INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

# January 2026 Pre-Election Newsletter

Topics:

INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

## Save The Date: Friday, January 30, 2026
**11 am (EST), 8 am (PST) and 5 pm (CET)**

Dear IGES members,

IGES hosts regular virtual journal clubs throughout the year to increase IGES members' familiarity with emerging and classic literature in genetic epidemiology and to foster discussion and networking among members. This month's journal club introduces joint sparse canonical correlation analysis (jsCCA), a multistage method that integrates multi-omics data (CNA, methylation, expression) with clinical outcomes to identify interpretable, outcome-associated molecular modules in cancer. Make plans to attend our next meeting!

**Title: "Identifying genes associated with disease outcomes using joint sparse canonical correlation analysis-An application in renal clear cell carcinoma" (*Genet Epidemiol*. 2024 Dec;48(8):414-43).**

**Article:** https://onlinelibrary.wiley.com/doi/10.1002/gepi.22566

**Abstract (adapted from the original abstract):**

Cancer genomics data often have multiple interconnected data modalities that are related but have captured different molecular features of the tumor. Connecting multiple such modalities jointly with a tumor-related outcome while maintaining interpretability has proven to be a difficult problem. We present joint sparse canonical correlation analysis (jsCCA), a multistage pipeline for integrating high-dimensional multi-omics data with clinical outcomes. jsCCA extends sparse canonical correlation analysis to simultaneously link patterns of multiple data modalities, namely copy number aberrations, DNA methylation, and gene expression, here, while retaining only small, interpretable sets of features in each layer. jsCCA detects potentially orthogonal gene components that are highly correlated with sets of methylation sites which in turn are correlated with sets of CNA sites. We then connect these multivariate "gene components" to the outcome. Applying jsCCA to TCGA clear cell renal cell carcinoma data (n = 515), we identify eight components representing coordinated CNA–methylation–expression modules. These components highlight regulatory relationships including a putative pathway

where CNAs on 10q25 and methylation near SIX5 influence ASAH1 expression, which is strongly associated with tumor stage. Two components also modify the association between smoking and tumor stage and are enriched for immune, inflammatory, and hypoxia pathways. Our framework offers a general, interpretable strategy for outcome-driven analysis of multimodal omics in cancer genetic epidemiology.

**Registration link:**

https://msm-edu.zoom.us/meeting/register/xxaG-AuOQ7CZa-NM5fOzMg

After registering, you will receive a confirmation email containing information about joining the meeting.

**Bio:**

Diptavo Dutta joined the Division of Cancer Epidemiology and Genetics as an Earl Stadtman tenure-track investigator in the Integrative Tumor Epidemiology Branch (ITEB) in August 2022. Before that, he earned his Ph.D. in biostatistics from the University of Michigan at Ann Arbor and subsequently was a postdoctoral fellow at Johns Hopkins University. Dr. Dutta's research program utilizes genetic, transcriptomic, proteomic, and other 'omics' data to study cancer etiology, especially focusing on kidney cancer and breast cancer.

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Do you have any suggestions for interesting topics, papers, or presenters for further talks? Or would you like to support us in organizing the Journal Club? Please contact Dr. Silke Szymczak (silke.szymczak@uni-luebeck.de)

On behalf of the organizing team of the IGES Journal Club,
Silke Szymczak
Heejong Sung
Cheryl Cropp

**Call for new members to the IGES ELSI Committee**

The IGES ELSI Committee brings together individuals committed to addressing ethical, legal, and social issues in genetic epidemiology and to supporting responsible research practices through guidelines, education, and outreach activities. We warmly invite IGES members at all career stages, and from diverse backgrounds, perspectives, and experiences, to express their interest by completing the following form:

https://forms.gle/P4Uq9YH5XZ8n52M97

Thanks!

Marie-Pierre Dube

**IGES Education Committee.**

SAVE THE DATE!

The next IGES educational workshop will occur on Tuesday 20th Oct 2026, immediately after the IGES 2026 annual meeting (Estérel Resort https://www.esterel.com/en, Quebec Saturday 17-Monday 19 October) at McGill University in downtown Montreal. Transportation from the IGES meeting to the education session will be arranged. The topic of the workshop will be 'AI in genetic epidemiology and genomics'.

**IGES Young Investigators Committee**

The new Chair of the IGES Young Investigators Committee (YIC) will be Ozvan Bocher with co-chair Anvita Kulshrestha.

And there are two new members for the YIC:

Sebastian Sendel (University of Kiel, Germany)

Peyton McClelland (McGill)

**IGES election candidates 2026**

(only one candidate for each position)

**President elect:** Elizabeth Blue (only one candidate)

**Treasurer:** Cheryl Cropp (only one candidate)

**Candidates for board** (select two from four candidates)**:**

Alexandre Bureau

Burcu Darst

Pingzhao Hu

Linda Kachuri

**President elect: Elizabeth Blue PhD**

Elizabeth Blue is a Professor of Medical Genetics and Associate Director of the Institute for Public Health Genetics at the University of Washington (UW). She trained in population genetics at the University of Utah, developing methods to test population histories of people and polymorphisms to earn a PhD in Anthropology. As a postdoc, Liz pivoted from populations to family structures, focusing on identity-by-descent, imputation, and Bayesian machine learning approaches for linkage and association testing.

The Blue lab incorporates tools from statistical genetics, genomics, and epigenetics to discover and evaluate genetic variants implicated in disease. Liz investigates the relationship between coding and non-coding causal variants, risk loci, and genetic modifiers of both rare Mendelian disorders and Alzheimer's disease. Her work has led to the identification of dozens of novel gene-phenotype relationships for rare diseases and molecular diagnoses for patients with long diagnostic odysseys by combining population genetics expertise with multi-omics data. Bridging the gap between complex traits and Mendelian disease, she identified genetic modifiers of cystic fibrosis-related phenotypes. She has incorporated family- and population-based approaches with functional annotations and pathogenicity predictions to identify novel loci associated with Alzheimer's disease risk and age-at-onset and better characterize known loci.

Liz's expertise in the genetic epidemiology of both rare and common disease genetics is internationally recognized, including leadership roles within IGES, the Alzheimer's Disease Sequencing Project, Centers for Mendelian Genomics, Cystic Fibrosis Genome Project, the Genome Sequencing Project, and the Pacific Northwest Undiagnosed Diseases Network Clinical Site. She is highly collaborative, leading to >400 publications to date.

Liz is deeply invested in teaching and community service. She mentors students and shapes the curriculum of the Institute for Public Health Genetics, teaches biostatistics for the UW Graduate Program in Genetic Counseling, and is a widely sought guest lecturer. Within IGES, Liz introduced the annual student-mentor lunch as chair of the Young Investigators Committee, maintained our Facebook page and organized the publication highlights while on the Communications Committee, developed our t-shirt fundraiser while on the Board of Directors, and now serves on the Scientific Program Committee.

Five selected publications:

1. Xue D., **Blue E.E.**, Fullerton S.M., Henrikson N.B., Knerr S., Laberge A.M., Parker L.S., Sabatello M., Shridhar N., Smith J.A., Wilfond B.S., Wojcik G.L., Yu J.H., Fohner A.E. (2025) Training competencies and recommendations for the next generation of public health genetics: Reflections from current leaders in the field. *Am J Hum Genet*, **112**, 2860-2869. PMID: 41265452.
2. **Blue E. E.**, Broome J., Xue D., Kingston H., Chapman N., Gogarten S., Alzheimer's Disease Genetics Consortium, Naj A., Wijsman E. (2025) Multi-ancestry meta-analysis identifies genetic modifiers of age-at-onset of Alzheimer's disease at known and novel loci. *Alzheimers Dement*, **21**, e70489. PMID: 40883957.
3. Faino A.V., Gordon W.W., Buckingham K., Stilp A.M., Pace R., Raraigh K.S., Collaco J.M., Zhou Y.H., Dang H., O'Neal W., Knowles M.K. Cutting G.R., Rosenfeld M., Bamshad M.J., Gibson R.L., **Blue E.E.** for the Cystic Fibrosis Genome Project. (2025) *CHP2* modifies chronic *Pseudomonas aeruginosa* airway infection risk in cystic fibrosis. *Ann Am Thorac Soc*, **22**, 715-723. PMID: 39746161.
4. **Blue E.E.**, Huang S.J., Khan A., Golden-Grant K., Boyd B., Rosenthal E.A., Gillentine M.A., Fleming L.R., Adams D.R., Wolfe L., Allworth A., Bamshad M.J., Caruana N., Chanprasert S., Chen J., Dargie N., Doherty D., Friederich M.W., Hisama F.M., Horike-Pyne M., Lee J.C., Donovan T.E., Hock D.H., Leppig K.A., Miller D.E., Mirzaa G., Ranchalis J., Raskind W.H., Michel C.R., Reisdorph R., Schwarze U., Sheppeard S., Strohbehn S., Straud D.A., Sybert V.P., Wener M., University of Washington Center for Rare Disease Research, Undiagnosed Diseases Network, Stergachis A.B., Lam C., Jarvik G.P., Dipple K.M., Van Hove J.L.K., Glass I.A. (2024) Dual Diagnosis of *UQCRFS1*-related Mitochondrial Complex III Deficiency and recessive *GJA8*-related Cataracts. *Rare*, **2**, 100040. PMID: 39421685.
5. **Blue E.E.**, White J.J., Dush M.K., Gordon W.W., Wyatt B.H., White P., Marvin C.T., Helle E., Ojala T., Priest J.R., Jenkins M.M., Almli L.M., Reefhuis J., Pangilinan F., Brody L.C., McBride K.L., Garg V., Shaw G.M., Romitti P.A., Nembhard W.N., Browne M.L., Werler M.M., Kay D.M., National Birth Defects Prevention Study, University of Washington Center for Mendelian Genetics, Mital S., Chong J.X., Nascone-Yoder N.M., Bamshad M.J. (2023) Rare variants in *CAPN2* increase risk for isolated hypoplastic left heart syndrome. *HGG Adv,* **4**, 100232. PMID: 37663545.

**Treasurer: Cheryl Cropp PhD**

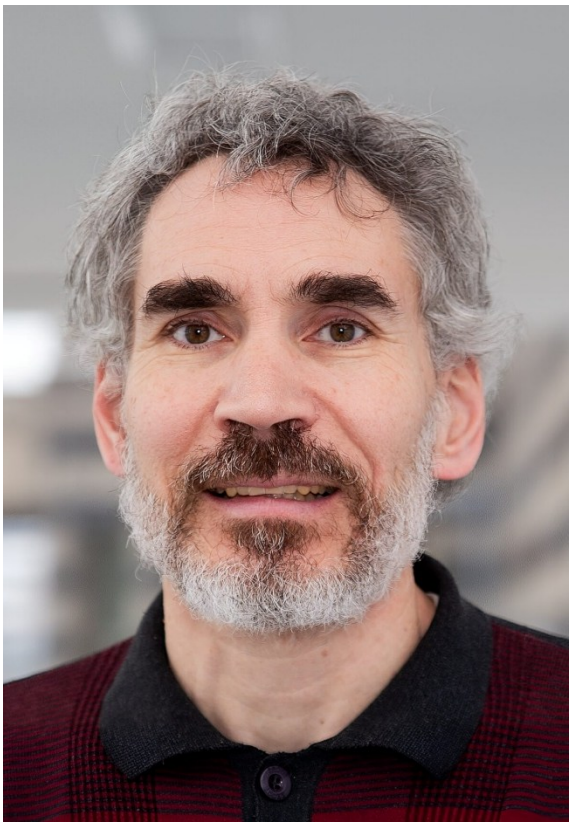
Dr. Cheryl D. Cropp is an Associate Professor at Morehouse School of Medicine. She holds a Doctor of Pharmacy degree from the University of Kentucky and a Ph.D. in Pharmaceutical Sciences and Pharmacogenomics from the University of California, San Francisco. Cheryl completed postdoctoral training in genetic epidemiology at the National Human Genome Research Institute (NHGRI), National Institutes of Health, under the mentorship of Dr. Joan E. Bailey-Wilson.

Dr. Cropp's research focuses on genome-wide linkage, association, and sequencing studies to identify rare, highly penetrant cancer susceptibility genes in populations of African descent and other health-disparate groups. Her work aims to advance understanding of genetic determinants that influence the efficacy of oncology pharmacotherapy. She leads ongoing projects in prostate, breast, and gastric cancer genetic epidemiology, pharmacogenomics, and pharmacokinetics.

In addition to her research, Dr. Cropp has extensive experience in academia and clinical pharmacy. She currently teaches pharmacology, pharmacokinetics, and pharmacogenomics, and developed and coordinates the graduate elective course "Topics in Pharmacogenomics and Precision Medicine" at Morehouse School of Medicine.

Cheryl is deeply committed to service, which she considers one of the most rewarding aspects of her career. She has been affiliated with the International Genetic Epidemiology Society (IGES) since her postdoctoral fellowship at NHGRI and currently serves on the IGES Journal Club and ELSI committees. She believes IGES provides an outstanding environment for collaboration and growth and pledges to continue her active engagement and enthusiasm in advancing the society's mission as Treasurer.

**Board Candidate: Alexandre Bureau PhD**



Alexandre Bureau is a faculty member in the Department of social and preventive medicine of Université Laval in Quebec City, Canada, since 2005 where he is now professor and chair of the biostatistics graduate programs and researcher at the CERVO Brain Research Centre. Alexandre earned a BSc in statistics from Université Laval in 1996 and a PhD in biostatistics from the University of California at Berkeley in 2001, training in statistical genetics with Terry Speed. He started his research career as senior scientist at Genome Therapeutics Corporation in Waltham, Massachusetts, under the supervision of Josée Dupuis and Paul Van Eerdewegh, where he was introduced to IGES. He has been a member of the society since 2001 and was nominated for the Neel award in 2002 for introducing the predictive method Random Forests in genetic epidemiology. Alexandre was a visiting scholar in the biostatistics department of the Johns Hopkins Bloomberg School of Public Health in Baltimore, Maryland, in 2013 and has established fruitful collaborations with researchers in Canada, China, France, Italy, the UK and the USA.

Alexandre develops statistical methods for human genetics, with a focus on familial studies and neurodevelopmental disorders. He has contributed methods to link rare genetic variants with complex disorders in familial sequencing studies and released software to make them available to the scientific community. He led a project leveraging genetic correlations among human traits to improve trait prediction with summary statistics. His involvement in the Schizophrenia and Bipolar Disorder Eastern Québec Kindred Study has led to several publications of genetic analyses of these disorders. In addition to Canadian students, Alexandre has trained graduate students from Burkina Faso, France, Guinea, Ivory Coast, Lebanon, Morocco and Senegal. He is an associate editor for Frontiers in Genetics and has served on grant review panels for research funding agencies from Romania and Italy and for what is now known as the European Partnership for Personalised Medicine numerous times. Alexandre has also served as board member, president and treasurer of local non-profit organizations.

Alexandre was a session moderator during the 2021 online IGES meeting and a mentor at the 2023 IGES meeting. Beyond these modest contributions to IGES, Alexandre has an extensive record of organizing scientific meetings and workshops in statistical genetics in Canada over the last ten years, including two events of international scope in 2018: a week-long summer school at Université Laval with 6 instructors from across Canada and the USA and a five-day workshop at the Banff International Research Station gathering recognized leaders in the field from Canada, the USA and the UK. He is currently one of the regional leads for Québec of a pan-Canadian training program in genetic epidemiology and statistical genetics.

Alexandre is committed to help IGES remain a strong and welcoming society at a time where its stance for international scientific collaboration and diversity is more important than ever.

Five selected publications:


1. Mangnier L, Ruczinski I , Ricard J, Moreau C , Girard S , Maziade M , **Bureau A.** (2025). RetroFun-RVS: A Retrospective Family-Based Framework for Rare Variant Analysis Incorporating Functional Annotations. Genetic epidemiology. 49(2): e70001
2. **Bureau A** , Tian Y , Levallois P , Giguère Y , Chen J , Zhang H. (2023). Methods and software to analyze gene-environment interactions under a case-mother - control-mother design with partially missing child genotype. Human heredity. 88(1): 38-49.
3. Bahda M, Ricard J, Girard SL , Maziade M , Isabelle M , **Bureau A.** (2023). Multivariate extension of penalized regression on summary statistics to construct polygenic risk scores for correlated traits. HGG advances. 4(3): 100209.
4. Chagnon YC, Maziade M, Paccalet T, Croteau J, Fournier A, Roy M-A, **Bureau A** (2020). A multimodal attempt to follow-up linkage regions using RNA expression, SNPs and CpG methylation in schizophrenia and bipolar disorder kindreds. European Journal of Human Genetics. 28:499–507.
5. **Bureau A,** Begum F, Taub M A, Hetmanski J B, Parker M M, Albacha-Hejazi H, Scott A F, Murray J C, Marazita M L, Bailey-Wilson J E, Beaty T H and Ruczinski I. (2019). Inferring Disease Risk Genes from Sequencing Data in Multiplex Pedigrees Through Sharing of Rare Variants. Genetic Epidemiology. 43(1): 37-49.

**Board Candidate: Burcu Darst PhD**

Dr. Burcu Darst is an Assistant Professor in the Epidemiology Program of the Public Health Sciences Division at the Fred Hutchinson Cancer Center. She is also a core faculty member of the Institute of Public Health Genetics and an affiliate faculty member in the Department of Epidemiology at the University of Washington. After completing her undergraduate studies at the University of California, San Diego, Dr. Darst completed her PhD in Epidemiology at the University of Wisconsin, Madison under the mentorship of Dr. Corinne Engelman and her postdoctoral training at the University of Southern California under the mentorship of Dr. Christopher Haiman and Dr. David Conti.

Dr. Darst's research is focused on identifying and understanding genetic and multi-omic risk factors of prostate cancer and other complex traits across multi-ancestry populations. This includes investigating the contribution of rare genetic variants to disease risk, developing and evaluating polygenic risk scores, and identifying metabolomic risk profiles, with a particular focus on how such risk factors could mitigate health disparities. She is highly collaborative and involved in several consortia and cohorts, including the Prostate Cancer Association Group to Investigate Cancer Associated Alterations in the Genome (PRACTICAL) Consortium, the Population Architecture Using Genomics and Epidemiology (PAGE) Study, the Polygenic Risk Methods Development (PRIMED) Consortium, and the Multiethnic Cohort (MEC). Dr. Darst has received multiple awards for her work, including the AACR NextGen Star Award, Prostate Cancer Foundation Young Investigator Award, Emerging Scholar in Genome Sciences Award, and an NCI Early Stage K99/R00, among others.

Dr. Darst has been an active member of IGES since her first IGES meeting in 2014 (held jointly with GAW19 in Vienna). Since 2018, she has been an engaged member of the IGES Ethical, Legal, and Social Issues Committee, contributing to guidelines on the reporting of race, ethnicity, and genetic ancestry in IGES abstracts, an IGES statement on racism and genetic epidemiology, and a perspective on conducting inclusive genetic epidemiology research published in *Genetic Epidemiology*. She received the IGES 2017 Ludmer Center Award for an outstanding trainee abstract. Beyond IGES, Dr. Darst has had relevant leadership and service experience through membership on the ASHG Training and Development Committee (2017-2019), ASHG Membership Engagement Committee (2020-2022), and PRIMED Agenda Planning Committee (2024-Present), among others. She would be honored to continue supporting our research community as a member of the IGES Board of Directors.

Five selected publications:

1. Guo, B., Cai, Y., Kim, D., Smit, R.A.J., Wang, Z., Iyer, K.R., Hilliard, A.T., Haessler, J., Tao, R., Broadaway, K.A., Wang, Y., Pozdeyev, N., Stæger, F.F., Yang, C., Vanderwerff, B., ..., The biobank at the Colorado Center for Personalized Medicine, VA Million Veteran Program, The Population Architecture using Genomics and Epidemiology (PAGE) study, Gignoux, C., North, K.E., Loos, R.J.F., Assimes, T.L., Peters, U., Kooperberg, C., Raghavan, S., H.M., **Darst, B.F.** (2025). Polygenic risk score for type 2 diabetes shows context-dependent effects across populations. *Nature Communications*.

2. Goss, L.B., Liu, M., Zheng, Y., Guo, B., Conti, D.V., Haiman, C.A., Kachuri, L., Catalona, W.J., Witte, J.S., Lin, D.W., Newcomb, L.F., **Darst, B.F.** (2024). Prostate cancer polygenic risk score associated with upgrading in patients on active surveillance. *JAMA Oncology*.

3. **Darst, B.F.***, Shen, J.*, Madduri, R.K., Rodriguez, A.A., Xiao, Y., Sheng, X., Saunders, E.J., Dadaev, T., Brook, M.N., Hoffmann, T.J., Muir, K., Wan, P., Le Marchand, L., Wilkens, L., ..., Crawford, D.C., Petrovics, G., Casey, G., Roobol, M.J., Hu, J.F., Berndt, S.I., Van Den Eeden, S.K., Easton, D.F., Chanock, S.J., Cook, M.B., Wiklund, F., Witte, J.S., Eeles, R.A., Kote-Jarai, S., Watya, S., Gaziano, J.M., Justice, A.C., Conti, D.V., Haiman, C.A. (2023). Evaluating approaches for constructing polygenic risk scores for prostate cancer in men of African and European ancestry. *American Journal of Human Genetics*.

4. Caliebe, A.*, Tekola-Ayele, F.*, **Darst, B.F.**, Wang, X., Song, Y.E., Gui, J., Sebro, R.A., Balding, D.J., Saad, M., Dubé, M., on behalf of the IGES ELSI committee (2022). Including diverse and admixed populations in genetic epidemiology research. *Genetic Epidemiology*.

5. Conti, D.V.*, **Darst, B.F.***, Moss, L., Saunders, E.J., Sheng, X., Chou, A., Schumacher, F.R., Al Olama, A.A., Benlloch, S., Dadaev, T., Brook, M.N., Sahimi, A., Hoffman, T.J., ..., Chanock, S.J., Cook, M.B., Wiklund, F., Nakagawa, H., Witte, J.S., Eeles, R.A., Kote-Jarai, Z., Haiman, C.A. (2021). Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. *Nature Genetics*.

* Indicates co-first authorship

Keywords: Genetic epidemiology, metabolomic epidemiology, prostate cancer, diversity

**Board Candidate: Pingzhao Hu PhD**

Dr. Pingzhao Hu is a tenured Associate Professor at Western University with appointments in the Departments of Biochemistry, Epidemiology and Biostatistics, Statistical and Actuarial Sciences, Oncology, and Computer Science, and a status-only Associate Professorship in Biostatistics at the University of Toronto. He holds a Tier 2 Canada Research Chair in Computational Approaches to Health Research. Dr. Hu received his PhD in Computer Science with a focus on bioinformatics and has more than two decades of experience at the intersection of genetic epidemiology, statistical genetics, and data science.

Dr. Hu's research focuses on developing and applying statistical and machine learning methods for genetic epidemiology, with emphasis on multi-omics data integration, survival and longitudinal modeling, radiogenomics, microbiome–host genetic interactions, and population-based disease studies. His work integrates genomic, imaging, microbiome, and electronic health record data to advance precision medicine in complex diseases, particularly cancer and immune-mediated disorders. He has published over 190 peer-reviewed articles in leading journals such as Nature Communications, Cell Reports, Bioinformatics, and PLOS Computational Biology.

Dr. Hu is an active member of IGES and currently serves as Co-Chair of the IGES Education Committee. He has delivered multiple oral presentations at recent IGES annual meetings and has been heavily involved in the Genetic Analysis Workshops (GAW15–GAW19). He also holds editorial leadership roles with PLOS Computational Biology (Academic Editor), Annals of Medicine (Associate Editor, Medical Genetics and Genomics), and Frontiers in Genetics (Associate Editor, Statistical Genetics and Methodology). A dedicated mentor, Dr. Hu has supervised more than 60 graduate trainees and directs the Western Bioinformatics Research Seminar Series. He would be honored to serve on the IGES Board of Directors and contribute to the society's mission of advancing rigorous, inclusive, and collaborative genetic epidemiology. More information about Dr. Hu's research and activities can be found at https://phulab.org.

Five Selected Publications:

Bolded names indicate trainees supervised by me as the primary supervisor; * denotes co-corresponding authorship.

1. **Khan MW**, Cruz de Jesus V, Mittermuller BA, Schroth RJ, Hu P*, Chelikani P*. Integrative analysis of taste genetics and the dental plaque microbiome in early childhood caries.
   *Cell Reports*. 2025 Sep 23;44(9):116245.

2. **Hadipour H**, **Li YY**, **Sun Y**, **Deng C**, **Lac L**, Davis R, Cardona ST, Hu P. GraphBAN: An inductive graph-based approach for enhanced prediction of compound-protein interactions. *Nature Communications*. 2025 Mar 18;16(1):2541.

3. **Chen L**, **Huang ZH**, **Sun Y**, Domaratzki M, Liu Q, Hu P. Conditional probabilistic diffusion model driven synthetic radiogenomic applications in breast cancer. *PLoS Computational Biology*. 2024 Oct 7;20(10):e1012490. **Cover Article.**

4. **Zhang JZ**, Xu W*, Hu P*. Tightly integrated multiomics-based deep tensor survival model for time-to-event prediction. *Bioinformatics*. 2022 Jun 13;38(12):3259-3266.

5. **Liu Q**, **Cheng B**, **Jin Y**, Hu P. Bayesian tensor factorization-drive breast cancer subtyping by integrating multi-omics data. *Journal of Biomedical Informatics*. 2022 Jan;125:103958.__Selected as a Translational Bioinformatics Year-in-Review Paper (American Medical Informatics Association Informatics Summit 2023).

**Keywords**: Genetic Epidemiology, Statistical Genetics, Multi-omics Integration, Survival Analysis, Interpretable Machine Learning, Radiogenomics

**Board Candidate: Linda Kachuri PhD**

Dr. Linda Kachuri is an Assistant Professor in the Department of Epidemiology and Population Health at Stanford University and a member of the Center for Computational, Evolutionary, and Human Genomics.

She earned her PhD in Epidemiology from the University of Toronto, where she was a fellow in the STAGE (Strategic Training for Advanced Genetic Epidemiology) Program, and spent time as a visiting scholar at the International Agency for Research on Cancer in Lyon, France. Her dissertation investigated the role of telomere length in lung risk, using methods for rare variant analysis and causal inference. After finishing her degree in 2018, Dr. Kachuri pursued postdoctoral training at the University of California in San Francisco, where she expanded her research interests into polygenic risk scores, genetic basis of immune function, and population genetics.

Dr. Kachuri's current research interests include developing genetically informed biomarkers for early detection of cancer and other diseases, improving methods for polygenic prediction in diverse populations, and enabling more equitable translation of tools in genomic medicine. Dr. Kachuri enjoys connecting with colleagues around the world and contributing to collaborative research endeavors. She is part of the NIH-funded Polygenic Risk Methods Development (PRIMED) Consortium and has chaired the PRIMED Methods Working Group since 2023. She has also contributed to research efforts focused on genetic regulation of molecular traits within the Trans-Omics for Precision Medicine (TOPMed) program.

Since first joining IGES as a PhD student, Dr. Kachuri has served a 3-year term on the Program Committee and helped organize the 2024 Annual IGES meeting in Denver as Program Committee chair. She would be honored to continue supporting the IGES community, increasing its visibility, and expanding professional opportunities for early-career researchers.

Five Selected Publications:

1. Nakase T, Guerra G, Ostrom QT, Ge T, Melin B, Wrensch M, Wiencke JK, Jenkins RB, Eckel-Passow JE, Bondy ML, Francis SS, **Kachuri L**. Genome-wide polygenic risk scores predict risk of glioma and molecular subtypes. Neuro-Oncology (2024) [PMID: 38916140]
2. **Kachuri L**, Chatterjee N, Hirbo J, Schaid DJ, Martin I, Kullo IJ, Kenny EE, Pasaniuc B, Polygenic Risk Methods Development (PRIMED) Consortium Methods Working Group, Witte JS, Ge T. Principles and methods for transferring polygenic risk scores across global populations. Nature Rev Genetics (2024) [PMID: 37620596]
3. **Kachuri L,** Hoffmann TJ, Jiang Y, Berndt SI, Shelley JP, Schaffer K, Machiela MJ, Freedman N, Huang W, Li S, Easterlin R, Goodman PJ, Till C, Thompson I, Lilja H, Van Den Eeden SK, Chanock SJ, Haiman CA, Conti DV, Klein R, Mosley JD, Graff RE, Witte JS. Genetically adjusted prostate-specific antigen (PSA) levels for prostate cancer screening. Nature Medicine (2023) [PMID: 37264206]
4. **Kachuri L**, Mak ACY, Hu D, Eng C, Huntsman S, Elhawary JR, Gupta N, Gabriel S, Xiao S, Gui H, Keys KL, Oni-Orisan A, Rodríguez-Santana JR, LeNoir M, Williams LK, Borrell LN, Gignoux CR, Zaitlen N, Burchard EG, Ziv E. Gene expression in African Americans, Puerto Ricans and Mexican Americans reveals ancestry-specific patterns of genetic architecture. Nature Genetics (2023) [PMID: 37231098]
5. **Kachuri L,** Francis SS, Morrison M, Wendt GA, Cavazos TB, Bossé Y, Rashkin SR, Ziv E, Witte JS. The landscape of host genetic factors involved in immune response to common viral infections. Genome Medicine (2020) [PMID: 33109261]