Date of Preparation of CV

10 April 2014

Personal data

William C. L. Stewart
20 June, 1970
Phoenix, AZ
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Academic Training

San Francisco State University	B.A.	05/99	Mathematics
University of Washington	M.S.	05/02	Statistics
University of Washington	Ph.D.	11/05	Statistics

Thesis: Alternative Models for Estimating Genetic Maps from Pedigree Data
Advisor: Dr. Elizabeth A. Thompson
Publication: UMI Microform 3198855

Postdoctoral Training

Statistical Genetics	University of Michigan	11/05 – 06/08

Military service

United States Air Force Academy	05/88 – 05/90

Professional organizations and societies

American Statistical Association (ASA)
American Society of Human Genetics (ASHG)
International Biometrics Society (IBS)
International Society of Epidemiology (IGES)

Academic Appointments

Principal Investigator, The Research Institute of NCH	08/12 – present
Assistant Professor of Pediatrics, Ohio State University	08/12 – present
Assistant Professor of Biostatistics, Columbia University	07/08 – 06/12

Honors

INVITED SPEAKER:

- Mathematical and Computational Medicine, Zing Conferences: "*The Limit Distribution of an Allele Sharing Statistic with Autoregressive Approximations for Small Samples*" – 10/2014
- Nationwide Children's Hospital/Ohio State University, Young Scientists Seminar Series: "Hard Work, Youth & Discipline: What Can Applied Math Do for Me?" – 07/2014
- Pennsylvania State University, StatGen Seminar: "*Combining Affected Families, Unrelated Cases & Controls: A More Powerful Test of Association*" – 08/2013

- Mathematical and Computational Medicine, Zing Conferences: "*Combining Affected Families, Independent Cases, and Controls to Obtain a Single, More Powerful Test of Association*" – 10/2012
- Joint Statistical Meetings: "*Imputing Copy Number Variants from Family-Based Signal Intensity Data*" – 07/2012
- University of Pavia, Department of Health Sciences, Section of Medical Statistics and Epidemiology: "*The Secondary Analysis of Existing Genetic Data*" – 10/2011
- 15th Grover Conference on Pulmonary Circulation: "*Identifying Novel Loci that Interact Epistatically with Bone Morphogenetic Protein Recptor 2 in FPAH*" – 09/2011
- Genetic Epidemiology Seminar, Columbia University: "*Increasing Power and Precision from Dense SNP Linkage Data*" – 12/2010
- International Conference on Statistics, Probability, Operations Research, Computer Science and Allied Areas: "*Multiple Subsampling Increases Precision*" – 12/2009
- Guelph University, Statistics Department: "*Detecting Short and Rare Copy Number Variants*" – 11/2007

CONFERENCE ORGANIZER:

- Topic Contributed Session: JSM (The Joint Statistical Meetings): *"The Secondary Analysis of Existing Genetic and Genomic Data"*

Fellowship Grant Support

R01 MH048858 (Subaward) **PI** 09/10 – 08/11 NIDA
Title: Biomarkers for Arsenic Toxicity: Genetics, Epigenetics and Folate

R21 NS070323 Co-Investigator 10/09 – 09/11 NIDA
Title: The Role of Genome Encoded ME2 in Epilepsy

R01 MH048858 Co-Investigator 09/10 – 08/11 NIDA
Title: Biomarkers for Arsenic Toxicity

R01 CA138750 Co-Investigator 07/09 – 06/10 NCI
Title: Genetic Factors and Nicotine Dependence in Adolescents

Calderone Prize **PI** 11/09 – 11/10 CU
Title: Subsampling Increases Power to Find Disease Genes

Profession Schools Fund **PI** 07/08– 07/09 CU
Title: A Flexible Method for Deletion Discovery from High-Throughput Genotype Data with Applications to BD

R01 DK031813 Co-Investigator 09/88 – 08/10 NIDDK
Title: Linkage and Segregation in Complex Genetic Diseases

R01 DK031775 Co-Investigator 04/03 – 02/07 NIDDK
Title: Two-Locus Models of Epistasis and Heterogeneity

Rackham Graduate School Co-Investigator 06/06 – 05/08 UM
Title: Rackham Interdisciplinary Workshop

Departmental and University Committees

RITAC (Research Information Technology

Advisory Committee) at NCH	06/01 – present
Steering Committee of MSPH at CU	09/09 – 05/12
RAC (Recruitment Advisory Committee) at CU	02/12 – 03/12

Teaching, Mentoring, and other Academic Responsibilities

Courses:	P8175 Principles of Genetics for Biostatisticians
Workshops:	Scientific Writing, Mathematical and Theoretical Biology, Statistical Genetics
Ph.D. Committee:	Nicole Scott, University of Michigan, Department of Human Genetics
Dr.Ph. Committees:	Anna Peljto, Gilberto Levy, and Esther Drill, Columbia University, Department of Biostatistics

Software Developed & Maintained: EAGLET, POPFAM, HAPLODROP, METAMAP, and HEMIZYG

BEST (Biostatistics Enrichment Summer Training) Mentor 06/09

Other Professional Activities

Review Editor for *Frontiers in Statistical Genetics and Methodology*
Reviewer for *Biomed Central*, *Human Heredity*, *Genetic Epidemiology*, and *European Journal of Human Genetics*, *Diabetes*, *Epilepsia*
Invited Panelist on *Meet the Methodologist: Genomics in Public Health*, at CU

Publications

A. *Peer-Reviewed Papers*

1. George A. W., Basu S., Li N., Rothstein J., Sieberts S. K., **Stewart W**., Wijsman E., Thompson E. A. (2003). Approaches to mapping genetically correlated complex traits. *BMC Genetics* 4 (Suppl 1): S71.

2. Sieh W., Basu S., Fu A., Rothstein J., Scheet P., **Stewart W**., Sung Y., Thompson E., Wijsman E. (2005). Comparison of marker types and map assumptions using MCMC-based linkage analysis of COGA data. *BMC Genetics* 6 (Suppl 1): S11.

3. **Stewart, W. C. L.** and Thompson, E. A. (2006). Improving estimates of genetic maps: A maximum likelihood approach. *Biometrics* 62: 728-734

4. **Stewart, W. C. L.** (2007) Improving estimates of genetic maps: A meta-analysis based approach. *Genetic Epidemiology* 31: 408-416

5. Matise T. C., Chen F., Chen W., De La Vega F. M., Hansen M., He C., Hyland F., Kennedy G. C., Kong X., Murray S., Ziegle J., **Stewart W. C. L.,** Buyske S. G. (2007). A Second-Generation Combined Linkage-Physical Map of the Human Genome. *Genome Research* 17: 1783-1786

6. Zöllner S., Su G., Chen Y., **Stewart W. C. L**., McInnis M. G., Burmeister M. (2009). Bayesian EM Algorithm for scoring polymorphic deletions from SNP

data and application to a common CNV on 8q24. *Genetic Epidemiology* 33(4): 357-68

7. Greenberg D. A., **Stewart W. C. L.,** Rowland P. L. (2009). Paraoxonase Genes and Susceptibility to ALS. *Neurology* 73: 11-12

8. Rodriguez-Murillo* L, Subaran* R, **Stewart* W. C. L**., Sreemanta* P., Marathe S., Barst, R. J., Chung W. K., Greenberg D. A. (2009) Novel Loci Interacting Epistatically with Bone Morphogenetic Protein Receptor 2 Cause Familial Pulmonary Arterial Hypertension. *Journal of Heart and Lung Transplantation*, 29(2): 174-180.

9. **Stewart W. C. L.,** Peljto A. L., Greenberg D. A. (2010). Multiple Subsampling of Dense SNP Data Localizes Disease Genes with Increased Precision. *Human Heredity* 69: 152-159

10. Chunsheng C, Weeks DE, Buyske S, Abecasis GR, **Stewart WC**, Matise TC, The Enhanced Map Consortium (2011). Enhanced genetic maps from family-based disease studies: population-specific comparisons, *BMC Medical Genetics*, 12(1):15.

11. **Stewart WCL**, Drill EN, Greenberg DA (2011). Finding disease genes: A fast and flexible approach for analyzing high-throughput data. *European Journal of Human Genetics*, 19(10): 1090-1094.

12. **Stewart WCL**, Subaran R (2012). Obtaining accurate p-values from a dense SNP linkage scan. *Human Heredity*, 74(1):12-16.

13. Greenberg DA, **Stewart WC** (2012). How should we be searching for genes for common epilepsy? A critique and a prescription, Epilepsia 53 Suppl 4:72–80.

14. Lipner EM, Tomer Y, Noble JA, Monti MC, Lonsdale JT, Corso B, Stewart WCL, Greenberg DA (2013). HLA class I and II alleles are associated with microvascular complications of type 1 diabetes. *Human Immunology*, 74(5):538-44.

15. **Stewart WCL**, Cerise J (2013). Increasing the Power of Association Studies with Affected Families, Unrelated Cases and Controls, Frontiers in Genetics. doi: 10.3389/fgene.2013.00200

16. Kambhampati S, Stewart C, **Stewart WCL**, Kelley J, and Ramnath R (2014). Managing Tiny Tasks for Efficient, Data-Parallel Subsampling. In *The Second IEEE Conference on Cloud Engineering*. March, 2014.

17. Heyer GL, Merison K, Rose SC, Perkins SQ, Lee EM, and **Stewart WCL** (2014). PedMIDAS-based scoring underestimates migraine disability on non-school days. *Headache*, 54(6):1048-53.

18. **Stewart WCL**, Huang Y, Greenberg DA, Vieland VJ (2014). Next Generation Linkage and Association Analysis Identifies OSBPL10 in Mexican-American Families with Hypertension, GAW18 Proceedings.

19. Subaran RL, Conte JM, **Stewart WCL**, Greenberg DA (2015). Pathogenic *EFHC1* mutations are tolerated in healthy individuals dependent on reported ancestry. *Epilepsia*.

B. *Book Chapters*

1. Greenberg DA, **Stewart WCL**. Remind me again what disease we are studying? A population genetics, genetic analysis, and real data perspective on why progress on identifying genetic influences on common epilepsies has been so slow in genetic analysis of idiopathic epilepsies: challenges and strategies. *In Steinlen, ed. Oxford: Elsevier* 2014.

C. *Technical Reports & Papers in Preparation*

1. **Stewart WCL,** and George AW and Thompson EA (2002). Using Markov chain Monte Carlo for multipoint linkage analysis: Improved estimates of lod scores. Technical Report No. 412, Dept. of Statistics, Univ. of Washington.

2. Roberts KE, Loyd JE, **Stewart WCL**, and Trembath R (*submitted*). Update and overview of genetic influences in pulmonary arterial hypertension. *Pulmonary Circulation*.

3. **Stewart WCL**, and Zoellner S (*in preparation*). Detecting carriers of a deletion using a single SNP.

4. **Stewart WCL**, and Ho YA (*in preparation*). A Secondary Analysis of Two Large FPAH Data Sets.