2019) A missense variant in CREBRF is associated with taller stature in Samoans. *bioRxiv*: <https://doi.org/10.1101/690586>
6. Taliun D, Harris D, Kessler M, Carlson J, Szpiech Z, Torres R, Taliun SG, Corvelo A, Gogarten S, Kang HM, Pitsillides A, LeFaive J, Lee S-b, Tian X, Browning B, Das S, Emde A-K, Clarke W, Loesch D, Shetty A, Blackwell T, Wong Q, Aguet F, Albert C, Alonso A, Ardlie K, Aslibekyan S, Auer P, Barnard J, Barr G, Becker L, Beer R, Benjamin E, Bielak L, Blangero J, Boehnke M, Bowden D, Brody J, Burchard E, Cade B, Casella J, Chalazan B, Chen Y-DI, Cho M, Choi SH, Chung M, Clish C, Correa A, Curran J, Custer B, Darbar D, Daya M, Andrade Md, DeMeo D, Dutcher S, Ellinor P, Emery L, Fatkin D, Forer L, Fornage M, Franceschini N, Fuchsberger C, Fullerton S, Germer S, Gladwin M, Gottlieb D, Guo X, Hall M, He J, Heard-Costa N, Heckbert S, Irvin M, Johnsen J, Johnson A, Kardia SLR, Kelly T, Kelly S, Kenny E, Kiel D, Klemmer R, Konkle B, Kooperberg C, Köttgen A, Lange L, Lasky-Su J, Levy D, Lin X, Lin K-H, Liu C, Loos RJJ, Garman L, Gerszten R, Lubitz S, Lunetta K, Mak ACY, Manichaikul A, Manning A, Mathias R, McManus D, McGarvey S, Meigs J, Meyers D, Mikulla J, Minear M, Mitchell B, Mohanty S, Montasser M, Montgomery C, Morrison A, Murabito J, Natale A, Natarajan P, Nelson S, North K, O'Connell J, Palmer N, Pankratz N, Peloso G, Peyser P, Post W, Psaty B, Rao DC, Redline S, Reiner A, Roden D, Rotter J, Ruczinski I, Sarnowski C, Schoenherr S, Seo J-S, Seshadri S, Sheehan V, Shoemaker B, Smith A, Smith N, Smith J, Sotoodehnia N, Stilp A, Tang W, Taylor K, Telen M, Thornton T, Tracy R, Berg DVD, Vasani R, Viaud-Martinez K, Vrieze S, Weeks D, Weir B, Weiss S, Weng L-C, Willer C, Zhang Y, Zhao X, Arnett D, Ashley-Koch A, Barnes K, Boerwinkle E, Gabriel S, Gibbs R, Rice K, Rich S, Silverman E, Qasba P, Gan W, Papanicolaou G, Nickerson D, Browning S, Zody M, Zöllner S, Wilson J, Cupples A, Laurie C, Jaquish C, Hernandez R, O'Connor T, Abecasis G, Trans-Omics for Precision Medicine Program (TOPMed) Population Genetics Working Group (2019) Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. *bioRxiv*: <https://doi.org/10.1101/563866>
7. Bick A, Weinstock J, Nandakumar S, Fulco C, Leventhal M, Bao E, Nasser J, Zekavat S, Szeto M, Laurie C, Taub M, Mitchell B, Barnes K, Moscati A, Fornage M, Redline S, Psaty B, Silverman E, Weiss S, Palmer N, Vasani R, Burchard E, Kardia SLR, He J, Kaplan R, Smith N, Arnett D, Schwartz D, Correa A, de Andrade M, Guo X, Konkle B, Custer B, Peralta J, Gui H, Meyers D, McGarvey S, Chen IY-D, Shoemaker B, Peyser P, Broome J, Gogarten S, Wang FF, Wong Q, Montasser M, Daya M, Kenny E, North K, Launer L, Cade B, Bis J, Cho M, Lasky-Su J, Bowden D, Cupples A, Mak ACY, Becker L, Smith J, Kelly T, Aslibekyan S, Heckbert S, Tiwari H, Yang I, Heit J, Lubitz S, Rich S, Johnsen J, Curran J, Wenzel S, Weeks D, Rao D, Darbar D, Moon J-Y, Tracy R, Buth E, Rafaels N, Loos RJJ, Hou L, Lee J, Kachroo P, Freedman B, Levy D, Bielak L, Hixson J, Floyd J, Whitsel E, Ellinor P, Irvin M, Fingerlin T, Raffield L, Armasu S, Rotter J, Wheeler M, Sabino E, Blangero J, Williams K, Levy B, Sheu WH-H, Roden D, Boerwinkle E, Manson J, Mathias R, Desai P, Taylor K, Johnson A, Auer P, Kooperberg C, Laurie C, Blackwell T, Smith A, Zhao H, Lange E, Lange L, Wilson J, Lander E, Engreitz J, Ebert B, Reiner A, Sankaran V, Jaiswal S, Abecasis G, Natarajan P, Kathiresan S, NHLBI Trans-Omics for Precision Medicine Consortium (2019) Inherited Causes of Clonal Hematopoiesis of Indeterminate Potential in TOPMed Whole Genomes. *bioRxiv*: <https://doi.org/10.1101/782748>
8. Taub M, Weinstock J, Iyer K, Yanek L, Conomos M, Brody J, Keramati A, Laurie C, Arvanitis M, Smith A, Lane J, Becker L, Bis J, Blangero J, Bleecker E, Burchard E, Celedon J, Chang YP, Custer B, Darbar D, de las Fuentes L, DeMeo D, Freedman B, Garrett M, Gladwin M, Heckbert S, Hidalgo B, Ingram C, Irvin M, Craig Johnson W, Kaab S, Launer L, Lee J, Liu S, Moscati A, North K, Peyser P, Rafaels N, Raffield L, Weeks D, Wheeler M, Keoki Williams L, Zhao W, Armanios M, Aslibekyan S, Auer P, Bowden D, Cade B, Yii-Der Chen I, Cho M, Cupples A, Curran J, Daya M, Deka R, Guo X, Hou L, Hwang S-J, Johnsen J, Kenny E, Levin A, Liu C, Minster R, Nouraei M, Sabino E, Smith J, Smith N, Lasky Su J, Telen M, Tiwari H, Tracy R, White M, Zhang Y, Wiggins K, Weiss S, Vasani R, Taylor K, Sinner M, Silverman E, Benjamin Shoemaker M, Sheu WHH, Rotter J, Redline S, Psaty B, Peralta J, Palmer N, Loos RJJ, Montgomery C, Mitchell B, Meyers D, McGarvey S, Mak ACY, Kumar R, Kooperberg C, Konkle B, Kelly S, Kardia SLR, Kaplan R, He J, Gui H, Fornage M, Ellinor P, de Andrade M, Correa A, Boerwinkle E, Barnes K, Ashley-Koch A, Arnett D, Albert C, Laurie C, Abecasis G, Aviv A, Nickerson D, Wilson J, Rich S, Levy D, Battle A, Blackwell T, Ruczinski I, Thornton T, O'Connell J, Perry J, Pankratz N, Reiner A, Mathias R, NHLBI Trans-Omics for Precision Medicine Consortium, TOPMed Hematology Hemostasis Working Group, TOPMed Structural Variation Working Group (2019) Novel genetic determinants of telomere length from a multi-ethnic analysis of 75,000 whole genome sequences in TOPMed. *bioRxiv*: <https://doi.org/10.1101/749010>

9. Yan Q, Jiang Y, Huang H, Swaroop A, Chew E, Weeks D, Chen W, Ding Y (2019) GWAS-based Machine Learning for Prediction of Age-Related Macular Degeneration Risk. medRxiv: <https://doi.org/10.1101/19006155>
10. Yan Q, Weeks D, Xin H, Huang H, Swaroop A, Chew E, Ding Y, Chen W (2019) Deep-learning-based Prediction of Late Age-Related Macular Degeneration Progression. medRxiv, <https://doi.org/10.1101/19006171>
11. Arockiaraj A[†], Liu D[†], Shaffer J, Koleck T, Crago E, Weeks D, Conley Y (2020) Methylation Data Processing Protocol & Comparison of Blood and Cerebral Spinal Fluid Following Aneurysmal Subarachnoid Hemorrhage. bioRxiv: <https://doi.org/10.1101/2020.03.24.005264>
12. Heinsberg LW[‡], Ray M[‡], Conley YP, Roberts JM, Jeyabalan A, Hubel CA, Weeks DE, Schmella MJ (2020) Racial Differences in DNA Methylation-Based Age Acceleration in Preeclamptic and Normotensive Pregnancy. medRxiv [Preprint] October 02, 2020 <https://doi.org/10.1101/2020.09.30.20204883>
13. Hindy G, Dornbos P, Chaffin MD, Liu DJ, Wang M, Aguilar-Salinas CA, Antonacci-Fulton L, Ardissino D, Arnett DK, Aslibekyan S, Atzmon G, Ballantyne CM, Barajas-Olmos F, Barzilai N, Becker LC, Bielak LF, Bis JC, Blangero J, Boerwinkle E, Bonnycastle LL, Bottinger E, Bowden DW, Bown MJ, Brody JA, Broome JG, Burtt NP, Cade BE, Centeno-Cruz F, Chan E, Chang Y-C, Chen Y-DI, Cheng C-Y, Choi WJ, Chowdhury R, Contreras-Cubas C, Córdova EJ, Correa A, Cupples LA, Curran JE, Danesh J, de Vries PS, DeFronzo RA, Doddapaneni H, Duggirala R, Dutcher SK, Ellinor PT, Emery LS, Florez JC, Fornage M, Freedman BI, Fuster V, Garay-Sevilla ME, García-Ortiz H, Germer S, Gibbs RA, Gieger C, Glaser B, Gonzalez C, Gonzalez-Villalpando ME, Graff M, Graham SE, Grarup N, Groop LC, Guo X, Gupta N, Han S, Hanis CL, Hansen T, He J, Heard-Costa NL, Hung Y-J, Hwang MY, Irvin MR, Islas-Andrade S, Jarvik GP, Kang HM, Kardia SLR, Kelly T, Kenny EE, Khan AT, Kim B-J, Kim RW, Kim YJ, Koistinen HA, Kooperberg C, Kuusisto J, Kwak SH, Laakso M, Lange LA, Lee J, Lee J, Lee S, Lehman DM, Lemaitre RN, Linneberg A, Liu J, Loos RJJ, Lubitz SA, Lyssenko V, Ma RCW, Martin LW, Martínez-Hernández A, Mathias RA, McGarvey ST, McPherson R, Meigs JB, Meitinger T, Melander O, Mendoza-Caamal E, Metcalf GA, Mi X, Mohlke KL, Montasser ME, Moon J-Y, Moreno-Macías H, Morrison AC, Muzny DM, Nelson SC, Nilsson PM, O'Connell JR, Orho-Melander M, Orozco L, Palmer CNA, Palmer ND, Park CJ, Park KS, Pedersen O, Peralta JM, Peyser PA, Post WS, Preuss M, Psaty BM, Qi Q, Rao D, Redline S, Reiner AP, Revilla-Monsalve C, Rich SS, Samani N, Schunkert H, Schurmann C, Seo D, Seo J-S, Sim X, Sladek R, Small KS, So WY, Stilp AM, Sunitha SM, Tai ES, Tam CHT, Taylor KD, Teo YY, Thameem F, Tomlinson B, Tsai MY, Tuomi T, Tuomilehto J, Tusié-Luna T, van Dam RM, Vasan RS, Viaud Martinez KA, Wang FF, Wang X, Watkins H, Weeks DE, Wilson JG, Witte DR, Wong T-Y, Yanek LR, AMP-T2D-GENES, Myocardial Infarction Genetics Consortium, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, NHLBI TOPMed Lipids Working Group, Kathiresan S, Rotter JI, Boehnke M, McCarthy MI, Willer CJ, Natarajan P, Flannick JA, Khera AV, Peloso GM (2020) Rare coding variants in 35 genes associate with circulating lipid levels – a multi-ancestry analysis of 170,000 exomes. bioRxiv [Preprint] December 23, 2020: Available from: <https://doi.org/10.1101/2020.12.22.423783>.
14. Kwong AM, Blackwell TW, LeFaive J, de Andrade M, Barnard J, Barnes KC, Blangero J, Boerwinkle E, Burchard EG, Cade BE, Chasman DI, Chen H, Conomos MP, Cupples LA, Ellinor PT, Eng C, Gao Y, Guo X, Irvin MR, Kelly TN, Kim W, Kooperberg C, Lubitz SA, Mak ACY, Manichaikul AW, Mathias RA, Montasser ME, Montgomery CG, Musani S, Palmer ND, Peloso GM, Qiao D, Reiner AP, Roden DM, Shoemaker MB, Smith JA, Smith NL, Su JL, Tiwari HK, Weeks DE, Weiss ST, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Analysis Working Group, Scott LJ, Smith AV, Abecasis GR, Boehnke M, Kang HM (2020) Robust, flexible, and scalable tests for Hardy-Weinberg Equilibrium across diverse ancestries. bioRxiv [Preprint] June 25, 2020: Available from: <https://doi.org/10.1101/2020.06.23.167759>.
15. Ray M[‡], Heinsberg LW[‡], Conley YP, Roberts JM, Jeyabalan A, Hubel CA, Weeks DE, Schmella MJ (2020) Utilization of Epigenome-wide DNA Methylation for Longitudinal Comparison of White Blood Cell Proportions Across Preeclamptic and Normotensive Pregnancy by Self-Reported Race. medRxiv [Preprint] September 20, 2020 <https://doi.org/10.1101/2020.09.18.20197491>

16. Stilp AM, Emery LS, Broome JG, Buth EJ, Khan AT, Laurie CA, Wang FF, Wong Q, Chen D, D'Augustine CM, Heard-Costa NL, Hohensee CR, Johnson WC, Juarez LD, Liu J, Mutalik KM, Raffield LM, Wiggins KL, de Vries PS, Kelly TN, Kooperberg C, Natarajan P, Peloso GM, Peyser PA, Reiner AP, Arnett DK, Aslibekyan S, Barnes KC, Bielak LF, Bis JC, Cade BE, Chen M-H, Correa A, Cupples LA, de Andrade M, Ellinor PT, Fornage M, Franceschini N, Gan W, Ganesh SK, Graffelman J, Grove ML, Guo X, Hawley NL, Hsu W-L, Jackson RD, Jaquish CE, Johnson AD, Kardia SL, Kelly S, Lee J, Mathias RA, McGarvey ST, Mitchell BD, Montasser ME, Morrison AC, North KE, Nouraei SM, Oelsner EC, Pankratz N, Rich SS, Rotter JI, Smith JA, Taylor KD, Vasani RS, Weeks DE, Weiss ST, Wilson CG, Yanek LR, Psaty BM, Heckbert SR, Laurie CC (2020) A system for phenotype harmonization in the NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. *bioRxiv* [Preprint] June 20, 2020 <https://doi.org/10.1101/2020.06.18.146423>
17. Wessel J, Majarian TD, Highland HM, Raghavan S, Szeto MD, Hasbani NR, de Vries PS, Brody JA, Sarnowski C, DiCorpo D, Yin X, Hidalgo B, Guo X, Perry J, O'Connell JR, Lent S, Montasser ME, Cade BE, Jain D, Wang H, Wu P, Bonàs-Guarch S, D'Oliveira Albanus R, Leong A, Miguel-Escalada I, Varshney A, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Anthropometry, DIAMANTE, Kinney GL, Yanek LR, Lange L, Almeida M, Peralta JM, Aslibekyan S, Baldrige AS, Bertoni AG, Bielak LF, Bowden DW, Chen C-S, Chen Y-DI, Choi SH, Choi WJ, Darbar D, Floyd JS, Freedman BI, Goodarzi MO, Irvin R, Kalyani RR, Kelly T, Lee S, Liu C-T, Loesch D, Manson JE, Nassir R, Palmer ND, Pankow JS, Rasmussen-Torvik LJ, Reiner AP, Selvin E, Shadyab AH, Smith JA, Weeks DE, Weng L-C, Xu H, Yao J, Yoneda Z, Zhao W, Ferrer J, Mahajan A, McCarthy MI, Parker S, Alonso A, Arnett DK, Blangero J, Boerwinkle E, Cho MH, Correa A, Cupples LA, Curran JE, Duggirala R, Ellinor PT, He J, Heckbert SR, Kardia SL, Kim RW, Kooperberg C, Liu S, Lubitz SA, Mathias RA, McGarvey S, Mitchell BD, Morrison AC, Peyser PA, Psaty BM, Redline S, Roden D, Shoemaker MB, Smith NL, Taylor KD, Vasani RS, Viaud-Martinez KA, Florez JC, Wilson JG, Sladek R, Dupuis J, Rich SS, Rotter JI, Meigs JB, Manning AK (2020) Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals Unexplained Heritability of Type 2 Diabetes. *medRxiv* [preprint] November 16, 2020: Available from: <https://doi.org/10.1101/2020.11.13.20221812>.
18. DiCorpo D, Gaynor SM, Russell EM[‡], Westerman KE, Raffield LM, Majarian TD, Wu P, Sarnowski C, Highland HM, Jackson A, Hasbani NR, de Vries PS, Brody JA, Hidalgo B, Guo X, Perry JA, O'Connell JR, Lent S, Montasser ME, Cade BE, Jain D, Wang H, D'Oliveira Albanus R, Varshney A, Yanek LR, Lange L, Palmer ND, Almeida M, Peralta JM, Aslibekyan S, Baldrige AS, Bertoni AG, Bielak LF, Chen C-S, Chen Y-DI, Choi WJ, Goodarzi MO, Floyd JS, Irvin MR, Kalyani RR, Kelly TN, Lee S, Liu C-T, Loesch D, Manson JE, Pankow JS, Rasmussen-Torvik LJ, Reiner AP, Selvin E, Smith JA, Weeks DE, Xu H, Yao J, Zhao W, Parker S, Alonso A, Arnett DK, Blangero J, Boerwinkle E, Correa A, Cupples LA, Curran JE, Duggirala R, He J, Heckbert SR, Kardia SL, Kim RW, Kooperberg C, Liu S, Mathias RA, McGarvey ST, Mitchell BD, Morrison AC, Peyser PA, Psaty BM, Redline S, Shuldiner AR, Taylor KD, Vasani RS, Viaud-Martinez KA, Florez JC, Wilson JG, Sladek R, Rich SS, Rotter JI, Lin X, Dupuis J, Meigs JB, Wessel J, Manning AK (2021) Whole Genome Sequence Association Analysis of Fasting Glucose and Fasting Insulin Levels in Diverse Cohorts from the NHLBI TOPMed Program. *medRxiv* [Preprint] January 04, 2021 <https://doi.org/10.1101/2020.12.31.20234310>
19. Hawley NL, Duckham RL, Carlson JC, Naseri T, Reupena MS, Lameko V, Pomer A, Wetzel A, Selu M, Lupematisila V, Unasa F, Vesi L, Fatu T, Unasa S, Faasalele-Savusa K, Viali S, Rivara AC, Russell EM[‡], Deka R, Kershaw EE, Minster RL, Weeks DE, McGarvey ST (2021) The association of CREBRF variant rs373863828 with body composition in adult Samoans. *medRxiv* [preprint] February 12, 2021 <https://doi.org/10.1101/2021.02.11.21251582>
20. Kanshana JS, Mattila PE, Ewing MC, Wood AN, Schoiswohl G, Meyer AC, Kowalski A, Rosenthal SL, Gingras S, Kaufman BA, Lu R, Weeks DE, McGarvey ST, Minster RL, Hawley NL, Kershaw EE (2021) A murine model of the human CREBRF^{R457Q} obesity-risk variant does not influence energy or glucose homeostasis in response to nutritional stress. *bioRxiv* [Preprint] May 06, 2021 <https://doi.org/10.1101/2021.05.06.442909>

21. Nakao T, Bick AG, Taub MA, Zekavat SM, Uddin MM, Niroula A, Carty CL, Lane J, Honigberg MC, Weinstock JS, Pampana A, Gibson CJ, Griffin GK, Clarke SL, Bhattacharya R, Assimes TL, Emery LS, Stilp AM, Wong Q, Broome J, Laurie CA, Khan AT, Smith AV, Blackwell TW, Yoneda ZT, Peralta JM, Bowden DW, Irvin MR, Boorgula M, Zhao W, Yanek LR, Wiggins KL, Hixson JE, Gu CC, Peloso GM, Roden DM, Reupena MaS, Hwu C-M, DeMeo DL, North KE, Kelly S, Musani SK, Bis JC, Lloyd-Jones DM, Johnsen JM, Preuss M, Tracy RP, Peyser PA, Qiao D, Desai P, Curran JE, Freedman BI, Tiwari HK, Chavan S, Smith JA, Smith NL, Kelly TN, Hildalgo B, Cupples LA, Weeks DE, Hawley NL, Minster RL, The Samoan Obesity, Lifestyle and Genetic Adaptations Study (OLaGA) Group, Deka R, Naseri TT, de las Fuentes L, Raffield LM, Tracy RP, Morrison AC, Vries PS, Ballantyne CM, Kenny EE, Rich SS, Whitsel EA, Cho MH, Shoemaker MB, Pace BS, Blangero J, Palmer ND, Mitchell BD, Shuldiner AR, Barnes KC, Redline S, Kardia SLR, Abecasis GR, Becker LC, Heckbert SR, He J, Post W, Arnett DK, Vasani RS, Darbar D, Weiss ST, McGarvey ST, de Andrade M, Chen Y-DI, Kaplan RC, Meyers DA, Custer BS, Correa A, Psaty BM, Fornage M, Manson JE, Boerwinkle E, Konkle BA, Loos RJF, Rotter JI, Silverman EK, Kooperberg C, Jaiswal S, Libby P, Ellinor PT, Pankratz N, Ebert BL, Reiner AP, Mathias RA, Do R, NHLBI Trans-Omics in Precision Medicine (TOPMed) Consortium, Natarajan P (2021) Bidirectional Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of intermediate potential. medRxiv [preprint] March 1, 2021. Available from: <https://doi.org/10.1101/2021.02.26.21252199>
22. Russell EM[‡], Carlson JC, Krishnan M, Hawley NL, Sun G, Cheng H, Naseri T, Sefuiva Reupena Ma, Viali Si, Tuitele J, Major TJ, Miljkovic I, Merriman TR, Deka R, Weeks DE, McGarvey ST, Minster RL (2021) CREBRF missense variant rs373863828 has both direct and indirect effects on type 2 diabetes and fasting glucose in Polynesians living in Samoa and Aotearoa New Zealand. medRxiv [Preprint] February 19, 2021. <https://doi.org/10.1101/2021.02.15.21251768>
23. Moors J, Krishnan M[‡], Sumpter N, Takei R, Bixley M, Cadzow M, Major TJ, Phipps-Green A, Topless R, Merriman M, Rutledge M, Morgan B, Carlson JC, Zhang JZ[†], Russell EM[‡], Sun G, Cheng H, Weeks DE, Naseri T, Reupena MS, Viali S, Tuitele J, Hawley NL, Deka R, McGarvey ST, Zoysa J de, Murphy R, Dalbeth N, Stamp L, Taumoepeau M, King F, Wilcox P, McCormick S, Minster RL, Merriman TR, Leask M. A population-specific missense variant rs159700001 in CETP promotes a favorable lipid profile and reduces CETP activity. medRxiv [Preprint]. 2021 Sep 15. <https://doi.org/10.1101/2021.09.11.21263438>
24. Li Z, Li X, Zhou H, Gaynor SM, Selvaraj MS, Arapoglou T, Quick C, Liu Y, Chen H, Sun R, Dey R, Arnett DK, Bielak LF, Bis JC, Blackwell TW, Blangero J, Boerwinkle E, Bowden DW, Brody JA, Cade BE, Conomos MP, Correa A, Cupples LA, Curran JE, Vries PS de, Duggirala R, Freedman BI, Göring HHH, Guo X, Kalyani RR, Kooperberg C, Kral BG, Lange LA, Manichaikul A, Martin LW, Mitchell BD, Montasser ME, Morrison AC, Naseri T, O'Connell JR, Palmer ND, Peyser PA, Psaty BM, Raffield LM, Redline S, Reiner AP, Reupena MS, Rice KM, Rich SS, Smith JA, Taylor KD, Vasani RS, Weeks DE, Wilson JG, Yanek LR, Zhao W, NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium, TOPMed Lipids Working Group, Rotter JI, Willer CJ, Natarajan P, Peloso GM, Lin X. A framework for detecting noncoding rare variant associations of large-scale whole-genome sequencing studies. bioRxiv [Preprint] 2021 Nov 8. <https://doi.org/10.1101/2021.11.05.467531>
25. Shan Y[†], Weeks D (2022) BayesRB: a markov chain Monte Carlo-based polygenic genetic risk score algorithm for dichotomous traits. bioRxiv [Preprint] 2022 March 2. <https://doi.org/10.1101/2022.02.27.482193>
26. Heinsberg LW[‡], Carlson JC, Pomer A, Cade BE, Naseri T, Reupena MS, Weeks DE, McGarvey ST, Redline S, Hawley NL. Correlates of Daytime Sleepiness and Insomnia among Adults in Samoa. medRxiv [Preprint] 2022 May 27. <https://doi.org/10.1101/2022.05.25.22275570>
27. Carlson JC, Krishnan M[‡], Rosenthal SL, Russell EM, Zhang JZ[†], Hawley NL, Moors J, Cheng H, Dalbeth N, Zoysa J de, Watson H, Qasim M, Murphy R, Naseri T, Reupena MS, Viali S, Stamp LK, Tuitele J, Kershaw EE, Deka R, McGarvey ST, Merriman TR, Weeks DE, Minster RL. A stop-gain variant in BTNL9 is associated with atherogenic lipid profiles. medRxiv [Preprint] 2022 Jun 23. <https://doi.org/10.1101/2022.06.22.22276448>
28. Zhang JZ[†], Heinsberg LW[‡], Krishnan M[‡], Hawley NL, Major TJ, Carlson JC, Hindmarsh JH, Watson H, Qasim M, Stamp LK, Dalbeth N, Murphy R, Sun G, Cheng H, Naseri T, Reupena MS, Kershaw EE, Deka R, McGarvey ST, Minster RL, Merriman TR, Weeks DE. Multivariate analysis of a missense variant in CREBRF reveals associations with measures of adiposity in people of Polynesian ancestries. medRxiv [preprint] 2022 Sep 9. <https://doi.org/10.1101/2022.09.08.22279720>

29. Treble-Barna A, Heinsberg LW[‡], Stec Z, Breazeale S, Davis TS, Kesbhat AA, Chattopadhyay A, VonVille HM, Ketchum AM, Yeates KO, Kochanek PM, Weeks DE, Conley YP (2022) Brain-Derived Neurotrophic Factor (BDNF) Epigenomic Modifications and Brain-Related Phenotypes in Humans: A Systematic Review. medRxiv [preprint] 2022 September 17. <https://doi.org/10.1101/2022.09.13.22279723>
30. Carlson JC, Krishnan M[‡], Liu S[†], Anderson KJ, Zhang JZ[†], Yapp TJ[†], Chiyka EA[†], Dikec DA[†], Cheng H, Naseri T, Reupena MS, Viali S, Deka R, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2023) Improving imputation quality in Samoans through the integration of population-specific sequences into existing reference panels. medRxiv [preprint] 2023 October 31 doi: <https://doi.org/10.1101/2023.10.31.23297835> PMID: PMC10635250
31. Heinsberg LW[‡], Niu S, Arslanian KJ, Chen R, Bedi M, Unasa-Apelu F, Fidow UT, Soti-Ulberg C, Conley YP, Weeks DE, Ng CA, Hawley NL (2023) Characterization of Per- and Polyfluoroalkyl Substance (PFAS) concentrations in a community-based sample of infants from Samoa. medRxiv [preprint] 2023 November 11 doi: <https://doi.org/10.1101/2023.11.10.23298357> PMID: PMC10659488
32. Heinsberg LW[‡], Pomer A, Cade BE, Carlson JC, Naseri T, Reupena MS, Viali S, Weeks DE, McGarvey ST, Redline S, Hawley NL (2023) Characterization of sleep apnea among a sample of adults from Samoa. medRxiv [preprint] 2023 November 16 doi: <https://doi.org/10.1101/2023.11.16.23298644> PMID: PMC10680886
33. Zhang X, Brody JA, Graff M, Highland HM, Chami N, Xu H, Wang Z, Ferrier K, Chittoor G, Josyula NS, Li X, Li Z, Allison MA, Becker DM, Bielak LF, Bis JC, Boorgula MP, Bowden DW, Broome JG, Buth EJ, Carlson CS, Chang KM, Chavan S, Chiu YF, Chuang LM, Conomos MP, DeMeo DL, Du M, Duggirala R, Eng C, Fohner AE, Freedman BI, Garrett ME, Guo X, Haiman C, Heavner BD, Hidalgo B, Hixson JE, Ho YL, Hobbs BD, Hu D, Hui Q, Hwu CM, Jackson RD, Jain D, Kalyani RR, Kardia SLR, Kelly TN, Lange EM, LeNoir M, Li C, Marchand LL, McDonald MN, McHugh CP, Morrison AC, Naseri T, NHLBI Trans-Omics for Precision Medicine Consortium, O'Connell J, O'Donnell CJ, Palmer ND, Pankow JS, Perry JA, Peters U, Preuss MH, Rao DC, Regan EA, Reupena SM, Roden DM, Rodriguez-Santana J, Sitlani CM, Smith JA, Tiwari HK, Vasani RS, Wang Z, Weeks DE, Wessel J, Wiggins KL, Wilkens LR, Wilson PWF, Yanek LR, Yoneda ZT, Zhao W, Zollner S, Arnett DK, Ashley-Koch AE, Barnes KC, Blangero J, Boerwinkle E, Burchard EG, Carson AP, Chasman DI, Chen YI, Curran JE, Fornage M, Gordeuk VR, He J, Heckbert SR, Hou L, Irvin MR, Kooperberg C, Minster RL, Mitchell BD, Nouraei M, Psaty BM, Raffield LM, Reiner AP, Rich SS, Rotter JI, Shoemaker MB, Smith NL, Taylor KD, Telen MJ, Weiss ST, Zhang Y, Heard-Costa N, Sun YV, Lin X, Adrienne Cupples L, Lange LA, Liu CT, Loos RJF, North KE, Justice AE (2023) Whole Genome Sequencing Analysis of Body Mass Index Identifies Novel African Ancestry-Specific Risk Allele. medRxiv [preprint] 2023 August 22 doi: <https://doi.org/10.1101/2023.08.21.23293271> PMID: PMC10473809
34. Erdogan-Yildirim Z, Carlson JC, Krishnan M[‡], Zhang JZ[†], Lambert-Messerlian G, Naseri T, Viali S, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2024) A genome-wide association study of anti-Mullerian hormone (AMH) levels in Samoan women. medRxiv. doi: <https://doi.org/10.1101/2024.12.05.24318457> PMID: PMC11643216
35. Liu S[†], Liu D, Bender CM, Erickson KI, Sereika SM, Shaffer JR, Weeks DE, Conley YP (2024) Associations between DNA methylation and cognitive function in early-stage hormone receptor-positive breast cancer patients. medRxiv. doi: <https://doi.org/10.1101/2024.11.17.24317299> PMID: PMC11601744
36. Heinsberg LW, Loia M, Tasele S, Faasalele-Savusa K, Carlson JC, Anesi S, Desobry K, Yuchongco E, Guevara BF, Sesaga A, Iloilo A, Tofaeono V, Bryan K, Tauasosi-Posiulai T, Kershaw EE, Conley YP, Weeks DE, Hawley NL, Muasau-Howard B (2025) Study Protocol for the Health Outcomes in Pregnancy and Early Childhood (HOPE) Study: A Mother-Infant Study in American Samoa. medRxiv. doi: <https://doi.org/10.1101/2025.06.04.25329013> PMID: PMC12155048
37. Heinsberg LW, Kesbhat A, Petersen B, Kaseman L, Stec Z, Anton N, Kochanek PM, Yeates KO, Weeks DE, Conley Y, Treble-Barna A (2025) Differential DNA Methylation of the Brain-Derived Neurotrophic Factor Gene is Observed after Pediatric Traumatic Brain Injury Compared to Orthopedic Injury. medRxiv doi: <https://doi.org/10.1101/2025.06.16.25329571> PMID: PMC12204258
38. Lee EY, Dinh BL, Tang J, Streicher S, Wang X, Biswas S, Tian H, Yu X, Tappara K, Naseri T, Viali S, Weeks DE, Carlson JC, Haiman CA, Marchand LL, Maskarinec G, Wilkens LR, Park SY, Chiang CWK (2025) Incorporating Dietary Information to Enhance Polygenic Prediction Models with Applications to Body Mass Index and Type 2 Diabetes. medRxiv. doi: <https://doi.org/10.1101/2025.10.03.25337287> PMID: PMC12687799

39. Dinh BL, Wang X, Sheng X, Wan P, Srivastava AK, Naseri T, Viali Si, Wilkens L, Marchand LL, Haiman C, Weeks DE, Chiang CWK, Carlson JC (2026) Meta-analysis of over 8,000 individuals from Hawai'i and Samoa for genetic associations to cardiometabolic phenotypes. medRxiv. doi: <https://doi.org/10.64898/2026.05.08.26352761>

Formal Online Comments:

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](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. Weeks DE, Sobel E, O'Connell JR, Lange K (1995) Computer programs for multilocus haplotyping of general pedigrees. Am J Hum Genet **56**:1506-1507

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. 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

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.

dbVOR: a database system for managing pedigree, phenotype, and genotype data.

Baron RV, Conley YP, Gorin MB, Weeks DE (2015) dbVOR: a database system for importing pedigree, phenotype and genotype data and exporting selected subsets. *BMC Bioinformatics* **16**:91. PMC4407391

Genetic ME: a visualization application for merging and editing pedigrees.

Bui DK, Jiang Y[†], Wei X, Ortube MC, Weeks DE, Conley YP, Gorin MB (2015) Genetic ME - a visualization application for merging and editing pedigrees for genetic studies. *BMC Res Notes* **8**:241. PMC4478623

RecCla: an R package for family relationship classification.

Zeng Z[†], Weeks DE, Chen W, Mukhopadhyay N, Feingold E (2016) A pipeline for classifying relationships using dense SNP/SNV data and putative pedigree information. *Genet Epidemiol* **40**:161-171. PMC514699

powerpkg: Power Analyses for the Affected Sib Pair and the TDT Design. DOI:

<https://doi.org/10.32614/CRAN.package.powerpkg>

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

Weeks DE, Baron RV and Stickel JR. The Mega2R R package: tools for accessing and processing common genetic data formats in R [version 1; not peer reviewed]. *F1000Research* 2017, **6**:1951 (poster)

(doi: <https://doi.org/10.7490/f1000research.1115046.1>)

dbGaPChecksum: 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.dbGaPChecksum>

Heinsberg LW[‡], Weeks DE (2023) dbGaPChecksum: pre-submission checks of dbGaP-formatted subject phenotype files. *BMC Bioinformatics* 24:77. PMID: PMC9985192

Abstracts:

[†]Graduate student; [‡]Post-doctoral trainee.

1. Gatti RA, DE Weeks, RS Sparkes, K Lange (1987) Genetic linkage studies of ataxia-telangiectasia: Phenotypic blood markers. *Am J Hum Genet* **41**:A166
2. Lange K, DE Weeks (1987) Preliminary ranking procedures for multilocus ordering. *Am J Hum Genet* **41**:A173
3. Weeks DE, K Lange (1987) The affected-pedigree-member method of linkage analysis. *Am J Hum Genet* **41**:A190
4. Weeks DE, K Lange (1988) Efficient computation of lod scores: Genotype elimination, genotype redefinition, and hybrid maximum likelihood algorithms. *Am J Hum Genet* **43**:A162
5. Smith M, K Dumars, R Baumann, K Yoshiyama, Y Nakamura, C Julier, JA Trofatter, DE Weeks, M Pandolfo, PM Conneally (1989) Evidence for genetic heterogeneity in tuberous sclerosis: one gene maps to the 9q34 region and a second gene maps in the 11q22-11q23 region. *Cytogenet Cell Genet* **51**:1082
6. Weeks DE, J Ott (1989) The regression approach to heterogeneity mapping. *Cytogenet Cell Genet* **51**:1104
7. Weeks DE, J Ott, GM Lathrop (1990) SLINK: a general simulation program for linkage analysis. *Am J Hum Genet* **47**:A204
8. Terwilliger JD, DE Weeks, J Ott (1990) Laboratory errors in the reading of marker alleles cause massive reductions in lod score and lead to gross overestimates of the recombination fraction. *Am J Hum Genet* **47**:A201
9. Li CC, Weeks DE, Ferrell RE, Chakravarti A (1991) A new measure of similarity of DNA fingerprints. *Am J Hum Genet (Supplement)* **49**:14
10. Nygaard TG, Weeks DE, Gilliam TC, Wilhelmsen KC (1991) Refinement of the pericentromeric localization of lubag (X-linked dystonia parkinsonism). *Am J Hum Genet (Supplement)* **49**:363
11. Straub RE, Baron M, Lehner T, Weeks D, Luo Y, Wexler SN, Ott J, Gilliam TC (1991) Genetic linkage analysis of bipolar affective illness. *Am J Hum Genet (Supplement)* **49**:361
12. Weeks DE, Ott J, Lathrop GM (1991) Multipoint mapping under different models of genetic interference using the LINKAGE programs. *Am J Hum Genet (Supplement)* **49**:372
13. Weeks DE, Harby LD (1992) Simulation studies of the Affected Pedigree Member method of linkage analysis. *Am J Hum Genet (Supplement)* **51**:205
14. Wilhelmsen KC, Weeks DE, Neystat M, Nygaard TG (1992) Linkage disequilibrium mapping of lubag (X-linked dystonia-parkinsonism) using simple sequence repeats. *Am J Hum Genet (Supplement)* **51**:205
15. Angrist M, Kauffman E, Matisse TC[‡], Slaugenhaupt SA, Bolk S, Puffenberger EG, Lipson A, Cass DT, Reyna T, Weeks DE, Weissenbach J, Chakravarti A (1993) A genetic locus for Hirschsprung disease in the pericentromeric region of human chromosome 10. *Am J Hum Genet (Supplement)* **53**, Abstract 134
16. Brown DL[†], Gorin MB, Weeks DE (1993) Optimal strategies for genomic searching using the affected pedigree member method of linkage analysis. *Am J Hum Genet (Supplement)* **53**, Abstract 981

17. Goldin LR, Weeks DE (1993) Two-locus models of disease: comparison of likelihood and non-parametric linkage methods. Am J Hum Genet (Supplement) **53**, Abstract 1006
18. Matisse TC[‡], Blaschak JE, Weeks DE, Chakravarti A. (1993) Analysis of interference and sex-specific recombination in the human genome. Am J Hum Genet (Supplement) **53**, Abstract 262
19. Valappil TI, Weeks DE (1993) The affected pedigree member method of linkage analysis for X-linked traits. Am J Hum Genet (Supplement) **53**, Abstract 1095
20. Weeks DE, Matisse TC[‡], Chakravarti A (1993) Detection of tandemly duplicated genetic markers and implications for linkage analysis. Am J Hum Genet (Supplement) **53**, Abstract 1100
21. Matisse TC[‡], Weeks DE, Chakravarti A (1993) Automated construction of human genomic linkage maps of microsatellites, VNTRs, and genes. Human Genome Mapping Workshop 93 (HGM 93)
22. Kramer RW, Weeks DE, Chiarulli DM (1994) Incremental computation of multipoint likelihoods in constructing genetic linkage maps. Am J Hum Genet **55**,A191
23. Matisse TC[‡], Schroeder MD, Chiarulli DM, Weeks DE (1994) Parallel computation of genetic likelihoods using CRI-MAP, PVM, and a network of distributed workstations. Am J Hum Genet **55**,A195
24. O'Connell JR, Chiarulli DM, Weeks DE (1994) Multipoint likelihoods for genetic linkage: the untyped founder problem. Am J Hum Genet **55**,A351
25. Davis S[†], Schroeder M, Goldin LR, Weeks DE (1995) Nonparametric simulation-based statistics for detecting linkage in general pedigrees. Am J Hum Genet **57**:A190
26. O'Connell JR, Weeks DE (1995) Rapid multilocus linkage analysis: Solving the untyped founder problem. Am J Hum Genet **57**:A199
27. Shannon WD[‡], Goldin LR, Chase GA, Weeks DE (1995) Distinguishing true and false positive peaks in allele-sharing statistics. Am J Hum Genet **57**:A35 (Slide presentation by Shannon)
28. Weeks DE, Young A[‡], Li CC (1995) DNA profile match probabilities in a subdivided population: When can subdivision be ignored? Am J Hum Genet **57**:A12 (Slide presentation)
29. Young A[‡], Weeks DE, Lathrop GM (1995) A new version of the LINKAGE analysis programs: dynamic memory allocation, amalgamation, and parallelization. Am J Hum Genet **57**:A206
30. Davis S[†], Weeks DE (1996) Comparison of nonparametric statistics for detecting linkage in affected-sib-pair data. Am J Hum Genet **59**:A216
31. O'Connell JR, Weeks DE (1996) Approximation methods for multipoint LOD scores. Am J Hum Genet **59**:A230
32. Terwedow H, Rimmler JB, Ter-Minassian M, Pritchard M, Weeks DE, Pericak-Vance MA, Haines JL (1996) A comparison of APM and SimIBD, two statistical methods of linkage analysis. Am J Hum Genet **59**:A238
33. Davis S[†], Weeks DE (1997) Improvements to SimIBD, a nonparametric method for detecting linkage in general pedigrees. Am J Hum Genet Suppl **61**:A272
34. Klauck S, Maestrini E, Weeks D, Nöthen M, Monaco A, Poustka F, Poustka A (1997) Association studies searching for candidate gene regions in a large collection of patients with autism German Society of Human Genetics, Innsbruck, April 1997

35. Marinov M, Sobel E, O'Connell JR, Lange K, Weeks DE (1997) Parallelization of SIMWALK2, a random walk program for analysis of general pedigrees. Am J Hum Genet Suppl **61**:A284
36. Nayak N, Weeks DE (1997) Mapping quantitative trait loci in humans: selected sampling by parental phenotypes only. Am J Hum Genet Suppl **61**:A287
37. O'Connell JR, Weeks DE (1997) PedCheck: A program for identifying marker typing incompatibilities in linkage analysis. Am J Hum Genet Suppl **61**:A288
38. Sinsheimer JS, Weeks DE, Duncan EL, Lathrop GM (1997) Designing a linkage study for a quantitative trait. Am J Hum Genet Suppl **61**:A294
39. Fisher SE, Marlow AJ, Lamb J, Maestrini E, Williams DF, Richardson AJ, Weeks DE, Stein JF, Monaco AP (1998) A quantitative trait locus on chromosome 6p influences different aspects of developmental dyslexia. Am J Hum Genet **63**:A326
40. O'Connell JR, Margetic N, Farrall M, Lathrop GM, Weeks DE, Demenais F, Martinez M, Durrieu G, Koch I, Rohde K (1998) Dissecting complex diseases with FINESSE. International Genetic Epidemiology Society, Arcachon, France
41. O'Connell JR, Weeks DE (1998) An optimal algorithm for automatic genotype elimination in the presence of loops. Am J Hum Genet **63**:A303
42. Sobel E, Weeks DE (1998) Multipoint IBD estimation at arbitrary locations using general pedigrees. Am J Hum Genet **63**:A309
43. Conley YP, Gorin MB, Mah TS, Weeks DE, Ferrell RE (1999) Glutathione peroxidase 3: Identification of promoter region polymorphisms and association with age-related maculopathy. Am J Hum Genet **65**:A104
44. Maestrini E, International Molecular Genetic Study of Autism Consortium (including D.E. Weeks) (1999) Search for autism susceptibility loci: genome screen follow-up and fine mapping of a candidate region on chromosome 7q. Am J Hum Genet **65**:A106
45. Mukhopadhyay N, Almasy L, Schroeder M, Mulvihill WP, Weeks DE (1999) Mega2, a data-handling program for facilitating genetic linkage and association analyses. Am J Hum Genet **65**:A436
46. McGarvey ST, Forrest W, Weeks DE, Deka R (2000) Human obesity gene (HOB) marker alleles and BMI in Samoans. North American Association for the Study of Obesity (Abstract)
47. Gorin MB, Weeks DE, Conley YS, Mah TS, Barnes LR, Rosenfeld PJ, Ferrell RE (2000) Results and comparison of 2 genome-wide scans for age-related maculopathy (ARM). Am J Hum Genet **67 (Suppl 2)**:47
48. Mukhopadhyay N, Finegold DN, Larson M, Cupples LA, Myers RH, Ferrell R, Weeks DE (2000) Heritability of height and assortative mating in the Framingham Study. Am J Hum Genet **67 (Suppl 2)**:235
49. Sengul H[‡], Weeks DE, Feingold E (2000) Affected-sibship statistics for nonparametric linkage analysis. Am J Hum Genet **67 (Suppl 2)**:309
50. Song K[‡], Weeks DE, Feingold E (2000) X chromosome statistics for nonparametric linkage analysis on general pedigrees. Am J Hum Genet **67 (Suppl 2)**:313
51. Gorin MB, Weeks DE, Conley YP, Tsai H-J[†], Mah TS, Rosenfeld PJ, Paul TO, Eller AW, Morse LS, Dailey JP, Ferrell RE (2001) Age-related maculopathy (ARM): an expanded genome-wide scan with evidence of susceptibility loci within the 1q31 and 17q25 regions. Am J Hum Genet **69 (Suppl)**:542

52. Mukhopadhyay N, Finegold DN, Larson M, Cupples LA, Myers RH, Ferrell R, Weeks DE (2001) Genome-wide scan for loci affecting normal adult height in the Framingham Study. Am J Hum Genet **69 (Suppl)**:402
53. Schmidt SA, Gorin MB, Klaver CCW, Small KW, Haines JL, Postel EA, Saunders AM, Duijn CMV, Weeks DE, Ferrell R, Agarwal A, Pericak-Vance MA (2001) Association of the apolipoprotein E (APOE) gene with age-related macular degeneration (AMD): a pooled case-control study. Am J Hum Genet **69 (Suppl)**:425
54. Sengul H[‡], Weeks DE, Feingold E (2001) Weighting pedigrees of varying sizes in nonparametric linkage analysis. Am J Hum Genet **69 (Suppl)**:535
55. Smelser DT, Sun G, He X, Indugula R, Wolujewicz M, Tsai H-J[†], Tufa J, Viali S, McGarvey ST, Weeks DE, Deka R (2002) Significant association of five candidate gene polymorphisms with Type 2 Diabetes in the Samoans. Am J Hum Genet **71 (Suppl)**:463
56. Song KK[‡], Weeks DE, Sobel E, Feingold E (2002) Efficient simulation of p-values for linkage analysis. Am J Hum Genet **71 (Suppl)**:570
57. Tsai H-J[†], Sun G, Smelser D, Weeks DE, McGarvey S, Deka R (2002) Genome-wide distribution of linkage disequilibrium in the Samoan population. Am J Hum Genet **71 (Suppl)**:451
58. Wicks J, Zabaneh D, Treloar SA, Hadfield R, Dawson G, Lambert A, Haddon B, MacKay I, Weeks DE, O'Connor DT, Schuette D, Gough N, Smith M, Douglas A, Montgomery G, Bennett S, Barlow DH, Martin NG, Kennedy SH (2002) International Endogene Study finds strong evidence of susceptibility loci for endometriosis at two genomic regions. Am J Hum Genet **71 (Suppl)**:215
59. Jones BL, Weeks DE (2003) Linkage testing of affected subjects when pedigree information is uncertain or ignored: A mixture model approach. The International Biometric Society, Eastern North American Region (ENAR) meeting, Tampa, Florida
60. Sengul H[‡], Weeks DE, Feingold E (2003) Weighting of pedigrees in genetic linkage analysis. The International Biometric Society, Eastern North American Region (ENAR) meeting, Tampa, FL
61. Deka R, McGarvey ST, Weeks DE, Indugula SR, Zhang G, Tsai H-J[†], Akey J, Wang N, Smelser D, Pal P, Kaushal R, Sun G, Viali S, Tufa J, Chakraborty R, Jin L (2003) Genetic variation in an isolated population, the Samoans of Polynesia: implications for mapping complex traits. Am J Hum Genet **73 Suppl**:187
62. Gorin MB, Rigatti BW, Demirci FY, Clarke SR, Mah TS, Weeks DE, Ferrell RE (2003) Refinement and candidate gene screening of the Cerulean cataract type 1 locus on 17q24-q25. Am J Hum Genet **73 Suppl**:503
63. Mukhopadhyay N, Buxbaum SG, Weeks DE (2003) Comparative study of multipoint methods for genotype error detection. Am J Hum Genet **73 Suppl**:607
64. Tsai H-J[†], Weeks DE (2003) Evaluating performance of the methods incorporating covariates into the affected sib pair linkage analysis. Am J Hum Genet **73 Suppl**:616
65. Weeks DE, Conley YP, Tsai H-J[†], Mah TS, Schmidt S, Pericak-Vance MA, Haines JL, Postel E, Rosenfeld PJ, Paul TO, Eller AW, Morse LS, Dailey JP, Ferrell RE, Gorin MB (2003) Age-related maculopathy: a third genome-wide scan with continued evidence of susceptibility loci within the 1q31 and 17q25 regions. Am J Hum Genet **73 Suppl**:481
66. MUSAAD S, Indugula SR, Kaushal R, McGarvey ST, Tufa J, Viali S, Weeks DE, Deka R (2004) An association study of 11B hydroxysteroid dehydrogenase type 1 (11HSD1) polymorphisms in Samoans with type 2 diabetes and obesity. American Journal Of Epidemiology **159**:S25

67. Brock G, Weeks D, Feingold E (2004) Simulation of P-Values in MCMC-based Non-parametric Linkage Analysis. Paper presented at the American Society of Human Genetics 54th Annual Meeting. Toronto, Ontario
68. Conley YP, Weeks DE, Thalamuthu A[‡], Mah TS, Ferrell RE, Gorin MB (2004) Positional Candidate Gene Evaluation for Age-Related Maculopathy. Paper presented at the American Society of Human Genetics 54th Annual Meeting. Toronto, Ontario
69. Gorin MB, Rigatti BW, Demirci FY, Clarke SR, Mah TS, Weeks DE, Ferrell RE (2004) Refinement of the Cerulean Cataract Type 1 Locus on 17q25.3 to a 0.5 Mb Critical Region. Paper presented at the American Society of Human Genetics 54th Annual Meeting. Toronto, Ontario
70. He C, Abecasis G, Kong X, Concannon P, Xu X, Buyske S, Weeks DE, Matise T (2004) Enhanced linkage maps from family-based genetics studies. Paper presented at the American Society of Human Genetics 54th Annual Meeting. Toronto, Ontario
71. Musaad S, Indugula SR, Kaushal R, McGarvey ST, Tufa J, Viali S, Weeks DE, Deka R (2004) An association study of 11B hydroxysteroid dehydrogenase type 1 (11HSD1) polymorphisms in Samoans with type 2 diabetes and obesity. Paper presented at the 37th Annual Meeting of the Society for Epidemiologic Research, Salt Lake City, Utah. *Am J Epidemiol* **159**:S25
72. Tsai H-J[†], Weeks DE (2004) Summarizing individual-level covariate information for covariate statistics for affected sib pair (ASP) linkage analysis. Paper presented at the American Society of Human Genetics 54th Annual Meeting. Toronto, Ontario
73. Conley YP, Jakobsdottir J[†], Weeks DE, Mah TS, Ferrell RE, Gorin MB (2005) No evidence of interaction between chromosomes 1q31 and 10q26 in age-related maculopathy (ARM). Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
74. Conley YP, Weeks DE, Thalamuthu A[‡], Mah TS, Ferrell RE, Gorin MB (2005) Association of the ELOVL4 gene with age-related maculopathy. *Investigative Ophthalmology & Visual Science* **46**:2287 Suppl. S
75. Dai F[†], Keighley ED, Sun G, Smelser D, Viali S, Tuitele J, Jin L, Deka R, Weeks DE, McGarvey ST (2005) Genome-wide scan for Adiposity-related Phenotypes in Adult Samoans. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
76. Deka R, Huang W, He Y, Wang H, Wang Y, Wang Y, Li H, Weeks DE, McGarvey ST, Jin L (2005) Portability of the HapMap: Linkage disequilibrium sharing between the continental populations and the Samoans of Polynesia. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
77. Indugula SR, Viali S, Tufa J, Xi H, Kaushal R, Pal P, Sun G, Smelser D, Jin L, Weeks DE, McGarvey ST, Deka R (2005) Association of ACDC, PPARG and LEP gene polymorphisms in type 2 diabetes and obesity among the Samoans. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
78. Jakobsdottir J[†], Conley YP, Weeks DE, Mah TS, Ferrell RE, Gorin MB (2005) Susceptibility genes for age related maculopathy (ARM) on chromosome 10q26. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
79. Jung J[‡], Weeks DE, Feingold E (2005) Gene dropping vs. empirical variance estimation: A comparative study of standardization methods for allele-sharing statistics. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah

80. McGarvey ST, Dai F[†], Weeks DE, Deka R, Viali S, Tufa J (2005) Heritability of cardiovascular disease (CVD) risk factors in adult Samoans. American Journal Of Human Biology **17**:250
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
83. Ray A[†], Weeks DE (2005) A linkage analysis test statistic which models relationship uncertainty. Paper presented at the annual meeting of The American Society of Human Genetics. Salt Lake City, Utah
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 Maculopathy: 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.
96. Gorin MB, Conley YP, Jakobsdottir J[†], Ferrell RE, Weeks DE (2007) C2 and BF genes in Age-Related Macular Degeneration and joint action with CFH and LOC387715 genes. Paper presented at the annual meeting of The American Society of Human Genetics. San Diego, California.
97. Mukhopadhyay I[‡], Thalamuthu A[‡], Feingold E, Weeks DE (2007) A powerful test of association of multiple markers with disease using kernel scores. Paper presented at the annual meeting of The American Society of Human Genetics. San Diego, California.
98. Mukhopadhyay I[‡], Thalamuthu A[‡], Feingold E, Weeks DE (2007) A powerful test of association of multiple genes with disease. *Genet Epidemiol* **31**:450-451. Presented at the 2006 annual meeting of the International Genetic Epidemiology Society. St. Petersburg, Florida.
99. Mukhopadhyay N, Bhattacharjee S, Kuo C-L, Reck BH, Weeks DE, Feingold E (2007) QTL-ALL: software for robust QTL linkage analysis in nuclear families. Paper presented at the annual meeting of The American Society of Human Genetics. San Diego, California.
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, Kambh 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, Anjomshoa 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, Diergaard 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*, *MGATI*, 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 *ICAMI* 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, Stitzel 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 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, March 2025.
217. Miller SL, Martinez DT, Liu C, Reilly PF, Weeks DE, Naseri T, Viali Si, Hawley NL, Minster RL, McGarvey ST, Tucci S (2025) The contribution of archaic introgression to local adaptation in Samoa. Paper presented at the Annual Meeting of The American Society of Human Genetics. Boston, Massachusetts, October 2025
218. Silva AN, Spor LM, Carlson JC, Yapp T-AJ, Zhang JZ, Krishnan M, Liu S, Cheng H, Naseri T, Reupena MS, Viali Si, Tuitele J, Deka R, Kershaw EE, Hawley NL, McGarvey ST, Weeks DE, Minster RL (2025) Genome-Wide Association Studies in Samoan Adults Identify Novel Adiponectin Loci. Paper presented at the Annual Meeting of The American Society of Human Genetics. Boston, Massachusetts, October 2025
219. Spor LM, Liau EM, Sanchis-Juan A, Cheng H, Naseri T, Reupena MS, Viali S, Tuitele J, Kershaw EE, Deka R, Hawley NL, McGarvey ST, Weeks DE, Carlson JC, Brand H, Minster RL (2025) Genome-wide analysis of structural variation and cardiometabolic traits in Samoans. Paper presented at the Annual Meeting of The American Society of Human Genetics. Boston, Massachusetts, October 2025
220. Dinh BL, Alatorre K, Tang J, Lee E, Sheng X, Wilkens LR, Le Marchand L, Haiman CA, Weeks DE, Carlson JC, Chiang CWK (2025) Genetic genealogy-based approach enhances the discovery of trait associated loci in small-sample populations. Paper presented at the Annual Meeting of The American Society of Human Genetics. Boston, Massachusetts, October 2025

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

2021-26 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.

2023-26 Member, Department of Human Genetics Curriculum Committee

School-wide (at the University of Pittsburgh)

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.
- 2022-26 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.
- 2026 Dean's Day Juror, evaluating students' posters, April 9, 2026.

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

Period: 9/09 - 9/12

Supplement

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

of Health

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 uncertainty.

“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: Wilhelmssen)
 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: Wilhelmssen)
 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.