

Sini Nagpal, Ph.D.

Academic Positions

- 2026–Present **Assistant Professor**, *Indian Institute of Technology (IIT)*, Bombay, India
Koita Centre for Digital Health
- 2022–2026 **Postdoctoral Fellow**, *Georgia Institute of Technology*, Atlanta, USA
Center for Integrative Genomics, School of Biological Sciences

Education

- 2019–2022 **Ph.D. in Bioinformatics**, *Georgia Institute of Technology*, Atlanta, USA
Advisor: Dr. Greg Gibson
Thesis: Genetic and Environmental Factors Influencing the Genomic Prediction of Complex Traits
Minor: Statistics
- 2017–2018 **M.S. in Bioinformatics**, *Georgia Institute of Technology*, Atlanta, USA
- 2011–2015 **B.Tech. in Biotechnology**, *Thapar University*, Patiala, India
Thesis: Predictive Analysis of Biomedical and Genomic Data for Better Diagnosis

Honors and Awards

- 2026 Petit Scholar Mentor, Petit Scholar Undergraduate Research Program, Georgia Tech, Atlanta, USA.
- 2023 Fellowship, Postdoctoral Leadership, Innovation and Project Management, Georgia Tech, Atlanta, USA.
- 2022 Postdoctoral Semifinalist for the 2022 Charles J. Epstein Award for Excellence in Human Genetics Research, The American Society of Human Genetics, Los Angeles, USA.
- 2022 Reviewer's Choice Abstract (selected in top 10% of all poster abstracts), The American Society of Human Genetics, Los Angeles, USA.
- 2021–2022 Project ENGAGES Mentor, serving minority high schools, Georgia Tech, Atlanta, USA.
- 2019 Scholarship, Advanced Statistical Genetics Workshop, Summer Institute of Statistical Genetics at the University of Washington, Seattle, USA.

Publications

- 2026 **Sini Nagpal** and Greg Gibson. Pervasive Interactions between Exposures and Polygenic Risk can Inform more Effective Clinical and Behavioral Intervention. *Nature Genetics*
- 2026 **Sini Nagpal**, Kosar Hooshmand, Piyushkumar Mundra, Mandy L. Ballinger, International Sarcoma Kindred Study (ISKS), Greg Gibson, David M. Thomas. A genome-wide association study of sarcoma suggests shared genetic overlap with rare variant susceptibility. *Under review*.
- 2026 CAR Warmerdam, Harm-Jan Westra, Adriaan van der Graaf, Marc Jan Bonder, Patrick Deelen, Tijs van Lieshout, Anke Jannie Landman, Mihkel Jesse, Benjamin J. Strober, Toni Boltz, Sandra Lapinska, **Sini Nagpal**, et al. Trans-eQTLs reveal the architecture of human gene regulatory networks. *Under review*.

- 2025 Kyle Gettler, **Sini Nagpal**, Savannah Washburn, Christopher Tastad, Jiayu Zhang, Ksenija Sabic, Mark Lazarev, Alain Bitton, Rita Cohen, Marc B. Schwartz, Arthur Barrie, Philip Gu, Philip Fleshner, Michelle Bao, Cristian Hernández-Rocha, Jacob McCauley, Maria Abreu, Subra Kugathasan, Dermot P. McGovern, Steven R. Brant, Richard H. Duerr, Mark S. Silverberg, John D. Rioux, Greg Gibson, Judy H. Cho. Post-operative ileum transcriptomics implicates sex-biased mechanisms of Crohn's disease recurrence. *Gastroenterology*.
- 2025 Adriaan van der Graaf, Robert Warmerdam, Chiara Auwerx, Urmo Vösa, Maria Carolina Borges, Lude Franke, Zoltán Kutalik, **eQTLGen Consortium**. MR-link-2: pleiotropy robust cis Mendelian randomization validated in three independent reference datasets of causality. *Nature Communications*.
- 2025 Krista Freimann, Anneke Brümmer, Robert Warmerdam, Tarran S. Rupall, Ana Laura Hernández-Ledesma, Joshua Chiou, Emily R. Holzinger, Joseph C. Maranville, Nikolina Nakic, Halit Ongen, Luca Stefanucci, Michael C. Turchin, **eQTLGen Consortium**, et al. Trans-eQTL mapping prioritises USP18 as a negative regulator of interferon response at a lupus risk locus. *Nature Communications*.
- 2024 Margaret Brown, Anne Dodd, Fang Shi, Emily Greenwood, **Sini Nagpal**, Vasantha L. Kolachala, Subra Kugathasan, Greg Gibson. Concordant B and T Cell Heterogeneity Inferred from the Multiomic Landscape of Peripheral Blood Mononuclear Cells in a Crohn's Disease Cohort. *Journal of Crohn's and Colitis*.
- 2023 Courtney Astore, Shivam Sharma, **Sini Nagpal**, NIDDK IBD Genetics Consortium, David J. Cutler, John D. Rioux, Judy H. Cho, Dermot P.B. McGovern, Steven R. Brant, Subra Kugathasan, I. King Jordan, Greg Gibson. The role of admixture in rare variant contributions to inflammatory bowel disease. *Genome Medicine*.
- 2022 Courtney Astore, **Sini Nagpal**, Greg Gibson. Mendelian Randomization Indicates a Causal Role for Omega-3 Fatty Acids in Inflammatory Bowel Disease. *International Journal of Molecular Sciences*.
- 2022 **Sini Nagpal**, Raghav Tandon, Greg Gibson. Canalization of the Polygenic Risk for Common Diseases and Traits in the UK Biobank Cohort. *Molecular Biology and Evolution*.
- 2021 Angela Mo*, **Sini Nagpal***, Kyle Gettler, Talin Haritunians, Mamta Giri, Yael Haberman, Rebekah Karns, Jarod Prince, Dalia Arafat, Nai-Yun Hsu, Ling-Shiang Chuang, Carmen Argmann, Andrew Kasarskis, Mayte Suarez-Farinas, Nathan Gotman, Emebet Mengesha, Suresh Venkateswaran, Paul A. Rufo, Susan S. Baker, Cary G. Sauer, James Markowitz, Marian D. Pfefferkorn, Joel R. Rosh, Brendan M. Boyle, David R. Mack, Robert N. Baldassano, Sapana Shah, Neal S. LeLeiko, Melvin B. Heyman, Anne M. Griffiths, Ashish S. Patel, Joshua D. Noe, Sonia Davis Thomas, Bruce J. Aronow, Thomas D. Walters, Dermot P.B. McGovern, Jeffrey S. Hyams, Subra Kugathasan, Judy H. Cho, Lee A. Denson, Greg Gibson. Stratification of Risk of Progression to Colectomy in Ulcerative Colitis via Measured and Predicted Gene Expression. *American Journal of Human Genetics*. (*Equal contribution)
- 2021 Hari K. Somineni, **Sini Nagpal**, Suresh Venkateswaran, David J. Cutler, David T. Okou, Talin Haritunians, Claire L. Simpson, Ferdouse Begum, Lisa W. Datta, Antonio J. Quiros, Jenifer Seminerio, Emebet Mengesha, et al. Whole-Genome Sequencing of African Americans Implicates Differential Genetic Architecture in Inflammatory Bowel Disease. *American Journal of Human Genetics*.
- 2021 James P. Stevens, Vasantha L. Kolachala, Gaurav N. Joshi, **Sini Nagpal**, Greg Gibson, Nitika A. Gupta. Angiotensin-converting Enzyme-2 (ACE2) Expression in Pediatric Liver Disease. *Applied Immunohistochemistry and Molecular Morphology*.

- 2020 Mark Pinese, Paul Lacaze, Emma M. Rath, Andrew Stone, Marie-Jo Brion, Adam Ameur, **Sini Nagpal**, Clare Puttick, Shane Husson, Dmitry Degreve, Tina Navin Cristina, Vivian F.S. Kahl, Aaron L. Statham, Robyn L. Woods, John J. McNeil, Moeen Riaz, Margo Barr, Mark R. Nelson, Christopher M. Reid, Anne M. Murray, Raj C. Shah, Rory Wolfe, Joshua R. Atkins, Chantel Fitzsimmons, Heath M. Cairns, Melissa J. Green, Vaughan J. Carr, Mark J. Cowley, Hilda A. Pickett, Paul A. James, Joseph E. Powell, Warren Kaplan, Greg Gibson, Ulf Gyllensten, Murray J. Cairns, Martin McNamara, Marcel E. Dinger, David M. Thomas. The Medical Genome Reference Bank Contains Whole Genome and Phenotype Data of 2570 Healthy Elderly. *Nature Communications*.
- 2019 **Sini Nagpal***, Xiaoran Meng*, Michael P. Epstein, Lam C. Tsoi, Matthew Patrick, Greg Gibson, Philip L. De Jager, David A. Bennett, Aliza P. Wingo, Thomas S. Wingo, Jingjing Yang. TIGAR: An Improved Bayesian Tool for Transcriptomic Data Imputation Enhances Gene Mapping of Complex Traits. *American Journal of Human Genetics*. (*Equal contribution)
- 2018 **Sini Nagpal**, Greg Gibson, Urko M. Marigorta. Pervasive Modulation of Obesity Risk by the Environment and Genomic Background. *Genes*.

Scientific Conferences and Meetings

- 2026 Poster, **Sini Nagpal** and Greg Gibson. Pervasive Interactions between Exposures and Polygenic Risk can Inform more Effective Clinical and Behavioral Intervention. *STATGEN 2026: Conference on Statistics in Genomics and Genetics, Emory University, Atlanta, USA*.
- 2025 **Sini Nagpal** and Greg Gibson. Dual Polygenic Score-by-Exposure Interactions Highlight Disparities across Social Groups in the Proportion Needed to Benefit. *American Society of Human Genetics, Boston, USA*.
- 2025 Workshop, BIRS Novel Statistical Approaches for Studying Multi-omics Data. *Banff International Research Station, Banff, Canada*.
- 2024 Talk, **Sini Nagpal**. Dual exposure-by-polygenic score interactions highlight disparities across social groups in the proportion needed to benefit. *Southern California Symposium on Polygenic Risk Scores*.
- 2023 Poster, **Sini Nagpal** and Greg Gibson. Interpreting decanalization as the amplification of polygenic signals. *Program in Quantitative Genomics – Diversity in Genetics and Genomics, Harvard T.H. Chan School of Public Health, Harvard University, Boston, USA*.
- 2023 Poster, Courtney Astore, Shivam Sharma, **Sini Nagpal**, et al. The role of admixture in rare variant contribution of inflammatory bowel disease. *American Society of Human Genetics, Washington DC, USA*.
- 2023 Participated in Integrative Genomics for Health Equity Workshop. *Georgia Tech, Atlanta, USA*.
- 2022 NIDDK Inflammatory Bowel Disease Genetics Consortium Meeting. *Bethesda, Washington DC, USA*.
- 2022 Poster, **Sini Nagpal**, Zheyang Xu, Greg Gibson, et al. Predicted polygenic transcriptional risk score supports the inference of canalization of polygenic risk for common disease and traits in the UK Biobank. *The American Society of Human Genetics, Los Angeles, USA*.
- 2022–2023 Participated in Atlanta Workshop on Single-Cell Omics (AWSOM). *Georgia Tech and Emory University, Atlanta, USA*.
- 2019 Poster, **Sini Nagpal**, Angela Mo, Jeffrey S. Hyams, et al. Tu1760 – Alterations in Expression Quantitative Trait Loci from Diagnosis to Recovery in Pediatric Ulcerative Colitis. *Gastroenterology – Digestive Diseases Week, San Diego, USA*.

- 2019 Poster, **Sini Nagpal**, Angela Mo, Jeffrey S. Hyams, et al. Alterations in Genetic Regulation of Rectal Gene Expression from Diagnosis to Recovery in Pediatric Ulcerative Colitis. *Annual Southeastern Pediatric Research Conference, Atlanta, USA*.
- 2018 Poster, Jingjing Yang, Xiaoran Meng, Aliza Wingo, Thomas Wingo, Lam C. Tsoi, Matthew Patrick, Michael Epstein, **Sini Nagpal**. Integrative functional genomics analysis of neuropathological features of Alzheimer's Disease reveals novel insights on GWAS loci. *American Society of Human Genetics, San Diego, USA*.

Invited Talks

- 2025 Polygenic and rare variant contributions to Sarcoma risk. *Center for Integrative Genomics, Georgia Tech, Atlanta, USA*.
- 2023 Polygenic risk score-by-exposure interactions are pervasive for cardiovascular diseases. *Emory Clinical Cardiovascular Research Conference, Emory University, Atlanta, USA*.
- 2023 Interpreting decanalization as the amplification of polygenic signals. *Center for Integrative Genomics, Georgia Tech, Atlanta, USA*.
- 2023 Integrative genomics for environmentally-informed precision medicine. *Department of Human Genetics, Emory University, Atlanta, USA*.

Research Experience

- 2018 **Research Intern**, *Emory University, Atlanta, USA*
Nonparametric Bayesian method for transcriptome-wide association studies (TWAS).
Advisor: Dr. Jingjing Yang
- 2017–2018 **Graduate Research Assistant**, *Georgia Institute of Technology, Atlanta, USA*
Effect of polygenic risk score-by-environment interactions on the risk of obesity.
Advisor: Dr. Greg Gibson; Postdoctoral Mentor: Dr. Urko M. Marigorta
- 2014 **Research Intern**, *CSIR-Institute of Genomics and Integrative Biology, Delhi, India*
Predictive analysis of biomedical and genomic data for better diagnosis.
Advisor: Dr. Tavpritesh Sethi
- 2013 **Research Intern**, *CSIR-Institute of Genomics and Integrative Biology, Delhi, India*
Protein expression and dynamic mitochondrial morphology during oxidative stress in Asthma.
Advisor: Dr. Anurag Agrawal

Teaching and Mentorship

Instructor

2024–2026 Bruce Weir Summer Institute in Statistical Genetics (SISG), Atlanta, USA. Quantitative Genetics Module: Introduction to R and Python.

Mentor, Gibson Lab, Georgia Tech, Atlanta, USA

- 2026 Aariz Jivani (BS Biology): The impact of indirect genetic effects of parents and siblings on the polygenic risk of diseases.
- 2026 Erin Yoon (BS Neuroscience): The evolution of eQTL architecture under linkage disequilibrium; Petit Scholar Mentorship.
- 2025–2026 Neha Suresh (MS Bioinformatics): Single cell transcriptional risk score for predicting Crohn's disease.
- 2024–2025 Mia Denning (MS Bioinformatics): Polygenic score by environmental interactions in All of Us.
- 2023–2024 Suraksha Vinod (MS Bioinformatics): Influence of admixture on polygenic risk assessment.
- 2022–2023 Jared Collins (BS-MS Biology): Coherence vs Incoherence of disease risk using integrative genomics approach of integrating single cell with GWAS. Jared successfully defended his MS thesis on this project.
- 2022–2023 Kate Xie (MS Bioinformatics): Development of predicted polygenic transcriptional risk score at single cell level to predict disease progression for autoimmune diseases.
- 2022–2023 Emily Hang (BS-MS Bioinformatics): Studying the effect of genetics on the expression of facial emotions and homophily.
- 2022 Zheyang Xu (MS Bioinformatics): Canalization of polygenic risk of common diseases and traits in the UK Biobank using predicted polygenic transcriptional risk scores.
- 2020 Kristine Lacek (MS Bioinformatics): Polygenic risk score-by-environment interactions for Inflammatory Bowel Disease in the UK Biobank cohort.
- 2020 Vidisha Goyal (MS Biomedical Engineering): Spatial Transcriptomics.

Project ENGAGES Mentor, Georgia Tech, Atlanta, USA

2021–2022 Jeremiah Longino (High School Student, South Atlanta High School): Predictive health genomics on Inflammatory Bowel Disease. Jeremiah won an award in district level science fair for this project.

Professional Service

Invited Peer Review

Invited Journal Reviewer – Nature Communications, Scientific Reports, Human Genetics and Genomics Advances, Journal of Crohn's and Colitis, Human Genomics, European Journal of Medical Research, BMC Medical Genomics, BMC Genomic Data, BMJ Open, International Journal of Obesity.

Reviewed applications for the 2022 President's Undergraduate Research Awards (PURA) at Georgia Tech.

Professional Memberships

Lead Analyst, NIDDK Inflammatory Bowel Disease Genetics Consortium.

Analyst, eQTLGen Consortium.

Member, American Society of Human Genetics.

Industry Experience

2015–2016 **Data Analyst**, *Elucidata*, Delhi, India

Metabolomics data analysis: Built python packages for mass isotopomer distribution analyses and correcting metabolomic data for naturally occurring isotopes. Delivered the tools to healthcare and pharmaceutical companies.