Agenda (only eligible sessions listed)

Please note as you are planning your agenda for the meeting, there is no partial credit for sessions. You may only claim credit for one full session per time block. Credits will <u>not</u> be available for on-demand content post-meeting. Credit hours are subject to change. Thank you for your understanding.

Time	Session	Session	Session Title	P.A.C.E.®	CME	NSGC	P.A.C.E.®
	Туре	Number		Program	Credit	Contact	Contact
				Number	Hours	Hours	Hours
Wednesday,	November 1						
11:00 am – 1:00 pm	Workshop	001	Genomic Analysis in the All of Us Researcher Workbench	603-001-23	2.00	2.00	
		002	Teaching Variant Curation through Team-based, Active Learning Approaches	603-002-23			2.00
2:00 pm –	Workshop	003	The Michigan Imputation Server: Data Preparation, Genotype Imputation, and Data Analysis	603-003-23	2.00	2.00	2.00
4:00 pm		004	Using UK Biobank to Scale up your Research	603-004-23			
4:30 pm – 5:00 pm	Plenary	005	Reflecting on our 75 years: Acknowledging our past, embracing our present, and dreaming about our future!	603-005-23	0.50	0.50	0.50
5:30 pm – 7:10 pm	Plenary	007	Featured Plenary Abstract Session I	603-007-23	1.75	1.75	1.50
Thursday, No	ovember 2						
	Platform	008	Advancing diagnoses for rare genetic diseases	603-008-23	1.50	1.50	1.50
		010	Multi-ancestry methods: This is the way	603-010-23			
		011	New advances in genome interpretation and functional studies	603-011-23			
8:30 am –		012	Novel genetic variations associated with cancer risk and outcomes	603-012-23			
10:00 am		013	Pharmacogenomics in the era of next-generation sequencing	603-013-23			
		014	Structural variation and the human genome	603-014-23			
		015	The health equity puzzle: Piecing together disparities for a fairer future	603-015-23			
	Platform	016	Advancing understanding of mechanisms in Alzheimer's Disease	603-016-23	1.50	1.50	1.50
		017	Causal noncoding variants and the genes they impact	603-017-23			
10:45 am – 12:15 pm		018	Chromatin connection to health and disease	603-018-23			
		019	Genetic basis of cardiovascular development and disease	603-019-23			
		020	Genetic tango: Dance between gene-gene and gene-environment interactions	603-020-23			
		021	Human genome evolving I	603-021-23			
		022	New treatments for some rare classics	603-022-23			
		023	Systematic analysis of variant functions	603-023-23			

Thursday, No	ovember 2						
		024	All about mom: Genetics and genomics of maternal outcomes	603-024-23			
1:45 – 2:45 pm	Platform	025	ARG! Ancestry-led reanalysis of genomes	603-025-23	1.00	1.00	
		026	CNVs in large-scale studies	603-026-23			
		027	Enemy within: Genetics of human autoimmune disorders	603-027-23			1.00
		028	Insights from systematic perturbation of the genome	603-028-23			1.00
		029	Life in the fast lane: Epigenetic aging and age acceleration in disease	603-029-23			
		030	New genetic insights into long-standing congenital phenotypes	603-030-23			
		031	Somatic mutation in health and disease	603-031-23			
5:30 pm – 7:10 pm	Plenary	047	Featured Plenary Abstract Session II	603-047-23	1.75	1.75	1.50
Friday, Nove	mber 3						
		048	Can we promise precision medicine to all?	603-048-23		1.50	
8:30 am – 10:00 am	Invited	049	Does size matter? Changing the rules of human genetics with miniproteins	603-049-23	1.50		
		050	Finding NEMO: Novel Enhanced Model Organism/Organs-on-chips platforms for translational genomics research	603-050-23			
		051	Genetic diagnosis of severe fetal and newborn conditions: Opportunities and challenges	603-051-23			
		052	RNA and nuclear structure: Perspective from the 4D nucleome program	603-052-23			1.50
		053	The ENCODE consortium: 2003 – 2023	603-053-23			
		054	The nature of nurture: The importance of modeling indirect genetic effects in large-scale genetic studies	603-054-23			
		055 Understanding huma	Understanding human genetic variation through the lens of germ cell biology	603-055-23			
		056	Use of race, ethnicity, and ancestry as population descriptors in genetics and genomics research	603-056-23	1		
10:45 am – 12:15 pm	Platform	057	Comparative omics to explore tumor landscapes	603-057-23	1.50	1.50	
		058	Mixtape of statistical genetics greatest hits	603-058-23			
		059	New mechanistic insights via diverse knockout models	603-059-23			1.50
		061	Scaling screening: A plethora of perspectives	603-061-23			
		062	Single-cell analyses across various tissues	603-062-23			
		063	Spatial omics: Resources and applications	603-063-23			
		064	Walking the dogma: Proteomics to inform genomic studies	603-064-23			

Friday, Nove	mber 3						
		065	Dysfunction of the power house: Mitochondrial disorders	603-065-23	.75	.75	.50
1:45 pm – 2:45 pm	Platform	066	Gene discovery from large-scale studies	603-066-23		1.00	1.00
		067	Genetic analysis of neurological disorders	603-067-23	1.00		
		068	More data, same problems: Bias in large-scale studies	603-068-23			
		069	Not fair and balanced: Learning about regulation from allelic bias	603-069-23			
		070	Sequencing, proceed with caution	603-070-23			1.00
		071	The mind's code: Unraveling neuropsychiatric disorders through genetics	603-071-23			
		072	Unraveling the genetic determinants of female infertility	603-072-23			
Saturday, No	vember 4						
8:30 am –	Invited	089	Al and machine learning in Alzheimer's disease genetics and genomics	603-089-23		1.50	1.50
		090	Deploying hundreds of mammalian genomes to understand human disease	603-090-23	1.50		
		091	Equitable access to genomics research: Australian Aboriginal leadership, expertise, and experience	603-091-23			
10:00 am		093	Male infertility – Mendelian traits with lifetime implications	603-093-23			
		094	Multiplexed assays of variant effect (MAVE): Generating, evaluating, and exploiting for improved clinical genetic diagnosis	603-094-23			
		095	Wrestling with social and behavioral genomics: Risks, potential benefits, and ethical responsibility	603-095-23			
10:30 am – 12:00 pm	Platform	096	Advancements in genome sequencing: Unraveling genetic factors in human health, disease, and phenotypic diversity	603-096-23	1.50	1.50	1.50
		097	Cell-type and context-dependent regulation of gene expression	603-097-23			
		098	Emerging tools for the genetic diagnostic toolbox	603-098-23			
		099	Epigenomics in neurodevelopmental disorders	603-099-23			
		100	Go beyond GWAS in type 2 diabetes, obesity and related metabolic disorders	603-100-23			
		102	Novel tools and data resources for genetic data analysis	603-102-23	1		
		103	Understanding kidney traits through genetics	603-103-23	1		

Saturday, No	vember 4						
		104	Addressing barriers to accessible genetic research and services	603-104-23			
1:00 pm – 2:00 pm	Platform	105	Epilepsy - new germline and somatic insights	603-105-23	1.00	1.00	1.00
		106	Human genome evolving II	603-106-23			
		107	Integrating functional annotation data in genetic association studies	603-107-23			
		108	Modifiers in neurological disease	603-108-23			
		109	New insights in inborn errors of metabolism	603-109-23			
		110	Omics, omics everywhere	603-110-23			
		111	Polygenic scores: Mediators, modifiers, and meanings	603-111-23			
5:00 pm – 6:40 pm	Plenary	127	Featured Plenary Abstract Session III	603-127-23	1.75	1.75	1.50
Sunday, Nov	ember 5					<u>'</u>	
		128	Advances in applied ancestry and admixture	603-128-23			
		129	Deep thoughts on brain genomics	603-129-23	1.00	1.00	
8:30 am –	Platform	130	Ode to tandem repeats in common disorders	603-130-23			1 00
9:30 am	Platform	131	RNA in action: Form and function	603-131-23			1.00
		132	Using proteomics to elucidate mechanisms underlying cardiometabolic traits and T2D	603-132-23	1.00		
		133	Al meets human genetics	603-133-23			
10:00 am – 11:00 am	Platform	134	Dollars and DNA: Financial considerations of genetic testing	603-134-23		1.00	1.00
		135	Genetic diagnosis of neurodevelopmental disorders beyond the exome	603-135-23			
		137	Rare germline variants and cancer susceptibility	603-137-23	1		
11:30 am – 1:00 pm	Plenary	138	Distinguished Speaker Symposium: The Future of Human Genetics and Genomics	603-138-23	1.50	1.50	1.50
TOTAL CREDIT COUNT				25.25	25.25	24.50	
TOTAL CREDIT COONT				CME	NSGC	P.A.C.E.®	