

## Curriculum Vitae

**Daniel E. Weeks**  
**Professor of Human Genetics and Biostatistics**

### 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

**Twitter:** @StatGenDan

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

**Citizenship:** United States of America

### Education:

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

### 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

Spring 1997	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 10 enrolled) Associate Professor, University of Pittsburgh, co-taught
Fall 1997	Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 21 enrolled) Associate Professor, University of Pittsburgh, organized and co-taught
Spring 1998	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 3 enrolled) Associate Professor, University of Pittsburgh, co-taught
Fall 1998	Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 15 enrolled) Associate Professor, University of Pittsburgh, co-taught
Fall 1999	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered) Associate Professor, University of Pittsburgh, co-taught
Fall 2000	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 8 registered) Associate Professor, University of Pittsburgh, co-taught
Spring 2001	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered) Associate Professor, University of Pittsburgh, co-taught
Fall 2001	Human Population Genetics (HUGEN 2022, 3 hrs/week, 3 credits, 18 registered) Associate Professor, University of Pittsburgh, co-taught half
Fall 2002	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 13 registered) Professor, University of Pittsburgh, co-taught half
Fall 2003	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 10 registered) Professor, University of Pittsburgh, co-taught more than half
Fall 2004	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 12 registered) Professor, University of Pittsburgh, co-taught half
Fall 2005	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 9 registered) Professor, University of Pittsburgh, co-taught half
Summer 2006	Linkage Analysis in Human Genetics (HUGEN 2048, 3 hrs/week, 3 credits, 9 registered) Professor, University of Pittsburgh, co-led a break-out discussion section
Fall 2006	Scientific Ethics (INTBP 2290, 4 hrs/week, 1 credit, May-June 2006) Professor, University of Pittsburgh, co-taught half
Summer 2007	Quantitative Genetics (HUGEN 2033, 3 hrs/weeks, 3 credits, 7 registered) 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
	Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 1 auditor)

November 2015	Professor, University of Pittsburgh, taught three lectures on sequencing in Introduction to Gene Mapping (HUGEN 2029, 3 hrs/week, 3 credits, 11 registered).
Spring 2016	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 4 registered, 2 auditors)
Fall 2016	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 13 registered, 3 auditors)
Spring 2018	Professor, University of Pittsburgh, co-taught half Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 10 registered, 8 auditors)
Fall 2018	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 16 registered, 4 auditors)
Fall 2019	Professor, University of Pittsburgh, co-taught half Bioinformatics for Human Genetics (HUGEN 2070, 3 hrs/week, 3 credits, 10 registered, 1 auditor)
Spring 2020	Professor, University of Pittsburgh, co-taught ~80% Statistical Genetics (HUGEN 2080, 3 hrs/week, 3 credits, 8 registered, 2 auditors)
Fall 2020	Professor, University of Pittsburgh, co-taught half Genomic Data Processing and Structure (HUGEN 2071, 3 hrs/week, 3 credits, 19 registered, 1 auditor)

**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).

### 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".
- 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- Frances M. Peterson-Burch, Ph.D., School of Nursing, "miRNAs Related to Age-Related Macular Degeneration, Given Genetic Susceptibility".
- 2020- Zeynep Erdogan-Yildirim, Ph.D., Human Genetics, "Identification of genetic factors involved in the etiology of polycystic ovary syndrome in Samoan women".
- 2021- 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".

### Graduate students

- 1994 Deborah L. Brown, M.S., Human Genetics, "Strategies for genomic searching using the affected pedigree member method of linkage analysis".
- 1997 Sean Davis, Ph.D., Human Genetics, "Nonparametric Statistics in Linkage Analysis".
- 2004 Hui-Ju Tsai, Ph.D., Human Genetics, "Comparison of methods incorporating covariates into affected sib pair linkage analysis".
- 2004 Feng Dai, M.S., Biostatistics, "Imprinting in variance components-based linkage analysis".
- 2007 Amrita Ray, Ph.D., Human Genetics, "Affected relative pair linkage statistics that model relationship uncertainty"
- 2007 Feng Dai, Ph.D., Biostatistics, "Variance components models in statistical genetics: extensions and applications".
- 2009 Johanna Jakobsdottir, Ph.D., Biostatistics, "Genetics of age-related maculopathy & score statistics for X-linked quantitative trait loci".
- 2015 Jia Jia, Ph.D., Biostatistics, "Association analysis between binary traits and common or rare genetic variants on family-based data".
- 2015 Yingda Jiang, Ph.D., Biostatistics, "Gene-based association testing of dichotomous traits using generalized functional linear mixed models for family data".
- 2016 Ying Shan, Ph.D., Biostatistics, "Statistical methods for genetic risk confidence intervals, Bayesian disease risk prediction, and estimating mutation screening saturation".
- 2018 Yunqi Li, M.S., Human Genetics, "Epigenome-wide association study of recovery outcomes of traumatic brain injury patients", co-supervised with Dr. John R. Shaffer.

2018	Richard J. Biedrzycki, M.S., Human Genetics, "Genome-wide association studies, false positives, and how we interpret them".
2018	Winston W. H. Eng, M.S., Biostatistics, "Exploring the genetic characteristics underlying a multidimensional latent chemotherapy symptom burden".
2019	Annie Arockiaraj, M.S., Human Genetics, "Epigenome-wide association studies in aneurysmal subarachnoid hemorrhage patients", co-supervised with Dr. John R. Shaffer.
2020	Chen' Ao Qian, M.S., Biostatistics, "Genome-wide association studies in Samoans give insight into obesity by investigating skinfold thickness".
2020-	Shuwei Liu, Ph.D., Human Genetics
2021-	Laura Stackhouse, M.S, 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-	Dr. Mohanraj Krishnan, co-supervised with Dr. Ryan Minster.
2020-	Dr. Lacey Heinsberg

### 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-	Co-mentor of Qi Yan on his K01 research project "Novel Methods for Analysis of Genetic and Epigenetic Studies of Childhood Asthma".
2020	Supervised Chen' Ao Qian, a Biostatistics M.S. student from the University of Pittsburgh.
2020-	Shuwei Liu, a Human Genetics Ph.D. student from the University of Pittsburgh, worked as a Graduate Student Researcher under my supervision.
2021-	Mentored Laura Stackhouse, a Human Genetics M.S. student from the University of Pittsburgh on her thesis project.

### Scholarly Oversight Committee Service

2016-2018	Erick Forno
2019-2020	Erica Stevens
2019-2020	Soyeon Kim

### 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.

### **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

**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.

**Bibliography**

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

**Peer-reviewed manuscripts:**

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  $\gamma$  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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup> (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<sup>†</sup> (1995) An X-linked version of the affected-pedigree-member method of linkage analysis. Hum Hered **45**:25-33
38. Weeks DE, Young A<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Sobel E, Marinov M, Weeks DE (1997) Analysis of bipolar disorder using affected relatives. Genetic Epidemiol **14**:605-610
43. Davis S<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Weeks DE (1997) Analysis of a complex oligogenic disease. Genetic Epidemiol **14**:861-866



48. Terwilliger JD, Shannon WD<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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 Ophthalmol **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, Udar 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<sup>‡</sup>, 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, Feingold 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<sup>‡</sup>, Weeks DE, Sobel E, Feingold E (2004) Efficient simulation of p values for linkage analysis. Genet Epidemiol **26**:88-96
92. Tsai H-J<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Jakobsdottir J<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Mukhopadhyay N, Tsai H-J<sup>†</sup>, 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<sup>‡</sup>, Mukhopadhyay I<sup>‡</sup>, Ray A<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Weeks DE, Feingold E (2006) Gene-dropping vs. empirical variance estimation for allele-sharing linkage statistics. Genet Epidemiol **30**:652-665

107. Mukhopadhyay I<sup>‡</sup>, 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<sup>†</sup>, Weeks DE (2006) Comparison of methods incorporating quantitative covariates into affected sib pair linkage analysis. Genet Epidemiol **30**:77-93
110. Brock GN<sup>‡</sup>, 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<sup>†</sup>, Keighley ED, Sun G, Indugula SR, Roberts ST, Åberg K<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, Dai F<sup>†</sup>, 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<sup>‡</sup>, Sun G, Smelser D, Indugula SR, Tsai H-J<sup>†</sup>, 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<sup>†</sup>, Sun G, Åberg K<sup>‡</sup>, 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<sup>‡</sup>, Weeks DE, Matthews AG<sup>‡</sup>, Mukhopadhyay I<sup>‡</sup> (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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Dai F<sup>†</sup>, 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<sup>‡</sup>, Dai F<sup>†</sup>, 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<sup>‡</sup>, Ferrell RE, Tekely K, Szatkiewicz JP, Ray A<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Feingold E, Weeks DE, Thalamuthu A<sup>‡</sup> (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, Zarepari 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<sup>†</sup>, 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<sup>†</sup>, Begum F<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Feingold E, Weeks DE (2015) Efficient identification of null-allele single nucleotide polymorphism markers. *Hum Hered* **80**:79-89
173. Yan Q<sup>‡</sup>, 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<sup>‡</sup>, 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, Hebbbring 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, Guymier RH, Johnson MP, Jiang Y<sup>†</sup>, 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<sup>†</sup>, Lin J<sup>†</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Sier AE<sup>†</sup>, Liu D<sup>†</sup>, Dreikorn EN<sup>†</sup>, 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. PMCID: PMC6303255

200. Carlson JC, Rosenthal SL<sup>‡</sup>, Russell EM<sup>†</sup>, 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, Celdon 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<sup>†</sup>, Liu D<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, Arockiaraj AI<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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* (in press)
211. 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
212. 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

213. Treble-Barna A, Heinsberg LW<sup>‡</sup>, 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*:15459683211028245

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

214. 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, Moscato 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 RJJ, 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
215. 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
216. 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
217. 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 RJJ, 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

218. 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 NHLBI Trans-Omics for Precision Medicine (TOPMed) Program. *Am J Epidemiol* (in press)
219. 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, Kardina 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 RJF, 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

#### 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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: Rimo 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 nonsynthetic 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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, Pongracic 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. PMCID: 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 RJF, 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 RJF, 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, Blecker 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 RJF, 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<sup>†</sup>, Liu D<sup>†</sup>, 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<sup>‡</sup>, 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, Vasana 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<sup>‡</sup>, 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, Vasana 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>R457Q</sup> 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, Hidalgo 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<sup>‡</sup>, 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>

#### 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:

<sup>†</sup>Graduate student; <sup>‡</sup>Post-doctoral trainee.

I have written or helped develop many software packages during my career. Several of these (SLINK, Mega2, VITESSE, PedCheck, SimWalk2) are very 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<sup>‡</sup>, 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<sup>†</sup>, 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

**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<sup>†</sup>, 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<sup>†</sup>, 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

**Mega2R:** an R package for loading and manipulating data frames containing genotype, phenotype, and family information from an SQLite database created by Mega2.

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>)

#### Abstracts:

<sup>†</sup>Graduate student; <sup>‡</sup>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<sup>‡</sup>, Slaughaupt 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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, Feingold 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<sup>‡</sup>, Weeks DE, Feingold E (2000) Affected-sibship statistics for nonparametric linkage analysis. Am J Hum Genet **67 (Suppl 2)**:309
50. Song K<sup>‡</sup>, 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<sup>†</sup>, 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, Feingold 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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 11 $\beta$  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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Weeks DE (2005) A linkage analysis test statistic which models relationship uncertainty. Genet Epidemiol **29**:275
83. Ray A<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Dai F<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Thalamuthu A<sup>‡</sup>, 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<sup>‡</sup>, Thalamuthu A<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>‡</sup>, Dai F<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, Tekely K, Ray A<sup>†</sup>, Szatkiewicz J, Weeks D (2009) Genetic epidemiology of Otitis Media. Paper presented at The 6th Extraordinary International Symposium on Recent Advances in Otitis Media. Seoul, Korea, May, 2009.
108. Sanghera DK, Begum MF, Mukerjee A, Ralhan S, Wander GS, Mehra NK, Singh JR, Ferrell RE, Kamboh MI, Weeks DE (2009) A genome-wide linkage scan for blood lipid phenotypes in the Khatri Sikh Diabetes Study (SDS). Paper presented at the 59th Annual Meeting of the American Society of Human Genetics. Honolulu, Hawaii
109. Kuo C, Weeks D, Mukhopadhyay N, Bhattacharjee S, Feingold E (2009) Robust Score Statistics for QTL Linkage Analysis Using Extended Pedigrees. Paper presented at the 59th Annual Meeting of the American Society of Human Genetics. Honolulu, Hawaii
110. Chen W, Stambolian D, Edwards AO, Branham KE, Othman M, Jakobsdottir J<sup>†</sup>, 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 60<sup>th</sup> 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Hawley NL, Medvedovic M, Minster RL, Sun G, Cheng H, Viali S, Deka R, Weeks DE, McGarvey ST (2013) A pilot study testing DNA methylation profiles in Samoan obese and lean young adult males. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA
144. Fung C, Trent K, Joyce S, Zhou P, Nukui T, Weeks DE, Diergaarde B, Ye YQ, Wu XF, Yuan JM, Grandis J, Weissfeld JL, Romkes M, Egloff AM (2013) Identification of epidermal growth factor receptor (EGFR) polymorphisms that modify risk for squamous cell carcinoma of the head and neck (HNSCC). Proceedings of the 104th Annual Meeting of the American Association for Cancer Research. *Cancer Research* **73** (8 Suppl), Abstract 1340.
145. Kollar CP, Baron RV, Mukhopadhyay N, Weeks DE (2013) Mega2: enhanced data-handling for facilitating genetic linkage and association analyses. Paper presented at the 63rd Annual Meeting of the American Society of Human Genetics. Boston, MA
146. Shan Y<sup>†</sup>, 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<sup>†</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Lin J<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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 42<sup>nd</sup> Annual Human Biology Association meeting, New Orleans, LA.
166. Weeks DE, Baron RV, Stichel 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<sup>‡</sup>, 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<sup>‡</sup>, 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<sup>†</sup>, 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<sup>†</sup>, Carlson JC<sup>‡</sup>, 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<sup>†</sup>, Zhang JZ<sup>†</sup>, 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<sup>†</sup>, 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. Krishnan M<sup>‡</sup>, 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

178. 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
179. Russell EM<sup>†</sup>, 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
180. Tiner J<sup>†</sup>, 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
181. 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
182. Zhang JZ<sup>†</sup>, 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
183. Russell E<sup>‡</sup>, Rivara AC, Fu H<sup>†</sup>, 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)
184. Minster RL, Carlson J, Zhang JZ<sup>†</sup>, 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)
185. Krishnan M<sup>‡</sup>, 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)
186. Fu H<sup>†</sup>, 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. Erdogan-Yildirim Z<sup>†</sup>, Carlson JC, Zhang JZ<sup>†</sup>, 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)
188. Carlson JC, Zhang JZ<sup>†</sup>, 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)

**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-   | 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-   | Chair, Strategic Planning Committee  |
| 2018-   | Chair, Computing Committee   |
| 2018-   | 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- Acting Chair, Department of Human Genetics

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 posters of students.  
 2012 Reviewed two grants for the Clinical and Translational Science Institute (CTSI), February 2012.  
 2012 Dean's Day Juror, evaluating posters of students, April 13, 2012.  
 2012-18 Member of the Faculty Appointment, Promotion, and Tenure Committee (FAPTC)  
 2013 Dean's Day Juror, evaluating posters of students, April 1, 2013.  
 2014 Dean's Day Juror, evaluating posters of students, 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 posters of students, April 1, 2015.  
 2016 Dean's Day Juror, evaluating posters of students, April 4, 2016.  
 2017 Dean's Day Juror, evaluating posters of students, April 6, 2017.  
 2017 Member, Department of Epidemiology Faculty Search Committee.  
 2019 Dean's Day Juror, evaluating posters of students, April 4, 2019.  
 2020- Faculty Mentoring Steering Committee  
 2021 Service on an *ad hoc* Faculty Appointment, Promotion, and Tenure Committee (FAPTC) committee, January 8, 2021.  
 2021 Judge, Department of Biostatistics Research Day Poster Session, March 4, 2021.  
 2021 Dean's Day Juror, evaluating posters of students, April 6, 2021.

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.

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://publons.com/researcher/1497688/daniel-e-weeks/peer-review/>

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**

##### **Grant Support:**

"Epigenomics of Neurocognitive Function in Breast Cancer" Annual Direct Costs: \$428,428

Principal Investigator: Conley, Yvette P.

Agency: NIH/NCI

R01 CA221882

Period: 7/18 - 6/23

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.



“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 - 3/22

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.

“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 - 1/22

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.

“Integrated cellular, mouse and human research on a novel missense variant influencing adiposity in Samoans”

Annual Direct Costs: \$735,219

Principal Investigator: McGarvey, Stephen T

Agency: NIH/NHLBI

R01 HL093093

Period: 9/09 - 4/21

The main goal of this project is to characterize a missense variant influencing adiposity in Samoans in cultured cell models, mouse models, and in Samoan adipose tissue, and to characterize the impact of the variant on metabolic and behavioral traits that impact energy homeostasis in deeply phenotyped Samoans selected based on genotype.

“DNA methylomic profiling of preeclampsia across pregnancy”

Annual Direct Costs: \$150,000

Principal Investigator: Schmella, Mandy

Agency: NIH/NICHD

R21 HD092770

Period: 7/17 – 8/20

The main goal of this project is to longitudinally characterize DNA methylation profiles across the three trimesters of pregnancy in the maternal blood at time points before and after clinically overt preeclampsia.

“Statistical methods for population and family-based whole-genome sequence data” Annual Direct Costs: \$241,427

Principal Investigator: Chen, Wei

Agency: NIH

R01 HG007358

Period: 4/14 - 7/19

The main goal of this project is to develop methods and software for family-based whole-genome sequencing association studies.

“Mega2: Manipulation Environment for Genetic Analysis”

Annual Direct Costs: \$207,633

Principal Investigator: Weeks

Agency: NIH/NIGMS

R01 GM076667

Period: 3/06 – 6/19

The main goal of this project is to improve and extend our Mega2 program for transforming genetic data into proper files for statistical analyses.

“Mapping Disease pathways in Biliary Atresia”

Annual Direct Costs: \$424,458

Principal Investigator: Rakesh, Sindhi

Agency: NIH/NIDDK

R01 DK109365

Period: 4/17 - 3/19

The main goal of this project is to carry out association tests to identify genes associated with biliary atresia, to evaluate the function of these genes using zebrafish models and liver tissue, and to examine pathways that these genes are involved in.

“Symptom Clusters in Oncology Patients Receiving Chemotherapy” Annual Direct Costs: \$54,717

Principal Investigator: Miaskowski, Christine

Agency: The Sharon Lamb

Period: 1/17 – 12/17

Endowed Chair Fund

The main goal of this project is to carry out genome-wide association analyses testing for association with clusters of symptom trajectories in oncology patients during the 4 weeks post-treatment.

“AMD genetics: methods and analysis for progression, prediction, and association” Annual Direct Costs: \$31,369 (subcontract)

Principal Investigator: Chen, Wei

Agency: NIH/NEI

R01 EY024226

Period: 4/14 - 3/18

The main goal of this project is to develop and apply novel statistical methods for the study of progression, association, and prediction of age-related macular degeneration (AMD), using existing data from our collaborators and public databases.

“Epigenomics of Patient Outcomes after Traumatic Brain Injury” Annual Direct Costs: \$32,640 (subcontract)

Principal Investigator: Conley, Yvette P

Agency: NIH/NR

R21 NR015142

Period: 8/14 - 7/17

The major goals of this project are to characterize the DNA methylome from samples representing the central nervous system environment post-traumatic brain injury and to use these methylation data to differentiate patient outcomes.

“Epigenetic Variation and Childhood Asthma in Puerto Ricans” Annual Direct Costs: \$21,065 (subcontract)

Principal Investigator: Celedon, Juan Carlos

Agency: NIH

R01 HL117191

Period: 7/13 - 6/18

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

"Post Genome-Wide Association Study of Food Allergy" Annual Direct Costs: \$13,387 (subcontract)

Principal Investigator: Wang

Agency: NIH/NIAID

U01 AI090727

Period: 7/10 – 6/15

The central focus of this study is to further replicate promising genetic variants identified by the ongoing GWAS and to conduct fine mapping to search for potential causative genes of food allergy.

“Epigenomics of Patient Outcomes after Aneurysmal SAH” Annual Direct Costs: \$251,780

Principal Investigator: Conley, Yvette P

Agency: NIH/NR

R01 NR013610

Period: 9/12 - 6/18

The main goal of this project is to study how methylation of the genome after aneurysmal subarachnoid hemorrhage (aSAH) impacts symptoms and complications in the aSAH survivor.

“Improving Vision and Preventing Visual Impairment in rural Amish and urban African Americans”

Principal Investigator: Stambolian, Dwight

Annual Direct Costs: \$69,411 (subcontract)

Agency: Pennsylvania Department of Health

State funding

Period: 6/10 - 5/14

The main goal of this project is to carry out gene and gene-environment studies, combined with modern imaging technology, in age-related macular degeneration in African Americans and Amish.

“Genome-Wide Association Studies of Adiposity in Samoans” Annual Direct Costs: \$127,898 (subcontract)

Principal Investigator: McGarvey

Total Direct Costs (TDC): \$1,161,658

Agency: NIH/NHLBI

R01 HL093093

Period: 9/09 - 12/15

The main goal of this project is to carry out a genome-wide association study of obesity and obesity-related phenotypes in adult Samoans.

“Genetics of age-related maculopathy” Annual Direct Costs: \$99,737 (subcontract)

Principal Investigator: Gorin

Agency: NIH/NEI

R01 EY009859

Period: 9/93 - 3/14

The main goal of this project is to map genes involved in age-related maculopathy via linkage and association analysis of marker data collected on disease families by my collaborators.

“Genetics of age-related maculopathy” Annual Direct Costs: \$80,207 (subcontract)

Principal Investigator: Gorin

Agency: NIH/NEI

R01 EY009859 Administrative Supplement

Period: 9/09 - 9/12

The major goals of this project are to map genes involved in age-related maculopathy via linkage and association analyses of marker data collected on disease families. Our efforts under this Supplement will be aimed at improving our databases that store and manage our genetic data.

“Utility of Genomic Data in Population Screening for Abdominal Aortic Aneurysm”

Principal Investigator: Carey, David J Annual Direct Costs: \$13,870 (subcontract)  
 Agency: Pennsylvania Department of Health PA CURE Period: 6/12 - 6/16

The main goal of this project is to create a risk stratification tool for abdominal aortic aneurysm screening that combines clinical and genetic risk factor data and to test the tool in a real-world clinical setting.

“Genomic variability and symptomatology after traumatic brain injury” Annual Direct Costs: \$281,851

Principal Investigator: Conley, Yvette P  
 Agency: NIH R01 NR013342 Period: 9/11 - 7/15

The main goal of this project is to determine the extent that variability in genes involved in the mitochondrial oxidative phosphorylation (OXPHOS) pathway, responsible for cellular energy production, is responsible for variability in symptoms related to cognition, behavior, and emotion after traumatic brain injury.

“Genetics of Emphysema: Extracellular Matrix and Growth Factor Signaling” Annual Direct Costs: \$25,000

Principal Investigator: Urban, Zsolt  
 Agency: University of Pittsburgh BaCCoR Period: 7/11 - 6/12

The main goal of this project is to investigate genetic risk factors of pulmonary emphysema using a candidate gene approach.

"Genome-Wide Association Study of Food Allergy" Annual Direct Costs: \$20,461 (subcontract)

Principal Investigator: Wang, Xiaobin  
 Agency: NIH/NIAID R56 AI080627 Period: 8/10 – 7/11

The major goals of this project are to carry out a genome-wide association study to identify susceptibility genes for food allergy.

“Genomic and Proteomic Biomarkers for Head and Neck Cancer Risk and Prognosis ”

Principal Investigator: Egloff, Ann Marie  
 Agency: NIH/NCI K07 CA137140 Period: 9/09 - 8/14

The main goal of this project is to evaluate the effect of Epidermal growth factor receptor (EGFR) and gastrin-releasing peptide receptor (GRPR) on head and neck squamous cell carcinoma development/progression.

“Dental caries: whole genome association and gene x environment studies” Annual Direct Costs: \$323,836

Principal Investigator: Marazita  
 Agency: NIH/NIDCR 5U01DE018903 Period: 8/07 - 5/10

The main goal of this project is to carry out genome-wide association and gene x environment studies of dental caries.

“Genome-wide association studies of prematurity and its complications”

Principal Investigator: Murray  
 Agency: NIH/NHGRI U01 HG004423 Period: 8/07 - 5/09

The main goal of this project is to carry out genome-wide association studies of preterm birth.

“Autism Genome Project” Annual Direct Costs: \$178,580

Principal Investigator: Devlin  
 Agency: Autism Speaks/Medical Research Council No number Period: 3/07-3/10

The main goal of this project is to fine-map genes for autism and to carry out a genome-wide association study of autism.

“Statistical Genetic Analysis of Orofacial Cleft Families” Annual Direct Costs: \$100,000

Principal Investigator: Maher  
 Agency: NIH/NIDCR R03DE016632 Period: 8/07 - 7/09

The main goal of this project is to study the genetics of nonsyndromic cleft lip with or without cleft palate, testing for gene x gene interaction, association, and to model diagnostic 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: Wilhelmsen)

Agency: Myoclonus Foundation

Period: 3/91 - 3/93

This grant supported linkage analysis of marker data collected on disease families by my collaborators at Columbia University.

"Genetic linkage study of dopa-responsive dystonia"

Principal Investigator: Daniel E. Weeks (on subcontract; PI: Wilhelmsen)

Agency: Dystonia Medical Research Foundation

Period: 3/91-3/92

This grant supported linkage analysis of marker data collected on the appropriate disease families by my collaborators at Columbia University.

"Linkage analysis methods for human gene mapping"

Co-Investigator: Daniel E. Weeks (Ott)

Agency: National Center for Human Genome Research R01HG00008

Period: 4/90 - 12/91

This grant supported the development of computer simulation methods in the area of human gene mapping. These simulation methods were used to investigate empirical significance levels of lod scores, interval estimation, the effects of unequal marker heterozygosity, and tests for heterogeneity of recombination fractions.