

APURBA SHIL

Computational Genomics Researcher

Aarhus, Denmark | apurba.shil316@gmail.com | Phone: +45 71577678 | [LinkedIn](#) | [Google Scholar](#) | [GitHub](#)

PROFESSIONAL SUMMARY

I solve large-scale human biomedical problems using statistical genetics and computational methods, translating genetic associations into biological mechanisms. With more than 7 years in human and complex-trait genomics, my work spans GWAS and rare-variant analysis, fine-mapping and effector-gene prioritization, polygenic scores, causal inference (colocalization, Mendelian randomization), and gene-environment interaction across neurodevelopmental, psychiatric, infection/immune, and cardiometabolic traits. I lead the Danish site of a multi-site international gene-environment consortium and contribute to the latest Autism GWAS, working with biobank- and national-registry-scale data in R, and HPC/Linux environments.

CORE TECHNICAL EXPERTISE

Human Genetics & Genomics: GWAS; whole-exome sequencing; rare-variant association; variant prioritization; fine-mapping; PGSs; genetic pleiotropy; colocalization; 2-sample Mendelian Randomisation; gene-environment interactions; effector-gene prioritization; functional annotation; pathway, cell types and tissue expression analyses; eQTL integration; biological interpretation

Statistical & Computational Methods: Generalised linear models; survival analysis; PCA; clustering; spatial statistics; machine learning/deep learning

Programming & Computing: R; Python; Linux/CLI; shell scripting; HPC/cluster environments; STATA; SPSS

Genomics Tools: PLINK, gsMap, PRSice, Magma, PoPs, FLAMES, PolyFun, SuSiE, PolarMorphism, coloc, HyPrColoc, TwosampleMR, LDSC, LAVA, MiXeR, GATK, bcftools, samtools, VEP, AnnoVar

Data: GWAS and eQTL summary statistics; WES; genotyping arrays; spatial transcriptomics, population-health registry data; large-scale biobank data

Current Data Access: iPSYCH; Statistics Denmark; All of Us; UK Biobank; SPARK; Israeli Biobank

PROFESSIONAL EXPERIENCE

Postdoctoral Researcher – Statistical Genetics | Aarhus University, Denmark | March 2024 – Present

- Developed post-GWAS statistical-genetics workflows to identify shared genetic architecture, pleiotropic variants, effector genes, genomic regions, and biological mechanisms (pathways, cell types, tissue expression, etc.) across complex human traits.
- Lead the Danish site of multi-site gene-environment interaction studies investigating how maternal and early-life exposures interact with genetic liability to influence neurodevelopmental, psychiatric and cognitive (NPCs) traits using iPSYCH Danish population health registry data.
- Lead analytical projects investigating cross-trait genetic pleiotropy and characterizing related biological mechanisms, drug targets between (a) infections/inflammation markers (CRP, IL6); (b) preterm birth (fetal and maternal); (c) subcortical brain volumes (d) cardiometabolic traits and NPCs.
- Contributing to the latest Autism GWAS analyses, including effector gene prioritization, pathway and spatially resolved cell-type mapping, tissue specific interpretation, colocalization with eQTLs and other traits, and common vs rare/common vs common genetic convergence across different NPCs, etc.
- Oral presentations at WCPG-2026 (ECIP Oral Finalist, Glasgow, Scotland), WCPG-2025 (Cancun, Mexico), Personalized Medicine Research 2025 (Aarhus, Denmark) and poster presentations at WCPG-2026 (Glasgow, Scotland) and INSAR-2026 (Prague, Czech Republic); collaborate with researchers at Karolinska Institutet and Johns Hopkins University.
- Supervise Junior researchers and MSc/BSc students and contribute to teaching in genetics and personalised medicine; contribute to grant development and collaborative research activities.

Ph.D. Researcher – Biostatistics & Genomics | Ben Gurion University of the Negev, Israel | Feb 2019 – 2024

- Developed *AutScore*, an integrative bioinformatics pipeline incorporating ACMG/AMP guidelines, public variant databases, and in-silico methods to prioritize rare autism candidate variants (SNVs/INDELs) from WES data across hundreds of Israeli simplex/multiplex families; published findings in Scientific Reports. The pipeline was subsequently used by the Azrieli National Centre for Neurodevelopment Research in Israel to support identification of clinically relevant variants in known and previously uncharacterised autism genes.
- Contributed to four peer-reviewed publications spanning rare variant prioritization, WES-based autism genetics, genetic variants and fetal anomalies, and diagnostic yield.
- Completed training in deep Learning in computational biology, biostatistical approaches, genetics and epidemiological data analysis using Python and R.
- Supervised junior researchers and an MS student through research projects. Presented findings at INSAR-2023 (Stockholm, Sweden), IGES-2022 (Paris, France), and I-MAR-2023 (Beersheba, Israel).

Junior Research Fellow | International Institute for Population Sciences, Mumbai, India | 2017 – 2019

- Applied geospatial, survival, and regression methods to large-scale survey datasets to investigate determinants of child health indicators, NCDs, and vaccination coverage at individual and district levels in India.
- Contributed to four peer-reviewed publications and presented research at the Population Association of America 2018 meeting.

Data Analyst | Karnataka Health Promotion Trust, Bangalore, India | 2017

- Analysed large-scale survey data on maternal and child health in Karnataka for a project jointly funded by the University of Manitoba and Karnataka Health Promotion Trust.
- Applied statistical and regression methods to survey data to inform program monitoring and evaluation of maternal and child health indicators.
- Supported additional research projects through data cleaning, analysis, and reporting.

EDUCATION

- Ph.D., Biostatistics & Genomics · Ben Gurion University of the Negev, Beersheba, Israel · 2024
- M.Phil., Biostatistics & Epidemiology · International Institute for Population Sciences, Mumbai, India · 2017
- M.Sc., Biostatistics · Banaras Hindu University, Varanasi, India · 2016
- B.Sc., Statistics · Visva Bharati University, Santiniketan, India · 2013

SELECTED GENOMICS PUBLICATIONS/MANUSCRIPTS

- **Shil, A.**, Ahlqvist, V.H., Ullah, A., ... & Schendel, D., Børglum, A., Grove, J. (2026). Mapping Shared Genetic Architecture between Infections/Immune Markers, and Neurodevelopmental, Psychiatric, and Cognitive Traits: A Multi-layered Genomic Analysis (Manuscript in preparation).
- **Shil, A.**, Ahlqvist, V.H., ... & Schendel, D., Børglum, A., Grove, J. (2026). Pervasive Pleiotropy between Preterm Birth and Neurodevelopmental, Psychiatric, and Cognitive Traits (Manuscript in preparation).
- **Shil, A.**, Arildskov, E. S., Maclean, H., Børglum, A., Benke, K., Volk, H., ... & Grove, J. (2025). Investigating cross-disorder gene-environment interactions in autism and related disorders: the role of different types of maternal infections and fever during pregnancy. *European neuropsychopharmacology*, 99, 8 (WCPG 2025 conference proceeding and working paper).
- Benke, K., Daniels, J., Chen, R., Cheng, T., Feinberg, J., Piven, J., ... & Ladd-Acosta, C. (2025). Prenatal maternal infection or fever effects on child ASD diagnosis do not differ by common polygenic liability for autism. *European Neuropsychopharmacology*, 99, 7-8 (WCPG 2025 conference proceeding and working paper).
- **Shil, A.**, Arava, N., Levi, N., Levine, L., Golan, H., Meiri, G., ... & Menashe, I. (2025). An integrative scoring approach for prioritization of rare autism spectrum disorder candidate variants from whole exome sequencing data. *Scientific Reports*, 15(1), 13024.
- Regev, O., **Shil, A.**, Bronshtein, T., Hadar, A., Meiri, G., Zigdon, D., ... & Menashe, I. (2024). Association between rare, genetic variants linked to autism and ultrasonography fetal anomalies in children with autism spectrum disorder. *Journal of Neurodevelopmental Disorders*, 16(1), 55.
- **Shil, A.**, Levin, L., Golan, H., Meiri, G., Michaelovski, A., Sadaka, Y., ... & Menashe, I. (2023). Comparison of three bioinformatics tools in the detection of ASD candidate variants from whole exome sequencing data. *Scientific Reports*, 13(1), 18853.
- Tal-Ben Ishay, R., **Shil, A.***, Solomon, S., Sadigurschi, N., Abu-Kaf, H., Meiri, G., ... & Menashe, I. (2021). Diagnostic Yield and Economic Implications of Whole-Exome Sequencing for ASD Diagnosis in Israel. *Genes*, 13(1), 36 (*co first author).

ADDITIONAL PUBLICATIONS

Peer-reviewed work in population health and epidemiology, including studies of vaccination coverage, child health outcomes, diabetes burden, blood pressure, and geospatial variation in non-communicable disease burden. Full publication list available via [Google Scholar](#).

AWARDS & FUNDING

Aarhus University Travel funding: WCPG 2026 (Scotland) · Kreitman Ph.D. Fellowship (2019–2024) · BGU Travel Awards: INSAR-2023 (Sweden) & IGES-2022 (France) · UNFPA, Statistics Korea - 2018 (South Korea) · Data Revolution Award, PAA - 2018 (USA) · UGC NET- JRF (2017)

Right to work: Indian national, currently resident in Denmark with a valid work and resident permit.