

Nicholas A. Furlotte (Nick)
Curriculum Vitae

CONTACT

Computer Science Department Mail Code: 1596
University of California, Los Angeles
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EDUCATION

The University of California Los Angeles (UCLA)

PhD, Computer Science
September 2008 – Present
Major: Computational Systems Biology
Minors: Algorithms and Human Genetics

The University Of Memphis

Master of Science, Bioinformatics
January 2007 – August 2008
Thesis: Literature-based evaluation of microarray normalization procedures

The University Of Memphis

Bachelor of Science, Computer Science, Minors in Mathematics and Physics
January 2001 – December 2005

RESEARCH INTERESTS

Computational and statistical genetics
Complex trait analysis
Machine Learning, Statistics and Data Mining
Linear Mixed Models

CURRENT POSITIONS

Graduate Research Assistant, September 2008 – Present
Dr. Eleazar Eskin's Lab, UCLA Computer Science
Principle Investigator: Dr. Eleazar Eskin

Computational Biology and Math Tutor, October 2010 – June 2012
Genomic Analysis Training Grant, UCLA Human Genetics

POSITIONS HELD

Software Developer / Research Assistant, May 2008 – September 2008
Clinical and Translational Science Institute (CTSI) at The University of Tennessee Health Science Center, Memphis, TN
Principle Investigator: Dr. Chanchai McDonald

Graduate Research Assistant, December 2007 – May 2008
The University of Memphis, Memphis, TN
Principle Investigator: Dr. Vinhthuy Phan

Graduate Research Assistant, June 2007 – May 2008
The University of Tennessee Health Science Center, Memphis, TN
Principle Investigator: Dr. Robert Williams

Graduate Research Assistant, January 2007 – May 2008
The University of Memphis, Memphis, TN
Principle Investigator: Dr. Ramin Homayouni

Partner / Lead Software Developer, January 2006 – December 2006
ShadeSpot.com, Memphis, TN

Undergraduate Research Assistant, September 2005 – December 2005
The University of Memphis, Memphis, TN
Principle Investigator: Dr. Max Garzon

Software Developer, December 2003 – December 2006
Apley Inc., Memphis, TN

Computer Technician, June 2001 – December 2001
Network and Computer Services (NCS), Memphis, TN

HONORS

Graduated Magna Cum Laude, December 2005
Northrup-Grumman Outstanding Graduate Student Research Award, May 2012

GRANTS

Neurobehavioral Genetics Training Grant (NINDS), June 2012 – May 2013
Includes payment of resident fees at UCLA plus a stipend.

Genomic Analysis Training Grant (NIH), September 2008 – June 2009 and July 2010 – June 2011

Includes payment of resident fees at UCLA plus a stipend.

INVITED SEMINARS

Speaker: Statistical Methods for Computational Genetics.

Center for Translational Informatics and Center for Translational and Integrative Genomics, University of Memphis and University of Tennessee. April 10th 2012.

ORAL AND POSTER PRESENTATIONS

Nicholas A. Furlotte. Mixed Model Coexpression (MMC): calculating gene coexpression while accounting for expression heterogeneity. ISMB 2011. **Talk.** Vienna Austria, July 2011.

Nicholas A. Furlotte. EMMA: Performing Genome-wide association mapping while accounting for population structure. Jackson Labs Short Course on Systems Genetics. **Talk.** Bar Harbor, Maine, Sept 23, 2010.

Nicholas A. Furlotte, Hyun Min Kang, Chun "Jimmie" Ye and Eleazar Eskin. Small-module-targeting (SMT) coexpression: prioritizing gene and module specific coexpressions by accounting for expression heterogeneity. UCLA Human Genetics Retreat 2009. **Talk,** Los Angeles, CA, Oct 8, 2009

Nick Furlotte, Dan He and Eleazar Eskin: Detection and reconstruction of copy number variations , The 59th Annual Meeting, the American Society of Human Genetics, (ASHG 2009) **Poster,** Honolulu, Hawaii, Oct. 20-24, 2009.

Dan He, **Nick Furlotte** and Eleazar Eskin: Detection and reconstruction of copy number variations , Personal Genomes meeting at Cold Spring Harbor Labs. **Poster,** Cold Springs Harbor, NY. Sept. 14-17, 2009.

Nicholas A. Furlotte, Hyun Min Kang, Chun "Jimmie" Ye and Eleazar Eskin. Small-module-targeting (SMT) coexpression: prioritizing gene and module specific coexpressions by accounting for expression heterogeneity. RECOMB 2009. **Poster,** Tuscon, AZ, March 18-21, 2009

Nicholas A. Furlotte, Hyun Min Kang, Chun "Jimmie" Ye and Eleazar Eskin. Small-module-targeting (SMT) coexpression: prioritizing gene and module specific coexpressions by accounting for expression heterogeneity. UCLA school of Engineering Techforum. **Poster,** Los Angeles, CA, April 2009.

Vinthuy Phan and **Nicholas A. Furlotte** dnaMotif: Managing and Analyzing DNA Motifs. The 4th Annual Computer Science Department Student Research Day. **Talk** Memphis, TN, March 2008.

WORKSHOPS ATTENDED

Short Course on Systems Genetics. Jackson Labs. October 2010.

PAPERS

2012

Nicholas A. Furlotte, Eleazar Eskin and Susana Eyheramendy. Genome-wide association mapping with longitudinal data. *Genetic Epidemiology*. May 2012.

Nicholas A. Furlotte, Eun Yong Kang, Atila Van Nas, Charles R. Farber, Aldons J. Lusis and Eleazar Eskin. Increasing association power and resolution in mouse genetic studies through the use of meta-analysis for structured populations. *Genetics*. April 2012.

2011

Nicholas Furlotte, Lijing Xu, Robert Williams, and Ramin Homayouni. Literature-based Evaluation of Microarray Normalization Procedures. Proceedings of BIBM 2011. Atlanta, Georgia. November 2011.

Thomas M. Keane, Leo Goodstadt, Petr Danecek, Michael A. White, Kim Wong, Binnaz Yalcin, Andreas Heger, Avigail Agam, Guy Slater, Martin Goodson, **Nicholas A. Furlotte**, Eleazar Eskin, Christoffer Nellaker, Helen Whitley, James Cleak, Deborah Janowitz, Polinka Hernandez-Pliego, Andrew Edwards, T. Grant Belgard, Peter L. Oliver, Rebecca E. McIntyre, Amarjit Bhomra, Jerome Nicod, Xiangchao Gan, Wei Yuan, Louise van der Weyden, Charles A. Steward, Sendu Bala, Jim Stalker, Richard Mott, Richard Durbin, Ian J. Jackson, Anne Czechanski, Jose Afonso Guerra-Assunção, Leah Rae Donahue, Laura G. Reinholdt, Bret A. Payseur, Chris P. Ponting, Ewan Birney, Jonathan Flint and David J. Adams. Mouse genomic variation and its effect on phenotypes and gene regulation. *Nature*. September 2011.

Nicholas A. Furlotte, Hyun Min Kang, Chun Ye and Eleazar Eskin. Mixed Model Coexpression: calculating gene coexpression while accounting for expression heterogeneity. *Bioinformatics*. July 2011.

Ghazalpour A, Bennett B, Petyuk VA, Orozco L, Hagopian R, Mungrue IN, Farber CR, Sinsheimer J, Kang HM, **Furlotte N**, Park CC, Wen PZ, Brewer H, Weitz K, Camp DG 2nd, Pan C, Yordanova R, Neuhaus I, Tilford C, Siemers N, Gargalovic P, Eskin E, Kirchgessner T, Smith DJ, Smith RD, Lusk AJ. Comparative analysis of proteome and transcriptome variation in mouse. *PLoS Genetics*. June 2011.

Dan He, Farhad Hormozdiari, **Nick Furlotte**, Eleazar Eskin: Efficient Algorithms for Tandem Copy Number Variation Reconstruction in Repeat-rich Regions, *Bioinformatics*. June, 2011.

Daria Van Tyne, Daniel J. Park, Stephen F. Schaffner, Daniel E. Neafsey, Elaine Angelino, Joseph F. Cortese, Kayla G. Barnes, David M. Rosen, Amanda K. Lukens, Rachel F. Daniels, Danny A. Milner, Charles A. Johnson, Ilya Shlyakhter, Sharon R. Grossman, Justin S. Becker, Daniel Yamins, Elinor K. Karlsson, Daouda Ndiaye, Ousmane Sarr, Souleymane Mboup, Christian Happi, **Nicholas A. Furlotte**, Eleazar Eskin, Hyun Min Kang, Daniel L. Hartl, Bruce W. Birren, Roger C. Wiegand, Eric S. Lander, Dyann F. Wirth, Sarah K. Volkman, Pardis C. Sabeti. Identification and Functional Validation of the Novel Antimalarial Resistance Locus *PF10_0355* in *Plasmodium falciparum*. *PLoS Genetics*. April 2011.

Charles R. Farber, Brian J. Bennett, Luz Orozco, Wei Zou, Ana Lira, Emrah Kostem, Hyun Min Kang, **Nicholas Furlotte**, Ani Berberyan, Anatole Ghazalpour, Jaijam Suwanwela, Thomas A. Drake, Eleazar Eskin, Q. Tian Wang, Steven L. Teitelbaum, Aldons J. Lusk. "Mouse Genome-Wide Association and Systems Genetics Identify *Asxl2* As a Regulator of Bone Mineral Density and Osteoclastogenesis." *PLoS Genetics*. April, 2011.

Lijing Xu, **Nicholas Furlotte**, Yunyue Lin, Kevin Heinrich, Michael W. Berry, Ebenezer O. George, Ramin Homayouni. "Functional Cohesion of Gene Sets Determined by Latent Semantic Indexing of Pubmed Abstracts." *PLoS ONE*. April, 2011.

2010

Dan He, **Nick Furlotte**, Eleazar Eskin. Detection and Reconstruction of Tandemly Organized de novo Copy Number Variations. *BMC Bioinformatics*. December 2010.

Andrew Kirby, Hyun Min Kang, Claire M. Wade, Chris J. Cotsapas, Emrah Kostem, Buhm Han, **Nick Furlotte**, Eun Yong Kang, Manuel Rivas, Molly A. Bogue, Kelly A. Frazer, Frank M. Johnson, Erica J. Beliharz, David R. Cox, Eleazar Eskin, Mark J. Daly. Fine Mapping in 94 Inbred Mouse Strains Using a High-density Haplotype Resource. *Genetics*. July 2010.

Bennett BJ, Farber CR, Orozco L, Min Kang H, Ghazalpour A, Siemers N, Neubauer M, Neuhaus I, Yordanova R, Guan B, Truong A, Yang WP, He A, Kayne P, Gargalovic P, Kirchgessner T, Pan C, Castellani LW, Kostem E, **Furlotte N**, Drake TA, Eskin E, Lusk AJ. A high-resolution association mapping panel for the dissection of complex traits in mice. *Genome Research*. January 2010.

2009

Viangteeravat, T., Brooks, I., **Furlotte, N.**, Vuthipadadon, S., Ketcherside, W., Homayouni, R., McDonald, C. Biomedical Informatics Unit (BMIU): Slim-Prim system bridges the gap between laboratory discovery and practice. *Clinical and Translational Science*. June 2009.

Viangteeravat, T., Brooks, I.M., Smith, E., **Furlotte, N.**, Vuthipadadon, S. Reynolds, R. & C.S. McDonald.. Slim-Prim: A biomedical informatics database to promote translational research Perspectives in Health Information Management. *Perspectives in Health Information Management*. May 2009.

2008

Vinhuy Phan and **Nicholas A. Furlotte** (2008) Motif Tool Manager: a web-based framework for motif discovery, *Bioinformatics*. December 2008.