# Bogdan Pasaniuc

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## Brief Bio

I am a Professor of Genetics and Director of Center for Computational Biomedicine in the Institute of Biomedical Informatics at Perelman School of Medicine at University of Pennsylvania. I am also serving as Professor of Computational Medicine; Pathology and Laboratory Medicine; and Human Genetics at UCLA. I develop statistical and computational methods to understand the genetic basis of disease, focusing on under-represented populations, integrative genomics, and biobank studies. My group develops innovative ML/AI methods to integrate genetics with multi-omic profiles (e.g., epigenetic/transcriptomic) and electronic health records to identify causal genes and pathways for human diseases. My group introduced transcriptome-wide association studies (TWAS) using predicted gene expression as a principled approach to identify disease genes for many traits such as Schizophrenia, Ovarian Cancer and Prostate Cancer. I have a long-standing interest in precision health using genomics to predict health outcomes; to stratify patients based on their genetic profiles; to identify undiagnosed rare diseases; and to translate computational algorithms to the clinic. I have a long-standing interest in the training the next generation of genomic and biomedical scientists, serving as PI of various NIH-funded training programs such as the NIH/NLM-T15 training program Biomedical Data Science Training Program for Precision Health Equity at UCLA.

## Positions

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| 2024 - | Professor of Genetics, Perelman School of Medicine, University of Pennsylvania, PA |
| 2024 - | Director, Center for Computational Biomedicine, Institute for Biomedical Informatics, University of Pennsylvania, PA |
| 2024 - | Member External Advisory Committee, Pacific Center for Genome Research, University of Hawaii Cancer Center, University of Hawaii, HI |
| 2022 - | Tenured Member, Genetics of Health and Disease Study Section, Center for Scientific Review, National Institutes of Health |
| 2023 - | Professor of Computational Medicine; Human Genetics; Pathology and Laboratory Medicine, David Geffen School of Medicine, UCLA |
| 2023 - 2024 | Director, Translational Polygenics for Health Equity (TransPHer), UCLA |
| 2022 - 2024 | Vice Chair, Department of Computational Medicine, David Geffen School of Medicine, UCLA |
| 2021 - 2024 | Associate Director, Population Genetics, Institute for Precision Health, UCLA |
| 2018 - 2023 | Associate Professor of Computational Medicine; Human Genetics; Pathology and Laboratory Medicine, David Geffen School of Medicine, UCLA |
| 2018 - 2022 | Associate Director, Bioinformatics Inter-departmental PhD program, UCLA |
| 2012 - 2018 | Assistant Professor of Pathology and Laboratory Medicine; Human Genetics, Geffen School of Medicine, UCLA |

## Education

2010 - 2012 Postdoctoral Fellow, Harvard School of Public Health and Broad Institute of Harvard and MIT

2008 - 2010 Postdoctoral Fellow, Algorithms Group, International Computer Science Institute, UC Berkeley

2004 - 2008 Ph.D. in Computer Science and Bioinformatics, University of Connecticut

1999 - 2003 B.Sc. in Computer Science, "A. I. Cuza" University of Iaşi, Iaşi, Romania

## Honors and Fellowships

- *2025 Nathan Kaufman Timely Topics Lecture* United States and Canadian Academy of Pathology (USCAP) 114th annual meeting, Boston 2025.
- *C.W. Cotterman Award* for the top trainee paper in Am J Hum Genet in 2015.
- *Ian Lawson Van Toch Memorial Award Best Student Paper Award*, 23rd Annual International Conference on Intelligent Systems for Molecular Biology, ISMB 2015.
- *STOP CANCER I.C.O.N. Seed Award* , Johnson Comprehensive Cancer Center 2014
- *Stellar Abstract Award*, 6th Annual Program in Quantitative Genetics Conference, Harvard School of Public Health, Boston, 2012
- *Charles J. Epstein Trainee Semifinalist,* American Society of Human Genetics, San Francisco, 2012
- *Best Poster Award,* 4th Int. Symposium on Bioinformatics Research and Applications, Atlanta, 2008
- *Summer Institute in Statistical Genetics Scholarship Award,* Department of Biostatistics, University of Washington, Seattle, 2007
- *Doctoral dissertation and pre-doctoral Fellowships,* University of Connecticut, 2006, 2007, 2008
- *Travel Fellowship,* Genetics of Complex Human Diseases Course, Cold Spring Harbor Laboratory, 2006
- *ERASMUS Fellowship,* Escuela Técnica Superior de Ingeniería Informática, University of Granada, Spain, 2003
- *Certificate of Distinction,* Canadian Euclid Mathematics Contest (1998), American High School Mathematics Examination (1999), American Invitational Mathematics Examination (1999)

## Representative Research Publications

- *Calibrated prediction intervals for polygenic scores across diverse contexts.*
  Hou K, Xu Z, Ding Y, Mandla R, Shi Z, Boulier K, Harpak A, Pasaniuc B. **Nat Genet.** 2024 Jul;56(7):1386-1396. doi: 10.1038/s41588-024-01792-w. Epub 2024 Jun 17. PMID: 38886587; PMCID: PMC11465192.
- *Polygenic scoring accuracy varies across the genetic ancestry continuum.*
  Ding Y, Hou K, Xu Z, Pimplaskar A, Petter E, Boulier K, Privé F, Vilhjálmsson BJ, Olde Loohuis LM, Pasaniuc B. **Nature.** 2023 Jun;618(7966):774-781. doi: 10.1038/s41586-023-06079-4. Epub 2023 May 17. PMID: 37198491
- *Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals.*
  Hou K, Ding Y, Xu X, Wu Y, Bhattacharya A, Mester R, Belbin G, Conti D, Darst BF, Fornage, Gignoux C, Guo X, Haiman X, Kenny E, Kim M, Kooperberg C, Lange L, Manichaikul A, North K, Nudelman N, Peters U, Rasmussen-Torvik L, Rich S, Rotter J, Wheeler H, Zhou Y, Sankararaman S, Pasaniuc B. **Nat Genet.** 2023 Apr;55(4):549-558. doi: 10.1038/s41588-023-01338-6. Epub 2023 Mar 20. PMID: 36941441
- *The UCLA ATLAS Community Health Initiative: Promoting precision health research in a diverse biobank.*
  Johnson R, Ding Y, Bhattacharya A, Knyazev S, Chiu A, Lajonchere C, Geschwind DH, Pasaniuc B. **Cell Genom.** 2023 Jan 11;3(1):100243. doi: 10.1016/j.xgen.2022.100243. eCollection 2023 Jan 11. PMID: 36777178

- *Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification.* Ding Y, Hou K, Burch KS, Lapinska S, Prive F, Vilhjalmsson B, Sankararaman S, Pasaniuc B. **Nat Genet.** 2022 Jan;54(1):30-39. doi: 10.1038/s41588-021-00961-5. Epub 2021 Dec 20. PMID: 34931067; PMCID: PMC8758557.
- *Accurate estimation of SNP-heritability from biobank-scale data irrespective of genetic architecture.* Hou K, Burch KS, Majumdar A, Shi H, Mancuso N, Wu Y, Sankararaman S, Pasaniuc B. **Nat Genet.** 2019 Aug;51(8):1244-1251. doi: 10.1038/s41588-019-0465-0. Epub 2019 Jul 29.
- *Probabilistic fine-mapping of transcriptome-wide association studies.* Mancuso N, Kichaev G, Shi H, Freund M, Gusev A, Pasaniuc B. **Nat Genet.** 2019 Apr;51(4):675-682. doi: 10.1038/s41588-019-0367-1. Epub 2019 Mar 29. PMID: 30926970
- *Integrative approaches for large-scale transcriptome-wide association studies.* Gusev A, Ko A, Shi H, Bhatia G, Chung W, Penninx BW, Jansen R, de Geus EJ, Boomsma DI, Wright FA, Sullivan PF, Nikkola E, Alvarez M, Civelek M, Lusis AJ, Lehtimki T, Raitoharju E, Kahanen M, Seppaa I, Raitakari OT, Kuusisto J, Laakso M, Price AL, Pajukanta P Pasaniuc B. **Nat Genet.** 2016 Mar;48(3):245-52. doi: 10.1038/ng.3506. Epub 2016 Feb 8. PMID: 26854917.
- *Contrasting the genetic architecture of 30 complex traits from summary association data.* Shi H, Kichaev G, Pasaniuc B. **Am J Hum Genet.** 2016 Jul 7;99(1):139-53. doi: 10.1016/j.ajhg.2016.05.013. PMID: 27346688.
- *Leveraging functional annotation data in trans-ethnic fine-mapping studies.* Kichaev G, Pasaniuc B. **Am J Hum Genet.** 2015 Aug 6;97(2):260-71. doi: 10.1016/j.ajhg.2015.06.007. Epub 2015 Jul 16. PMID: 26189819.
- *Extremely low-coverage sequencing and imputation increases power for genome-wide association studies.* Pasaniuc B, Rohland N, McLaren PJ, Garimella K, Zaitlen N, Li, H, Gupta N, Neale B, Daly M, Sklar P, Sullivan P, Bergen S, Moran J, Hultman C, Lichtenstein P, Magnusson P, Purcell S, Haas DW, Liang L, Sunyaev S, Patterson N, de Bakker PIW, Reich D, Price AL. **Nat Genet**, 2012 May 20;44(6):631-5. doi: 10.1038/ng.2283.

## Funding

- Principal Investigator
  - T15-LM013976: *Biomedical Data Science Training Program for Precision Health Equity*, 2022-2027
  - U01-HG011715: *PRS Center for Admixed Populations and Health Equity (CAPE)*, 2021-2026
  - R01-AI153827: *Collaborative Multi-site Project to Speed the Identification and Management of Rare Genetic Immune Diseases*, 2021-2026
  - R01-CA251555: *Elucidation of the genetic mechanisms driving prostate tumorigenesis through integrative computational and functional approaches*, 2021-2026
  - R01-HG009120: *Integrative approaches for mapping the genetic risk of complex traits*, 2017-2022
  - R01-MH115676: *Joint genomic and statistical analyses of schizophrenia and bipolar to decipher genetic susceptibility*, 2018-2023
  - R21-CA220078: *The Role of Splice Quantitative Traits in Ovarian Cancer Pathogenesis*, 2017-2019
  - R03-CA162200: *Metrics and methods for cross-population fine mapping*, 2012-2014
- Co-Investigator
  - U19-AI166059: *Machine-assisted Approach to Accelerating the Diagnosis of Inborn Errors of Immunity*, 2022-2026
  - R01-CA244670: *Integration of Genetic, Gene Expression and Environmental Data to Inform Biological Basis of Mammographic Density*, 2021-2025
  - R01-HG006399: *Leveraging Functional Data to Predict Disease Risk in Multi-Ethnic Populations*, 2021-2026

- R01-MH125252: *Single-Cell Multi-Omic Approaches to Mechanistically Characterize Psychiatric Disorder Risk Loci in the Human Brain*, 2021-2026
- R01-HL151152: *Polygenic Risk Scores for Diverse populations Bridging Research and Clinical Care*, 2020-2024
- R01-MH123922: *Population-level and mechanistic dissection of 17Q21 Structural variant association with psychiatric traits*, 2020-2025
- R01-CA194393: *Leveraging cross-cancer shared heritability to better understand the genetic architecture of cancer*, 2020-2024
- R01-HG010505: *Methods for genomics analysis in heterogeneous tissues.* 2019-2023
- R01-MH121521: *Isoform-level probabilistic transcriptome-wide association to uncover neurogenetic mechanisms underlying complex psychiatric traits*, 2018-2023
- R01-MH100027: *Autism Genetics, Phase II: Increasing Representation of Human Diversity*, 2018-2023
- R01-AC058484: *Genetics of CSF metabolites in Alzheimer Disease and other Brain Disorders*, 2017-2022
- R01-HG006399: *Methods for Disease Mapping in Multi-ethnic Populations*, 2017-2021
- R01-MH107250: *Genetic Risk for Developmental Expression of Neuropsychiatric Intermediate Traits*, 2015-2018
- R01-HL095056: *Genetics of High Serum Triglycerides and Related Metabolic Traits in Mexicans*, 2015-2020
- U01-CA194393: *Quantifying and Characterizing the shared genetic contribution to common cancers*, 2015-2019
- U01-CA188392: *Imputation-based Approach to Identify Low Frequency Variants in Prostate Cancer*, 2014-2017
- R21-CA182821: *Prioritizing Follow-up of GWAS Loci Using Genetic and Functional Annotation Data*, 2014-2016
- R01-GM053275: *Statistical methods for gene mapping*, 2013-2022

## Peer-reviewed Journal Publications

148. *The Germline and Somatic Origins of Prostate Cancer Heterogeneity.*
Yamaguchi TN, Houlahan KE, Zhu H, Kurganovs N, Livingstone J, Fox NS, Yuan J, Sietsma Penington J, Jung CH, Schwarz T, Jaratlerdsiri W, van Riet J, Georgeson P, Mangiola S, Taraszka K, Lesurf R, Jiang J, Chow K, Heisler LE, Shiah YJ, Ramanand SG, Clarkson MJ, Nguyen A, Espiritu SMG, Stuchbery R, Jovelin R, HuangV, Bell C, O'Connor E, McCoy PJ, Lalansingh CM, Cmero M, Salcedo A, Chan EKF, Liu LY, Stricker PD, Bhandari V, Bornman RMS, Sendorek DH, Lonie A, Prokopec SD, Fraser M, Peters JS, Foucal A, Mutambirwa SBA, Mcintosh L, Orain M, Wakefield M, Picard V, Park DJ, Hovington H, Kerger M, Bergeron A, Sabelnykova V, Seo JH, Pomerantz MM, Zaitlen N, Waszak SM, Gusev A, Lacombe L, Fradet Y, Ryan A, Kishan AU, Lolkema MP, Weischenfeldt J, Têtu B, Costello AJ, Hayes VM, Hung RJ, He HH, McPherson JD, Pasaniuc B, van der Kwast T, Papenfuss AT, Freedman ML, Pope BJ, Bristow RG, Mani RS, Corcoran NM, Reimand J, Hovens CM, Boutros PC. **Cancer Discov.** 2025 Feb 13. doi: 10.1158/2159-8290.CD-23-0882. Epub ahead of print. PMID: 39945744.

147. *The PRIMED Consortium: Reducing disparities in polygenic risk assessment.*
Kullo IJ, Conomos MP, Nelson SC, Adebamowo SN, Choudhury A, Conti D, Fullerton SM, Gogarten SM, Heavner B, Hornsby WE, Kenny EE, Khan A, Khera AV, Li Y, Martin I, Mercader JM, Ng M, Raffield LM, Reiner A, Rowley R, Schaid D, Stilp A, Wiley K, Wilson R, Witte JS, Natarajan P, Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium. **Am J Hum Genet.** 2024 Dec 5;111(12):2594-2606. doi: 10.1016/j.ajhg.2024.10.010. Epub 2024 Nov 18. PMID: 39561770; PMCID: PMC11639095.

146. *Evaluating Performance and Agreement of Coronary Heart Disease Polygenic Risk Scores.*
Abramowitz SA, Boulier K, Keat K, Cardone KM, Shivakumar M, DePaolo J, Judy R, Bermudez F, Mimouni N, Neylan C, Kim D, Rader DJ, Ritchie MD, Voight BF, Pasaniuc B, Levin MG, Damrauer SM; Penn Medicine BioBank. **JAMA.** 2025 Jan 7;333(1):60-70. doi: 10.1001/jama.2024.23784. PMID: 39549270; PMCID: PMC11569413.

145. *Advancing Mental Health Research Through Strategic Integration of Transdiagnostic Dimensions and Genomics.*
Doyle AE, Bearden CE, Gur RE, Ledbetter DH, Martin CL, McCoy TH Jr, Pasaniuc B, Perlis RH, Smoller JW, Davis LK. **Biol Psychiatry.** 2025 Mar 1;97(5):450-460. doi: 10.1016/j.biopsych.2024.10.006. Epub 2024 Oct 16. PMID: 39424167.

144. *Temporally distinct 3D multi-omic dynamics in the developing human brain.*
Heffel MG, Zhou J, Zhang Y, Lee DS, Hou K, Pastor-Alonso O, Abuhanna KD, Galasso J, Kern C, Tai CY, Garcia-Padilla C, Nafisi M, Zhou Y, Schmitt AD, Li T, Haeussler M, Wick B, Zhang MJ, Xie F, Ziffra RS, Mukamel EA, Eskin E, Nowakowski, TJ, Dixon JR, Pasaniuc B, Ecker JR, Zhu Q, Bintu B, Paredes MF, Luo C. **Nature.** 2024 Nov;635(8038):481-489. doi: 10.1038/s41586-024-08030-7. Epub 2024 Oct 9. PMID: 39385032; PMCID: PMC11560841.

143. *Improving genetic risk modeling of dementia from real-world data in underrepresented populations.*
Fu M, Valiente-Banuet L, Wadhwa SS, Pasaniuc B, Vossel K, Chang TS. **Commun Biol.** 2024 Aug 25;7(1):1049. doi: 10.1038/s42003-024-06742-0. PMID: 39183196; PMCID: PMC11345412.

142. *Splicing-specific transcriptome-wide association uncovers genetic mechanisms for schizophrenia.*
Hervoso JL, Amoah K, Dodson J, Choudhury M, Bhattacharya A, Quinones-Valdez G, Pasaniuc B*, Xiao X*. **Am J Hum Genet.** 2024 Aug 8;111(8):1573-1587. doi: 10.1016/j.ajhg.2024.06.001. Epub 2024 Jun 25. PMID: 38925119; PMCID: PMC11339621.

141. *Calibrated prediction intervals for polygenic scores across diverse contexts.*
Hou K, Xu Z, Ding Y, Mandla R, Shi Z, Boulier K, Harpak A, Pasaniuc B. **Nat Genet.** 2024 Jul;56(7):1386-1396. doi: 10.1038/s41588-024-01792-w. Epub 2024 Jun 17. PMID: 38886587; PMCID: PMC11465192.

140. *INVENT Consortium. Multi-ancestry polygenic risk scores for venous thromboembolism.*
Jee YH, Thibord F, Dominguez A, Sept C, Boulier K, Venkateswaran V, Ding Y, Cherlin T, Verma SS, Faro VL, Bartz TM, Boland A, Brody JA, Deleuze JF, Emmerich J, Germain M, Johnson AD, Kooperberg C, Morange PE, Pankratz N, Psaty BM, Reiner AP, Smadja DM, Sitlani CM, Suchon P, Tang W, Trégouët DA, Zöllner S, Pasaniuc B, Damrauer SM, Sanna S, Snieder H; Lifelines Cohort Study; Kabrhel C, Smith NL, Kraft P; **Hum Mol Genet.** 2024 Sep 3;33(18):1584-1591. doi: 10.1093/hmg/ddae097. PMID: 38879759; PMCID: PMC11373328.

139. *Cross-ancestry atlas of gene, isoform, and splicing regulation in the developing human brain.*
Wen C, Margolis M, Dai R, Zhang P, Przytycki PF, Vo DD, Bhattacharya A, Matoba N, Tang M, Jiao C, Kim M, Tsai E, Hoh C, Aygün N, Walker RL, Chatzinakos C, Clarke D, Pratt H; PsychENCODE Consortium†; Peters MA, Gerstein M, Daskalakis NP, Weng Z, Jaffe AE, Kleinman JE, Hyde TM, Weinberger DR, Bray NJ, Sestan N, Geschwind DH, Roeder K, Gusev A, Pasaniuc B, Stein JL, Love MI, Pollard KS, Liu C, Gandal MJ, PsychENCODE Consortium. **Science.** 2024 May 24;384(6698):eadh0829. doi: 10.1126/science.adh0829. Epub 2024 May 24. PMID: 38781368.

138. *Developmental isoform diversity in the human neocortex informs neuropsychiatric risk mechanisms.*
Patowary A, Zhang P, Jops C, Vuong CK, Ge X, Hou K, Kim M, Gong N, Margolis M, Vo D, Wang X, Liu C, Pasaniuc B, Li JJ, Gandal MJ, de la Torre-Ubieta L. **Science.** 2024 May 24;384(6698):eadh7688. doi: 10.1126/science.adh7688. Epub 2024 May 24. PMID: 38781356.

137. *Brain cell-type shifts in Alzheimer's disease, autism, and schizophrenia interrogated using methylomics and genetics.*
Yap CX, Vo DD, Heffel MG, Bhattacharya A, Wen C, Yang Y, Kemper KE, Zeng J, Zheng Z, Zhu Z, Hannon E, Vellame DS, Franklin A, Caggiano C, Wamsley B, Geschwind DH, Zaitlen N, Gusev A, Pasaniuc B, Mill J, Luo C, Gandal MJ. **Sci Adv.** 2024 May 24;10(21):eadn7655. doi: 10.1126/sciadv.adn7655. Epub 2024 May 23. PMID: 38781333; PMCID: PMC11114225.

136. *Generalizability of PGS313 for breast cancer risk in a Los Angeles biobank.*
Shang H, Ding Y, Venkateswaran V, Boulier K, Kathuria-Prakash N, Malidarreh PB, Luber JM, Pasaniuc B. **HGG Adv.** 2024 Jul 18;5(3):100302. doi: 10.1016/j.xhgg.2024.100302. Epub 2024 May 3. PMID: 38704641; PMCID: PMC11137525.

135. *Electronic health record signatures identify undiagnosed patients with common variable immunodeficiency disease.*
Johnson R, Stephens AV, Mester R, Knyazev S, Kohn LA, Freund MK, Bondhus L, Hill BL, Schwarz T, Zaitlen N, Arboleda VA, A Bastarache L, Pasaniuc B*, Butte MJ*. **Sci Transl Med.** 2024 May;16(745):eade4510. doi: 10.1126/scitranslmed.ade4510. Epub 2024 May 1. PMID: 38691621; PMCID: PMC11402387.

134. *Admix-kit: an integrated toolkit and pipeline for genetic analyses of admixed populations.*
Hou K, Gogarten S, Kim J, Hua X, Dias JA, Sun Q, Wang Y, Tan T; Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium Methods Working Group; Atkinson EG, Martin A, Shortt J, Hirbo J, Li Y, Pasaniuc B, Zhang H. **Bioinformatics**. 2024 Mar 29;40(4):btae148. doi: 10.1093/bioinformatics/btae148. PMID: 38490256; PMCID: PMC10980565.

133. *Cell-type deconvolution of bulk-blood RNA-seq reveals biological insights into neuropsychiatric disorders.*
Boltz T, Schwarz T, Bot M, Hou K, Caggiano C, Lapinska S, Duan C, Boks MP, Kahn RS, Zaitlen N, Pasaniuc B, Ophoff R. **Am J Hum Genet.** 2024 Feb 1;111(2):323-337. doi: 10.1016/j.ajhg.2023.12.018. PMID: 38306997; PMCID: PMC10870131.

132. *Polygenic scores for tobacco use provide insights into systemic health risks in a diverse EHR-linked biobank in Los Angeles.*
Venkateswaran V, Boulier K, Ding Y, Johnson R, Bhattacharya A, Pasaniuc B. **Transl Psychiatry.** 2024 Jan 18;14(1):38. doi: 10.1038/s41398-024-02743-z. PMID: 38238290; PMCID: PMC10796315.

131. *Isoform-level transcriptome-wide association uncovers genetic risk mechanisms for neuropsychiatric disorders in the human brain.*
Bhattacharya A, Vo DD, Jops C, Kim M, Wen C, Hervoso JL, Pasaniuc B*, Gandal MJ*. **Nat Genet.** 2023 Dec;55(12):2117-2128. doi: 10.1038/s41588-023-01560-2. Epub 2023 Nov 30. PMID: 38036788; PMCID: PMC10703692.

130. *Inferring disease architecture and predictive ability with LDpred2-auto.*
Privé F, Albiñana C, Arbel J, Pasaniuc B, Vilhjálmsson BJ. **Am J Hum Genet.** 2023 Dec 7;110(12):2042-2055. doi: 10.1016/j.ajhg.2023.10.010. Epub 2023 Nov 8. PMID: 37944514; PMCID: PMC10716363.

129. *A second update on mapping the human genetic architecture of COVID-19.*
COVID-19 Host Genetics Initiative. **Nature**. 2023 Sep;621(7977):E7-E26. doi: 10.1038/s41586-023-06355-3. Epub 2023 Sep 6. PMID: 37674002

128. *A Bayesian method for estimating gene-level polygenicity under the framework of transcriptome-wide association study.*
Majumdar A, Pasaniuc B. Stat Med. 2023 Aug 29. doi: 10.1002/sim.9892. Online ahead of print. PMID: 37643728

127. *Principles and methods for transferring polygenic risk scores across global populations.*
Kachuri L, Chatterjee N, Hirbo J, Schaid DJ, Martin I, Kullo IJ, Kenny EE, Pasaniuc B; Polygenic Risk Methods in Diverse Populations (PRIMED) Consortium Methods Working Group; Witte JS, Ge T. **Nat Rev Genet**. 2023 Aug 24. doi: 10.1038/s41576-023-00637-2. Online ahead of print. PMID: 37620596

126. *Genotype error due to low-coverage sequencing induces uncertainty in polygenic scoring.*
Petter E, Ding Y, Hou K, Bhattacharya A, Gusev A, Zaitlen N, Pasaniuc B. **Am J Hum Genet**. 2023 Aug 3;110(8):1319-1329. doi: 10.1016/j.ajhg.2023.06.015. Epub 2023 Jul 24. PMID: 37490908

125. *Disease risk and healthcare utilization among ancestrally diverse groups in the Los Angeles region.*
Caggiano C, Boudaie A, Shemirani R, Mefford J, Petter E, Chiu A, Ercelen D, He R, Tward D, Paul KC, Chang TS, Pasaniuc B, Kenny EE, Shortt JA, Gignoux CR, Balliu B, Arboleda VA, Belbin G, Zaitlen N. **Nat Med**. 2023 Jul;29(7):1845-1856. doi: 10.1038/s41591-023-02425-1. Epub 2023 Jul 18. PMID: 37464048

124. *Impact of cross-ancestry genetic architecture on GWASs in admixed populations.*
Mester R, Hou K, Ding Y, Meeks G, Burch KS, Bhattacharya A, Henn BM, Pasaniuc B. **Am J Hum Genet**. 2023 Jun 1;110(6):927-939. doi: 10.1016/j.ajhg.2023.05.001. Epub 2023 May 23. PMID: 37224807

123. *Polygenic scoring accuracy varies across the genetic ancestry continuum.*
Ding Y, Hou K, Xu Z, Pimplaskar A, Petter E, Boulier K, Privé F, Vilhjálmsson BJ, Olde Loohuis

LM, Pasaniuc B. **Nature.** 2023 Jun;618(7966):774-781. doi: 10.1038/s41586-023-06079-4. Epub 2023 May 17. PMID: 37198491

122. *twassim, a Python-based tool for simulation and power analysis of transcriptome-wide association analysis.*
Wang X, Lu Z, Bhattacharya A, Pasaniuc B, Mancuso N. **Bioinformatics**. 2023 May 4;39(5):btad288. doi: 10.1093/bioinformatics/btad288. PMID: 37099718

121. *Causal effects on complex traits are similar across segments of different continental ancestries within admixed individuals.*
Hou K, Ding Y, Xu X, Wu Y, Bhattacharya A, Mester R, Belbin G, Conti D, Darst BF, Fornage, Gignoux C, Guo X, Haiman X, Kenny E, Kim M, Kooperberg C, Lange L, Manichaikul A, North K, Nudelman N, Peters U, Rasmussen-Torvik L, Rich S, Rotter J, Wheeler H, Zhou Y, Sankararaman S, Pasaniuc B. **Nat Genet.** 2023 Apr;55(4):549-558. doi: 10.1038/s41588-023-01338-6. Epub 2023 Mar 20. PMID: 36941441

120. *The UCLA ATLAS Community Health Initiative: Promoting precision health research in a diverse biobank.*
Johnson R, Ding Y, Bhattacharya A, Knyazev S, Chiu A, Lajonchere C, Geschwind DH, Pasaniuc B. **Cell Genom.** 2023 Jan 11;3(1):100243. doi: 10.1016/j.xgen.2022.100243. eCollection 2023 Jan 11. PMID: 36777178

119. *Optimized high-throughput screening of non-coding variants identified from genome-wide association studies.*
Morova T, Ding Y, Huang CF, Sar F, Schwarz T, Giambartolomei C, Baca SC, Grishin D, Hach F, Gusev A, Freedman ML, Pasaniuc B, Lack NA. **Nucleic Acids Res.** 2022 Dec 22:gkac1198. doi: 10.1093/nar/gkac1198. Online ahead of print. PMID: 36546757

118. *Best practices for multi-ancestry, meta-analytic transcriptome-wide association studies: Lessons from the Global Biobank Meta-analysis Initiative.*
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15. *Admixture Mapping Identifies Loci on 6q25 and 11p15 Associated with Breast Cancer Risk in US Latinas.* Fejerman L, Chen G, Huntsman S, Hu D, Williams A, Pasaniuc B, John E, Via M, Gignoux C, Ingles S, Marchand L, Kolonel L, Torres-Meja G, Parez-Stable E, Burchard EG, Eng C, Henderson BE, Haiman C, Ziv E. . **Human Molecular Genetics** 2012 Jan 19. doi:10.1093/hmg/ddr617.

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11. *Combining effects from rare and common genetic variants in an exome-wide association study of sequence data.* Aschard H, Qiu W, Pasaniuc B, Zaitlen N, Cho M and Carey V. **BMC Proceedings** 2011, 5(Suppl 9):S44

10. *Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal.* Wang J, Geesman G, Hostikka S, Atallah M, Blackwell B, Lee E, Cook P, Pasaniuc B, Shariat G, Halperin E, Dobke M, Rosenfield MG, Jordan IK, Lunyak VV. **Cell Cycle.** 2011, Sept 1; 10:17

9. *Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments.* Pasaniuc B, Zaitlen N, Halperin E. **Journal of Computational Biology.** 2011 Mar;18(3):459-68.
8. *Genotyping common and rare variation using overlapping pool sequencing.* He D, Zaitlen N, Pasaniuc B, Eskin E, Halperin E. **BMC Bioinformatics.** 2011, 12(Suppl 6):S2
7. *Optimal Testing of Digital Microfluidic Biochips.* Pasaniuc B, Garfinkel R, Mandoiu I, Zelikovsky A. **INFORMS Journal on computing.** 2011.
6. *A Generic Coalescent-based Framework for the Selection of a Reference Panel for Imputation.* Pasaniuc B, Avinery, R, Gur T, Skibola CF, Brooks PM, Halperin E. **Genetic Epidemiology.** 2010 Dec;34(8):773-82.
5. *Leveraging genetic variability across populations for the identification of causal variants.* Zaitlen N*, Pasaniuc B*, Gur T, Ziv E, Halperin E. **Am J Hum Genet.** 2010 Jan;86(1):23-33.
4. *Imputation-Based Local Ancestry Inference in Admixed Populations.* Pasaniuc B, Kennedy J, Mandoiu I. **Proc. 5th International Symposium on Bioinformatics Research and Applications**, pp. 221-233, 2009.
3. *Inference of locus-specific ancestry in closely related populations.* Pasaniuc B*, Sankararaman S*, Kimmel G, Halperin E. **Bioinformatics** (special edition of ISMB 2009). 2009 Jun 15;25(12):i213-21.
2. *Genotype error detection using Hidden Markov Models of haplotype diversity.* Kennedy J, Mandoiu I, Pasaniuc B. **Journal of Computational Biology.** 2008 Nov;15(9):1155-71.
1. *Highly scalable genotype phasing by entropy minimization.* Gusev A, Mandoiu II, Pasaniuc B. **IEEE/ACM Transactions on Computational Biology and Bioinformatics.** 2008 Apr-Jun;5(2):252-61. (conference version: *Highly scalable genotype phasing by entropy minimization.* Pasaniuc B, Mandoiu I. **Conf Proc IEEE Eng Med Biol Soc.** 2006;1:3482-6.)

* denotes equal contribution.

## Teaching

- Computational Methods in Genomics (HUM GEN M265/COM SCI M225/BIOINFO M265), 2016, 2017, 2018, 2019, 2020, 2021.
- Advanced Methods in Computational Biology (BIOINFO M252), 2013, 2014, 2015.
- Current Topics in Bioinformatics (HUM GEN M229S/COM SCI M229S/BIOL CH M229S), 2013, 2014, 2015.
- Advances in Human Genetics A, 2015, 2016.
- Medical population genetics and GWAS for complex diseases, H3ABioNet, University of Cape Town, South Africa, 2015.
- Bruins-In-Genomics (B.I.G.) Summer Institute, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022.
- Computational Genomics Summer Institute, 2016, 2017, 2018, 2019, 2020, 2021, 2022.
- American Association for Cancer Research (AACR): Integrative Molecular Epidemiology Workshop, 2016, 2017, 2018, 2019, 2020, 2021.
- Advanced Gene Mapping Course, Rockefeller University, 2020.
- Statistical fine-mapping of GWAS signals, Karolinska Institute, 2022.
- Welcome Trust's Advanced Courses: Genetic Analysis of Mendelian and Complex Disorders, 2022.

## Trainees

- Postdoctoral fellowss
  - Igor Mandric, 2018-2020, currently data scientist at Illumina, Inc.
  - Arunabha Majumdar, 2018-2020, currently Assistant Professor in the Department of Mathematics at Indian Institute of Technology (IIT), Hyderabad.
  - Yan Guo, 2018-2019, currently Professor at Xi'an Jiaotong University in China.

  - Claudia Giambartolomei, 2016-2019, currently Marie Curie Fellow in Genoa, Italy.
  - Nicholas Mancuso, 2016-2019, currently Assistant Professor at USC.
  - Valerie Arboleda, 2016-2017, currently Associate Professor at UCLA.
  - Steven Gazal, visiting postdoctoral researcher (2016), currently Assistant Professor at USC.
  - Alexander Gusev, visiting postdoctoral researcher (2015), currently Associate Professor at Harvard Medical School.

- Chair of doctoral committee
  - Alex Flynn-Carroll, Bioinformatics, UCLA, 2026 (expected).
  - Ella Petter, Computer Science, UCLA, 2025 (expected).
  - Rachel Mester, Biomathematics, UCLA, 2025 (expected).
  - Kangcheng Hou, Bioinformatics, UCLA, 2024 (expected).
  - Jonatan Hervoso, Bioinformatics, UCLA, 2024 (expected).
  - Kristin Boulier, Bioinformatics, UCLA, 2024 (expected).
  - Ruth Johnson, Computer Science, UCLA, 2023 (expected).
  - Yi Ding, Bioinformatics, UCLA, 2023 (expected).
  - Vidhya Venkaterasewan, UCLA, 2023.
  - Tommer Schwarz, Bioinformatics, UCLA, 2022.
  - Kathryn Burch, Bioinformatics, UCLA, 2021.
  - Malika Kumar, Genetics and Genomics, UCLA, 2020.
  - Megan Roytman, Bioinformatics, UCLA, 2018.
  - Gleb Kichaev, Bioinformatics, UCLA, 2018.
  - Huwenbo Shi, Bioinformatics, UCLA, 2018.
  - Robert Brown, Bioinformatics, UCLA, 2017.
- Member of doctoral committee
  - Ekaterina Maksimova, Institute of Science and Technology Austria, 2025 (expected).
  - Ekaterina Maksimova, Institute of Science and Technology Austria, 2025 (expected).
  - Dennis Grishin, Harvard Medical School, 2022.
  - Alec Chiu, Bioinformatics, UCLA, 2022.
  - Mike Thompson, Bioinformatics, UCLA, 2022.
  - Minsoo Kim, Bioinformatics, UCLA, 2022.
  - Lingyu Zhang, Bioinformatics, UCLA, 2021.
  - Jennifer Zou, Computer Science, UCLA, 2021.
  - Yonatan Cooper, Bioinformatics, UCLA, 2021.
  - James Boocock, Genetics and Genomics, UCLA, 2021.
  - Helian Feng, Harvard School of Public Health, 2020.
  - Jillian De Bree, Neuroscience, UCLA, 2020.
  - Adriana Arneson, Bioinformatics, UCLA, 2020.
  - Ivette Zelaya, Bioinformatics, UCLA, 2019.
  - Chris Hartl, Bioinformatics, UCLA, 2019.
  - Kristina Garske, Genetics and Genomics, UCLA, 2019.
  - Liangke Gou, Genetics and Genomics, UCLA, 2019.
  - Rebecca Walker, Bioinformatics, UCLA, 2019.
  - Alden Huang, Bioinformatics, UCLA, 2018.
  - Farhad Hormozdiari, Computer Science, UCLA, 2015.
  - Jong Wha Joo, Computer Science, UCLA, 2015.
  - Wen-Yun Yang, Computer Science, UCLA, 2013.

Last Updated February 2025.