CURRICULUM VITAE
Noah Simon
November 23 , 2015

1.   Biographical Information

Work Address:

University of Washington

Department of Biostatistics F-650 Health Sciences Building Box 357232
Seattle, WA 98195

Phone: (202) 277-5346
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2.   Education

Pomona College, Claremont CA, B.A. Mathematics, 2008
Stanford University, Stanford CA, Ph.D., Statistics, 2013 *Advisor:* Prof. Robert Tibshirani

Dissertation Title: High Dimensional Interaction Testing and Estimation

3.   Licensure   Not applicable

4.   Professional Positions

Graduate Student, Department of Statistics, Stanford University, 2008-2013
Assistant Professor, Department of Biostatistics, University of Washington 2013 - present

5.   Honors, Awards, Scholarships

Academic Awards and Honors
- Jaeger Prize in Mathematics from Pomona College (2005)
- Llewellyn Bixby Mathematics Prize from Pomona College (2006)
- TA Award from Department of Statistics, Stanford University (2009)
- National Science Foundation Graduate Research Fellowship Honorable Mention (2010)
- Yahoo Key Scientific Challenges Award (2012)
- Weiland Fellowship (2011-13)

Popular Awards
- Forbes 30 under 30 in Science (2015)

6.   Professional Activities (outside of UW)

Referee Service:

BMC Bioinformatics; Biometrika; Biostatistics; Journal of the American Statistical Association

(Theory and Methods); Journal of Computational and Graphical Statistics; Journal of

Machine Learning Research; Journal of the Royal Statistical Society, Series B; Statistical Applications

in Genetics and Molecular Biology, Journal of Statistical Software, R Journal

Professional Memberships:

American Statistical Association, 2010-present
International Chinese Statistical Association, 2013-present

7. Bibliography Refereed Research Articles

1. Garcia SR, Selhorst-Jones V, Poore DE, & **Simon N** (2011). Quotient Sets and Diophantine Equations. *American Mathematical Monthly*, *118*(8), 704-711.

2. **Simon N**, Friedman JH, Hastie T, and Tibshirani R (2011). Regularization Paths for Cox's Proportional Hazards Model via Coordinate Descent. *Journal of Statistical Software*, 39(5), 1-13.

3. Simon R, and **Simon N** (2011). Using randomization tests to preserve type I error with response adaptive and covariate adaptive randomization. *Statistics & probability letters*, *81*(7), 767-772.

4. Harshman L, Manda S, Hansel D, McKenney J, Oliveria V, **Simon N**, Dreicer R, Srinivas S, Bepler G, (2011). ERCC1 and RRM1 expression patterns in synchronous primary and metastatic urothelial cancer lesions. *Journal of Clinical Oncology* 29:2011 (suppl; abstr e15035)

5. Tibshirani R, Bien J, Friedman J, Hastie T, **Simon N**, Taylor J, and Tibshirani R (2012). Strong rules for discarding predictors in lasso-type problems. *Journal of the Royal Statistical Society: Series B (Statistical Methodology)*, *74*(2), 245-266.

6. **Simon N**, and Tibshirani R (2012). Standardization and the group Lasso penalty. *Statistica Sinica*, *22*(3), 983.

7. Witten DM, Friedman JH, and **Simon N** (2011). New insights and faster computations for the graphical lasso. *Journal of Computational and Graphical Statistics*, *20*(4), 892-900.

8. Harshman L, Bepler G, Quinn D, McKenney J, Hawes D, **Simon N**, Srinivas S, Dorff (2012).Evaluation of ERCC1 and RRM1 as prognostic biomarkers in urothelial cancer (UC) treated with adjuvant platinum and gemcitabine chemotherapy *Journal of Clinical Oncology 30,*2012 (suppl; abstr e15005)

9. **Simon N**, Friedman J, Hastie T, and Tibshirani R (2012). A sparse-group lasso. *Journal of Computational and Graphical Statistics*, 22.2 (2013): 231-245.

10. **Simon N**, and Simon R (2013). Adaptive enrichment designs for clinical trials. *Biostatistics,* 14.4 (2013): 613-625.

11. Furman D, Hejblum, B. P., **Simon N**, Jojic V, Dekker C L., Thiébaut R, …, Davis, M. M. (2013). Systems analysis of sex differences reveals an immunosuppressive role for testosterone in the response to influenza vaccination. *Proceedings of the National Academy of Sciences*, 201321060.

12. Moore H E, Andlauer O, **Simon N**, Mignot E (2014). Exploring medical diagnostic performance using interactive, multi-parameter sourced receiver operating characteristic scatter plots. *Comp. in Bio. and Med*. 47: 120-129

13. Li X, Battle A, Karczewski KJ, Zappala Z, Knowles DA, Smith KS, Kukurba KR, Wu E, **Simon N**, Montgomery SB (2014). Transcriptome Sequencing of a Large Human Family Identifies the Impact of Rare Noncoding Variants. *American Journal of Human Genetics* 4;93(3):245-56.

14. Bien J, **Simon N**, and Tibshirani R (2015). Convex Hierarchical Testing of Interactions. *Annals of Applied Statistics*. 9(1): 27-42.

15. de Sisternes L, **Simon N**, Leng T, Tibshirani R, and Rubin D (2014). Quantitative SD-OCT Imaging Biomarkers as Indicators of Age-Related Macular Degeneration Progression *Investigative Ophthalmology and Visual Science*. 55(11):7093-7103

16. **Simon N**, Tibshirani R (to appear 2015). A Permutation Approach to Testing Interactions for Binary Response by Comparing Correlations Between Classes. *Journal of the American Statistical Association*.

17. **Simon N,** (2015). Adaptive Enrichment Designs: Applications and Challenges. *Future Medicine*. 5(4), 383-391

18. Haris A, Witten D, **Simon N** (to appear 2015). Convex Modeling of Interactions with Strong Heredity. *Journal of Computational and Graphical Statistics*.

19. Petersen A, Witten D, **Simon N** (to appear 2015). Fused Lasso Additive Model. *Journal of Computational and Graphical Statistics*.

Patents and Other Intellectual Property

Publicly Available Software

1. **sgl**, an R library for fitting the sparse group lasso for a variety of losses, available at "http://cran.r-project.org/"http://cran.r-project.org/web/packages/SGL/index.html.

2. **standGL**, an R library for fitting the standardized group lasso (and ridged-group lasso) available at http://cran.r-project.org/web/packages/standGL/index.html.

3. **Interact**, an R library for testing for interactions in high dimensions with binary response (with FDR estimates based on permutations), available at http://cran.r-project.org/web/packages/Interact/index.html.

9.   **Funding History**

1. NIH Director's Early Independence Award; Role: PI; 1 DP5OD019820-01
Title: "Data-Driven Statistical Learning, with Applications to Genomics"
9/18/2014 – 2019; $250,000/year in direct costs

2. Google Computing Grant; Role: PI;
Title: "Detecting Differentially Methylated Regions in Developing Muscle Cells"
2/16/2015 – 2016; $5000 computing costs on google compute engine.

3. NSF conference Grant; Role: co-PI; 1506255
Title: "17th IMS New Researchers Conference"
6/15/2015 – 5/31/2016; $23,000 in costs

4. NIH conference Grant; Role: co-PI; 1R13CA200282-01
Title: "17th IMS New Researchers Conference"
7/17/2015 – 6/30/2016; $16,140 in direct costs

5. Amazon Computing Grant; Role: PI;
Title: "Biomarkers Which Inform Treatment: Searching for Qualitative Interactions"
10/2015 – 2016; $8500 computing costs on AWS.

10. **Public Health Practice Activities** (None)

11. **Conferences and Symposiums**

Contributed Oral Presentations

1. *Coordinate Descent For Lasso Problems: The good, the bad, and the ugly*. JSM, Miami, FL. (08/11)

2. *The Sparse-group Lasso and Structured Learning: Sometimes Less is More.* Stanford Department of Statistics Industrial Affiliates Meeting. Stanford, CA. (03/11)

3. *Adaptive Enrichment in Clinical Trials and A/B Testing.* Stanford Department of Statistics Industrial Affiliates Meeting. Stanford, CA. (03/13)

Invited Oral Presentations and Seminars

1. *Permutation Approach to High Dimensional Interaction Testing*. Stanford University, Workshop in Biostatistics, Department of Health Research & Policy. Stanford, CA. (10/12)

2. *A Permutation Approach to High Dimensional Interaction Testing*. University of California at Berkeley, Biostatistics Seminar, Department of Biostatistics. Berkeley, CA. (11/12)

3. *A Permutation Approach to High Dimensional Interaction Testing*. University of California at Davis, Statistics Seminar, Department of Statistics. Davis, CA. (1/13)

4. *A Permutation Approach to High Dimensional Interaction Testing*. University of Washington, Biostatistics Seminar, Department of Biostatistics. Seattle, WA. (2/13)

5. *A Sparse-group Lasso, Computation, and GPUs*. JSM, Montreal, Canada. (8/13)

6. Estimating Many Effect-sizes Bayesian Estimation as a Frequentist. Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine, Banff, Canada (8/13)

7. *Adaptive Enrichment Designs for Clinical Trials.* Bayesian Biostatistics and Bioinformatics *Conference* 2014. The University of Texas, and M.D. Anderson. Houston, Texas. (2/14)

8. *Adaptive Enrichment Designs for Clinical Trials.* Pacific Coast Statisticians and Pharmacometricians Innovation Conference. Cal Poly San Luis Obispo. San Luis Obispo, CA. (2/14)

9. Adaptive Enrichment Designs for Clinical Trials. Eastern North American Region Meeting. Baltimore, MD. (3/14)

10. Adaptive Enrichment Designs for Clinical Trials. International Chinese Statistics Association Meeting. Portland, OR. (6/14)

11. Adaptive Enrichment Designs for Clinical Trials. International Indian Statistics Association Meeting. Riverside, CA. (7/14)

12. *Workshop on Building Biomarkers using High Dimensional Data.* Deming Conference, Atlantic City, NJ (12/14)

13. *Learn and confirm phase 3 clinical trials.* Takeda Pharmaceutical. Deerfield IL. (12/14)

14. *A Flexible Framework for Sparse Additive Modeling.* Eastern North American Region Meeting, Miami, FL. (3/15)

15. *Adjusting Point Estimates and Confidence Intervals for Selection Bias in High Dimensions as a Frequentist.* Workshop on Statistical Inference for Large Scale Data, Vancouver, Canada. (invited for 4/15)

16. *Stratification Free Adaptive Enrichment.* International Chinese Statistics Association Meeting. Fort Collins, CO. (6/15)

17. *Selection Bias in Adaptive Enrichment Designs.* JSM, Seattle WA (8/15)

18. *Correcting for Selection Bias in High-Throughput Experiments.* Department of Genome Sciences Seminar, University of Washington (10/15)

19. *Adaptive Enrichment Designs for Clinical Trials.* Biomath Group Department Seminar, Fred Hutchinson (10/15)

20. *Additive Modeling in High Dimensions (estimation and testing).* Department of Biostatistics Seminar, University of Pennsylvania (10/15)

12.   University Service:

Department of Biostatistics

- Communications committee, Member (2014)
- Admissions Committee, Member (2014)
- Diversity Committee, Member (2014)

- MS theory committee, Member (2014)
- Department Seminar Organizer (2014)

13.   Professionally-Related Community Service: None

14.   [Other Pertinent Information As Needed]

Other Work Experience:
- Research Intern at Genentech, San Francisco CA (Summer 2008)

15.   Teaching History

Formal Courses at The University of Washington
- BIOST 561 Computational Tools for Biostatistics I
Enrollment 33 (Fall 2013)
Enrollment 21 (Fall 2014)
- BIOST 562 Computational Tools for Biostatistics II
Enrollment 21 (Winter 2014)
Enrollment 20 (Winter 2015)

Independent Study
- Brenda Price (Fall 2013 – Fall 2014)
- Jeremy Roth (Winter 2014 – Winter 2015)
- Katie Wilson (Fall 2014 – Winter 2015)
- Anna Plantinga (Fall 2014)
- Brayan Ortiz (Fall 2014 – Winter 2015)
- Phuong Vu (Fall 2014)
- Yatong Li (Fall 2014)

Formal Courses at Stanford University
- Statistics 390, Consulting Workshop
- Enrollment 6 (Summer 2010)
- Enrollment 5 (Summer 2011)
- Enrollment 24 (Winter 2011)
- Enrollment 8 (Summer 2012)
- Enrollment 17 (Fall 2012)

Teaching Assistantships at Stanford University
- Statistics 60, Introduction to Statistics
  - Winter 2008, Summer 2009, Fall 2009, Spring 2010
- Statistics 191, Introduction to Applied Statistics (Winter 2010)
- Statistics 306B, Unsupervised Statistical Learning (Winter 2011)
- Statistics 290, Statistical Computing (Fall 2011)
- Statistics 306a, Exponential Families (Winter 2012)

16.   Advising and Formal Mentoring

Thesis Advising

- Ashley Petersen, Biostatistics PhD student (co with Daniela Witten)

- JooYoon Han, Biostatistics PhD student (co with Andrew Zhou)
- Jean Morrison, Biostatistics PhD student

Project Supervision

- Asad Harris, Biostatistics PhD student (co with Daniela Witten)
- Jeremy Roth, Biostatistics PhD student
- Anna Plantinga, Biostatistics PhD student
- Katie Wilson, Biostatistics Phd student
- Richard Robinson, Mathematics PhD student