Kunal Bhutani, PhD

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EDUCATION

University of California, San Diego, La Jolla, California
Doctor of Philosophy, Bioinformatics & Systems Biology   *February 2017*

University of Texas at Austin, Austin, Texas
Bachelor of Science, Biomedical Engineering   *May 2011*

RESEARCH INTERESTS

Applied Bayesian Statistics, Heterogeneity, Measurement Error, Variant Calling, Transcriptome-wide Association Studies, N-of-1 Studies, Genomics, Transcriptomics, Metabolomics

PUBLICATIONS

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". *Genome biology.* 14(8). 2013

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". *Nature Communications.* 7. 2016.

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". *Nature protocols.* 11(3). 2016.

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". *bioRxiv.* 2016.

Bhutani K*, Sarkar A*, Park Y, Kellis M, Schork NJ. "Modeling prediction error improves power of transcriptome-wide association studies". *bioRxiv.* 2017.

Park Y*, Sarkar A*, **Bhutani K**, Kellis M "Multi-tissue polygenic models for transcriptome-wide association studies". *bioRxiv.* 2017.

Bhutani K*, Magnuson V*, Buckley A, Quarless D, Goetz L, Schork NJ. "Longitudinal metabolome, microbiome, and transcriptome profiling of a germline TP53 mutation carrier". *In Preparation.* 2017.

PRESENTATIONS

Modeling prediction error improves power of transcriptome-wide association studies
Talk   *Leena Peltonen School of Human Genomics - August 2016*

Propagating uncertainty of predicted expression in transcriptome-wide association studies
Poster *American Society of Human Genetics - Oct 2016, The Biology of Genomes - May 2016*

Quantifying DNA heterogeneity in a population of cells
Talk   *J. Craig Venter Institute Informatics Seminar - September 2014*

Whole genome sequencing of Li-Fraumeni families reveals heterogeneous de-novo mutation signatures
Poster   *American Society of Human Genetics - October 2013*

WORK
EXPERIENCE

Illumina, Inc., La Jolla, CA
Bioinformatics Intern   *July 2012 - September 2012*

Flok, Austin, TX
A Social Geo-location Startup, Co-Founder   *January 2010 - September 2011*

TEACHING
EXPERIENCE

Introduction to Bioinformatics
Curriculum Creator, Lecturer   *July 2013*

Introduction to Biological Algorithms and Databases
Teaching Assistant   *September 2012 - December 2012*

AWARDS &
ACHIEVEMENTS

Invited to Leena Peltonen School of Human Genomics
National Science Foundation Graduate Research Fellowship
Texas Exes Award for Scholarship and Leadership

TECHNICAL
SKILLS

Programming Languages: Python, R, Bash
Statistics: Bayesian Inference, Generalized Linear Models, Mixed Models, Mixture Models, Measurement Error, Dimensionality Reduction, Outlier Detection, Changepoint Detection
Bioinformatics:
Whole Genome Sequencing: processing, quality control, variant calling: germline and somatic, and annotation
Population Genetics: imputation, genome-wide association studies, transcriptome-wide association studies
RNA-Seq: processing, quality control, and differential expression for single cell and population transcriptomics
Familiarity with metabolomics and microbiome data.

REFERENCES

Nicholas J. Schork, Ph.D., Director of Human Biology, JCVI

Manolis Kellis, Ph.D., Professor of Computer Science, MIT

Erick Scott, M.P.H., M.D., Ph.D., Assistant Professor of Genetics and Genomic Sciences, Mount Sinai