

Po-Ru Loh

CONTACT INFORMATION	Brigham and Women's Hospital Harvard Medical School 77 Avenue Louis Pasteur, NRB 250F Boston, MA 02115	Phone: 617-525-4065 E-mail: poruloh@broadinstitute.org http://statgen.hms.harvard.edu
ACADEMIC POSITIONS	Brigham and Women's Hospital / Harvard Medical School Assistant Professor of Medicine Instructor in Medicine	March 2018–present August 2017–March 2018
	Broad Institute of MIT and Harvard Associate Member	March 2018–present
	Harvard T.H. Chan School of Public Health Postdoctoral Research Associate, Epidemiology Mentor: Alkes Price	June 2013–July 2017
EDUCATION	Massachusetts Institute of Technology Ph.D., Applied Mathematics Advisor: Bonnie Berger	June 2013
	California Institute of Technology B.S., Mathematics	June 2007
GRANTS & FELLOWSHIPS	NIH New Innovator Award Glenn Foundation for Medical Research and AFAR Grant for Junior Faculty Burroughs Wellcome Fund Career Award at the Scientific Interface NIH Ruth L. Kirschstein NRSA Postdoctoral Research Fellowship NSF Mathematical Sciences Postdoctoral Research Fellowship NSF Graduate Research Fellowship National Defense Science and Engineering Graduate Fellowship	2018–2023 2018–2020 2017–2022 2014–2017 (declined 2013) 2010–2012 2007–2010
PUBLICATIONS	53. Kichaev G, Bhatia G, Loh P-R , Gazal S, Burch K, Freund MK, Schoech A, Pasaniuc B, Price AL. Leveraging polygenic functional enrichment to improve GWAS power. <i>American Journal of Human Genetics</i> 2019, in press. 52. Galinsky KJ, Reshef YA, Finucane HK, Loh P-R , Zaitlen N, Patterson NJ, Brown BC, Price AL. Estimating cross-population genetic correlations of causal effect sizes. <i>Genetic Epidemiology</i> 2019, in press. 51. Gazal S, Loh P-R , Finucane HK, Ganna A, Schoech AP, Sunyaev S, Price AL. Low-frequency variant functional architectures reveal strength of negative selection across coding and non-coding annotations. <i>Nature Genetics</i> 50(11), 2018.	

50. Reshef YA, Finucane HK, Kelley DR, Gusev A, Kotliar D, . . . , **Loh P-R**, . . . , Palamara PF, Pinello L, Patterson N, Adams R, Price AL. Detecting genome-wide directional effects of transcription factor binding on polygenic disease risk. *Nature Genetics* 50(10), 2018.
49. **Loh P-R**^{*}, Genovese G^{*}, Handsaker RE, Finucane HK, Reshef YA, Francesco PF, Birman BM, Talkowski ME, Bakhoun SF, McCarroll SA, Price AL. Insights into clonal haematopoiesis from 8,342 mosaic chromosomal alterations. *Nature* 559(7714), 2018.
48. Hormozdiari F, Gazal S, van de Geijn B, Finucane HK, Ju CJ-T, **Loh P-R**, . . . , Liu X, O'Connor L, Gusev A, Eskin E, Price AL. Leveraging molecular quantitative trait loci to understand the genetic architecture of diseases and complex traits. *Nature Genetics* 50(7), 2018.
47. **Loh P-R**, Kichaev G, Gazal S, Schoech AP, Price AL. Mixed-model association for biobank-scale data sets. *Nature Genetics* 50(7), 2018.
46. Zhu Z, Lee PH, Chaffin MD, Chung W, **Loh P-R**, Lu Q, Christiani DC, Liang L. A genome-wide cross-trait analysis from UK Biobank highlights the shared genetic architecture of asthma and allergic diseases. *Nature Genetics* 50(6), 2018.
45. Finucane HK, Reshef YA, Anttila V, Slowikowski K, Gusev A, . . . , **Loh P-R**, . . . , Bernstein BE, Raychaudhuri S, McCarroll S, Neale BM, Price AL. Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. *Nature Genetics* 50(4), 2018.
44. Weng LC, Choi SH, Klarin D, Smith JG, **Loh P-R**, . . . , Benjamin EJ, Newton-Cheh C, Kathiresan S, Ellinor PT, Lubitz SA. Heritability of atrial fibrillation. *Circulation: Cardiovascular Genetics* 10(6), 2017.
43. Marquez-Luna C, **Loh P-R**, South Asian Type 2 Diabetes (SAT2D) Consortium, SIGMA Type 2 Diabetes Consortium, Price AL. Multiethnic polygenic risk scores improve risk prediction in diverse populations. *Genetic Epidemiology* 41(8), 2017.
42. Gazal S, Finucane HK, Furlotte NA, **Loh P-R**, Palamara PF, . . . , Schoech A, Bulik-Sullivan B, Neale BM, Gusev A, Price AL. Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. *Nature Genetics* 49(10), 2017.
41. Willems SM, Wright DJ, Day FR, Trajanoska K, Joshi PK, . . . , **Loh P-R**, . . . , Rivadeneira F, Langenberg C, Perry JRB, Wareham NJ, Scott RA. Large-scale GWAS identifies multiple loci for hand grip strength providing biological insights into muscular fitness. *Nature Communications* 8:16015, 2017.
40. Day FR, Thompson DJ, Helgason H, Chasman DI, Finucane H, . . . , **Loh P-R**, . . . , Murray A, Murabito JM, Stefansson K, Ong KK, and Perry JRB. Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics* 49(6), 2017.

39. Hill A, **Loh P-R**, Bharadwaj R, Pons P, Shang J, Guinan E, Lakhani K, Kilty I, and Jelinsky S. Stepwise distributed open innovation contests for software development: acceleration of genome-wide association analysis. *GigaScience* 6(5), 2017.
38. Hayeck T, **Loh P-R**, Pollack S, Gusev A, Patterson N, Zaitlen NA, and Price AL. Mixed model association with family-biased case-control ascertainment. *American Journal of Human Genetics* 100(1), 2017.
37. Galinsky K, **Loh P-R**, Mallick S, Patterson N, and Price AL. Population structure of UK Biobank and ancient Eurasians reveals adaptation at genes influencing blood pressure. *American Journal of Human Genetics* 99(5), 2016.
36. **Loh P-R**, Danecek P, Palamara PF, Fuchsberger C, Reshef YA, . . . , Forer L, McCarthy S, Abecasis GR, Durbin R, and Price AL. Reference-based phasing using the Haplotype Reference Consortium panel. *Nature Genetics* 48(11), 2016.
35. Horikoshi M, Beaumont RN, Day FR, Warrington NM, Kooijman MN, . . . , **Loh P-R**, . . . , Timpson NJ, Perry JRB, Evans DM, McCarthy MI, and Freathy RM. Genome-wide associations for birth weight and correlations with adult disease. *Nature* 538, 2016.
34. Das S, Forer L, Schoenherr S, Sidore C, Locke AE, . . . , **Loh P-R**, . . . , Cucca F, Kronenberg F, Boehnke M, Abecasis GR, and Fuchsberger C. Next generation genotype imputation service and methods. *Nature Genetics* 48(10), 2016.
33. **Loh P-R**, Palamara PF, and Price AL. Fast and accurate long-range phasing in a UK Biobank cohort. *Nature Genetics* 48(7), 2016.
32. Day FR, Helgason H, Chasman DI, Rose LM, **Loh P-R**, . . . , Ridker PM, Sulem P, Stefansson K, Ong KK, and Perry JRB. Physical and neurobehavioral determinants of reproductive onset and success. *Nature Genetics* 48(6), 2016.
31. Galinsky KJ, Bhatia G, **Loh P-R**, Georgiev S, Mukherjee S, Patterson NJ, and Price AL. Fast principal components analysis reveals independent evolution of *ADH1B* gene in Europe and East Asia. *American Journal of Human Genetics* 98(3), 2016.
30. Day FR, **Loh P-R**, Scott RA, Ong KK, and Perry JRB. A robust example of collider bias in a genetic association study. *American Journal of Human Genetics* 98(2), 2016.
29. **Loh P-R**, Bhatia G, Gusev A, Finucane HK, Bulik-Sullivan BK, . . . , Kendler KS, O'Donovan MC, Neale BM, Patterson N, and Price AL. Contrasting genetic architectures of schizophrenia and other complex diseases using fast variance components analysis. *Nature Genetics* 47(12), 2015.
28. Tucker G*, **Loh P-R***, MacLeod IM, Hayes BJ, Goddard ME, Berger B, and Price AL. Two variance component model improves genetic prediction in family data sets. *American Journal of Human Genetics* 97(5), 2015.
27. Lipson M, **Loh P-R**, Sankararaman S, Patterson N, Berger B, and Reich D. Calibrating

the human mutation rate via ancestral recombination density in diploid genomes. *PLOS Genetics* 11(11), 2015.

26. Vilhjálmsón BJ, Yang J, Finucane HK, Gusev A, Lindstrom S, Ripke S, Genovese G, **Loh P-R**, . . . , Goddard M, Visscher PM, Kraft P, Patterson N, and Price AL. Modeling linkage disequilibrium increases accuracy of polygenic risk scores. *American Journal of Human Genetics* 97(4), 2015.
25. Finucane HK, Bulik-Sullivan BK, Gusev A, Trynka G, Reshef Y, **Loh P-R**, . . . , Raychaudhuri S, Daly MJ, Patterson N, Neale BM, and Price AL. Partitioning heritability by functional category using GWAS summary statistics. *Nature Genetics* 47(11), 2015.
24. Bulik-Sullivan BK, Finucane HK, Anttila V, Gusev A, Day FR, **Loh P-R**, . . . , Patterson N, Robinson E, Daly MJ, Price AL, and Neale BM. An atlas of genetic correlations across human diseases and traits. *Nature Genetics* 47(11), 2015.
23. Hayeck T, Zaitlen NA, **Loh P-R**, Vilhjálmsón BJ, Pollack S, Gusev A, Yang J, Chen G-B, Coddard ME, Visscher PM, Patterson N, and Price AL. Mixed model with correction for case-control ascertainment increases association power. *American Journal of Human Genetics* 96(5), 2015.
22. **Loh P-R**, Tucker G, Bulik-Sullivan BK, Vilhjálmsón BJ, Finucane HK, Salem RM, Chasman DI, Ridker PM, Neale BM, Berger B, Patterson N, and Price AL. Efficient Bayesian mixed model analysis increases association power in large cohorts. *Nature Genetics* 47(3), 2015.
21. Bulik-Sullivan B, **Loh P-R**, Finucane H, Ripke S, Yang J, Schizophrenia Working Group of the PGC, Patterson N, Daly M, Price A, and Neale B. LD Score regression distinguishes confounding from polygenicity in genome-wide association studies. *Nature Genetics* 47(3), 2015.
20. Price AL and **Loh P-R**. Genomic prediction and genome wide association in humans with whole genome sequence data. *Proceedings of the 10th World Congress of Genetics Applied to Livestock Production (WCGALP)*, 2014.
19. Lipson M, **Loh P-R**, Patterson N, Moorjani P, Ko Y-C, Stoneking M, Berger B, and Reich D. Reconstructing Austronesian population history in Island Southeast Asia. *Nature Communications* 5:4689, 2014.
18. Pickrell J, Patterson N, **Loh P-R**, Lipson M, Berger B, Stoneking M, Pakendorf B, and Reich D. Ancient west Eurasian ancestry in southern and eastern Africa. *Proc Nat Acad Sci* 111(7), 2014.
17. Meyer P, Cokelaer T, Chandran D, Kim K, **Loh P-R**, . . . , Timmer J, Bilal E, Sauro HM, Stolovitzky G, and Saez-Rodriguez J. Network topology and parameter estimation: from experimental design methods to gene regulatory network kinetics using a community based approach. *BMC Systems Biology* 8(1), 2014.

16. Tucker G*, **Loh P-R***, and Berger B. A sampling framework for incorporating quantitative mass spectrometry data in protein interaction analysis. *BMC Bioinformatics* 14(1), 2013.
15. Moorjani P, Thangaraj K, Patterson N, Lipson M, **Loh P-R**, Govindaraj P, Berger B, Reich D, and Singh L. Genetic evidence for recent population mixture in India. *American Journal of Human Genetics* 93(3), 2013.
14. Lipson M*, **Loh P-R***, Levin A, Reich D, Patterson N, and Berger B. Efficient moment-based inference of admixture parameters and sources of gene flow. *Molecular Biology and Evolution* 30(8), 2013.
13. **Loh P-R***, Lipson M*, Patterson N, Moorjani P, Pickrell J, Reich D, and Berger B. Inferring admixture histories of human populations using linkage disequilibrium. *Genetics* 193(4), 2013.
12. Moorjani P, Patterson N, **Loh P-R**, Lipson M, Kisfali P, Melegh B, Bonin M, Kádaši L', Rieß O, Berger B, Reich D, and Melegh B. Reconstructing Roma history from genome-wide data. *PLOS ONE* 8(3), 2013.
11. Lakhani KR, Boudreau KJ, **Loh P-R**, Backstrom L, Baldwin C, Lonstein E, Lydon M, MacCormack A, Arnaout RA, and Guinan EC. Prize-based contests can provide solutions to computational biology problems. *Nature Biotechnology* 31(2), 2013.
10. Pickrell JK, Patterson N, Barbieri C, Berthold F, Gerlach L, Lipson M, **Loh P-R**, . . . , Tishkoff S, Henn B, Stoneking M, Reich D, and Pakendorf B. The genetic prehistory of southern Africa. *Nature Communications* 3:1143, 2012. chance J, Güldemann T, Kure B, Mpoloka SW, Nakagawa H, Naumann C, Mountain J, Bustamante C, Berger B,
9. **Loh P-R***, Baym M*, and Berger B. Compressive genomics. *Nature Biotechnology* 30(7), 2012.
8. Chindelevitch L, **Loh P-R**, Enayetallah A, Berger B, and Ziemek D. Assessing statistical significance in causal graphs. *BMC Bioinformatics* 13(1), 2012.
7. **Loh P-R**, Tucker G, and Berger B. Phenotype prediction using regularized regression on genetic data in the DREAM5 Systems Genetics B Challenge. *PLOS ONE* 6(12), 2011.
6. Garcia-Reyero N, Escalon BL, **Loh P-R**, Laird JG, Kennedy AJ, Berger B, and Perkins, EJ. Assessment of chemical mixtures and groundwater effects on *Daphnia magna* transcriptomics. *Environmental Science & Technology* 46(1), 2011.
5. Gong P, **Loh P-R**, Barker ND, Tucker G, Wang N, Zhang C, Escalon BL, Berger B, and Perkins EJ. Building quantitative prediction models for tissue residue of two explosives compounds in earthworms from microarray gene expression data. *Environmental Science & Technology* 46(1), 2011.

4. Demaine E, Demaine M, Hawksley A, Ito H, **Loh P-R**, Manber S, and Stephens O. Making polygons by simple folds and one straight cut. *Proceedings of the 2010 China-Japan Joint Conference on Computational Geometry, Graphs and Applications (CGGA)*, 2011.
3. **Loh P-R**, Oskooi AF, Ibanescu M, Skorobogatiy M, and Johnson SG. Fundamental relation between phase and group velocity, and application to the failure of perfectly matched layers in backward-wave structures. *Physical Review E* 79(6), 2009.
2. **Loh P-R**. Stepping to infinity along Gaussian primes. *American Mathematical Monthly* 114(2), 2007.
1. **Loh P-R** and Rhoades RC. p -adic and combinatorial properties of modular form coefficients. *International Journal of Number Theory* 2(2), 2006.

INVITED
SEMINARS

University of Michigan Genome Science Training Program	Oct 2018
23andMe Research Seminar	Oct 2018
Harvard Medical School Department of Biomedical Informatics	Apr 2018
UCLA Computational Genomics Winter Institute	Feb 2018
MIT Bioinformatics Seminar	Feb 2018
Broad Institute Models, Inference & Algorithms Seminar	Feb 2018
Brigham and Women's Hospital Channing Division of Network Medicine	Nov 2017
Princeton Department of Computer Science	Apr 2017
Broad Institute Special Seminar	Apr 2017
Boston Children's Hospital Division of Genetics & Genomics	Mar 2017
Dana-Farber Cancer Institute Center for Cancer Genome Discovery	Mar 2017
Princeton Lewis-Sigler Institute for Integrative Genomics	Mar 2017
Brigham and Women's Hospital Division of Genetics	Mar 2017
Harvard Medical School Department of Biomedical Informatics	Feb 2017
MIT Department of Mathematics	Feb 2017
Stanford Department of Statistics	Jan 2017
Broad Institute Models, Inference & Algorithms Seminar	Mar 2016
University of Pennsylvania MathBio Seminar	Feb 2016
MIT Bioinformatics Seminar	Feb 2016
MIT Bioinformatics Seminar	Feb 2015
University of Chicago Department of Statistics	May 2014
Harvard T.H. Chan School of Public Health Department of Epidemiology	Jan 2013
UCSF Institute for Human Genetics	Jan 2013
UCLA Bioinformatics Program	Jan 2013
UC Berkeley Center for Theoretical Evolutionary Genomics	Nov 2012

CONFERENCE
TALKS

Mosaic chromosomal alterations increase proliferative loads from rare coding variants and common polygenic risk. *68th Annual Meeting of the American Society of Human Genetics*, San Diego, CA, Oct 17, 2018.

An atlas of 8,342 mosaic structural variants reveals strong inherited drivers of clonal hematopoiesis. Plenary talk at *67th Annual Meeting of the American Society of Human Ge-*

netics, Orlando, FL, Oct 17, 2017.

Contrasting regional architectures of schizophrenia and other complex diseases using fast variance components analysis. *65th Annual Meeting of the American Society of Human Genetics*, Baltimore, MD, Oct 7, 2015.

Efficient Bayesian mixed model analysis increases association power in large cohorts. *64th Annual Meeting of the American Society of Human Genetics*, San Diego, CA, Oct 20, 2014.

Divide-and-conquer game tree heuristics for iterative network parameter inference. *5th Annual Joint Conference on Systems Biology, Regulatory Genomics, and Reverse Engineering Challenges*, San Francisco, CA, Nov 14, 2012.

Targeted stepwise maximum-likelihood estimation of gene regulatory network parameters. *4th Annual Joint Conference on Systems Biology, Regulatory Genomics, and Reverse Engineering Challenges*, IDIBELL, Barcelona, Spain, Oct 14, 2011.

A numerical linear algebra look at smallest singular value universality. *Householder Symposium XVIII on Numerical Linear Algebra*, Tahoe City, CA, Jun 14, 2011.

Max-correlation min-redundancy and other regression variants predict phenotype in the DREAM5 contest. *3rd Annual Joint Conference on Systems Biology, Regulatory Genomics, and Reverse Engineering Challenges*, Columbia University, New York, Nov 16, 2010.

When PML isn't P: The failure of perfectly matched layers. *Progress In Electromagnetics Research Symposium*, Cambridge, MA, Jul 5, 2010.

An NLA look at smallest singular value universality and the stochastic differential operator. *Workshop on Sparse Random Structures: Analysis and Computation*, Banff International Research Station, Alberta, Canada, Jan 28, 2010.

HONORS & AWARDS

Research

- Harvard Program in Quantitative Genomics (HSPH PQG) Stellar Abstract Award, 2018
- American Society of Human Genetics (ASHG) Charles J. Epstein Trainee Award for Excellence in Human Genetics Research, 2017
- Harvard Program in Quantitative Genomics (HSPH PQG) Stellar Abstract Award, 2016
- Probabilistic Modeling in Genomics (ProbGen) Best Poster Prize, 2016
- American Society of Human Genetics (ASHG) Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist, 2015
- American Society of Human Genetics (ASHG) Charles J. Epstein Trainee Award for Excellence in Human Genetics Research – Semifinalist, 2014
- Postdoc Travel Award, Program in Quantitative Genetics, Harvard T.H. Chan School of Public Health, 2014
- Broad Institute Next Generation Fund Award, 2017

Mathematics

- Putnam Fellow, William Lowell Putnam Mathematics Competition, 2006

- Caltech Mathematics Department Undergraduate Awards
 - Scott Russell Johnson Prize for Graduating Senior, 2007
 - Robert P. Balles Prize, 2006
 - Herbert J. Ryser Scholarship, 2005 and 2006
 - Fredrick J. Zeigler Memorial Award, 2005
 - Morgan Ward Prize, 2004 and 2005
- International Mathematical Olympiad (IMO)
 - Gold medalist and top-scorer on USA team, 2002 and 2003
 - Silver medalist, 2000

Computational Biology and Computer Science Competitions

- Dialogue for Reverse Engineering Assessments and Methods for research in computational biology (DREAM Challenges)
 - Best performer, DREAM7 Network Parameter Inference Challenge, 2012
 - Best performer, DREAM6 Model Parameter Estimation Challenge, 2011
 - Second-best performer, DREAM6 Alternative Splicing Challenge, 2011
 - Best performer, DREAM5 Systems Genetics Challenge B, 2010
- Computer Programming Competitions
 - TopCoder Marathon Match six-time winner, 2008–2010
 - ACM-ICPC World Finals Bronze Medal team member, 2007
 - TopCoder Open 2nd-place finisher, 2005
 - Google Code Jam 2nd-place finisher, 2004

Miscellaneous

- Teaching Assistant Award, Associated Students of Caltech, 2006
- Jack E. Froehlich Memorial Award, Caltech Division of Physics, Mathematics, and Astronomy, 2006
- Hixon Writing Prize, Caltech Humanities Department, 2004
- Doris S. Perpall SURF Speaking Competition Finalist, Caltech, 2003
- Lucent Global Science Scholar, 2003
- National Merit Scholar, 2003
- Robert C. Byrd Scholar, 2003

TEACHING EXPERIENCE

California Institute of Technology, Department of Mathematics

- Teaching Assistant, Linear Algebra (Math 1b–Analytic), Winter 2006
Received institute-wide teaching assistant award
- Teaching Assistant, Number Theory for Beginners (Math 7), Spring 2004

MENTORING EXPERIENCE

Ronen E. Mukamel: Instructor, Harvard Medical School (2019–)

Alison Barton: Ph.D. student, HMS Bioinformatics and Integrative Genomics (BIG) program (2018–)

Maxwell A. Sherman: Ph.D. student, MIT EECS (2018–)

Ramya Rangan: High school student, Research Science Institute at MIT (2011)

- “*De Novo* Splice Site Discovery Using RNA-Seq Data” project received Intel Science Talent Search Semifinalist, Siemens Regional Finalist, and DREAM6 Alternative Splicing Challenge Best-Performer awards

Dissertation advisory committee (DAC) service:

- Craig Bohrson, HMS BIG Ph.D. program (2018–)
- Margaux Hujoel, HSPH Biostatistics Ph.D. program (2018–)
- Tiffany Amariuta, HMS BIG Ph.D. program (2018–)
- Rebeca Borges Monroy, HMS BIG Ph.D. program (2017–)

PROFESSIONAL
EXPERIENCE

Consultant, TopCoder, Inc. and Babbage Analytics & Innovation 2013–14

Independent consultant for development of bioinformatics crowdsourcing competitions. Designed contest that produced logistic regression algorithm used by PLINK software.

Interactive Supercomputing, Waltham, MA Summer 2008

Software Engineering Intern. Implemented mathematical function optimization routines emulating the MATLAB Optimization Toolbox.

Google, Irvine, CA Summer 2007

Software Engineering Intern. Developed algorithms for audio ad forecasting.

ACADEMIC
SERVICE

Referee Service

- *Bioinformatics*
- *BMC Bioinformatics*
- *BMC Genetics*
- *eLife*
- *Genetics*
- *Genetic Epidemiology*
- *Genome Research*
- *GigaScience*
- *Nature Communications*
- *Nature Genetics*
- *New England Journal of Medicine*
- *PLOS Computational Biology*
- *PLOS Genetics*

Conference Service

- RECOMB 2019 Program Committee
- RECOMB-Genetics 2018 and 2019 Program Committee
- ISMB 2016 Program Committee, Population Genomics
- ISMB 2014 and 2015 Program Committee, Applied Bioinformatics

Seminar Organization

- Harvard T.H. Chan School of Public Health: Program in Quantitative Genetics Working Group Seminar, 2014–15