

# Prasad Patil

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## EDUCATION

Ph.D. in Biostatistics  
Johns Hopkins University, Baltimore, MD, 2011-2016 (expected)  
Advisor: Jeffrey Leek, Co-advisor: Michael Rosenblum

B.A. in Mathematics  
New York University, New York, NY, 2005-2008  
Concentration: Applied Mathematics  
Minor: Computer Science

## RESEARCH EXPERIENCE

*Graduate Research* 2012-  
*Department of Biostatistics, Johns Hopkins University, Baltimore, MD*

With Jeff Leek,

- Identified and described bias due to data normalization in the prediction of breast cancer subtypes using gene expression information.
- Formalized feature selection and modeling with Top-Scoring Pairs for simple, decision-tree-based classifiers.
- Developed R packages for standardized analysis templating (**tdsm**) and interactive health visualizations (**healthvis**).
- Suggested 95% prediction intervals as a means of assessing whether a study result has been replicated.

With Jeff Leek and Michael Rosenblum,

- Used RCT baseline covariate adjustment methods to assess the additional value a genomic prediction can provide beyond standard clinical measurements in improving the precision of a treatment effect estimator.
- Examined the benefit of using machine learning methods to summarize the predictive value of large numbers of baseline covariates in an RCT setting.

*Scientific Programmer* 2009-2011  
*Center for Biomedical Informatics, Harvard Medical School, Boston, MA*

- Developed synthetic patient simulation platform predicated on Bayesian networks, and accompanying web service.
- Built clinical trial simulation framework using synthetic patients, stochastic PK-PD models for drug clearance, and coded clinical trial protocols.
- Fostered collaboration with Beth Israel Deaconess Medical Center and Genome-Quest, Inc. to create a commercial, clinical-grade omics analysis pipeline intended for hospital use.
- Administered a cloud computing environment via Amazon Web Services for day-to-day lab operations and omics pipeline deployment.

- Collaborated with the Center for Biomedical Informatics at Harvard Medical School to develop an open-source pipeline using next-generation sequencing (NGS) technology to detect and clinically annotate all variants in an individual human genome.
- Evaluated and tested NGS tools and restructured code for parallelization via Hadoop/MapReduce.
- Developed a comprehensive data model and modular scripted pipeline for variant annotation and reporting.

## PUBLICATIONS

1. **Patil P**, Peng RD, Leek JT (2015). A glass half-full interpretation of replicability in psychological science. Under revision, *Perspectives on Psychological Science*.
2. **Patil P**, Colantuoni E, Rosenblum MA, Leek JT (2015). Genomic and clinical predictors for improving estimator precision in randomized trials of breast cancer treatments. Revised and resubmitted, *Contemporary Clinical Trials Communications*.
3. **Patil P**, Leek JT (2015). Discussion of “Visualizing statistical models: Removing the blindfold”. *Statistical Analysis and Data Mining: The ASA Data Science Journal*, 8(4), 240-241.
4. **Patil P**, Bachant-Winner PO, Haibe-Kains B, Leek JT (2015). Test set bias affects reproducibility of gene signatures. *Bioinformatics*, btv157.
5. Hyland PL, Burke LS, Pfeiffer RM, Rotunno M, Sun D, **Patil P**, Wu X, Tucker MA, Goldstein AM, Yang XR (2014). Constitutional promoter methylation and risk of familial melanoma. *Epigenetics*, 9(5), 685-692.
6. Fusaro, VA, **Patil P**, Chi CL, Contant CF, Tonellato PJ (2013). A Systems Approach to Designing Effective Clinical Trials Using Simulations. *Circulation*, 127(4), 517-526.
7. Fusaro VA, **Patil P**, Gafni E, Wall DP, Tonellato PJ (2011). Biomedical Cloud Computing Using Amazon Web Services. *PLoS Computational Biology*. 7(8):e1002147.
8. Wall DP, Kudtarkar P, Fusaro VA, Pivovarov R, **Patil P**, Tonellato PJ (2010). Cloud computing for comparative genomics. *BMC Bioinformatics* 11:259.

## PRESENTATIONS AND POSTERS

1. **Patil P\***, Alquicira J, Leek JT. Measuring the value of GWAS results in a clinical trial setting. ASHG 2015 [poster].
2. **Patil P\***. What to expect when you’re replicating. Hopkins Biostatistics Journal Club 2015 [talk].
3. **Patil P\***, Leek JT. Reproducibility and value of genomic signatures. JSM 2015 [talk].
4. **Patil P\***. On organization. Hopkins Biostatistics Computing Club 2015 [talk].
5. **Patil P\***, Leek JT. Assessing the reproducibility and value of genomic signatures. ENAR 2015 [talk].
6. **Patil P\***, Haibe-Kains B, Leek JT. Cross-platform gene signature development using Top-Scoring Pairs. JSM 2014 [talk].
7. **Patil P\***. Cross-validation in the presence of many features. Hopkins Biostatistics Journal Club 2014 [talk].

8. **Patil P\***, Haibe-Kains B, Leek JT. Cross-platform gene signature development using Top-Scoring Pairs. ENAR 2014 [talk].
9. Chi CL, Fusaro VA, **Patil P**, Crawford MA, Contant CF, Tonellato PJ. An approach to optimal individualized warfarin treatment through clinical trial simulations. Proceedings of IEEE Cairo International Biomedical Engineering Conference (CIBEC) 2010, Cairo, Egypt [talk].
10. Chi, CL, **Patil P**, Fusaro VA, Kos PJ, Pivovarov R, Contant CF, Tonellato PJ. A Simulation Platform to Examine Heterogeneity Influence on Treatment. Proceedings of the 2010 American Medical Informatics Association Annual Symposium, Washington, DC [talk].
11. Chi CL, Kos PJ, Fusaro VA, Pivovarov R, **Patil P**, Tonellato PJ. Mining personalized medicine algorithms with surrogate algorithm tags. Proceedings of the First ACM International Health Informatics Symposium 2010 [poster].
12. **Patil P\***, Heus H, Arnaout R, Tonellato PJ. Refining a method for processing an individuals whole genome to clinical utility. CSHL Personal Genomes Meeting 2010. Cold Spring Harbor, N.Y [talk].
13. **Patil P\***, Tonellato PJ. Individual Whole Genome Mapping: from NGS reads to clinical variants, American Medical Informatics Association Clinical Research Informatics Summit 2010, San Francisco, CA [poster].
14. Fusaro VA, Kos PJ, Tector M, Tector A, **Patil P**, Tonellato PJ. Electronic Medical Record Analysis Using Cloud Computing, American Medical Informatics Association Clinical Research Informatics Summit 2010, San Francisco, CA [poster].
15. **Patil P\***. Clinical algorithms for whole genome data Partners Health Care Information Systems Research Council Symposium 2009, Harvard Medical School, Boston, MA [talk].
16. **Patil P\***. Clinical annotation of an individual whole genome assembly, Center for Biomedical Informatics Research Day 2009, Harvard Medical School, Boston, MA [talk].

\* - Presenter

<b>TEACHING</b>	Guest lecturer, BIO622	2015
	Conducted daily lecture for 500+ student course	
	Lead TA, BIO621-623	2014-2015
	Prepared and held 2-3 sections per week, 40-60 students each	
	Beta-tested, proctored, and graded exams	
	TA, BIO611-612, 615, 621-624, AS.280.35	2012-2014
	Graded homework and exams, held small sections and office hours	

## SERVICE

Refereeing: Biometrics, Genome Biology, PLOS ONE

### Organization

- Session chair, Next Generation Sequencing. ENAR 2014.
- Organizer (2012), Hopkins Biostatistics Computing Club.

<b>AWARDS</b>	JHSPH Student Assembly Teaching Assistant Recognition Award	2015
	One of two voted on by students across all courses in JHSPH	
	NYU Honors Scholar	2008
	NYU Deans List	2006-2007
	National Merit Scholarship	2005-2008

<b>SOFTWARE</b>	R Packages (submitted to Bioconductor):	
	<b>healthvis</b> ( <a href="https://github.com/prpatil/healthvis">https://github.com/prpatil/healthvis</a> )	
	Interactive health visualizations. Built using <b>d3</b> , <b>shiny</b> , <b>htmlWidgets</b> .	
	<b>tdsm</b> ( <a href="https://github.com/prpatil/tdsm">https://github.com/prpatil/tdsm</a> )	
	Templated Deterministic Statistical Machines. Automated analysis templates and standardized reports that can be edited and compared.	
	Languages:	
	R, Javascript, C/C++, Java, Perl, MATLAB, Stata, Hadoop, Shell scripting	

<b>REFERENCES</b>	Available upon request.
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