

CURRICULUM VITAE

ANDREW E. JAFFE

Lieber Institute for Brain Development
855 North Wolfe Street, Suite 300, Baltimore, MD 21205
Phone: (847)-644-2766 - Email: andrew.jaffe@libd.org
[My Webpage](#) - [My Google Citations](#)

Affiliations

2013-Present: Investigator, Bioinformatics, Genetics and Epigenetics, Clinical Sciences Division, Lieber Institute for Brain Development, Baltimore, MD 21205.

2014-Present: Assistant Professor, Department of Mental Health, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD 21205.

2013-Present: Affiliated Faculty, Wendy Klag Center for Autism & Developmental Disabilities, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD 21205.

2013-Present: Faculty, Johns Hopkins Center for Computational Biology, McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins School of Medicine, Baltimore, MD 21205.

2012-Present: Associate, Department of Biostatistics, Johns Hopkins Bloomberg School of Public Health, Baltimore, MD 21205.

Education

2011: PhD in Epidemiology (Human Genetics/Genetic Epidemiology)
Johns Hopkins Bloomberg School of Public Health, Department of Epidemiology

2011: MHS in Bioinformatics
Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics and Department of Molecular Microbiology and Immunology

2008: BA (with Departmental and University Honors) in Public Health Studies
Johns Hopkins University

Publications

[1] Marioni RE, Shah S, McRae AF, Chen BH, Colicino E, Harris SE, Gibson J, Henders AK, Redmond P, Cox SR, Pattie A, Corley J, Murphy L, Martin NG, Montgomery GW, Feinberg AP, Fallin MD, **Jaffe AE**, Multhaup ML, Joehanes R, Schwartz J, Just AC,

Lunetta KL, Murabito JM, Starr JM, Horvath S, Baccarelli AA, Levy D, Visscher PM, Wray NR, Deary IJ. Epigenetic signatures of age predict all-cause mortality in later life. *Genome Biol.* 2015 Jan 30;16(1):25. PMID: 25633388

[2] Feinberg, JI, Bakulski KM, **Jaffe AE**, Trygvadottir R, Brown SC, Goldman LR, Croen LA, Hertz-Picciotto I, Newschaffer CJ, Fallin MD, Feinberg AP. Paternal sperm DNA methylation associated with early signs of autism risk in an autism-enriched cohort. *International Journal of Epidemiology*. In Press.

[3] **Jaffe AE**⁺, Shin J, Collado-Torres L, Leek JT, Tao R, Li C, Gao Y, Jia Y, Maher BJ, Hyde TM, Kleinman JE, Weinberger DR⁺. Developmental regulation of human cortex transcription and its clinical relevance at base resolution. *Nature Neuroscience*. 2014 Dec 15. PMID: 25501035 +corresponding author

[4] Multhaup ML*, Seldin M*, **Jaffe AE***, Lei X, Kirchner H, Mondal P, Li P, Rodriguez V, Drong A, Hussain M, Lindgren C, McCarthy M, Nslund E, Zierath JR, Wong GW, Feinberg AP. Mouse-human experimental epigenetic analysis unmasks dietary targets and genetic liability for diabetic phenotypes. *Cell Metab.* 2015 Jan 6;21(1):138-49. PMID: 25565211 *These authors contributed equally to this work.

[5] **Jaffe AE***, Deep-Soboslay A*, Tao R, Hauptman DT, Kaye WH, Weinberger DR, Hyde TM, Kleinman JE. Genetic Neuropathology of Obsessive Psychiatric Syndromes. *Translational Psychiatry*. 2014 Sep 2;4:e432. PMID: 25180571. *These authors contributed equally to this work.

[6] **Jaffe AE**⁺, Irizarry RA⁺. Accounting for cellular heterogeneity is critical in epigenome-wide association studies. *Genome Biol.* 2014 Feb 4;15(2):R31 (Epub). PMID: 24495553. ⁺corresponding author

[7] Birnbaum R, **Jaffe AE**, Qiang Chen, Hyde TM, Kleinman JE, Weinberger DR. Investigation of the Prenatal Expression Patterns of 108 Schizophrenia-Associated Genetic Loci. *Biological Psychiatry*. October 21, 2014. PMID: 25592863.

[8] Frazee AC, Pertea G, **Jaffe AE**, Langmead B, Salzberg SL, Leek JT. Flexible isoform-level differential expression analysis with Ballgown. *Nature Biotechnology*, In Press. Available on bioRxiv.

[9] Aryee MJ, **Jaffe AE**, Corrada-Bravo H, Ladd-Acosta C, Feinberg AP, Hansen KD, Irizarry, RA. Minfi: A flexible and comprehensive Bioconductor package for the analysis of Infinium DNA Methylation microarrays. *Bioinformatics*. 2014 Jan 28 (Epub). PMID: 24478339

[10] Birnbaum R, **Jaffe AE**, Hyde TM, Kleinman JE, Weinberger DR. Investigating the prenatal expression patterns of genes associated with neuropsychiatric disorders. *Am J*

Psychiatry. 2014 May 30. PMID: 24874100

[11] Tao R, Cousijn H, **Jaffe AE**, Burnet PW, Edwards F, Eastwood SL, Shin JH, Lane TA, Walker MA, Maher B, Weinberger DR, Harrison PJ, Hyde TM, Kleinman JE. ZNF804A Expression in Human Brain: A Novel Transcript Fetally Regulated by the Psychosis Risk SNP rs1344706, and Alterations in Schizophrenia, Bipolar Disorder and Major Depression. *JAMA Psychiatry*. 2014 Oct 1;71(10):1112-20. PMID: 25162540

[12] Michailidi C, Soudry E, Brait M, Maldonado L, **Jaffe A**, Ili-Gangas C, Brebi-Mieville P, Perez J, Kim MS, Zhong X, Yang Q, Valle BL, Meltzer SJ, Torbenson MS, Irizarry RA, Esteller M, Sidransky D, Preston RG. Genome-wide and gene-specific epigenomic platforms for biomarker development trials. *Gastroenterol Res Pract*. 2014;2014:597164. Epub 2014 Apr 17. 24829571

[13] **Jaffe AE**, Storey JD, Ji HK, Leek JT. Gene set bagging for estimating the probability a statistically significant result will replicate. *BMC Bioinformatics*, 2013 Dec 12;14(1):360. PMID: 24330332

[14] Gnanakkan VP, **Jaffe AE**, Dai L, Fu J, Wheelan SJ, Levitsky HI, Irizarry RA, Boeke JD, Burns KH. TE-array - a high-throughput tool to study transposon transcription. *BMC Genomics*. 2013 Dec 10;14(1):869. PMID: 24325565

[15] Oliver VF, Franchina M, **Jaffe AE**, Branham KE, Othman M, Heckenlively JR, Swaroop A, Campochiaro B, Vote BJ, Craig JE, Saffery R, Mackey DA, Qian J, Zack DJ, Hewitt AW, Merbs SL. Hypomethylation of the IL17RC Promoter in Peripheral Blood Leukocytes is Not A Hallmark of Age-Related Macular Degeneration. *Cell Reports*, 2013 Dec 26;5(6):1527-35. PMID: 24373284

[16] **Jaffe AE**, Eaton WW, Marenco S, Straub RE, Weinberger DR. Paternal age, de novo mutations and schizophrenia. *Molecular Psychiatry*, advance online publication, 11 June 2013; doi:10.1038/mp.2013.76. PMID: 23752248

[17] Schwartzman A, **Jaffe AE**, Gavrilov Y, Meyer CA. Multiple testing of local maxima for detection of peaks in ChIP-seq data. *Ann. Appl. Stat.* Volume 7, Number 1 (2013), 471-494. PMID: 25411587

[18] Horiuchi Y, Kano S, Ishizuka K, Cascella NG, Ishii S, Talbot CC, **Jaffe AE**, Okano H, Pevsner J, Colantuoni C, Sawa A. Olfactory cells via nasal biopsy reflect the developing brain in its expression profiles: utility and limitation of the surrogate tissues in research for brain disorders. *Neuroscience Research*, 2013 Oct 11. pii: S0168-0102(13)00207-1. PMID: 24120685

[19] **Jaffe AE**, Murakami P, Lee H, Fallin MD, Leek JT, Feinberg AP, Irizarry RA. Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies.

Int. J. Epidemiol. (2012) 41 (1):200-209. PMID: 22422453

[20] Lee H*, **Jaffe AE***, Feinberg JI, Tryggvadottir R, Brown S, Montano C, Aryee MJ, Irizarry RA, Herbstman J, Witter FR, Goldman LR, Feinberg AP, Fallin MD. DNA methylation shows genome-wide association of NFIX, RAPGEF2, and MSRB3 with Gestational Age at Birth. Int. J. Epidemiol. (2012) 41 (1):188-199. PMID: 22422452.

*These authors contributed equally to this work.

[21] Leek JT, Johnson WE, Parker HS, **Jaffe AE**, Storey JD. The sva package for removing batch effects and other unwanted variation in high-throughput experiments. Bioinformatics. January 17, 2012 (Epub). PMID: 22257669

[22] **Jaffe AE**, Feinberg AP, Irizarry RA, Leek JT. Significance analysis and statistical dissection of variably methylated regions. Biostatistics. 2012; 13(1): 166-178. PMID: 21685414

[23] Bliss LA, Sams MR, Deep-Soboslay A, Ren-Patterson R, **Jaffe AE**, Chenoweth JG, Jaishankar A, Kleinman JE, Hyde TM. Use of postmortem human dura mater and scalp for deriving human fibroblast cultures. PLoS ONE 7(9): e45282 (2012). PMID: 23028905

[24] **Jaffe A***, Wojcik G*, Chu A, Golozar A, Maroo A, Duggal P, Klein AP. Identification of functional genetic variation in exomic sequence analysis. Genetic Analysis Workshop 17. October 13-16, 2010. Boston, MA. BMC Proceedings 2011, 5(Suppl 9):S13 (29 November 2011). PMID: 22373437

[25] Vincent A, Omura N, Hong S, **Jaffe A**, Eshleman J, Goggins M. Genome-wide analysis of promoter methylation associated with gene expression profile in pancreatic adenocarcinoma. Clinical Cancer Research, 2011 June 28. PMID: 21610144.

[26] Guerrero-Preston R, Soudry E, **Jaffe A**, Ili-Gangas C, Brebi-Mieville P, Zhong X, Yang Q, Meltzer S, and Sidransky, D. NID2 and HOXA9 promoter hypermethylation as biomarkers for prevention and early detection in oral cavity squamous cell carcinoma tissues and saliva. Cancer Prevention Research. 2011 May 10. PMID: 21558411

[27] Guerrero-Preston R, Goldman L, Brebi-Mieville P, Ili-Gangas C, LeBron C, Hernandez-Arroyo M, Witter F, Apelberg B, Roystacher M, **Jaffe A**, Halden R, Sidransky D. Global DNA hypomethylation is associated with in utero exposure to cotinine and perfluorinated alkyl compounds. Epigenetics. 2010 Aug 14;5(6). PMID: 20523118

[28] Ganesh SK, Zakai NA, van Rooij FJ, Soranzo N, Smith AV, Nalls MA, Chen MH, Kottgen A, Glazer NL, Dehghan A, Kuhnle B, Aspelund T, Yang Q, Tanaka T, **Jaffe A**, Bis JC, Verwoert GC, Teumer A, Fox CS, Guralnik JM, Ehret GB, Rice K, Felix JF, Rendon A, Eiriksdottir G, Levy D, Patel KV, Boerwinkle E, Rotter JI, Hofman A, Sambrook JG, Hernandez DG, Zheng G, Bandinelli S, Singleton AB, Coresh J, Lumley T, Uitterlinden AG, Vangils JM, Launer LJ, Cupples LA, Oostra BA, Zwaiginga JJ, Ouwehand

WH, Thein SL, Meisinger C, Deloukas P, Nauck M, Spector TD, Gieger C, Gudnason V, van Duijn CM, Psaty BM, Ferrucci L, Chakravarti A, Greinacher A, O'Donnell CJ, Witteman JC, Furth S, Cushman M, Harris TB, Lin JP. Multiple loci influence erythrocyte phenotypes in the CHARGE consortium. *Nature Genetics*, 2009 Nov;41(11):1191-8. PMID: 19862010

Book Chapters

[1] Fertig EJ, Stein-O'Brien G, **Jaffe A**, Colantuoni C. Pattern Identification in Time-Course Gene Expression Data with the CoGAPS Matrix Factorization. *Methods Mol Biol*. 2014;1101:87-112. PMID: 24233779

[2] Frazee AC, Torres LC, **Jaffe AE**, Langmead B, Leek JT. Measurement, Summary, and Methodological Variation in RNA-sequencing. *Statistical Analysis of Next Generation Sequencing Data*. 2014: 115-128.

Publications in Progress

[1] **Jaffe AE**⁺, Gao Y, Tao R, Hyde TM, Weinberger DR, Kleinman JE. The epigenetic landscape of the human frontal cortex across development. Under Review. Available on bioRxiv. ⁺corresponding author

[2] Collado-Torres L, Frazee AC, MI Love, Irizarry RA, **Jaffe AE**⁺ Leek JT⁺. derfinder: Software for annotation-agnostic RNA-seq differential expression analysis. Under Review. ⁺corresponding author

[3] Oliver V, **Jaffe AE**^{*}, Song J, Wang G, Zhang P, Branham KE, Swaroop A, Campochiaro B, Eberhart CG, Zack DJ, Qian J, Merbs SL. Differential DNA Methylation Identified in the Blood and Retina of AMD Patients. Under Review.

[4] **Jaffe AE**, Chenoweth J, McKay R, Leek JT, Colantuoni C. Practical Impacts of Genomic Data "Cleaning" on Biological Discovery. Under Review.

[5] Frazee AC, **Jaffe AE**, Langmead B, Leek JT. Polyester: simulating RNA-seq datasets with differential transcript expression. Under Review. Available on bioRxiv.

[6] **Jaffe AE**. "Bump hunting" for DNA methylation data analysis: applications to variably and differentially methylated regions. *CpG Islands: Methods and Protocols*. Submitted.

[7] Bakulski KM, Lee HJ, Feinberg JI, Wells EM, Brown S, Herbstman JB, Witter FR, Halden RU, Caldwell K, Mortensen ME, **Jaffe AE**, Moye J, Caulfield LE, Pan Y, Goldman LR, Feinberg AP, Fallin MD. Prenatal mercury concentration is associated with changes in DNA methylation at TCEANC2 in newborns. Under Review.

Software Development

FlowSorted.Blood.450k: An R package containing flow sorted blood experimental data. Available on Bioconductor.

sva: An R package for surrogate variable analysis. Available on Bioconductor.

GeneSetBagging: An R package for gene set bagging. Available on GitHub

derfinder: An R package for fast differential expression analysis of RNA-seq data at base-pair resolution. Available on GitHub

Research

2013-Present: Investigator, Functional Genomics and Developmental Neurobiology, Lieber Institute for Brain Development (working on integrating genomic measurements in the human brain)

2011-2013: Postdoctoral Fellow in Genome Informatics, Lieber Institute for Brain Development, Baltimore, Maryland. Mentors: Carlo Colantuoni, PhD, Thomas Hyde, MD PhD, and Daniel Weinberger, MD (worked on identifying molecular signatures in the developing and aging human brain)

2009-2011: Research Assistant, Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics. Mentors: Jeffery Leek, PhD and Rafael Irizarry, PhD (worked on novel discovery methods for DNA methylation)

2009-2011: Research Assistant, Johns Hopkins School of Medicine Epigenetics Center, Mentors: M Daniele Fallin, PhD and Andrew Feinberg, MD (analyzed high-throughput DNA methylation data for environment and autism study)

2009-2011: Research Assistant, Johns Hopkins School of Medicine, Department of Otolaryngology, Laboratory of David Sidransky MD. Mentor: Rafael Guerrero-Preston, DrPH (assisted in ongoing studies involving DNA methylation and gene expression in neck cancers)

2008-2010: Research Assistant, Johns Hopkins School of Medicine, National Familial Pancreas Tumor Registry, Sidney Kimmel Cancer Center. Mentor: Alison Klein, PhD (helped to validate the BayesMendel R software package, which models familial pancreatic cancer risk)

2008-2009: Research Assistant, Johns Hopkins Bloomberg School of Public Health, Department of Epidemiology. Mentor: Linda Kao, PhD (conducted genetic association analyses for Atherosclerosis Risk In Communities [ARIC] study)

Honors and Awards

2013: The James V. Neel Young Investigator Award for Best Platform Presentation, 22nd Annual Conference of the International Genetic Epidemiology Society

2012: Young Investigator Award, Statistics in Epidemiology Section, American Statistical Association

2011: The Louis I. and Thomas D. Dublin Award for the Advancement of Epidemiology and Biostatistics (Department of Biostatistics and Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health)

2010: Fellowship in Biostatistics for Genetics/Genomics (NIH, National Institute of General Medical Sciences T32 training grant)

2009: Fellowship in Genetic Epidemiology of Cancer (NIH, National Cancer Institute, Cancer Epidemiology, Prevention, and Control T32 training grant)

2008: Outstanding Senior Award, Johns Hopkins University, Krieger School of Arts and Sciences, Undergraduate Program in Public Health Studies

2007 and 2008: Chris Watson Academic Achievement Award, Johns Hopkins Mens Varsity Lacrosse Team

Teaching

2013-2014: Instructor, Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics: 140.866 Introduction to R for Public Health Researchers

- Summer Institute (2014)
- Winter Institute (2014)
- Summer Institute (2013)
- Winter Institute (2013)

2012: Teaching Assistant, Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics: 140.688 Statistics for Genomics

2010-2011: Instructor, Introduction to R for Epidemiologists (340.840 - Special Studies, 1 unit). Johns Hopkins Bloomberg School of Public Health, Department of Epidemiology

2009-2011: Teaching Assistant, Johns Hopkins Bloomberg School of Public Health, Graduate Summer Institute in Epidemiology and Biostatistics

- 340.661.11 - Family Based Genetic Epidemiology (2009 and 2010)
- 140.613.11 - Data Analysis Workshop I (2011)
- 140.614.11 - Data Analysis Workshop II (2011)

2008-2009: Teaching Assistant, Johns Hopkins Bloomberg School of Public Health, Department of Epidemiology:

- 340.644 - Introduction To Genetic Epidemiology
- 340.649 - Population Genetics And Genetic Epidemiology
- 340.632 - Methods For Linkage Analysis In Genetic Epidemiology

Ongoing Research Support

- 2014-2015: 1R21MH102791 from NIMH (PI: Andrew Jaffe)

This project will bisulfite sequence 60 postmortem human brains to better characterize normal patterns of DNA methylation during the first three decades of life.

- 2012-2016: 1R01EY023188 from NEI (PI: Shannath Merbs).

This project will develop novel computational tools to integrate existing diverse types of datasets in order to identify genetic and epigenetic variations associated with age-related macular degeneration, which will ultimately lead to new biomarkers and possibly to therapeutic targets.

Presentations

Conference Papers

[1] **Jaffe AE**. The methylome of the human frontal cortex across development and schizophrenia. Epigenomics of Common Disease. October 27-31, 2014. Cambridge, UK.

[2] **Jaffe AE**, Shin J, Collado-Torres L, Leek JT, Tao R, Li C, Gao Y, Jia Y, Maher BJ, Hyde TM, Kleinman JE, Weinberger DR. Developmental regulation of human cortex transcription at base-pair resolution. World Congress of Psychiatric Genetics. October 12-16, 2014. Copenhagen, DK.

[3] **Jaffe AE**, Shin J, Collado-Torres L, Gao Y, Leek JT, Hyde TM, Weinberger DR, Kleinman JE. Characterizing the transcriptome of the developing human prefrontal cortex. Society for Biological Psychiatry. May 8-10, 2014. New York, NY.

[4] **Jaffe AE**. Characterizing the transcriptome of the developing human prefrontal cortex. Winter Conference on Brain Research. January 25-30, 2014. Steamboat Springs, CO.

[5] **Jaffe AE**, Shin J, Gao Y, Tao R, Hyde TM, Weinberger DR, Kleinman JE. Issues in the integration of genome and transcriptome data in the human brain. American College of Neuropsychopharmacology Annual Meeting. December 8-12, 2013. Hollywood, FL.

[6] **Jaffe AE**, Maher B, Shin J, Gao Y, Tao R, Hyde TM, Kleinman JE, Weinberger DR. Leveraging RNAseq to Identify Molecular Mechanisms of Risk from GWAS-positive Genomic Regions. Molecular Psychiatry Meeting. November 8-10, 2013. San Francisco, CA.

- [7] **Jaffe AE**, Gao Y, Tao R, Hyde TM, Weinberger DR, Kleinman JE. The role of DNA methylation in development and neuropsychiatric disorders of the human brain. World Congress of Psychiatric Genetics. Early Career Investigator Award Finalist and International Society of Psychiatric Genetics Travel Award Winner. October 17-21, 2013. Boston, MA.
- [8] **Jaffe AE**, Irizarry RA. Accounting for Cellular Heterogeneity is Critical in Epigenome-Wide Association Studies. James V. Neel Young Investigator Award for Best Platform Presentation, International Genetic Epidemiology Society Annual Meeting. September 15-17, 2013. Chicago, IL.
- [9] **Jaffe AE**, Fertig EJ, Marchionni L, Ochs MF, Lipska BK, Weinberger DR, Kleinman JE, Hyde TM, Colantuoni C. Fundamental patterns of gene expression in the developing human brain. Society for Neuroscience Annual Meeting. October 13-17, 2012. New Orleans, LA.
- [10] **Jaffe AE**, Murakami P, Lee H, Fallin MD, Leek JT, Feinberg AP, Irizarry RA. Bump hunting to identify differentially methylated regions in epigenetic epidemiology studies. Joint Statistical Meeting, Statistics in Epidemiology Young Investigator Award winner. July 29-August 2, 2012. San Diego, CA.
- [11] **Jaffe AE**, Feinberg AP, Irizarry RA, Leek JT. Significance analysis and statistical dissection of variably methylation regions. International Genetic Epidemiology Society, Roger W. Williams Award Finalist. September 19-21, 2011. Heidelberg, Germany

Talks

- [1] Incorporating high-throughput DNA methylation data in epidemiological studies. 5th Annual Young Investigator Symposium on Genomics & Bioinformatics, Johns Hopkins University Center for Computational Genomics, September 23, 2011. Baltimore, Maryland.
- [2] The statistical analysis of variably methylated regions. Seminar in Computational Genomics, Johns Hopkins University Center for Computational Genomics. May 2, 2011. Baltimore, MD.

Conference Posters

- [1] **Jaffe AE**, Murakami P, Lee H, Fallin MD, Leek JT, Feinberg AP, Irizarry RA. Bump hunting in genomics data from large epidemiological studies. Delta Omega Poster Competition, 3rd Place: Basic/Lab Science Category.
- [2] **Jaffe AE**, Lee H, Feinberg AP, Goldman LR, Leek JT, Fallin MD, Irizarry RA. Statistical methods for identifying epigenetic regions of interest in epidemiological studies. Epigenomics of Common Disease, September 13-16, 2011. Hinxton, Cambridge, UK.

[3] **Jaffe AE**, Feinberg AP, Irizarry RA, Leek JT. Significance analysis and statistical dissection of variably methylation regions. Joint Statistical Meeting, July 31 - August 4, 2011. Miami, FL.

Service

Referee for: Biometrics, Bioinformatics, BMC Bioinformatics, Nucleic Acids Research, PLoS Genetics

Epidemiology Student Organization, Johns Hopkins Bloomberg School of Public Health

- President (2010-2011)
- Sports Chair (2009-2010)
- Information Chair (2009-2010)

Volunteer, Health Education Across Languages [HEAL] project, Johns Hopkins Bloomberg School of Public Health (2010-2011).

Extracurricular

2008-present: Member, Falls Road Running Club: raced the Baltimore, Philadelphia, Boston, Washington DC, Chicago, and New York marathons (PR: 2:38), North Face 2011 Endurance Challenge 50k - Washington DC (2nd place)

2005-2008: Midfielder, Johns Hopkins Varsity Mens Lacrosse Team (NCAA Division I National Champions in 2007 and National Championship Runners-Up in 2008)