

BIOGRAPHICAL SKETCH

NAME Steve Horvath	POSITION TITLE Professor, Human Genetics, David Geffen School of Medicine; Biostatistics, School of Public Health, University of California, LA		
eRA COMMONS USER NAME Horvath2			
EDUCATION/TRAINING			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
University of Berlin, Germany	BSc	1989	Mathematics/Physics
University of North Carolina, Chapel Hill	PhD	1995	Mathematics
Harvard School of Public Health	ScD	2000	Biostatistics

A. Personal Statement

I am a Professor in Human Genetics and Biostatistics at UCLA. My methodological research area lies at the intersection of biostatistics, bioinformatics, computational biology, cancer research, genetics, epidemiology, machine learning, and systems biology. My group applies data mining methods to study a broad spectrum of diseases (including age related diseases such as cancer and neurodegeneration). We develop methods for analyzing and integrating gene expression-, DNA methylation-, microRNA, genetic marker-, and complex phenotype data. In particular, we developed weighted correlation network analysis (also known as weighted gene co-expression network analysis WGCNA), which is a systems biologic data analysis method for analyzing high dimensional "-omics" data. My group works on all aspects of biomarker development. I have a long standing interest in machine learning methods (e.g. the random GLM predictor) and allelic association tests (e.g. the FBAT software). A major interest is the analysis of epigenomic data, e.g. DNA methylation data.

B. Positions and Honors

Positions

12/1999–10/2000	Visiting Scientist (Postdoc level), Inst. for Medical Statistics University of Bonn
11/2000–7/2006	Assistant Professor in the Depts of Hum Genetics & Biostats, Uni of Calif., LA
8/2006-6/2009	Tenured Associate Professor in the Depts of Hum Genetics & Biostats, Uni of Calif., LA
7/2009- present	Full Professor in the Depts of Hum Genetics & Biostats, Uni of Calif., LA

Honors

2006 Joint first authored article is elected as "Nature Milestone". Nature, PMID: 15988529

2007 Elected to the top 100 author list at BioMed Central

2007 The brain tumor research portal (at www.braintumour.net) elects the following paper as the second most influential brain tumor publication in the year 2006: Horvath et al. (2006) PMID: 17090670

C. Selected peer-reviewed publications out of 162 total publications

1. Xue Z, Huang K, Cai C, Cai L, Jiang CY, Feng Y, Liu Z, Zeng Q, Cheng L, Sun YE, Liu JY, Horvath S, Fan G. (2013) Genetic programs in human and mouse early embryos revealed by single-cell RNA?sequencing. Nature. 2013 Jul 28. doi: 10.1038/nature12364 PMID: 23892778
2. Langfelder P, Mischel PS, Horvath S (2013) When Is Hub Gene Selection Better than Standard Meta-Analysis? PLoS ONE 8(4): e61505. PMID: 2361386 PMCID: PMC3629234
3. Ranola JM, Langfelder P, Lange K, Horvath S Cluster and propensity based approximation of a network. BMC Syst Biol. 2013 Mar 14;7(1):21 PMID: 23497424 PMCID: PMC3663730
4. Song L, Langfelder P, Horvath S (2013) Random generalized linear model: a highly accurate and interpretable ensemble predictor. BMC Bioinformatics. PMID: 23323760 PMCID: PMC3645958
5. Horvath S, Zhang Y, Langfelder P, Kahn RS, Boks MP, van Eijk K, van den Berg LH, Ophoff RA. Aging effects on DNA methylation modules in human brain and blood tissue. Genome Biol. 2012 Oct 3;13(10):R97. PMID: 23034122. PMCID: Not yet available.
6. Hawrylycz MJ, Lein ES, Guillozet-Bongaarts AL, Shen EH, Ng L, Miller JA, van de Lagemaat LN, Smith KA, Ebbert A, Riley ZL, Abajian C, Beckmann CF, Bernard A, Bertagnolli D, Boe AF, Cartagena PM,

- Chakravarty MM, Chapin M, Chong J, Dalley RA, Daly BD, Dang C, Datta S, Dee N, Dolbeare TA, Faber V, Feng D, Fowler DR, Goldy J, Gregor BW, Haradon Z, Haynor DR, Hohmann JG, Horvath S, Howard RE, Jeromin A, Jochim JM, Kinnunen M, Lau C, Lazarz ET, Lee C, Lemon TA, Li L, Li Y, Morris JA, Overly CC, Parker PD, Parry SE, Reding M, Royall JJ, Schulkin J, Sequeira PA, Slaughterbeck CR, Smith SC, Sodt AJ, Sunkin SM, Swanson BE, Vawter MP, Williams D, Wohnoutka P, Zielke HR, Geschwind DH, Hof PR, Smith SM, Koch C, Grant SG, Jones AR (2012) An anatomically comprehensive atlas of the adult human brain transcriptome. *Nature*. 2012 Sep 20;489(7416):391-9. doi: 10.1038/nature11405. PMID: 22996553.
7. van Eijk KR, de Jong S, Boks MP, Langeveld T, Colas F, Veldink JH, de Kovel CG, Janson E, Strengman E, Langfelder P, Kahn RS, van den Berg LH, Horvath S, Ophoff RA (2012) Genetic analysis of DNA methylation and gene expression levels in whole blood of healthy human subjects *BMC Genomics*. 2012 Nov 17;13(1):636 PMID: 23157493
 8. Voineagu I, Wang X, Johnston P, Lowe JK, Tian Y, Horvath S, Mill J, Cantor R, Blencowe BJ, Geschwind DH (2011) Transcriptomic analysis of autistic brain reveals convergent molecular pathology. *Nature*. 25;474(7351):380-4 PMID: 21614001
 9. Langfelder P, Luo R, Oldham MC, Horvath S (2011) Is my network module preserved and reproducible? *PLoS Comp Biol*. 7(1): e1001057. PMID: 21283776
 10. Langfelder P, Horvath S (2008) WGCNA: an R package for Weighted Correlation Network Analysis. *BMC Bioinformatics*. 2008 Dec 29;9(1):559. PMID: 19114008 PMCID: PMC2631488
 11. Oldham MC, Konopka G, Iwamoto K, Langfelder P, Kato T, Horvath S, Geschwind DH (2008) Functional organization of the transcriptome in human brain. *Nature Neuroscience*. 11(11):1271-82. PMID: 18849986
 12. Horvath S, Dong J (2008) Geometric Interpretation of Gene Co-Expression Network Analysis. *PLoS Computational Biology*. 4(8): e1000117. PMID: 18704157
 13. Langfelder P, Zhang B, Horvath S (2008) Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. *Bioinformatics*. 2008 Mar 1;24(5):719-20. PMID: 18024473
 14. Seligson DB, Horvath S, Shi T, Yu H, Tze S, Grunstein M, Kurdistani SK (2005) Global histone modification patterns predict risk of prostate cancer recurrence. *Nature* 435, 1262-1266 PMID: 15988529
 15. Zhang B, Horvath S (2005) A General Framework for Weighted Gene Co-Expression Network Analysis. *Statistical Applications in Genetics and Molecular Biology*. Vol. 4: No. 1, Article 17. PMID: 16646834

D. Research Support

Ongoing Research Support

5R01AG042511-02 (Horvath) 07/01/2013 – 06/30/2017
 RO1 Systems genetic and reverse phenotypic analysis of age and retirement
 Role: PI. In this application, we propose to apply/develop state of the art computational, statistical, and bioinformatic approaches with which to investigate the association between genetic data and aging-related phenotypes. Specifically, the study uses data from the Health and Retirement Study (HRS) and a systems biology approach to identifying relevant SNPs and genetic pathways and machine learning techniques and reverse phenotyping methods to better understand the complex relationship between genetics and aging outcomes including cognition and wealth.

1R25GM103774-01 (Papp, co-PI Horvath) 01/01/2013-12/31/2017
 R25: "Statistical Genomics and Systems Biology Workshop"
 National Institute of General Medical Sciences
 Role: As co-PI, I am in charge of organizing several week-long network analysis workshops to be held at UCLA.

UCLA CFAR/AIDS Institute /CTSI seed grant (PI Horvath) 09/01/2012-01/08/2014
 Diagnostic and prognostic biomarkers for HIV-Associated Non-AIDS (HANA) conditions
 Role: As PI, I will direct the generation of DNA methylation data and the analysis of these data.

Biostatistics Core Director: Steve Horvath

Prostate SPORE Director: Robert Reiter

Grant Duration: 2007-2012

Project Title: UCLA Specialized Program of Research Excellence (SPORE) in Prostate Cancer.

1R01DA030913-01 (Levine, co-PI Horvath)

09/17/10-07/31/15

National Institute on Drug Abuse (NIDA)

Title: Pathways to HIV-associated neurocognitive disorders: a systems biology approach.

In the proposed study, we will apply innovative systems biology approaches to the investigation of mild HIV-associated neurocognitive disorders (HAND) pathogenesis. We focus our investigation on circulating blood monocytes, as these cells are an early and key component of this pathogenesis. We will use integrated weighted gene co-expression network analysis (IWGCNA), developed by the co-PI (Horvath), to develop meaningful biological pathways derived from monocyte-specific gene expression microarrays, HAND-associated genetic markers, and clinical diagnosis of HAND.

Completed Research Support

S058980 (Ophoff)

09/15/2008 – 06/30/2013

NIH/NATIONAL INSTITUTE OF NEUROLOGICAL DISORDERS & STROKE

Title: Genetics of gene expression and gene mapping for amyotrophic lateral sclerosis

The main goal of this project is to perform a genome-wide gene expression profiling in peripheral blood in a sample of Amyotrophic Lateral Sclerosis (ALS) patients and matched controls, all from a relatively homogeneous population in The Netherlands. Next the expression data are used to find genetic sequence variations the expression data (eQTLs) and to find SNPs for subtypes of the disease.