

Kunal Bhutani

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EDUCATION	University of California, San Diego , La Jolla, California <i>Doctor of Philosophy, Bioinformatics & Systems Biology</i> <i>February 2017 (Expected)</i>
	University of Texas at Austin , Austin, Texas <i>Bachelor of Science, Biomedical Engineering</i> <i>May 2011</i>

RESEARCH INTERESTS	Applied Bayesian Statistics, Heterogeneity, Measurement Error, Variant Calling, Transcriptome-wide Association Studies, N-of-1 Studies, Genomics, Transcriptomics, Metabolomics
PUBLICATIONS	<p>Kim S*, Jeong K*, Bhutani K, Lee JH, Patel A, Scott E, Nam H, Lee H, Gleeson JG, Bafna V. "Virmid: accurate detection of somatic mutations with sample impurity inference". <i>Genome biology</i>. 14(8). 2013</p> <p>Bhutani K, Nazor KL, Williams R, Tran H, Dai H, Dzakula Z, Cho EH, Pang AW, Rao M, Cao H, Schork NJ, Loring JF. "Whole-genome mutational burden analysis of three pluripotency induction methods". <i>Nature Communications</i>. 7. 2016.</p> <p>Krishnaswami SR*, Grindberg RV*, Novotny M, Venepally P, Lacar B, Bhutani K, et al. "Using single nuclei for RNA-seq to capture the transcriptome of postmortem neurons". <i>Nature protocols</i>. 11(3). 2016.</p> <p>Buckley AR, Standish KA, Bhutani K, Ideker T, Harismendy O, Carter H, Schork NJ. "Pan-Cancer Analysis Reveals Technical Artifacts in The Cancer Genome Atlas (TCGA) Germline Variant Calls". <i>bioRxiv</i>. 2016.</p> <p>Bhutani K*, Sarkar A*, Park Y, Kellis M, Schork NJ. "Modeling prediction error improves power of transcriptome-wide association studies". <i>bioRxiv</i>. 2017.</p> <p>Park Y*, Sarkar A*, Bhutani K, Kellis M "Multi-tissue polygenic models for transcriptome-wide association studies". <i>bioRxiv</i>. 2017.</p> <p>Bhutani K*, Magnuson V*, Buckley A, Quarless D, Goetz L, Schork NJ. "Longitudinal metabolome, microbiome, and transcriptome profiling of a germline TP53 mutation carrier". <i>In Preparation</i>. 2017.</p>

PRESENTATIONS	<p>Modeling prediction error improves power of transcriptome-wide association studies Talk <i>Leena Peltonen School of Human Genomics - August 2016</i></p> <p>Propagating uncertainty of predicted expression in transcriptome-wide association studies Poster <i>American Society of Human Genetics - Oct 2016, The Biology of Genomes - May 2016</i></p> <p>Quantifying DNA heterogeneity in a population of cells Talk <i>J. Craig Venter Institute Informatics Seminar - September 2014</i></p> <p>Whole genome sequencing of Li-Fraumeni families reveals heterogeneous de-novo mutation signatures Poster <i>American Society of Human Genetics - October 2013</i></p>
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WORK EXPERIENCE	Illumina, Inc. , La Jolla, CA Bioinformatics Intern	<i>July 2012 - September 2012</i>
	Flok , Austin, TX Co-Founder	<i>January 2010 - September 2011</i>

TEACHING EXPERIENCE	Introduction to Bioinformatics Lecturer, Curriculum Creator	<i>July 2013</i>
	Introduction to Biological Algorithms and Databases Teaching Assistant	<i>September 2012 - December 2012</i>

AWARDS & ACHIEVEMENTS	Invited to Leena Peltonen School of Human Genomics National Science Foundation Graduate Research Fellowship Texas Exes Award for Scholarship and Leadership
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REFERENCES	Nicholas J. Schork, Ph.D. , Director of Human Biology, JCVI nschork@jcv.org, 858-200-1813
	Manolis Kellis, Ph.D. , Professor of Computer Science, MIT manoli@mit.edu, 617-253-2419
	Erick Scott, M.P.H., M.D., Ph.D. , Assistant Professor of Genetics and Genomic Sciences, Mount Sinai erick.scott@mssm.edu
