Bogdan Pasaniuc

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Vice Chair, Department of Computational Medicine
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Brief Bio

I am an associate professor of Computational Medicine, Human Genetics and Pathology&Laboratory Medicine 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 developed machine learning methods to integrate epigenetic profiles within trans-ethnic studies to localize genetic variants that cause disease; more recently, 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 am actively involved in the Institute of Precision Health at UCLA that links the genetics of more than 150k patients with their electronic health record to predict health outcomes, to stratify patients based on their genetic risk to disease and to translate computational algorithms to the clinic. I main focus of research is equity and inclusion in computational methods for large-scale genomic studies.

Positions

2022 -	Vice Chair, Department of Computational Medicine, David Geffen School of Medicine, UCLA
2021 -	Associate Director, Population Genetics, Institute of Precision Health, UCLA
2018 -	Associate Professor of Computational Medicine; Human Genetics; Pathology and Laboratory Medicine, David Geffen School of Medicine, UC:LA
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; Broad Institute of Harvard and MIT, Boston MA
2008 - 2010	Postdoctoral Fellow, Algorithms Group, International Computer Science Institute, UC Berkeley, CA
2004 - 2008	Ph.D. in Computer Science and Bioinformatics, University of Connecticut, Storrs, CT
1999 - 2003	B.Sc. in Computer Science, "A. I. Cuza" University of Iaşi, Iaşi, Romania

Honors and Fellowships

- *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

- *Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes.* Burch KS, Hou K, Ding Y, Wang Y, Gazal S, Shi H, Pasaniuc B. **Am J Hum Genet.** 2022 Apr 7;109(4):692-709. doi: 10.1016/j.ajhg.2022.02.012. Epub 2022 Mar 9. PMID: 35271803; PMCID: PMC9069080.
- *Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification.* Ding Y, Hou K, Burch KS, Lapinska S, Priv F, Vilhjlmsson 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.
- *On powerful GWAS in admixed populations.* Hou K, Bhattacharya A, Mester R, Burch KS, Pasaniuc B. **Nat Genet.** 2021 Dec;53(12):1631-1633. doi: 10.1038/s41588-021-00953-5. Epub 2021 Nov 25. PMID: 34824480; PMCID: PMC8939372.
- *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, Khnen M, Sepp 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

113. *Multi-ancestry fine-mapping improves precision to identify causal genes in transcriptome-wide association studies.* Lu Z, Gopalan S, Yuan D, Conti DV, Pasaniuc B,, Gusev A, Mancuso N. **Am J Hum Genet.** 2022 Aug 4;109(8):1388-1404. doi: 10.1016/j.ajhg.2022.07.002. PMID: 35931050.

112. *Drug-induced epigenomic plasticity reprograms circadian rhythm regulation to drive prostate cancer towards androgen-independence.* Linder S, Hoogstraat M, Stelloo S, Eickhoff N, Schuurman K, de Barros H, Alkemade M, Bekers EM, Severson TM, Sanders J, Huang CF, Morova T, Altintas UB, Hoekman L, Kim Y, Baca SC, Sjostrom M, Zaalberg A, Hintzen DC, de Jong J, Kluin RJC, de Rink I, Giambartolomei C, Seo JH, Pasaniuc B,, Altelaar M, Medema RH, Feng FY, Zoubeidi A, Freedman ML, Wessels LFA, Butler LM, Lack NA, van der Poel H, Bergman AM, Zwart W. **Cancer Discov.** 2022 Jun 27:candisc.0576.2021-5-3 12:14:47.513. doi: 10.1158/2159-8290.CD-21-0576. Epub ahead of print. PMID: 35754340.

111. *Combining SNP-to-gene linking strategies to identify disease genes and assess disease omnigenicity.* Gazal S, Weissbrod O, Hormozdiari F, Dey KK, Nasser J, Jagadeesh KA, Weiner DJ, Shi H, Fulco CP, O'Connor LJ, Pasaniuc B, Engreitz JM, Price AL. **Nat Genet.** 2022 Jun;54(6):827-836. doi: 10.1038/s41588-022-01087-y. Epub 2022 Jun 6. PMID: 35668300.

110. *Powerful eQTL mapping through low-coverage RNA sequencing.* Schwarz T, Boltz T, Hou K, Bot M, Duan C, Loohuis LO, Boks MP, Kahn RS, Ophoff RA, Pasaniuc B. **HGG Adv.** 2022 Apr 2;3(3):100103. doi: 10.1016/j.xhgg.2022.100103. PMID: 35519825; PMCID: PMC9062329.

109. *Unlocking capacities of genomics for the COVID-19 response and future pandemics.* Knyazev S, Chhugani K, Sarwal V, Ayyala R, Singh H, Karthikeyan S, Deshpande D, Baykal PI, Comarova Z, Lu A, Porozov Y, Vasylyeva TI, Wertheim JO, Tierney BT, Chiu CY, Sun R, Wu A, Abedalthagafi MS, Pak VM, Nagaraj SH, Smith AL, Skums P, Pasaniuc B, Komissarov A, Mason CE, Bortz E, Lemey P, Kondrashov F, Beerenwinkel N, Lam TT, Wu NC, Zelikovsky A, Knight R, Crandall KA, Mangul S. **Nat Methods.** 2022 Apr;19(4):374-380. doi: 10.1038/s41592-022-01444-z. PMID: 35396471.

108. *Phenome-Wide Association Study of Polygenic Risk Score for Alzheimer's Disease in Electronic Health Records.* Fu M; UCLA Precision Health Data Discovery Repository Working Group; UCLA Precision Health ATLAS Working Group, Chang TS. **Front Aging Neurosci.** 2022 Mar 15;14:800375. doi: 10.3389/fnagi.2022.800375. PMID: 35370621; PMCID: PMC8965623.

107. *Partitioning gene-level contributions to complex-trait heritability by allele frequency identifies disease-relevant genes.* Burch KS, Hou K, Ding Y, Wang Y, Gazal S, Shi H, Pasaniuc B. **Am J Hum Genet.** 2022 Apr 7;109(4):692-709. doi: 10.1016/j.ajhg.2022.02.012. Epub 2022 Mar 9. PMID: 35271803; PMCID: PMC9069080.

106. *Genetically regulated multi-omics study for symptom clusters of posttraumatic stress disorder highlights pleiotropy with hematologic and cardio-metabolic traits.* Pathak GA, Singh K, Wendt FR, Fleming TW, Overstreet C, Koller D, Tylee DS, De Angelis F, Cabrera Mendoza B, Levey DF, Koenen KC, Krystal JH, Pietrzak RH, O' Donell C, Gaziano JM, Falcone G, Stein MB, Gelernter J, Pasaniuc B, Mancuso N, Davis LK, Polimanti R. **Mol Psychiatry**. 2022 Mar;27(3):1394-1404. doi: 10.1038/s41380-022-01488-9. Epub 2022 Mar 3. PMID: 35241783; PMCID: PMC9210390.

105. *A summary-statistics-based approach to examine the role of serotonin transporter promoter tandem repeat polymorphism in psychiatric phenotypes.* Majumdar A, Patel P, Pasaniuc B, Ophoff RA. **Eur J Hum Genet**. 2022 May;30(5):547-554. doi: 10.1038/s41431-021-00996-6. Epub 2021 Dec 23. PMID: 34949768; PMCID: PMC9091198.

104. *Large uncertainty in individual polygenic risk score estimation impacts PRS-based risk stratification.* Ding Y, Hou K, Burch KS, Lapinska S, Priv F, Vilhjlmsson 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.

103. *Fast estimation of genetic correlation for biobank-scale data.* Wu Y, Burch KS, Ganna A, Pajukanta P, Pasaniuc B, Sankararaman S. **Am J Hum Genet**. 2022 Jan 6;109(1):24-32. doi: 10.1016/j.ajhg.2021.11.015. Epub 2021 Dec 2. PMID: 34861179; PMCID: PMC8764132.

102. *On powerful GWAS in admixed populations.* Hou K, Bhattacharya A, Mester R, Burch KS, Pasaniuc B. **Nat Genet.** 2021 Dec;53(12):1631-1633. doi: 10.1038/s41588-021-00953-5. Epub 2021 Nov 25. PMID: 34824480; PMCID: PMC8939372.

101. *H3K27ac HiChIP in prostate cell lines identifies risk genes for prostate cancer susceptibility.* Giambartolomei C, Seo JH, Schwarz T, Freund MK, Johnson RD, Spisak S, Baca SC, Gusev A, Mancuso N, Pasaniuc B*, Freedman ML*. **Am J Hum Genet.** 2021 Dec 2;108(12):2284-2300. doi: 10.1016/j.ajhg.2021.11.007. Epub 2021 Nov 24. PMID: 34822763; PMCID: PMC8715276.

100. *Predicting master transcription factors from pan-cancer expression data.* Reddy J, Fonseca MAS, Corona RI, Nameki R, Segato Dezem F, Klein IA, Chang H, Chaves-Moreira D, Afeyan LK, Malta TM, Lin X, Abbasi F, Font-Tello A, Sabedot T, Cejas P, Rodrguez-Malav N, Seo JH, Lin DC, Matulonis U, Karlan BY, Gayther SA, Pasaniuc B, Gusev A, Noushmehr H, Long H, Freedman ML, Drapkin R, Young RA, Abraham BJ, Lawrenson K. **Sci Adv.** 2021 Nov 26;7(48):eabf6123. doi: 10.1126/sciadv.abf6123. Epub 2021 Nov 24. PMID: 34818047; PMCID: PMC8612691.
99. *Estimation of regional polygenicity from GWAS provides insights into the genetic architecture of complex traits.* Johnson R, Burch KS, Hou K, Paciuc M, Pasaniuc B*, Sankararaman S*. **PLoS Comput Biol.** 2021 Oct 21;17(10):e1009483. doi: 10.1371/journal.pcbi.1009483. PMID: 34673766; PMCID: PMC8562817.
98. *Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals.* Chen H, Majumdar A, Wang L, Kar S, Brown KM, Feng H, Turman C, Dennis J, Easton D, Michailidou K, Simard J; Breast Cancer Association Consortium (BCAC), Bishop T, Cheng IC, Huyghe JR, Schmit SL; Colorectal Transdisciplinary Study (CORECT); Colon Cancer Family Registry Study (CCFR); Genetics and Epidemiology of Colorectal Cancer Consortium (GECCO), O'Mara TA, Spurdle AB; Endometrial Cancer Association Consortium (ECAC), Gharahkhani P, Schumacher J, Jankowski J, Gockel I; Esophageal Cancer GWAS Consortium, Bondy ML, Houlston RS, Jenkins RB, Melin B; Glioma International Case Control Consortium (GICC), Lesseur C, Ness AR, Diergaarde B, Olshan AF; Head-Neck Cancer GWAS Consortium, Amos CI, Christiani DC, Landi MT, McKay JD; International Lung Cancer Consortium (ILCCO), Brossard M, Iles MM, Law MH, MacGregor S; Melanoma GWAS Consortium, Beesley J, Jones MR, Tyrer J, Winham SJ; Ovarian Cancer Association Consortium (OCAC), Klein AP, Petersen G, Li D, Wolpin BM; Pancreatic Cancer Case-Control Consortium (PANC4); Pancreatic Cancer Cohort Consortium (PanScan), Eeles RA, Haiman CA, Kote-Jarai Z, Schumacher FR; PRACTICAL consortium; CRUK; BPC3; CAPS; PEGASUS, Brennan P, Chanock SJ, Gaborieau V, Purdue MP; Renal Cancer GWAS Consortium, Pharoah P, Hung RJ, Amundadottir LT, Kraft P, Pasaniuc B, Lindstrm S. **HGG Adv.** 2021 Jul 8;2(3):100041. doi: 10.1016/j.xhgg.2021.100041. Epub 2021 Jun 12. PMID: 34355204; PMCID: PMC8336922.
97. *Integrative genomic analyses identify susceptibility genes underlying COVID-19 hospitalization.* Pathak GA, Singh K, Miller-Fleming TW, Wendt FR, Ehsan N, Hou K, Johnson R, Lu Z, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B, Polimanti R, Davis LK, Mancuso N. **Nat Commun.** 2021 Jul 27;12(1):4569. doi: 10.1038/s41467-021-24824-z. PMID: 34315903; PMCID: PMC8316582.
96. *Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data.* Rondel FM, Hosseini R, Sahoo B, Knyazev S, Mandric I, Stewart F, Mandoiu II, Pasaniuc B, Porozov Y, Zelikovsky A. **J Comput Biol.** 2021 Aug;28(8):842-855. doi: 10.1089/cmb.2021.0053. Epub 2021 Jul 14. PMID: 34264744; PMCID: PMC8575064.
95. *Mapping the human genetic architecture of COVID-19.* COVID-19 Host Genetics Initiative. **Nature.** 2021 Dec;600(7889):472-477. doi: 10.1038/s41586-021-03767-x. Epub 2021 Jul 8. PMID: 34237774; PMCID: PMC8674144.
94. *Multi-trait transcriptome-wide association study (TWAS) tests.* Feng H, Mancuso N, Pasaniuc B, Kraft P. **Genet Epidemiol.** 2021 Sep;45(6):563-576. doi: 10.1002/gepi.22391. Epub 2021 Jun 3. PMID: 34082479.
93. *Leveraging eQTLs to identify individual-level tissue of interest for a complex trait.* Majumdar A, Giambartolomei C, Cai N, Haldar T, Schwarz T, Gandal M, Flint J, Pasaniuc B. **PLoS Comput Biol.** 2021 May 21;17(5):e1008915. doi: 10.1371/journal.pcbi.1008915. PMID: 34019542; PMCID: PMC8174686.
92. *CDK4/6 inhibition reprograms the breast cancer enhancer landscape by stimulating AP-1 transcriptional activity.* Watt AC, Cejas P, DeCristo MJ, Metzger-Filho O, Lam EYN, Qiu X, BrinJones H, Kesten N, Coulson R, Font-Tello A, Lim K, Vadhi R, Daniels VW, Montero J, Taing L, Meyer CA, Gilan O, Bell CC, Korthauer KD, Giambartolomei C, Pasaniuc B, Seo JH, Freedman ML, Ma C, Ellis MJ, Krop I, Winer E, Letai A, Brown M, Dawson MA, Long HW, Zhao JJ, Goel S. **Nat Cancer.** 2021 Jan;2(1):34-48. doi: 10.1038/s43018-020-00135-y. Epub 2020 Nov 9. PMID: 33997789; PMCID: PMC8115221.
91. *Leveraging expression from multiple tissues using sparse canonical correlation analysis and aggregate tests improves the power of transcriptome-wide association studies.* Feng H, Mancuso N, Gusev A, Majumdar A, Major M, Pasaniuc B, Kraft P. **PLoS Genet.** 2021 Apr 8;17(4):e1008973. doi: 10.1371/journal.pgen.1008973. PMID: 33831007; PMCID: PMC8057593.

90. *Quantifying the contribution of dominance deviation effects to complex trait variation in biobank-scale data.* Pazokitoroudi A, Chiu AM, Burch KS, Pasaniuc B, Sankararaman S. **Am J Hum Genet.** 2021 May 6;108(5):799-808. doi: 10.1016/j.ajhg.2021.03.018. Epub 2021 Apr 2. PMID: 33811807; PMCID: PMC8206203.

89. *Reprogramming of the FOXA1 cistrome in treatment-emergent neuroendocrine prostate cancer.* Baca SC, Takeda DY, Seo JH, Hwang J, Ku SY, Arafeh R, Arnoff T, Agarwal S, Bell C, O'Connor E, Qiu X, Alaiwi SA, Corona RI, Fonseca MAS, Giambartolomei C, Cejas P, Lim K, He M, Sheahan A, Nassar A, Berchuck JE, Brown L, Nguyen HM, Coleman IM, Kaipainen A, De Sarkar N, Nelson PS, Morrissey C, Korthauer K, Pomerantz MM, Ellis L, Pasaniuc B, Lawrenson K, Kelly K, Zoubeidi A, Hahn WC, Beltran H, Long HW, Brown M, Corey E, Freedman ML. **Nat Commun.** 2021 Mar 30;12(1):1979. doi: 10.1038/s41467-021-22139-7. PMID: 33785741; PMCID: PMC8010057.

88. *Gene Expression Imputation Across Multiple Tissue Types Provides Insight Into the Genetic Architecture of Frontotemporal Dementia and Its Clinical Subtypes.* Reus LM, Pasaniuc B, Posthuma D, Boltz T; International FTD-Genomics Consortium, Pijnenburg YAL, Ophoff RA. . **Biol Psychiatry**. 2021 Apr 15;89(8):825-835. doi: 10.1016/j.biopsych.2020.12.023. Epub 2021 Jan 9. PMID: 33637304; PMCID: PMC8415425.

87. *Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors.* Chang TS, Ding Y, Freund MK, Johnson R, Schwarz T, Yabu JM, Hazlett C, Chiang JN, Wulf DA; UCLA Precision Health Data Discovery Repository Working Group, Geschwind DH, Butte MJ, Pasaniuc B. **iScience.** 2021 Mar 19;24(3):102188. doi: 10.1016/j.isci.2021.102188. Epub 2021 Feb 12. PMID: 33615196; PMCID: PMC7879099.

86. *A two-step approach to testing overall effect of gene-environment interaction for multiple phenotypes.* Majumdar A, Burch KS, Haldar T, Sankararaman S, Pasaniuc B, Gauderman WJ, Witte JS. **Bioinformatics.** 2021 Jan 16:btaa1083. doi: 10.1093/bioinformatics/btaa1083. Epub ahead of print. PMID: 33453114.

85. *PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics.* Lee CH, Shi H, Pasaniuc B, Eskin E, Han B. **Am J Hum Genet.** 2021 Jan 7;108(1):36-48. doi: 10.1016/j.ajhg.2020.11.017. Epub 2020 Dec 21. PMID: 33352115; PMCID: PMC7820744.

84. *Integrative analyses identify susceptibility genes underlying COVID-19 hospitalization.* Pathak GA, Singh K, Miller-Fleming TW, Wendt FR, Ehsan N, Hou K, Johnson R, Lu Z, Gopalan S, Yengo L, Mohammadi P, Pasaniuc B, Polimanti R, Davis LK, Mancuso N. medRxiv [Preprint]. 2020 Dec 8:2020.12.07.20245308. doi: 10.1101/2020.12.07.20245308. Update in: **Nat Commun.** 2021 Jul 27;12(1):4569. PMID: 33330876; PMCID: PMC7743085.

83. *Optimized design of single-cell RNA sequencing experiments for cell-type-specific eQTL analysis.* Mandric I, Schwarz T, Majumdar A, Hou K, Briscoe L, Perez R, Subramaniam M, Hafemeister C, Satija R, Ye CJ, Pasaniuc B, Halperin E. **Nat Commun.** 2020 Oct 30;11(1):5504. doi: 10.1038/s41467-020-19365-w. PMID: 33127880; PMCID: PMC7599215.

82. *Transcriptomic Insights Into the Polygenic Mechanisms Underlying Psychiatric Disorders.* Hernandez LM, Kim M, Hoftman GD, Haney JR, de la Torre-Ubieta L, Pasaniuc B, Gandal MJ. **Biol Psychiatry.** 2020 Jun 12:S0006-3223(20)31674-7. doi: 10.1016/j.biopsych.2020.06.005. Online ahead of print. PMID: 32792264

81. *Efficient variance components analysis across millions of genomes.* Pazokitoroudi A, Wu Y, Burch KS, Hou K, Zhou A, Pasaniuc B, Sankararaman S. **Nat Commun.** 2020 Aug 11;11(1):4020. doi: 10.1038/s41467-020-17576-9. PMID: 32782262; PMCID: PMC7419517.

80. *Prostate cancer reactivates developmental epigenomic programs during metastatic progression.* Pomerantz MM, Qiu X, Zhu Y, Takeda DY, Pan W, Baca SC, Gusev A, Korthauer KD, Severson TM, Ha G, Viswanathan SR, Seo JH, Nguyen HM, Zhang B, Pasaniuc B, Giambartolomei C, Alaiwi SA, Bell CA, O'Connor EP, Chabot MS, Stillman DR, Lis R, Font-Tello A, Li L, Cejas P, Bergman AM, Sanders J, van der Poel HG, Gayther SA, Lawrenson K, Fonseca MAS, Reddy J, Corona RI, Martovetsky G, Egan B, Choueiri T, Ellis L, Garraway IP, Lee GM, Corey E, Long HW, Zwart W, Freedman ML. **Nat Genet.** 2020 Aug;52(8):790-799. doi: 10.1038/s41588-020-0664-8. Epub 2020 Jul 20. PMID: 32690948.

79. *Localizing Components of Shared Transethnic Genetic Architecture of Complex Traits from GWAS Summary Data.* Shi H, Burch KS, Johnson R, Freund MK, Kichaev G, Mancuso N, Manuel AM, Dong

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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.
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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 currently 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).
  - Yi Ding, Bioinformatics, UCLA, 2024 (expected).
  - Kristin Boulier, Bioinformatics, UCLA, 2024 (expected).
  - Ruth Johnson, Computer Science, UCLA, 2023 (expected).
  - 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).
  - Dennis Grishin, Harvard Medical School, 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.