



INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Annual Meeting • October 18-20, 2026
Estérel Resort • Estérel, Quebec

Saturday, October 17

4:00pm-7:00pm	Registration	Salon Fridolin Hall
6:00pm	IGES Board Meeting	Salon du Lac-Lake Level

Sunday, October 18

IGES Annual Meeting-Day 1

7:00am-5:30pm	Registration	Salon Fridolin Hall
7:00am-8:15am	Complimentary Breakfast (for hotel guests)	Le Voilier Restaurant
8:15am-8:55am	Opening Session	Salon Fridolin ABC
8:15am-8:20am	Welcome	
8:20am-8:50am	Presidential Address: Emmanuelle Génin	
8:50am-8:55am	CANSSI Remarks - Jinko Graham	
8:55am-9:55am	Session 1 - Roger Williams Award	Salon Fridolin ABC

Chair: Hae Kyung Im

	Presentation	Abstract	Author
8:55am-9:10am	The Landscape and Phenotypic Impact of Mobile Element Variations in the UK Biobank	45	Dandan Tan
9:10am-9:25am	Can I Borrow Your Instruments? Robust and Efficient Mendelian Randomization by Sharing Across Outcome Traits	92	Anagh Chattopadhyay
9:25am-9:40am	Investigating Allele Count Cutoffs for Safe Sharing of Sequencing-Based Genome-Wide Association Study Summary Statistics	94	Hongyu Xiao
9:40am-9:55am	Multi-Ancestry GWAS of Triglyceride-to-HDL Ratio in 1.2 Million Individuals Reveals Distinct Mechanisms of Insulin Resistance and Cardiometabolic Risk	135	Urvashi Singh

9:55am-10:00am	ELSI activity: Whole-conference Online Workshop on AI for Genetic Epidemiology	Marie-Pierre Dubé
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10:00am-10:20am	Refreshment Break	Salon Fridolin Hall
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10:20am-11:50am	Session 2 - James Neel Award	Salon Fridolin ABC
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Chair: Mohamad Saad

10:20am-10:50am	Keynote Presentation: Josée Dupuis Unravelling the Genetic Architecture of Type 2 Diabetes Using Novel Statistical Approaches	
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	Presentation	Abstract	Author
10:50am-11:05am	Can Generative AI Learn Gene Expression Like Language? A Framework for Self-Supervised Representation Learning for Cancer Genomics	153	SeyedMohsen Hosseini
11:05am-11:20am	Robust Mendelian Randomization Estimation Using Weighted Quantile Regression	38	Julien St-Pierre
11:20am-11:35am	Low-Dimensional Linkage Disequilibrium Matrices as a Scalable Framework for Multi-Ancestry Fine-Mapping	111	Nadia Alipour
11:35am-11:50am	Estimation of Joint SNP Effects from GWAS Summary Statistics: Use of Reference Panel Genotype Frequencies	138	Fatemeh Yavartanoo

11:50am-1:20pm	Buffet Lunch (included for IGES registrants, you must wear your badge) IGES Committee Meetings -Pick up lunch at the <i>Le Voilier Restaurant</i> before going to your meeting room Young Investigator Committee Salon Du Nord Scientific Program Committee Salon Masson ELSI Committee Salon Exécutif		Le Voilier Restaurant
1:20pm-3:05pm	Session 3 - From GWAS to Biological Mechanisms and Drug Discovery Chair: Marie-Pierre Dubé		Salon Fridolin ABC
1:20pm-1:50pm	Keynote Presentation: Mike Inouye Multi-omic Approaches for Elucidating Aetiology and Enhancing Risk Prediction		
	Presentation	Abstract	Author
1:50pm-2:05pm	The Developmental GTEx Resource Enables the Discovery of Disease-Associated Genes	105	Sofia Salazar-Magaña
2:05pm-2:20pm	A Pangenomic Approach Reveals New Structural Variants Associated with Gene Expression in the CARTaGENE Cohort	101	Rose Laflamme
2:20pm-2:35pm	TL-TWAS: Transfer Learning for TWAS Using Large-Scale Transcriptomic Resources in Underpowered Target Context	93	Dongsoo Lee
2:35pm-2:50pm	Genetic Similarity Among 178 Disease Phenotypes Predicts Therapeutic and Side Effects for 1,711 Drugs	155	Rachel Melamed
2:50pm-3:05pm	Genetic Architecture of Pathway-Specific Metabolomic Aging Clocks in the Canadian Longitudinal Study on Aging	96	Thomas Zheng
3:05pm-3:20pm	Poster Highlights 1 Chair: Anvita Kulshrestha		
	Poster	Abstract	Author
	Phenome-Wide Atlas of HLA-regulated T-cell Receptor Variation Underlying Immune-mediated Traits and Diseases	76	Aaron Meyers
	SOLAMAME: Software for Large-scale MultiAllelic Variant and MEta Analyses	60	Yuriko Katsumata
	Statistical Behavior of Ratio Traits in Genetic Studies: Impact of Distribution and Correlation	16	Chao Xing
	Shared Genetic Architecture and Novel Pleiotropic Variants Across Solid Cancers	97	Stacey Winham
	Cell-Type-Aware Transcriptome-wide Association Studies Using Paired Bulk Gene Expression and Digital Pathology	161	Nicholas Larson
3:20pm-4:20pm	Poster Session 1 & Refreshments <i>The Dupuis room will be open starting Saturday, October 17th after 9:30pm. On Sunday, the room will be open at 7am.</i>		Salon Dupuis
4:20pm-5:35pm	Session 4 - Novel Statistical Methods in Genetic Epidemiology Chair: Peter Kraft		Salon Fridolin ABC
	Presentation	Abstract	Author
4:20pm-4:35pm	TorchGWAS2: Cost-Effective Phenome- and Genome-Wide Association Testing in Related Samples	48	Mengyu Zhang
4:35pm-4:50pm	Fast and Powerful Gene Discovery Using pQTL Weights: A Summary-Statistics-Based Method for Complex Trait Analysis	132	Xuexia Wang
4:50pm-5:05pm	VACANT: A Tool for Annotation-Stratified Rare Variant Association Analysis and Effect Size Estimation	150	Shu-Hsien Cho
5:05pm-5:20pm	Indirect-Direct Genetic Association Utilizing Partitioned Family-Based SNP Effects in MoBa Reveals Parental Genetic Nurture Traits Putatively Influencing Offspring Birth Weight while Controlling for Assortative Mating and Population Stratification	83	Annabel Perry
5:20pm-5:35pm	Population-Scale DNA Methylation Profiling from Long-Read Sequencing Data and EWAS of Aging in the All of Us Cohort	120	Sarbani Thakur

Monday, October 19		IGES Annual Meeting-Day 2	
7:00am-5:30pm	Registration	Salon Fridolin Hall	
7:00am-8:30am	Complimentary Breakfast (for hotel guests)	Le Voilier Restaurant	
8:30am-9:00am	Robert Elston Award for Best Paper 2025	Salon Fridolin ABC	
9:00am-10:00am	Session 5 - Polygenic Risk Prediction and Disease Stratification	Salon Fridolin ABC	
	Chair: Burcu Darst		
	Presentation	Abstract	Author
9:00am-9:15am	Polygenic Mapping and CRISPR-Based Imaging of Latent Mechanisms Underlying Type 2 Diabetes Reveal Distinct Disease Risk and Cellular Programs	53	Satoshi Yoshiji
9:15am-9:30am	Personalized Polygenic Score Through Genetic Ancestry Continuum	57	Chuan Fu Yap
9:30am-9:45am	Phenome-Derived Polygenic Scores and Social Determinants Jointly Shape Context-Dependent Disease Risk	28	Ying Wang
9:45am-10:00am	Identifying Shared and Distinct Biology Across Cancers Using Pathway-Based Polygenic Risk Scores	54	Jiachen Zhang
10:00am-10:15am	Poster Highlights 2		
	Chair: Andrew Paterson		
	Poster	Abstract	Author
	Multi-Ancestry Genome-Wide Association Meta-Analysis of Wearable-Derived Physical Activity Identifies Novel Loci in up to 214,000 Individuals	125	Charilaos Zisou
	Fine-Scale Regional Ancestry Classification: A Genealogically Validated Benchmark With Applications to Rare Variant Enrichment	61	Gilles-Philippe Morin
	New Proteomic and Rare Variant Analyses to Map Genetic Variants Associated with Lung Function to Causal Genes and Pathways	81	Nick Shrine
	Cerebrovascular Age to Map the Trajectory of Brain and Vascular Diseases	84	Cienna Gin-Naccarato
	Identification of Novel Genetic Associations with COVID-19 Severity Through Analysis of Mobile Element Variants	95	Jasmin Junseo Lee
10:15am-11:20am	Poster Session 2 & Refreshments	Salon Dupuis	
	Please have all posters down by 2:30pm		
11:20am-12:50pm	Buffet Lunch (included for IGES registrants, you must wear your badge)	Le Voilier Restaurant	
	Young Investigators Mentoring Lunch (Advance sign-up required)	ROK Restaurant	
	IGES Committee Meetings-Pick up lunch at the Le Voilier Restaurant before going to your meeting room		
	Education Committee	Salon Exécutif	
	Communications Committee	Salon Du Lac	
12:50pm-2:20pm	Session 6 - Causal Inference and GxE Interaction	Salon Fridolin ABC	
	Chair: Hongyu Zhao		
12:50pm-1:20pm	Keynote Presentation: Sriram Sankararaman		
	Understanding the Genetic Architecture of Complex Traits from Biobank-Scale Data: Statistical and Computational Challenges		
	Presentation	Abstract	Author
1:20pm-1:35pm	The Protective Effect of Education on Mental Health is Driven by Cognition	9	Stephanie Sheir
1:35pm-1:50pm	CaPri: A Bayesian Mendelian Randomization Method Robust to Widespread Horizontal Pleiotropy	22	Ou Ren
1:50pm-2:05pm	Deep Learning for Gene-Environment Interaction Analysis of Complex Traits	110	Jessica George
2:05pm-2:20pm	Disentangling Phenotype Scale, Amplification, and Effect Heterogeneity in Polygenic Gene-by-Environment Architecture	29	Zhengdong Liu

Monday, October 19

IGES Annual Meeting-Day 2

2:20pm-3:50pm	Session 7 - Diverse Populations and Deeper Insights in Human Genetics		Salon Fridolin ABC
	Chair: Anthony Herzig		
2:20pm-2:50pm	Keynote Presentation: Sasha Gusev Leveraging Large-Scale Data to Identify Novel Context-Specific Disease Mechanisms		
	Presentation	Abstract	Author
2:50pm-3:05pm	AfriGWAtlas: An Atlas of Genome-Wide Associations in African-Ancestry Populations	69	Mateus Gouveia
3:05pm-3:20pm	Large-Scale Multi-Omics Analyses of Cardiometabolic Traits in the Middle East	65	Areeba Irfan
3:20pm-3:35pm	Objective Multi-Criteria Optimisation Yields a Fine-Scale, Validated Ancestry Reference Panel That Improves Local Ancestry Inference for Admixed and Underrepresented Populations	124	Taghrid Aloraini
3:35pm-3:50pm	Longitudinal GWAS Reveals the Genetic Architecture of Kidney Function Across the Life Course in the Population and Disease	80	Iris Heid
3:50pm-4:05pm	Refreshment Break		Salon Fridolin Hall
4:05pm-5:30pm	Business Meeting and Awards		Salon Fridolin ABC
6:00pm-7:00pm	Networking Reception		Salon Dupuis
7:15pm-10:00pm	Annual Dinner Banquet		Salon Fridolin ABC

Tuesday, October 20

Education Workshop

7:30am-10:30am	Complimentary Breakfast (for hotel guests)	Le Voilier Restaurant
9:30am	Bus Departure for McGill University and Montreal Airport This will be the only bus departure from the resort.	Outside of Hotel Lobby
12:00pm-6:00pm	AI for Genomic Research: From Genomic Language Models to Agentic Workflows	McGill University
Workshop Chairs: Pingzhao Hu and Tae-Hwi Schwantes-An <i>This is separate from the IGES Annual Meeting, advance registration and payment required.</i>		

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Canada-wide training program in molecular epidemiology and statistical -omics

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INTERNATIONAL GENETIC EPIDEMIOLOGY SOCIETY

Annual Meeting • October 18-20, 2026

INVITED SPEAKERS



Josée Dupuis, PhD

McGill University, Montreal, Canada

Unravelling the Genetic Architecture of Type 2 Diabetes Using Novel Statistical Approaches

Josée Dupuis is Professor and Chair of the Department of Epidemiology, Biostatistics and Occupational Health at McGill University. Prior to joining McGill in 2022, she was Chair of the Department of Biostatistics at Boston University. Professor Dupuis's research focuses on the development of statistical methods for genome-wide association, rare variant analysis, gene-environment interaction, fine-mapping and colocalization, multi-omics integration, and their applications to diabetes and lung diseases. She served as IGES president and was honoured with the Society's Leadership Award for her substantial contributions to the field. She also received the 2020 American Society of Human Genetics Mentorship Award.



Mike Inouye, PhD

University of Cambridge, Cambridge, UK

Multi-omic Approaches for Elucidating Aetiology and Enhancing Risk Prediction

Mike Inouye is currently Professor of Systems Genomics and Population Health at the University of Cambridge, Theme Lead for Data Science and Population Health at the NIHR Cambridge Biomedical Research Centre, Director of Data Sciences at the Baker Heart and Diabetes Institute, and Director of the Cambridge Baker Systems Genomics Initiative. His lab has four main research programmes: (I) improving the prediction, prevention and management of common diseases with polygenic scores, (II) Uncovering insights into disease aetiology through integrative analysis of high-dimensional multi-omics data, (III) Developing open computational methods, tools and resources for translational research, and (IV) Developing green computing through the Green Algorithms Initiative.



Sriram Sankararaman, PhD

University of California, Los Angeles, USA

Understanding the Genetic Architecture of Complex Traits from Biobank-Scale Data: Statistical and Computational Challenges

Sriram Sankararaman is a Professor in the Departments of Computer Science, Human Genetics, and Computational Medicine at UCLA. His research interests lie at the interface of computer science, statistics, and biology. His lab develops machine learning algorithms to analyze genomic and biomedical data with the broad goal of understanding the interplay between evolution, genomes, and traits. He is a recipient of a NSF Career Award, a NIH Outstanding Investigator Award, a NIH Pathway to Independence Award, and fellowships from Microsoft Research, the Sloan Foundation, the Okawa Foundation and the Simons Institute as well as multiple teaching awards at UCLA.



Alexander (Sasha) Gusev, PhD

Harvard Medical School, Boston, USA

Leveraging Large-Scale Data to Identify Novel Context-Specific Disease Mechanisms

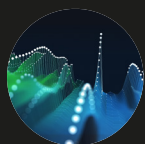
Alexander Sasha Gusev is a statistical geneticist and an Associate Professor of Medicine at the Dana Farber Cancer Institute in the Population Sciences Division. He received his PhD training in Computer Science from Columbia University, followed by a postdoctoral fellowship focused on developing computational methods to understand disease heritability at the Harvard School of Public Health. His lab has led the development of methods for deciphering biological mechanisms from genome-wide association studies, identifying germline-somatic interactions, and characterizing the germline influences on response to treatment. This work includes the development of the Transcriptome-Wide Association Study and related methods for integrating molecular and GWAS data.



CANSSI ONTARIO

Mission: To strengthen and enhance research and training in statistical science by developing programs that promote interdisciplinary research and enable multidisciplinary collaborations.

Funding & Other Opportunities

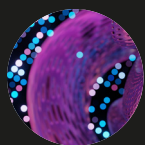


POSTDOCTORAL FELLOWSHIP IN STATISTICS

For postdoctoral fellows undertaking full-time research projects on theoretical or other areas of statistical sciences at CANSSI Ontario [partner universities](#) or at their affiliated research institutes. See [here](#) for details.

Postdoc Recruitment: NOV 21, 2026-JAN 16, 2027.

up to \$70,000 for two years



POSTDOCTORAL FELLOWSHIP IN GENOME DATA SCIENCE

To support postdoctoral research in genomics and data science, particularly projects involving new genomic technologies or multi-omic integration. The fellowship is open to postdocs based at CANSSI Ontario [partner universities](#) or at their affiliated research institutes. See [here](#) for details.

Deadline: MAR 1, 2027.

up to \$50,000 for two years



BANTING-CANSSI DISCOVERY AWARDS IN BIOSTATISTICS

These awards are intended to support early-career biostatisticians who work and collaborate with other scientists in biomedicine, occupational health, or environmental health. A total of four awards are available, two of the four awards are reserved for biostatisticians based in Ontario. See [here](#) for details.

Applications accepted on a rolling basis.

up to \$30,000 for one year

STAGE TRAINING PROGRAM

STAGE (Strategic Training for Advanced Genetic Epidemiology) is a Canada-wide training Fellowship in genetic epidemiology and statistical -omics that brings together experts in genetic epidemiology, statistical genetics, computer science, AI, population health and other research areas to train master's and doctoral graduate students and postdoctoral fellows at Canadian institutions to work across disciplinary boundaries.



Research Allowance



Travel Awards



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Courses and training

Deadline to apply: October 30, 2026

Details and application:
<https://stage.utoronto.ca>



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3:20pm-4:20pm Poster Session 1 with *Poster Highlights		
Presenter	Poster	Title
*Chao Xing	16	Statistical Behavior of Ratio Traits in Genetic Studies: Impact of Distribution and Correlation
*Yuriko Katsumata	60	SOLAMAME: S oftware for L arge-scale M ultiAllelic Variant and M Eta Analyses
* Aaron Meyers	76	Phenome-Wide Atlas of HLA-Regulated T-Cell Receptor Variation Underlying Immune-mediated Traits and Diseases
*Stacey Winham	97	Shared Genetic Architecture and Novel Pleiotropic Variants Across Solid Cancers
*Nicholas Larson	161	Cell-Type-Aware Transcriptome-Wide Association Studies Using Paired Bulk Gene Expression and Digital Pathology
Jingxian Wu	10	Uncovering Novel Atrial Fibrillation Genetics Through Pleiotropic Overlap with Life's Essential 8
Chiemela S. Odoemelam	13	Investigating Age-Dependent Genetic Associations with Lung Function
Hyunkyu Lee	15	GLEN: A Deep Learning Framework for Genetic Liability Prediction From Multimodal Data
Richard Howey	18	An End-to-End Implementation of KnockoffGWAS with Application to Primary Biliary Cholangitis Data
Elizabeth Blue	23	Local Ancestry Effects on the Relationship Between APOE Variation and Lipids and Inflammatory Markers
Anna Lorenz	24	The Genetic Architecture of Blood-based Biomarkers of the Central Nervous system – Insights from a Diverse Population-based Cohort
Jinko Graham	27	Prioritizing Variants in Familial Cancer Exome Sequencing Using Transmission Patterns
Claudia Moreau	31	Reconstructing the Haplotype Transmission Dynamics of Myotonic Dystrophy Type 1 in a Founder Population
Jonathan Bennet Krause	32	Epigenetic Aging Is Accelerated In Patients With X-linked Dystonia-Parkinsonism
Heejong Sung	33	Genetic Influences on Dimensional Psychopathology and Its Correlation with Bipolar Disorder Liability in the Amish Mennonite Bipolar Genetics Study
Xiaofeng Zhu	35	Partitioned Blood Pressure Polygenic Risk Reveals Differential Genetic Effects of Tissue-Specific Enhancers
Steven Buyske	39	Development of a New US Large-Scale Online Study on the Genetics of Breast Cancer Risk
Victor Vera Frazão	40	HapEyrie: Enlarging Population-Scale Genotype-Phenotype Simulations
Shili Luo	41	Effects of Polygenic Risk Scores and Physical Activity on Blood Pressure Trajectories in Childhood, Adolescence, and Young Adulthood
Rebecca Darlay	42	Investigating the Genetic Basis of HCC in the Context of MASLD
Alun Jones	43	Proteomic Profiling of Disease State and Treatment Response in Primary Biliary Cholangitis
Sara Lago	44	Genomic Viewer: Visual Integration of Multi-Omics Data for Functional Validation of Genome-Wide Association Study Risk Loci
Jayati Sharma	46	Polygenic Risk for Lung Cancer is Amplified by Current Smoking: A Comparison of Two PGS in the PLCO Cohort
Ghislain Rocheleau	47	Optimizing the Use of Longitudinal Data in Electronic Health Records for Genome-Wide Association Studies
Sergio Ordonez Beltran	49	Is It How Tall You Are as a Child or How Tall You End Up That Influences Socio-Economic Outcomes? A Life-Course Mendelian Randomization Analysis
Chen-Yang Su	50	Disentangling Adiposity-Related and Non-Adiposity-Related Pathways for Type 2 Diabetes
Tianyuan Lu	51	Dissecting Glycemic and Non-Glycemic Genetic Components of HbA1c Improves Diabetes Risk Stratification in Prediabetes
Aida Eslami	52	Power Comparison of X-Chromosome Association Methods - Application in Asthma
Anthony Herzig	55	A Methodological Framework for a Pan-European Genomic Reference Resource: Data Harmonization, Federated Analyses, and Early Results from the Genome of Europe Project

Presenter	Poster	Title
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Inti Pagnuco	58	Cross-Tissue Ancestry-Specific TWAS refines Type 2 Diabetes GWAS Loci
Hayley Power	59	An Assessment of the Contribution of Structural Variation to Known Pulmonary Fibrosis Loci
Katherine Fawcett	62	Gene-Based and Set-Based Tests of Primary Ciliary Dyskinesia Gene Variants and Asthma Susceptibility in UK Biobank
Roxana Moslehi	66	Integrative Multi-Omic and Epidemiologic Analyses Reveal Convergent Immune and Transcriptomic Dysregulation in Myalgic Encephalomyelitis/Chronic Fatigue Syndrome
Ohanna C. L. Bezerra	67	Novel Regulatory X-Chromosome Cpg Loci Associated With Recurrent Venous Thromboembolism Are Not Explained by Variable Escape From X-Chromosome Inactivation
Shihui Peng	68	Genetic Evidence Supports a Protective Role of Immunoglobulin M in Alzheimer's Disease
Jennifer Zevounou	71	Menopause-Associated Biological Age Acceleration and Its Contribution to Increased Blood Pressure
Zeluan LI	72	Interaction Index: A Novel Unified Measure for Interaction
Ariane T. Ange	74	Retrospective Modeling of Rare Variants: Impact of Including Unaffected Individuals and Functional Prioritization in a Founder Effect Family Cohort
Isabelle Foote	75	Multivariate Analysis of Frailty Improves Genomic Discovery and Provides New Insights Into How Frailty Influences Brain Aging
Matt Saward	78	Pleiotropic Effects of Asthma Genetic Risk Scores Partitioned Using Cell Specific Epigenomic Profiles
Jean-François Nepveu	82	Genotype-Phenotype Associations in Parkinson's Disease: A Systematic Review with Identification of Biological Pathways
Alexander Tinworth	85	Proteome-wide Genetic Analyses Identify ASGR1 as a Potential Mediator of Smoking on Ischaemic Heart Disease
Elyse Faucher	86	Effects of Extreme Temperatures on Cardiovascular and Pharmacogenomic Responses to Beta-Blocker Use
Michelle Yau	88	Leveraging a Multivariate Genomic Framework to Identify the Shared Genetic Architecture Between Osteoarthritis and Alzheimer's Disease
Peter Kraft	91	Multi-Ancestry Fine-Mapping in Two Million Participants Improves Breast-Cancer Credible Set Resolution
Benedikt Fröhlich	98	Age-Informed Finemapping Improves Prioritization of Likely Causal Variants for Kidney Function Decline
Jeewoen Shin	99	Multi-Omic Integration Reveals Rare Variant Effects on Blood DNA Methylation and Gene Expression in Alzheimer's Disease Loci
Shuyan Cheng	100	Rare Population-Specific HOXB13 Variants and Prostate Cancer Risk in The All of Us Research Program
Michael J. Betti	103	Multi-Ancestry Genome-Wide Association Study Identifies Novel Genetic Contributors to Dyslipidemia Risk in Childhood Cancer Survivors
Dominic Sayers	104	Single-Variant and Gene-based Rare Variant Analyses Identify Novel Associations with Survival in Idiopathic Pulmonary Fibrosis
Cristian Riccio	107	Polygenic Scores for Targeted Atrial Fibrillation Screening: Prime Time for the Clinic?
Shuangyu Zhao	108	Cell-Type-Informed DNA Methylation Clocks Reveal Immune Aging Signatures Across Immune-Mediated Diseases
Peyton McClelland	109	Pleiotropic Effects of HLA Alleles on Immune, Thyroid, and Lipid Traits in a Population-Based Canadian Cohort
Yan Sun	112	Multi-Ancestry Genome-Wide Association Study of Longitudinal BMI Variability and Trajectory
Brendan Newton	113	Investigating the Genetic Architecture of Juvenile Myoclonic Epilepsy Through Genome-Wide Association Meta-Analysis
Abhinav Kansal	117	Genetic Architecture of Height in Longitudinally Phenotyped Canadians from the Canadian Longitudinal Study on Aging (CLSA)

10:15am-11:20am Poster Session 2 with *Poster Highlights		
Presenter	Poster	Title
*Gilles-Philippe Morin	61	Fine-Scale Regional Ancestry Classification: A Genealogically Validated Benchmark With Applications to Rare Variant Enrichment
*Nick Shrine	81	New Proteomic and Rare Variant Analyses to Map Genetic Variants Associated with Lung Function to Causal Genes and Pathways
*Cienna Gin-Naccarato	84	Cerebrovascular Age to Map the Trajectory of Brain and Vascular Diseases
*Jasmin Junseo Lee	95	Identification of Novel Genetic Associations with COVID-19 Severity through Analysis of Mobile Element Variants
*Charilaos Zisou	125	Multi-Ancestry Genome-Wide Association Meta-Analysis of Wearable-Derived Physical Activity Identifies Novel Loci in up to 214,000 Individuals
Liuyan Zheng	11	Neurobehavioral Related Genes Exert Indirect Genetic Effects on Blood Lipid Profiles Through Behaviors: A Family-Based Study
Ana Luiza Arruda	19	The Genetic Architecture of Premature Ovarian Insufficiency is Mostly Shared with Common Variation Driving Age at Natural Menopause
Maggie Haitian Wang	26	Evolutionary Trait of the Mpox Virus in Its Recent Epidemics in Shenzhen and Clinical Association
Geetha Chittoor	30	Large-Scale Genome-Wide Association Meta-Analysis of Coronary Heart Disease in Hispanic/Latino Adults
Juan Pablo Tabja Bortesi	34	Genetic Confounding in Lipid-Cognition Associations: Evidence from the Canadian Longitudinal Study on Aging
Alyssa Green	36	Context-Specific Polygenic Risk Scores Provide Limited Improvement Over Traditional Approaches
Despoina Manousaki	37	Assessing the Causal Role of Maternal BMI in the Risk of Dysglycemia in Offspring: A Mendelian Randomization Study
Mohamad Saad	63	Leveraging Runs of Homozygosity to Identify Rare Susceptibility Loci for Cardiometabolic Traits in Middle Eastern Individuals
Sara Gunderson	70	Characterizing Sex Differences in the Effect of APOE on Lipid Profiles and Cognitive Trajectories
Christelle Nguenda Kemda	77	Towards Robust Epigenetic Age Estimation from Incomplete DNA-Methylation Data
Ozvan Bocher	79	Feature Stability in Multi-Omics Integration Models: A Comparative Study of MOFA and DIABLO
Peter Kraft	87	Links Between Prediagnostic Exposures, Germline Genetics, and Somatic Mutational Profiles in Triple-Negative Breast Cancer
Fasil Tekola-Ayele	89	Genetic Contributions to Early Life Growth Progression
John Baierl	106	S4-Oligo: Optimizing Polygenic Scores for Clinical Deployment
Anna Zaidi	115	A Multi-Organ Vascular Aging Clock to Map Trajectories of Systemic Disease
Sam Pedro Galilee Ayivi	116	Reduced Cancer Incidence Associated with Metformin use in <i>DNMT3A</i> -mutant Clonal Hematopoiesis: An Entropy Balancing Approach
Sebastian Sendel	119	Subtype-Specific Polygenic Scores Reveal Genetic Heterogeneity Across Dystonia Phenotypes
Iqra Tabassum	121	Genetic Epidemiology of Rare Genetic Diseases in the Punjabi Population
Marc Gros La Faige	122	Nationwide Insights Into Pharmacogenomics and Medication Use in France
Yasmeen Ehsan	123	Real-World Impact of Comprehensive β -Thalassemia Prevention Services in Punjab
Bowei Xiao	126	Copula Regression Improves the Ability to Detect Modulation of Promoter-Enhancer Dependence
Saa Moussa Tenguiano	127	Accounting for the Moderating Effect of Polygenic Risk Scores in Association Studies of Rare Variants With a Trait in Families

10:15am-11:20am Poster Session 2 continued		
Presenter	Poster	Title
Maurel Dylane Tchuisse Il Mbiagoup	128	Linear Mixed and Threshold Linear Mixed Model Analyses of <i>DNMT3A</i> -Associated <i>TET2</i> Clonal Expansion in Clonal Hematopoiesis Under Colchicine Treatment
Wendy Shue	129	GWAS of Quantitative Traits with Repeated Measures: Alanine Aminotransferase (ALT) Levels in the Canadian Longitudinal Study on Aging (CLSA)
Mykhaylo M. Malakhov	130	Accounting for Selected Genetic Regulators of Prostate-Specific Antigen Levels Enhances Prostate Cancer Prediction
Zhaotong Lin	131	MR2G: A Novel Framework for Causal Network Inference Using GWAS Summary Data
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Anvita Kulshrestha	140	Identifying Genes Associated with Occurrence of Leg Ulcers in Sickle Cell Disease Patients
Heather M Highland	142	Multi-Omic Signatures of Hepatic Steatosis in an Underrepresented Hispanic/Latino Population
Yu Shi	144	Bridging Ancestry Gaps in Polygenic Risk Scores with Linkage Disequilibrium-Aware Optimal Transport
Ting-Chen Wang	145	Brain Single-Nucleus and Multi-Omic Integration Reveals Female-Predominant <i>MS4A</i> Locus for AD CSF Biomarkers
Mohan Rakesh	146	Effects of Homozygosity on Fitness-Related Traits in the Taiwan Biobank
Alejandro Mejia Garcia	147	Genetic Architecture and Disease Tracking of a Multi-Ancestry Biological Aging Clock
Hsuan (Megan) Tsao	148	Genomic Atlas of Cardiac and Adiposity Imaging Phenotypes
Qihuang Zhang	149	Identifying Density-Correlated Genes from Single-Cell-Resolution Spatial Transcriptomics With DenMark: A Bayesian Hierarchical Model
Amandeep Kaur	151	Refined Phenotyping and Cross-Biobank GWAS Meta-Analysis Reveals New Genetic Insights into Multisite Chronic Pain
Denitsa Vasileva	152	BRIDGE: A New Epigenetic Clock for Mid-to-Late Life
Lap Sum Chan	156	Coxformer-Surv: transformer-based survival modelling of longitudinal health records for calibrated multi-disease risk prediction
Jinling Liu	157	Novel Alzheimer's Disease-Associated Variants and Genetic Interactions Identified from UK Biobank Whole-Exome Sequencing Data Using IBI-DT
Wiame Belbellaj	159	A Multi-Ancestry Optimization of Polygenic Risk Prediction for Type 1 Diabetes
Samaneh Mansouri	160	A Novel Statistical Method for Unmasking Sex-Specific Genomics Signatures in Complex Traits
Yaxin Luo	162	Genomic Analysis Highlights Polygenic and Region-Specific Contributions to ADHD-Migraine Comorbidity
Lavinia Paternoster	163	Using the Genotype-Phenotype Map (GPMaP) to Uncover Shared Skin Biology and Prioritise drug targets

Poster Sessions - Salon Dupuis

Salon Dupuis Hours

Saturday, October 17: 9:30 pm • Sunday, October 18: 7:00 am

All posters should be displayed before your assigned poster session and removed by 2:30 pm on Monday, October 19.

Pushpins will be provided.

Poster Session 1

Sunday 3:20pm-4:20pm

Poster Session 2

Monday 10:15am-11:20am

*Poster Highlights

