

## Ian J. Barnett

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CONTACT INFORMATION	Website: <a href="http://scholar.harvard.edu/ibarnett">http://scholar.harvard.edu/ibarnett</a> Email: <a href="mailto:ianjamesbarnett@gmail.com">ianjamesbarnett@gmail.com</a> Phone: 650-799-7868
RESEARCH INTERESTS	Digital phenotyping, signal detection theory, analysis of high dimensional and correlated data, longitudinal data analysis, network science, statistical genetics
EDUCATION	<b>Harvard University</b> , Boston, MA  Ph.D., Biostatistics, Spring 2014 <ul style="list-style-type: none"><li>• Thesis Title: <i>SNP-set tests for sequencing and genome-wide association studies</i></li><li>• Advisor: Xihong Lin, Ph.D</li></ul> <b>Stanford University</b> , Stanford, CA  B.S., Mathematical and Computational Sciences , June 2010 <ul style="list-style-type: none"><li>• <i>Departmental honors</i></li></ul>
RESEARCH EXPERIENCE	<b>Postdoctoral Researcher</b> Jun 2014 to present Department of Biostatistics, Harvard University Supervisors: Jukka-Pekka Onnela, Ph.D (primary) Xihong Lin, Ph.D (secondary) <b>Research Assistant</b> Mar 2013 to Jun 2013 Division of Computational Biology, Dana Farber Cancer Institute Supervisors: John Quackenbush, Ph.D <b>NSF REU Student Researcher</b> Jun 2009 to Sep 2009 Department of Mathematics, Mount Holyoke College Supervisors: Jessica Sidman, Ph.D <b>NSF REU Student Researcher</b> Jun 2008 to Sep 2008 Department of Statistics, Stanford University Supervisors: Susan Holmes, Ph.D
REFEREED JOURNAL PUBLICATIONS	<ul style="list-style-type: none"><li>• <b>Barnett, I.</b>, Lee, S., and Lin, X. “Detecting rare variant effects using extreme phenotype sampling in sequencing association studies.” <i>Genetic Epidemiology</i>, 37(2):142–151. 2013.</li><li>• <b>Barnett I.</b>, Lin, X. “Analytical p-values calculation for the higher criticism test in finite-d problems.” <i>Biometrika</i>, 101(4):964-970. 2014.</li><li>• Fan, T., Fang, S. C., Cavallari, J. M., <b>Barnett, I. J.</b>, Wang, Z., Su, L., ... and Christiani, D. C. “Heart rate variability and DNA methylation levels are altered after short-term metal fume exposure among occupational welders: a repeated-measures panel study.” <i>BMC public health</i>, 14(1), 1. 2014.</li></ul>

	<ul style="list-style-type: none"> <li>• <b>Barnett I.</b>, Onnela, J-P. “Change point detection in correlation networks.” <i>Scientific Reports</i>, 6. 2016.</li> <li>• <b>Barnett, I.</b>, Mukherjee, R., and Lin, X. “The Generalized Higher Criticism for testing SNP-sets in genetic association studies.” <i>Journal of the American Statistical Association: Case Studies and Applications</i>. 2016.</li> <li>• <b>Barnett, I.</b>, Khanna, T., and Onnela, J-P. “Social and Spatial Clustering of People at Humanity’s Largest Gathering’.” <i>PloS one</i>, 11(6). 2016.</li> </ul>	
PREPRINTS UNDER REVIEW	<ul style="list-style-type: none"> <li>• <b>Barnett, I.</b>, Onnela, J-P. “Inferring mobility measures from GPS traces with missing data.” <i>arXiv preprint arXiv:1606.06328</i> (2016).</li> <li>• <b>Barnett, I.</b>, Malik, N., Kuijjer, M., Mucha, P., and Onnela, J-P. “Feature-based classification of networks.” <i>arXiv preprint arXiv:1610.05868</i> (2016).</li> </ul>	
IN PREPARATION	<ul style="list-style-type: none"> <li>• <b>Barnett, I.</b>, Onnela, J-P. “Estimating air pollution exposure from call detail records.”</li> <li>• <b>Barnett, I.</b>, Calfee, C., ... Lin, X., Christiani, D., and Wurfel, M. “A Genome-Wide Association Study identifies genetic variation in MBP that is associated with Ventilator-Free Days in patients with ARDS in the iSPAAR Consortium”</li> <li>• <b>Barnett, I.</b>, Liu, Z., and Lin, X. “On principal component methods in genetic epidemiology.”</li> <li>• Shen, Y., <b>Barnett, I.</b>, Lin, X. “Identifying sparse predictive markers for personalized treatment selection.”</li> </ul>	
AWARDS	<ul style="list-style-type: none"> <li>• ASA Section in Epidemiology Young Investigators Award for “The Generalized Higher Criticism for testing SNP-sets in genetic association studies.’”</li> <li>• ENAR Student Paper Award for “The Generalized Higher Criticism for testing SNP-sets in genetic association studies.”</li> <li>• Program in Quantitative Genomics Travel Award</li> <li>• Harvard Horizons Finalist</li> </ul>	<p>Aug 2014</p> <p>March 2014</p> <p>May 2013</p> <p>Mar 2013</p>
PRESENTATIONS	<p>Statistical Meetings</p> <ul style="list-style-type: none"> <li>• Joint Statistical Meetings, Seattle, WA</li> <li>• NetMob, Boston, MA</li> <li>• ENAR, Baltimore, MD</li> <li>• Joint Statistical Meetings, Montreal, CA</li> <li>• American Society of Human Genetics, San Francisco, CA</li> </ul> <p>Harvard University</p> <ul style="list-style-type: none"> <li>• P01/Environmental Statistics Retreat</li> <li>• PQG Annual Retreat</li> </ul>	<p>Aug 2015</p> <p>Apr 2015</p> <p>Mar 2014</p> <p>Aug 2013</p> <p>Nov 2012</p> <p></p> <p>Oct 2012</p> <p>Apr 2012</p>
TEACHING EXPERIENCE	<p>Teaching Assistant</p> <p>BIO 245 - Analysis of Multivariate and Longitudinal Data</p> <p>Instructor: Xihong Lin, Ph.D.</p>	<p>Spring 2014</p>

