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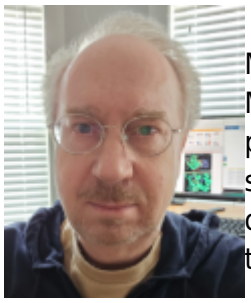
Shamil Sunyaev is a Professor of Biomedical Informatics at Harvard Medical School and Professor of Medicine at Brigham & Women's Hospital. He is also an Institute Member at the Broad Institute of MIT and Harvard. Shamil is a computational geneticist interested in many aspects of genetic variation from the evolutionary, functional and medical genetics perspectives. He is interested in population and statistical genetics, mutagenesis and the functional effect of allelic variants.

Lab Members



Ivan Adzhubey, Ph.D. is a Research Associate in Biomedical Informatics at Harvard Medical School. He obtained his Ph.D. in Molecular Biology from the Lomonosov Moscow State University and worked on co-translational protein folding, designing protein 3D structural databases and studying long-term evolution of the protein sequences. Ivan helps develop methods and software for interpreting functional impact of protein coding genomic variants using machine learning approaches, among them tools like PolyPhen-2 and DeMAG.

Daniel Balick, Ph.D. is an Instructor in the Division of Biomedical Informatics at Harvard Medical School, an Associate Geneticist at Brigham and Women's Hospital, and a Visiting Researcher at the Icahn School of Medicine at Mount Sinai. He earned is doctorate in theoretical physics at the University of California, Santa Barbara under the guidance of Boris Shraiman at the KITP. Dan is interested in the mathematical modeling of non-equilibrium phenomena in population genetics and in the nature and evolution of genetic dominance. His recent work focuses on the development of statistical methods to infer recessive purifying selection from natural population data, modeling transient allele frequency dynamics in population genetics, and the evolutionary impact of genetic dominance on human orthologs in divergent species. Resources relevant to Dan's research can be found here.

Alex Berg is a Ph.D. candidate in the Bioinformatics and Integrative Genomics program.

Carles Boix, Ph.D. completed his Ph.D. at MIT in the laboratory of Manolis Kellis, where he studied disease progression and the role of DNA damage in neurodegeneration as well as developing epigenomic references and methods for understanding gene regulation and complex disease. His current interests include understanding context-specific proximal and biological mechanisms of disease-associated variation and how selection on multiple traits influences disease risk.

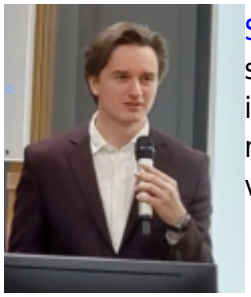
Colby Chiang is a Clinical Fellow in the Medical Genetics and Genomics at Boston Children's Hospital. He completed his MD-PhD at Washington University in St. Louis and his Pediatrics residency at Boston Children's Hospital. His doctoral work studied the functional impact of structural variation in humans. Current research interests include the genetics of complex disease, disease subtypes, epistasis, and two-locus dynamics in populations under selection.

Evan Koch, Ph.D. obtained his Ph.D. from the University of Chicago where he worked on mutation rate estimation and the various population genetics impacts of nonequilibrium demography. He is currently interested in the validation and application of fine-scale mutation rate maps, methods for estimating negative selection, and population genetics models of complex traits and GWAS.

Daniel Lee is a Ph.D. Student in the Bioinformatics and Integrative Genomics Program.

Ryan McGinty, Ph.D. received his Ph.D. from Tufts University in the laboratory of Sergei Mirkin, studying microsatellite repeat expansion and complex genomic rearrangements. Current interests involve combining computational and experimental approaches to uncover mechanisms of mutagenesis in humans, especially those involving unusual DNA secondary structures.

Jonathan Mitchel is currently a Ph.D. candidate in the Harvard-MIT Health Sciences and Technology program. He received his undergraduate degree in biomedical engineering from Georgia Tech in 2019. Jonathan is interested in studying inter-individual variation in gene expression and uncovering the processes that mediate the effects of genotype on phenotype.



Misha (Mikhail) Moldovan, Ph.D. completed his Ph.D. at Skolkovo Institute for Science and Technology in the laboratory of Prof. Mikhail Gelfand. During the Ph.D., he studied evolutionary features of processes involved in the transmission of biological information such as mRNA editing, ribosomal frameshifting and post-translational modifications of proteins. His current interests are in the field of prediction of gene variants causing Mendelian diseases

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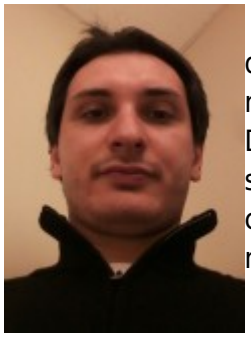
Sumaiya Nazeen, Ph.D. is a postdoctoral research fellow with a joint appointment between Sunyaev and Khurana labs. She obtained her Ph.D. in Computer Science at MIT under the supervision of Prof. Bonnie Berger. Her research focuses on the development of computational and statistical models for the interpretation of the genetic foundation of complex human diseases. Her current projects include network-based rare variant analysis, patient stratification, and biomarker discovery for Lewy body pathologies.

Maha Shady is a Ph.D. student in the Bioinformatics and Integrative Genomics (BIG) program at Harvard Medical School. She is jointly advised by Dr. Shamil Sunyaev and Dr. Eliezer Van Allen. One direction of her research focuses on understanding and modeling tumorigenesis and tumor progression. Another direction of her work focuses on building machine learning models that can inform clinical decision making for cancer patients. She is generally interested in using computational methods to understand human diseases and to develop clinically relevant models.



Vova (Vladimir) Seplyarskiy, Ph.D. graduated from Moscow State University and did his Ph.D. research in Georgii Bazykin's lab at IITP. Vladimir is interested in mutational patterns and underlying biological mechanisms. He is trying to measure DNA repair preferences by comparing mutational profiles between cancers with very specific deficiencies in repair or replication. Current projects also include characterization of sources for heritable mutations and investigation of evolution of mutation rates.

Administrative Coordinator

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Former Lab Members

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