BIOGRAPHICAL SKETCH

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NAME: Jonathan L. Haines

eRA COMMONS USER NAME (credential, e.g., agency login): Hainesjl

POSITION TITLE: Chair and Professor, Department of Population & Quantitative Health Sciences

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Colby College, Waterville, ME	BA	05/1979	Biology
University of Minnesota, Minneapolis, MN	PhD	10/1984	Genetics & Cell Biology

A. Personal Statement

Jonathan Haines, Ph.D., is a genetic epidemiologist and computational biologist, Mary W. Sheldon M.D. Professor of Genomic Sciences, Chair of Department of Population & Quantitative Health Sciences, and Director of the Cleveland Institute for Computational Biology at Case Western Reserve University. Dr. Haines has extensive experience in all aspects of human genetic studies including clinical ascertainment, statistical and computational analysis, molecular genetics and studies of unique and diverse populations. He has a particular interest in developing and applying statistical genetic methods of analysis to complex clinical and genomic data, including GWAS, whole exome and whole genome DNA sequencing data. He has applied these methods to the genetics and genomics of over 30 different diseases most recently focusing on Alzheimer disease and age-related macular degeneration (AMD). He fosters collaboration through integration and promoting access to multiple data types, including structured and unstructured EHR and genomic data. He has ascertained and enrolled participants for large case-control and family-based datasets that include clinical, co-morbidity (e.g., diabetes, cardiovascular disease, etc.), genomic, and environmental data with a focus on diverse (African-American) and unique (Amish) populations. He is a founding member of multiple national and international research consortia. He has worked with the Amish communities in central Ohio for the past 22 years and his strong positive relationship enables a high level of participation.

B. Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2016-2021	Member, National Advisory Council for Human Genome Research, NHGRI/NIH
2015-2018	Member, Board of Directors for the National Organization for Rare Disorders (NORD)
2014-Present	Professor, Department of Ophthalmology & Visual Sciences, Case Western Reserve University, Cleveland, OH
2013-Present	Director, Cleveland Institute for Computational Biology, Case Western Reserve University, Cleveland, OH
2013-Present	Professor & Chair, Department of Population & Quantitative Health Sciences, Case Western Reserve University, Cleveland, OH
2013-Present	Professor, Department of Genetics and Genome Sciences, Case Western Reserve University, Cleveland, OH
2013-Present	Mary W. Sheldon, M.D. Professor of Genomic Sciences, Case Western Reserve University, Cleveland, OH
2013-2015	Member, Multi-Council Working Group for BD2K initiatives, NIH
2011-2015	Member, National Advisory Eye Council, NEI/NIH

2011-2013	Professor, Department of Neurology, Vanderbilt University School of Medicine, Nashville, TN
2011-2013	Professor, Department of Ophthalmology & Visual Sciences, Vanderbilt University School of Medicine, Nashville, TN
2011-2013	Louise B. McGavock Professor of Human Genetics, Vanderbilt University School of Medicine, Nashville, TN
2010-Present	Fellow, American Association for the Advancement of Science
2009-2013	Annual Meeting Program Committee, American Society of Human Genetics
2008-2013	Chief, Division of Human Genetics, Department of Molecular Physiology & Biophysics, Vanderbilt University School of Medicine, Nashville, TN
2004-2013	Director, Center for Human Genetics Research, Vanderbilt University School of Medicine, Nashville, TN
2003-2011	T.H. Morgan Professor of Human Genetics, Vanderbilt University School of Medicine, Nashville, Tennessee
1999-2013	Professor, Molecular Physiology & Biophysics, Vanderbilt University School of Medicine, Nashville, TN
1998-2003	Director, Program in Genetics, Brain & Behavioral Development, Kennedy Center, Vanderbilt University, Nashville, TN
1997-2003	Director, Program in Human Genetics, Vanderbilt Univ. School of Medicine, Nashville, TN
1997-1999	Associate Professor, Molecular Physiology & Biophysics, Vanderbilt University School of Medicine, Nashville, TN
1996-1997	Associate Professor in Biostatistics, Harvard School of Public Health, Boston, MA
1995-1997	Associate Professor in Neurology (Genetics), Harvard Medical School, Boston, MA
1989-1995	Assistant Professor in Neurology (Genetics), Harvard Medical School, Boston, MA
1987-1997	Assistant Geneticist, Neurology Service, Massachusetts General Hospital, Boston, MA
1987-1989	Instructor in Neurology (Genetics), Harvard Medical School, Boston, MA
1984-1987	Postdoctoral Fellow, Department of Medical Genetics, Indiana University School of Medicine, Indianapolis, IN
1981-1984	Pre-doctoral Fellow, Behavioral Genetics Training Grant, University of Minnesota, Minneapolis, Minnesota
1979-1981	Teaching Assistant, Dept. of Genetics & Cell Biology, University of Minnesota, Minneapolis, MN

Honors

2019	Faculty Distinguished Research Award, Case Western Reserve University, Cleveland, OH
2005	Sidney P. Colowick Award for Research in Diverse Areas, Vanderbilt University School of Medicine, Nashville, TN
1993	Best of What's New Award (Science & Technology), Popular Science Magazine: "Discovery of Alzheimer Gene"
1993	Zenith Award for Excellence in Alzheimer's Disease Research, Alzheimer's Association
1992	Distinguished Alumnae Award, Department of Medical Genetics, Indiana University

C. Contributions to Science

1. Data Aggregation, Integration, and analysis. With the explosion of data generation, capture, and storage technologies, the era of "Big Data" is upon us. Collaborative teams are required to harness the vast potential of these data. I have been developing and applying methods and/or directing such studies both locally and internationally with a focus on genomic data.
    a. Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorff LA, et al. Finding the missing heritability of complex diseases. Nature. 2009 Oct 8;461(7265):747-53. PMID: 19812666; PMCID: PMC2831613
    b. Bush WS, Sawcer SJ, de Jager PL, Oksenberg JR, McCauley JL, et al. Evidence for polygenic susceptibility to multiple sclerosis--the shape of things to come. Am J Hum Genet. 2010 Apr 9;86(4):621-5. PMID: 20362272; PMCID: PMC2850422

c. Butkiewicz M, Blue E, Leung F, Jian X, Marcora E, Renton A, Kuzma A, Wang LS, Koboldt D, Haines JL, Bush WS. Functional Annotation of genomic variants in studies of Late-Onset Alzheimer's Disease. Bioinformatics. 2018 Mar 24. PMID: 29590295; PMCID: PMC6084586
d. Wheeler NR, Benchek P, Kunkle BW, Hamilton-Nelson KL, Warfe M, Fondran JR, Haines JL, Bush WS. Hadoop and PySpark for reproducibility and scalability of genomic sequencing studies. Pac Symp Biocomput. 2020;25:523-534. PMID: 31797624; PMCID: PMC6956992.

2. Genetics of Common Diseases: By the early 1990's I could leverage the developing tools of the human genome project to start deconstructing the genetic architecture of common human diseases, with a particular focus on late onset neurological and ophthalmological diseases. This led to multiple seminal discoveries, including identifying that the common polymorphism in the APOE gene greatly modulates the risk of late-onset Alzheimer disease and that common variation in the CFH gene greatly modulates the risk of age-related macular degeneration. We were among the first to demonstrate that the theoretical approach of Genome-Wide Association Studies (GWAS) was indeed both practical and useful by applying it to numerous different traits. We have identified hundreds of highly significantly associated loci across numerous diseases and further demonstrated that collectively these loci identify underlying biological pathways important in these diseases.
    a. Corder EH, Saunders AM, Strittmatter WJ, Schmechel DE, Gaskell PC, et al. Gene dose of apolipoprotein E type 4 allele and the risk of Alzheimer's disease in late onset families. Science. 1993 Aug 13;261(5123):921-3. PMID: 8346443
    b. Haines JL, Hauser MA, Schmidt S, Scott WK, Olson LM, et al. Complement factor H variant increases the risk of age-related macular degeneration. Science. 2005 Apr 15;308(5720):419-21. PMID: 15761120
    c. Fritsche LG, Igl, W, Bailey JN, Grassmann F, Sengupta S, et al. A large genome-wide association study of age-related macular degeneration highlights contributions of rare and common variants. Nat Genet. 2016 Feb;48(2):134-43. PMID: 26691988; PMCID: PMC4745342
    d. Bellenguez C, Küçükali F, Jansen IE, Kleineidam L, Moreno-Grau S, Amin N, Naj AC, et al. New insights into the genetic etiology of Alzheimer's disease and related dementias. Nat Genet. 2022 Apr;54(4):412-436. PMID: 35379992; PMCID: PMC9005347

3. Genetic Analysis of Diverse and Founder Populations. The vast majority of genetic studies have been done in datasets of European descent. Few studies have been performed in datasets that include diverse ancestries (e.g., African, Asian, Native American) or in founder populations. Such studies are critical for equity and inclusion, and provide a broader understanding of human biology. I have been active in recruiting and analyzing participants from diverse (African-American) and founder (Amish) populations.
    a. Pericak-Vance MA, Johnson CC, Rimmler JB, Saunders AM, Robinson LC, D'Hondt EG, Jackson CE, Haines JL. Alzheimer's disease and apolipoprotein E-4 allele in an Amish population. Ann Neurol. 1996 Jun;39(6):700-4. PMID: 8651641.
    b. Oksenberg JR, Barcellos LF, Cree BA, Baranzini SE, Bugawan TL, …(8)… Thomson G, Reich DE, Pericak-Vance MA, Haines JL, Hauser SL. Mapping multiple sclerosis susceptibility to the HLA-DR locus in African Americans. Am J Hum Genet. 2004 Jan;74(1):160-7. PMID: 14669136; PMCID: PMC1181903.
    c. D'Aoust LN, Cummings AC, Laux R, Fuzzell D, Caywood L, Reinhart-Mercer L, Scott WK, Pericak-Vance MA, Haines JL. Examination of candidate exonic variants for association to Alzheimer disease in the Amish. PLoS One. 2015 Feb 10;10(2):e0118043. PMID: 25668194; PMCID: PMC4323242.
    d. Rajabli F, Feliciano BE, Celis K, Hamilton-Nelson KL, Whitehead PL, …(18)…Martin ER, Haines JL, Byrd GS, Beecham GW, Pericak-Vance MA. Ancestral origin of ApoE ε4 Alzheimer disease risk in Puerto Rican and African American populations. PLoS Genet. 2018 Dec 5;14(12):e1007791. PMID: 30517106; PMCID: PMC6281216.

4. Electronic Health Records (EHRs) Linked to Biospecimens. The ongoing implementation of electronic health records in clinical medicine provides a vast pool of already collected detailed phenotypic data in very large datasets. Through numerous collaborative efforts, I have explored both the use of EHR data to define research-level phenotypes and the linkage of EHR data to genomic data to explore genetic

associations. These efforts have demonstrated that EHR data are a rich and valuable source of information and that EHR-linked biobanks can greatly increase power at reduced research costs.

a. Ritchie MD, Denny JC, Crawford DC, Ramirez AH, Weiner JB, et al. Robust replication of genotype-phenotype associations across multiple diseases in an electronic medical record. Am J Hum Genet. 2010 Apr 9;86(4):560-72. PMID: 20362271; PMCID: PMC2850440
b. Davis MF, Sriram S, Bush WS, Denny JC, Haines JL. Automated extraction of clinical traits of multiple sclerosis in electronic medical records. J Am Med Inform Assoc. 2013 Dec;20(e2):e334-40. PMID: 24148554; PMCID: PMC3861927
c. Denny JC, Bastarache L, Ritchie MD, Carroll RJ, Zink R, et al. Systematic comparison of phenome-wide association study of electronic medical record data and genome-wide association study data. Nat Biotechnol. 2013 Dec;31(12):1102-10. PMID: 24270849; PMCID: PMC3969265
d. Butkiewicz M, Restrepo NA, Haines JL, Crawford DC. Drug-Drug Interaction Profiles of Medication Regimens Extracted From A De-Identified Electronic Medical Records System. AMIA Jt Summits Transl Sci Proc. 2016 Jul 20;2016:33-40. eCollection 2016. PMID: 27570646; PMC5001747

5. Genetics of Rare Genetic Disorders: By the early 1980's the development of recombinant DNA technology and PCR opened the human genome to exploration and the mapping of genes and disease-causing mutations. I combined my training in biostatistics, computer science, biology, and genetics to provide the critical analytical expertise in multiple collaborative efforts to map and ultimately identify mutations in over 30 different diseases, with a focus on neurological disorders including Huntington disease, early-onset Alzheimer disease, amyotrophic lateral sclerosis, and tuberous sclerosis. In addition to advancing our understanding of these diseases, this research provided working paradigms of how to approach these difficult problems.
    a. Gilliam TC, Tanzi RE, Haines JL, Bonner TI, Faryniarz AG, et al. Localization of the Huntington's disease gene to a small segment of chromosome 4 flanked by D4S10 and the telomere. Cell. 1987 Aug 14;50(4):565-71. PMID: 2886227
    b. St George-Hyslop PH, Haines JL, Farrer LA, Polinsky R, Van Broeckhoven C, et al. Genetic linkage studies suggest that Alzheimer's disease is not a single homogeneous disorder. Nature. 1990 Sep 13;347(6289):194-7. PMID: 2395471
    c. Rosen DR, Siddique T, Patterson D, Figlewicz DA, Sapp P, et al. Mutations in Cu/Zn superoxide dismutase gene are associated with familial amyotrophic lateral sclerosis. Nature. 1993 Mar 4;362(6415):59-62. PMID: 8446170
    d. Sherrington R, Rogaev EI, Liang Y, Rogaeva EA, Levesque G, et al. Cloning of a gene bearing missense mutations in early-onset familial Alzheimer's disease. Nature. 1995 Jun 29;375(6534):754-60. PMID: 7596406

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http://www.ncbi.nlm.nih.gov/myncbi/1j78fQ_Yhzw5g/bibliography/47703218/public/?sort=date&direction=ascending