Start Time	End Time	517d	518	519	521	522	520a	520b	520c	524ab	524c
						Friday, July 12					
9:00 AM	10:45 AM		Tutorial IP1: Advanced machine learning methods for modeling, analyzing, and interpreting single-cell omics and spatial transcriptomics data	Tutorial IP6: Creating and running cloud-native pipelines with WDL, Dockstore, and Terra	Tutorial IP5: Modelling Multi-Modal Biomedical Data Using Networks	Tutorial IP4: Quantum-enabled multi-omics analysis	SCS	SCS Posters	YBS	Tutorial IP3: Multi-omic data integration for microbiome research using scikit-bio	Tutorial IP2: Just-in-time compiled Python for bioinformatics research
10:45 AM	11:00 AM	Coffee Break									
11:00 AM	1:00 PM		Tutorial IP1: Advanced machine learning methods for modeling, analyzing, and interpreting single-cell omics and spatial transcriptomics data	Tutorial IP6: Creating and running cloud-native pipelines with WDL, Dockstore, and Terra	Tutorial IP5: Modelling Multi-Modal Biomedical Data Using Networks	Tutorial IP4: Quantum-enabled multi-omics analysis	SCS	SCS Posters	YBS	Tutorial IP3: Multi-omic data integration for microbiome research using scikit-bio	Tutorial IP2: Just-in-time compiled Python for bioinformatics research
1:00 PM	2:00 PM	Lunch Break									
2:00 PM	4:00 PM		Tutorial IP1: Advanced machine learning methods for modeling, analyzing, and interpreting single-cell omics and spatial transcriptomics data	Tutorial IP7: Federated Ensemble Learning for Biomedical Data	Tutorial IP5: Modelling Multi-Modal Biomedical Data Using Networks	Tutorial IP4: Quantum-enabled multi-omics analysis	SCS	SCS Posters	YBS	Tutorial IP3: Multi-omic data integration for microbiome research using scikit-bio	Tutorial IP2: Just-in-time compiled Python for bioinformatics research
4:00 PM	4:15 PM	Coffee Break									
4:15 PM	6:00 PM		Tutorial IP1: Advanced machine learning methods for modeling, analyzing, and interpreting single-cell omics and spatial transcriptomics data	Tutorial IP7: Federated Ensemble Learning for Biomedical Data	Tutorial IP5: Modelling Multi-Modal Biomedical Data Using Networks	Tutorial IP4: Quantum-enabled multi-omics analysis	SCS	SCS Posters	YBS	Tutorial IP3: Multi-omic data integration for microbiome research using scikit-bio	Tutorial IP2: Just-in-time compiled Python for bioinformatics research
4:00 PM	6:00 PM	Career Fair in 517c (pre-registration required)									
6:15 PM	6:30 PM	Welcome in 517d									
6:30 PM	7:30 PM	Keynote - Fiona Brinkman in 517d									
7:30 PM	9:00 PM	Welcome Reception in 517c									

		Saturday, July 13									
Start Time	End Time	517d	518	519	521	522	520a	520b	520c	525	524c
		HitSeq	RegSys	iRNA	Eduation	BioOntologies	NIH/ODSS	Function	Microbiome	CompMS	Tech Talks
7:30 AM	8:00 AM	Serene Stretch Symposium - Yoga in Level 2, Hall Viger									
8:40 AM	9:00 AM	Welcome in 517d									
9:00 AM	10:00 AM	Keynote - Tandy Warnow in 517d									
10:00 AM	10:40 AM	Caffeinate and Connect with Exhibitors - Coffee Break									
10:40 AM	11:00 AM	Unsupervised learning approaches for genomics to decipher structure and dynamics of 3D genome organization and gene regulatory networks - Sushmita Roy	Continual improvement of cis-regulatory models - Carl de Boer	SPLASH is a reference-free statistical algorithm, unifying biological discovery in RNA-seq, single cell sequencing and beyond - TBD	Expanding data science training and health innovations in Africa: the DS-I Africa Consortium - Rolanda Julius	COSI Opening Remarks Learning from our collective scientific ignorance: How can ontologies help us determine what isn't yet? - Mayla Boguslav	Opening Remarks AI/ML to Identify and Stratify Non-Clinical Factors Contributing to Cancer Health Disparity in Rural Appalachia - Aisha Montgomery	Roll Call and Introduction to the Function COSI	Towards fully genome-resolved metagenomics - Christopher Quince	Disruption of ClpX reverses antifungal resistance - Jennifer Geddes-McAlister	Tech Talk: HPC-AI Support for Singapore's Bioinformaticians and Computational Biologists - Shoba Ranganathan
11:00 AM	11:20 AM						Estimating and Controlling for Fairness in Radiology with Missing Sensitive Information Confirmed Presenter: Jeremias Sulam Ethical Development of Imaging Biomarkers for Colorectal Biomarkers - Rina Khan	Linking Gene and function in the post-genomic era: issues and opportunities - Valerie de Crécy-Lagard			Tech Talk: Traversing the mouse-human interface with a knowledge graph of analytic and data services - Robyn Ball
11:20 AM	11:40 AM		Interpreting Cis-Regulatory Interactions from Large-Scale Deep Neural Networks for Genomics - Peter Koo	Hybrid exons build genome-wide proteomic complexity - Zachary Wakefield	Expanding the ISCB competency framework to describe professionals in bioinformatics core facilities - Marta Lloret-Llinares		Examining how social and behavioral determinants affect the prevalence, severity, and outcomes of Long-COVID-19 and health disparity - Deborah Mudali An Ethical Framework-Guided Tool for Assessing Bias in EHR based Big Data Studies - Bankole Olatosi		Effective binning of metagenomic contigs using contrastive multi-view representation learning - Shanfeng Zhu	Perception and reality of FDR control, data completeness and quantitative precision in (single-cell proteomics) DIA data - Martin Frejno A novel supervised learning algorithm for real-time collision energy selection to optimize peptide fragmentation in mass spectrometry - Mathieu Lavallée-Adam	Tech Talk: Network analyses for functional annotation with FunCoup tools - Erik Sonnhammer
11:40 AM	12:00 PM	An Adaptive K-Nearest Neighbor Graph Optimized for Single-cell and Spatial Clustering - Qi Liu	Chromatin accessibility is driven by intra-nucleosomal pioneer cooperativity that includes low affinity motifs - Melanie Weilert	Splicing-derived neo-epitopes in pediatric high-grade glioma - Priyanka Sehgal	Seven Domain Topics in Bioinformatics Education - Refining the ISCB Core Competencies to Access Diversity in Training - Nilson Coimbra		Modern, Intuitive Tools for Managing AI/ML Data in Health Equity-Focused Multiomic and Population Studies - Victor Nwankwo Use Explainable AI to Improve the Trust of and Detect the Bias of AI Models - Senait Tekle	Unveiling the Functional Fate of Duplicated Genes Through Expression Profiling - Alex Warwick Vesztrocy	Floria: Fast and accurate strain haplotyping in metagenomes - Jim Shaw	A learned score function improves the power of mass spectrometry database search - Varun Ananth	Tech Talk: Advances towards comprehensive and accurate whole genome analysis at scale using DRAGEN accelerated algorithms - Rami Mehio
12:00 PM	12:20 PM	A mechanistic and predictive model of the splicing status of scRNA-seq reads - Yuan Gao	Flash Talks (w/ Q&A) - Fangxin Cai, Cyrus Tam, Pedro Tomaz de Silva, Yusen Hou, Shamim Ashrafiyan	Flash Talks - Athma Pai	Support consistent, competent practice for data science in pathogen genomics: the development of an innovative competency framework - Dusanka Nikolic	Poster Madness - Tiffany Callahan	Panel: Discussion	Leveraging deep learning for characterization of malaria parasite PUFs — proteins of unknown function - Harsh R. Srivastava	The impact of transitive annotation on the training of taxonomic classifiers - Mihai Pop Sensitive, specific association of microbial functions with host phenotypes using Phylogenize2 - Patrick Bradley	Multi-Omic Data Workflows for Drug Discovery and Development - Matthew Glover	
12:20 PM	2:20 PM	Poster Session with Lunch Bioinformatics Advances Editorial Board meeting in 523b									

Start	End	Track 1	Track 2	Track 3	Track 4	Track 5	Track 6	Track 7	Track 8	Track 9	Track 10
2:20 PM	2:40 PM	Sigmoni: classification of nanopore signal with a compressed pangenome index - Vikram Shivakumar	Integrative modeling of multiscale single-cell spatial epigenome - Jian Ma	Accurate Assembly of Multiple RNA-seq Samples with Aletsch - Qian Shi	Bridging Education and Research: Data Hunters Workshop Empowering Bioinformatics Education via Microbiome Studies - Sara Fumagalli	Integration of Background Knowledge for Automatic Detection of Inconsistencies in Gene Ontology Annotation - Jiyu Chen	Deep LTMLE: Scalable Causal Survival Analysis with Transformer - Toru Shirakawa Cloud exploration and AI/ML-readiness of CAZyme annotation in human gut microbiome - Yanbin Yin Wearable Biosensing to Predict Imminent Aggressive Behavior in Psychiatric Inpatient Youths with Autism - Matthew Goodwin Improve speed, scalability, inter-operability of core C++ modules for Stan - a tool doing Bayesian modeling and statistical inference - Mitzi Morris	Crowdsoursing the Fifth Critical Assessment of Protein Function Annotation Algorithms (CAFA 5) - M. Clara De Paolis Kaluza	Reference-free Structural Variant Detection in Microbiomes via Long-read Co-assembly Graphs - Kristen Curry	A unified LC-MS metabolomics framework for multi-omics and systems biology - Jianguo Xia	Tech Talk: Enhancing Clinical Trial Outcomes with AI-based Predictive Biomarker Discovery via Contrastive Learning - Etai Jacob
2:40 PM	3:00 PM	Label-guided seed-chain-extend alignment on annotated De Bruijn graphs - Harun Mustafa		Detecting differential transcript usage in heterogenous populations with SPIT - Beril Erdogdu	Increasing training access with a new Distributed workshop model - Nia Hughes		LinkML: A FAIR data modeling framework for the biosciences and beyond - Nomi L Harris PubTator 3.0: an AI-powered Literature Resource for Unlocking Biomedical Knowledge - Robert Leaman Leveraging Language Models for Enhanced Biocuration and User Interaction in Reactome: A Pathway Towards Community-Driven Knowledge Enrichment - Nancy Li ToxPipe: Harnessing AI and Cloud Computing for Toxicological Data Exploration and Interpretation - Trey Saddler		Targeted Sequencing and Triplet Loss classification allow for microbiome-based inference of soil sample origin - Paweł P. Łabaj		Tech Talk: Miqa: Automating bioinformatics testing, evaluation and validation for real-time performance data & instant bug detection on every code change - Gwenn Berry
3:00 PM	3:20 PM	Compressed Indexing for Pangenome Substring Queries - Stephen Hwang	Enhancing Hi-C contact matrices for loop detection with Capricorn, a multi-view diffusion model - William Noble	Flash Talks - Ana Victoria Conesa Cegarra, Yu-Jen Lin, Eraj Khokhar	Learning through play: using games in bioinformatics training - Anna Swan	The cyclic nature of biases against understudied genes and diseases in knowledge graph embedding link prediction models - Michael Bradshaw	Panel: Discussion	StarFunc: interplaying template-based and deep learning approach for accurate protein function prediction - Chengxin Zhang MC-Funcformer: A foundational model of microbial community metabolism - Ananthan Nambiar	Integration and analysis of 168,000 human gut microbiome samples - Samantha Graham Assessing Microbial Genome Representation Across Various Reference Databases: A Comprehensive	waveome: characterizing temporal dynamics of metabolites in longitudinal studies - Ali Rahnavard AI-driven de novo structural candidate generation for mass spectra annotation - Margaret Martin	Tech Talk: UniProt: The Universal Protein resource: new features, access and tools for protein data - Aurélien Luciani
3:20 PM	3:40 PM	Sequence-to-graph alignment based copy number calling using a flow network	Ultra-long-range and interchromosomal loops link T cell superenhancers - Gabriel Dolsten	Deciphering Transcriptional Bursting Using Single-Cell Metabolic Labeling Data - Teresa Rummel	Empowering Global Genomic Innovation: The BioDev Network's Educational Blueprint for Cutting-Edge Science and Inclusion - Priyanka Surana	Prioritizing Causative Genomic Variants by Integrating Molecular and Functional Annotations from Multiple Biomedical Ontologies - Azza Althagafi		ProtBoost: Prediction of functional properties of the proteins by Py-Boost and protein language models (CAFA5 top2) - Alexander Chervov		A consensus serum metabolome by large-scale data mining reveals major gaps in metabolomic	
3:40 PM	4:00 PM	Targeted genotyping of complex polymorphic genes using short and long reads - Timofey Prodanov	scGrapHiC: Deep learning-based graph deconvolution for Hi-C using single cell gene expression - Ghulam Murtaza	Coordinated regulation by lncRNAs results in tight lncRNA-target couplings - Pavel Sumazin	Report from New York City: Bioinformatics Education Summit 2024			GORetriever: Reranking protein-description-based GO candidates by literature-driven deep information retrieval for precise protein function annotation - Huiying Yan	A rigorous benchmarking of methods for SARS-CoV-2 lineage abundance estimation in wastewater - Victor Gordeev	The sky is the limit: a cloud-based proteomics platform for the masses - Martin Frejno	
4:00 PM	4:40 PM	Caffeinate and Connect with Exhibitors - Coffee Break									

4:40 PM	5:00 PM	VISTA: An integrated framework for structural variant discovery - Varuni Sarwal	Cross-species and tissue imputation of species-level DNA methylation samples across mammalian species - Emily Maciejewski	SWARM: Single-molecule Workflow for Analysing RNA Modifications - Stefan Prodic	Teaching Bioinformatics through the Analysis of SARS-CoV-2: Project-Based Training for Computer Science Students - Pavlin G. Poličar	Taking AIIM at antibiotic resistance: harmonizing the nomenclature for aminoglycoside inactivating enzymes - Emily Bordeleau	Multi-Context Graph Neural Networks for Enhanced Multivariate Time-Series Analysis in Healthcare - Luciano Nocera Clustering-Informed Shared-Structure Variational Autoencoder for Missing Data Imputation in Large-Scale Healthcare Data - Yasin Khadem Charvadeh	InterLabelGO+: Unraveling label correlations in protein function prediction - Quancheng Liu	Towards more accurate microbial source tracking via non-negative matrix factorization (NMF) - Yanni Sun	SpecEncoder: Deep Metric Learning for Accurate Peptide Identification in Proteomics - Haixu Tang
5:00 PM	5:20 PM	Long-read sequencing and pangenome perspective of structural variation - TBD	Ontology-aware prediction of tissue-specific DNA methylation - Mirae Kim	Refinement of SARS-CoV-2 Intra-host Mutations Using Explainable Representations - Fatima Mostefai	Closing the computational biology "knowledge gap": Spanish Wikipedia as a case study - Nelly Sélem-Mojica	Investigating Food Composition Components in Cancer Prevention and Therapy using Knowledge Graphs - Hande McGinty	SCH: Predicting and Preventing Adverse Pregnancy Outcomes in Nulliparous Women - Ansaf Salleb-Aouissi SCH: Graph-based Spatial Transcriptomics	Discovery of PETases using a computational classification system - Joel Roca Martinez	Carbohydrate-active enzyme annotation in microbiomes using dbCAN3 - Yanbin Yin NUTRIclock, NEURAL NETWORKS ANALYSIS OF MICROBIOME FOR IMPLEMENTING PRECISSION NUTRITION IN AGING - Adrian Martin-Segura MIOSTONE: Modeling microbiome-trait associations with taxonomy-adaptive neural networks - Yifan Jiang	FLASHTagger: An open-source web application for ion type- and precursor mass-free protein identification in top-down mass spectrometry - Kyowon Jeong Imputation of cancer proteomics data with a deep model that learns jointly from many datasets - Lincoln Harris Proteogenomics analysis of human tissues using pangenomes - Husen
5:20 PM	5:40 PM		Virtual ChIP-seq: predicting transcription factor binding by learning from the transcriptome - Michael Hoffman	Tackling the genotype-to-phenotype problem in cancer evolution - Ashley Laughney	Celebrating 25 Years of Bioinformatics.ca - Francis Ouellette		AI/ML Ready mHealth and Wearable Data for Dyadic HCT - Bengie L Ortiz Enhancing the AI-readiness of	Plastic-MI-Tool, a machine learning tool for discovering and optimising plastic degrading enzymes - David Medina-Ortiz		
5:40 PM	6:00 PM					COSI Day 1 Wrap-up	Enhancing Imputation for Clinical Research: The Path for a Flexible Toolkit - Vida Abedi Closing Remarks	A BLAST from the past: revisiting BLAST's E-value - Yang Lu	Critical Assessment of Metagenome Interpretation - Updates and Future Benchmarking Challenges - Alice McHardy	An algorithm for decoy-free false discovery rate estimation in XL-MS/MS - Shantanu Jain
6:00 PM	8:00 PM	Celebrating 25 years of Bioinformatics.ca Ticketed event in room 710a								
6:00 PM	10:00 PM	Explore Montreal								

Sunday, July 14

Start Time	End Time	517d	518	519	521	522	520a	520b	520c	525	524ab	524c
		HitSeq	RegSys	iRNA	BioVis	Bio-Ontologies	Bioinformatics in Canada	Function	MICROBIOME	BioInfo Core	Text Mining	iCn3D
7:30 AM	8:00 AM	Serene Stretch Symposium - Yoga in Level 2, Hall Viger										
8:40 AM	9:00 AM	Welcome in 517d										
9:00 AM	10:00 AM	Keynote - Guillaume Bourque in 517d										
10:00 AM	10:40 AM	Caffeinate and Connect with Exhibitors - Coffee Break										
10:40 AM	11:00 AM	Why and how long reads are used to improve gene isoform quantification	Single-cell and single-molecule computational epigenomics - Maria Colomé Tatché	Interpretable models to understand regulation of RNA splicing - Christopher Burge	Opening When Visualization Meets AI: Exploring Opportunities	COSI Announcements Invited Presentation: Exploring Multiple Perspectives for Associative Knowledgebases - Karin Slater	The Silent Genomes Project: Building the path to equitable genomic care for Indigenous patients, one variant at a time. - Laura Arbour	Fast, high-performance biophysics-based computational methods in function prediction - Rafael Najmanovich	Sequence-based interrogation of soil microbiomes and their ecosystem benefits - Susannah Tringe	Building a Future-Proof Resource: The Comprehensive Modernization of TAIR - Swapnil Sawant	Combining computational pipelines and text mining to build a cell type knowledge graph resource - Richard Scheuermann	Introduction: "Visualizing Protein Function from Genes to Biology: Back to the Future" - Philippe Youkharibache Predicting Protein-Protein Interactions - Barry Honig
11:00 AM	11:20 AM											
11:20 AM	11:40 AM		REUNION: transcription factor binding prediction and regulatory association inference from single-cell multi-omics data - Yang Yang	IsoCLR: Contrastive learning for RNA foundation models - Ruian Shi			From Sequences to Reports: A Controlled Approach to Pipeline Validation in Cancer Genomics - Beatriz Lujan Toro	Energetic Local Frustration Through Time and Species - R. Gonzalo Parra	Understanding the small proteins from the global microbiome - Luis Pedro Coelho	Invited Presentation title TBA - Yann Fang	Enhancing Machine Learning Based Drug Response Prediction Models via Text Mining-Driven Feature Selection Approach - Arvind Mer Streamlining Drug Development with Conversational AI-Powered Knowledge Graphs: From Preclinical Discovery to Clinical Trials - Maaly Nassar	Critical assessment in Computational Structural Biology - John Moult 11:50 Protein Structure Accuracy Estimation Using Geometry-Complete Graph Neural Networks - Jianlin Cheng 12:10 The NSF Funded iCn3D POSE Project for Collaborative Research and Education in Mechanistic Biology - Ravi Abrol
11:40 AM	12:00 PM	Telomere-to-telomere assembly by preserving contained reads - Sudhanva Shyam Kamath	scHOCMO: Higher Order Correlation Model for Single-cell Multi-omics - Reetika Ghag	Explaining Deep Neural Networks for the Prediction of Translation Initiation - Uwe Ohler	PRIMAVO: Precision Immune Monitoring Assay Visualization Online - Zeynep H. Gümüş		The Canadian Genomic Data Commons (CGDC): A Platform for National Genomic Data Sharing - Erika Frangione	Function Prediction of Intrinsically Disordered Proteins and Regions: A Graph Auto-Encoder Approach - Mahta Mehdiabadi	Multi-level analysis of the gut–brain axis shows autism spectrum disorder-associated molecular and microbial profiles - James Morton	Panel: AI and LLMs in cores: How are we using them now?	eMIND: Enabling automatic collection of protein variation impacts in Alzheimer's disease from the literature - Cathy Wu	
12:00 PM	12:20 PM	Rawsamble: Overlapping and Assembling Raw Nanopore Signals using a Hash-based Seeding Mechanism - Can Firtina	Flash Talks (w/ Q&A) - Habib Daneshpajouh, Océane Cassan, Jianfeng Ke, Delaram Pouyabahar, Shaun Mahony	Translational efficiency covariation across cell types is a conserved organizing principle of mammalian transcriptomes - Can Cenik	The Best of Both Worlds: Blending Mixed Reality and 2D displays in an Hybrid Approach for Visual analysis of 3D Tissue Maps - Eric Mörth	Extracting Clinical Significance for Drug-Gene Interactions using FDA Label Packages - Matthew Cannon	Binomify: Unified normalization of ChIP-seq data through negative binomial regression - Abdul Rahman Diab	Mapping the affinity of protein-protein interactions with multiple amino acid mutations using deep neural networks - Yaron Orenstein	Metagenomic Mining Reveals Niche-Specific Bilirubin Reductases in the Gut Microbiome - Xiaofang Jiang		Poster Flash Presentations	
12:20 PM	2:20 PM	Poster Session with Lunch Fellows Workshop by invitation in 523b										

Start	End	(T1)	(T2)	(T3)	(T4)	(T5)	(T6)	(T7)	(T8)	(T9)	(T10)	(T11)
2:20 PM	2:40 PM	Conway-Bromage-Lyndon (CBL): an exact, dynamic representation of k-mer sets - Igor Martayan	A count-based model for delineating cell-cell interactions in spatial transcriptomics data - Hirak Sarkar	CellRBP: Improving Protein-RNA Binding Prediction In Vivo Using Cell-Type-Specific Features - Yaron Orenstein	Understanding Visualization Authoring for Genomics Data through User Interviews - Sehi L'Yi; New BioCyc Visualization Tools for Genome Exploration and Comparison - Suzanne Paley; Matreex: compact and interactive visualisation of large gene families - Yannis Nevers; Interactive visualisation of raw nanopore signal data with Squigualiser - Hiruna Samarakoon; Aggregate Annotated Single-Cell Heatmap Visualizations - Devin Lange	Predicting protein functions using positive-unlabeled ranking with ontology-based priors - Fernando Zhapa-Camacho	Bioinformatics and AI for precision farming - Abdoulaye Diallo	Utilising Large Language Models for GO Term Extraction in UniProt Annotation - Vishal Joshi	Scalable de novo Classification of Antimicrobial Resistance of Mycobacterium Tuberculosis - Christina Boucher	Streamlining Bioinformatics Pipelines with Nextflow: A Scalable, Portable, Reproducible, and Collaborative Solution. - Francesco Lescai	An informatic path to better understanding of cardiovascular biology and medicine - Peipei Ping	The impact of comparative structure analysis on protein classification at NCBI - Aron Marchler-Bauer; 14:35 From Immersive Visualization to Interdisciplinary Communication - Chris Henn; 14:50 Visualizing Immune Epitope Data: The Innovations of IEDB-3D 2.0 - Marcus De Almeida Mendes
2:40 PM	3:00 PM	Learning Locality-Sensitive Bucketing Functions - Xin Yuan	Mapping lineage-resolved scRNA-seq data with spatial transcriptomics using TemSOMap - Xinhai Pan	Reconstructing the sequence specificities of RNA-binding proteins across eukaryotes - Kaitlin Laverty				ProstGOPred: Advancing Protein Function Prediction through Graph Contrastive Learning and Structure-Aware Protein Language Model Embeddings - Weining Lin	Genomic analysis reveals dysregulation of the intratumor microbiome related to immune response in lung cancer - Youping Deng; Bioinformatics exploration of bacterial communities and plastic-degrading laccase from the gut microbiomes of plastic degrading beetle larvae - Jithin Sunny	Leveraging the NF-Core Framework for sharable institutional Nextflow modules at Memorial Sloan Kettering Cancer Center - Nikhil Kumar		
3:00 PM	3:20 PM	Fast Multiple Sequence Alignment via Multi-Armed Bandits - Kayvon Majoozi	Enhancing spatial transcriptomics analysis using deep learning-based batch effect mitigation - Rian Pratama	A novel NLP-based RBP binding motif and context discovery method using multiple-instance learning - Shaimae Elhajjajy; snoFlake: Discovery of a snoRNA-guided splicing regulatory complex via the snoRNA-RBP interactome - Kristina Sungeun Song; scTail: precise polyadenylation site detection and its alternative usage analysis from reads 1 preserved 3' scRNA-seq data - Ruiyan Hou		Protein Function: how much do we know and how much do we care? - An Phan; Harmonizing human and microbial datasets to explore mechanisms of the gut microbiome in disease - Brook Santangelo	UseGalaxy Canada now in production - Pierre-Étienne Jacques	Evaluation of large language models for discovery of gene set function - Mengzhou Hu		UTAP2: User-friendly Transcriptome and Epigenome Analysis Pipeline - Leshkowitz Dena; Managing Big Data in a High-Throughput Genomics Pipeline - Grace Pigeau	The Netherlands Neurogenetics Database: Reveiling clinical, neuropathological and genetic heterogeneity of brain-disorders - Inge Holtman; GeneAgent: Self-verification Language Agent for Gene Set Knowledge Discovery - Zhiyong Lu	New iCn3D tools for educators: color keys and collections - Sandra Porter; 15:10 iCn3D: visualization, analysis & sharing of protein structures and interactions - Jiyao Wang; 15:25 Using iCn3D to address molecular structure/function and to bridge the biology and chemistry educational communities - Henry Jakubowski
3:20 PM	3:40 PM	Contrasting and Combining Transcriptome Complexity Captured by Short and Long RNA Sequencing Reads - Seong Woo Han	Gene Regulatory Networks analysis from single cell multi-omics data - Zhana Duren		Aardvark: Composite Visualizations of Trees, Time-Series, and Images - Devin Lange	Apollo: A comprehensive GPU-powered Within-host Viral simulator with tissue and cellular hierarchies for studying viral evolutionary and infection dynamics. - Deshan Perera		Transformer based data mining for predicting moonlighting in proteins and comparison with first principle annotation - Dana Varghese	NetBio Towards semantic representation and causal inference in biomedicine. Challenges and - applications - Sergio Baranzini	Novel Linux-style code helps us all down the road - George Bell; Panel: New technologies in cores: single-cell, spatial, etc.	MolLM: A Unified Language Model for Integrating Biomedical Text with 2D and 3D Molecular Representations - Andrew Tran	
3:40 PM	4:00 PM	Quantum Computing for Genomic Analysis - Sergii Strelchuk	Dynamic Gene Regulatory Network Inference with Interpretable, Biophysically-Motivated Neural ODEs - Maggie Beheler-Amass	G4mer: Transcriptome-wide prediction of RNA G-quadruplexes with a deep RNA language model - Farica Zhuang	Boosting Data Interpretation with GiBOOST to Enhance Visualization of High-Dimensional Data - Komlan Atitey	Utanos: A general-purpose shallow whole genome sequencing analysis toolkit identifies interpretable copy number signatures - J Maxwell Douglas		Gene families of unknown function conserved across Fungi - Asaf Salamov			BioCoder: A Benchmark for Bioinformatics Code Generation with Large Language Models - Xiangru Tang	RCSB.org: a one-stop shop to explore biology in 3D - Jose Duarte; Advancing Molecular Graphics: MolviewSpec and Recent Enhancements in Molstar - Marcelo Querino Lima Afonso
4:00 PM	4:40 PM	Caffeinate and Connect with Exhibitors - Coffee Break										

4:40 PM	5:00 PM	Adaptive Digital Tissue Deconvolution - Franziska Görtler	Optimal sequencing budget allocation for trajectory reconstruction of single cells - Noa Moriel	Fast and accurate RNA virtual screening using non-canonical RNA base pair interaction networks and graph machine learning - Jérôme Waldispühl	Unveil Cis-acting Combinatorial mRNA Motifs by Interpreting Deep Neural Network - Xiaocheng Zeng	Using ontologies to make bioassay protocols machine readable - Alex Clark	The Quebec Genomic Data Center - Vincent Ferretti	Improved prediction of DNA and RNA binding proteins with deep learning models - Jun-Tao Guo	Modeling metastatic progression from cross-sectional cancer genomics data - Kevin Rupp	Short Talks, Various topics	Improving Medical Reasoning through Retrieval and Self-Reflection with Retrieval-Augmented Large Language Models - Minbyul Jeong	Envisioning the OSE for Biology Research and Education - Philippe Youkharibache Community Hackathons - Allissa Dillman
5:00 PM	5:20 PM	Maximizing accuracy of cellular deconvolution. (ACeD) - Jonathan Bard	Charting the role of RNA binding proteins in tissue-specific alternative splicing using machine explanations - Ayan Paul		The Insight's in the Details: Challenges and Opportunities in Visually Exploring High-Dimensional BioMedical Data - Fritz Lekschas	Knowledge graphs in Cancer Genomics: The Case of Mutational Signatures - Ulrike Steindl COSI Closing Remarks		Analysing multifunctional proteins with MultifacetedProtDB - Giulia Babbi	Multi-omics systems biology approach identifies novel signature genes for neuropsychiatric disorders - TBD		Panel: Leveraging AI, text mining and large language models to advance biology and medicine	Panel: Round Table Discussion
5:20 PM	5:40 PM	Evolution of genomic and epigenomic heterogeneity in prostate cancer from tissue and liquid biopsy - Marjorie Roskes	Harnessing deep learning to amplify insights from GWAS - Hae Kyung Im	Partial RNA Design - Frederic Runge	Award Ceremony & Closing		FraGNNet: A Deep Probabilistic Model for Mass Spectrum Prediction - Fei Wang	Dynamic network analysis of multi-scale -omics data for protein function prediction - Siyu Yang	Improved community detection through signed graphs in single-cell co-expression networks - Luis Augusto Eijy Nagai	Panel: Breakout Groups		
5:40 PM	6:00 PM	Accurate and robust bootstrap inference of single-cell phylogenies by integrating sequencing read counts - Rija Zaidi		High resolution deconvolution of RNA secondary structure via long read nanopore technology - J. White Bear Conclusion/Awards			Formation of the Canadian Artificial Intelligence and Mass Spectrometry Consortium (CAN-AIMS) - Jennifer Geddes-McAlister	Enhanced Functional Annotation for Genome-Scale Metabolic Models Using an Omics-Informed Integrated Pipeline - Jason McDermott	Fast Gene Regulatory Network Inference in Single-cell RNA-Seq with RegDiffusion - Hao Zhu			
6:00 PM	7:30 PM	Success Circles Ticketed Event in room 517c										18:00 - 19:30 iCn3D Workshop
7:30 PM	11:00 PM	President's Reception INVITE ONLY in room 720a										

Monday, July 15

Start Time	End Time	517d MLCSB	518 EvolCompGen	519 Gen Comp Biol	521 VarI	522 EDI	520a 3D	520b CAMDA	520c NetBio	525 WEB	524ab BOSC	524c Tech Talks
7:30 AM	8:00 AM	Serene Stretch Symposium - Yoga in Level 2, Hall Viger Green Task Force Meeting in 523b										
8:40 AM	9:00 AM	Welcome in 517d										
9:00 AM	10:00 AM	Keynote - Martin Steinegger in 517d										
10:00 AM	10:40 AM	Caffeinate and Connect with Exhibitors - Coffee Break										
10:40 AM	11:00 AM	How generative AI can transform biomedical research - James Zou SPRITE: improving spatial gene expression imputation with gene and cell networks - Eric Sun	Median and Small Parsimony Problems on RNA trees - Bertrand Marchand	An Empirical Study on KDIGO-Defined Acute Kidney Injury Prediction in the Intensive Care Unit - Xinrui Lyu	Opening Remarks Exploring the landscape of regulatory uORFs in BMPR2 and their potential as therapeutic targets - Danielle Gutman	Epidemiological topology data analysis links severe COVID-19 to RAAS and hyperlipidemia associated metabolic syndrome conditions - Aritra Bose	50 Years of Protein Structures & Structural Bioinformatics - Janet M Thornton	Welcome & Overview	Using proximity-dependent biotinylation to understand dynamic cell organization - Anne-Claude Gingras	WEB 2024: Experiential Learning on How to Implement AI in Bioinformatics Training	Opening Remarks Open Bioinformatics Foundation Update CoFest Intro Platinum and Gold Sponsor Videos	Utilizing Pre-Treatment Lab Values & Whole-Lung Radiomics for Modeling Survival Risk for ICB in the mNSCLC Setting - Kedar Patwardhan
11:00 AM	11:20 AM		Inferring transcript phylogenies based on precomputed groups of conserved transcripts - Wend Yam Donald Davy Ouedraogo	Mapping spatial omics when tissue architecture doesn't match - Patrick Martin	Beyond the sequence: interpreting missense variants with structure context - Jun Cheng	Disparate radiomic imaging features are predictive of recurrence events and molecular subtype in Black and White breast cancer patients - George Acquaah-Mensah	Democratizing Protein Language Models with Parameter-Efficient Fine-Tuning - Samuel Sledzieski	CAMDA Keynote: Exploring drivers of gut microbiome compositional differences in disease and mechanistic pathways to recovery using big data - Catherine Lozupone	GraphCompass: Spatial metrics for differential analyses of cell organization across conditions - Merel Kuijs		Gemma: Curation, re-analysis and dissemination of 18,000 gene expression studies - Paul Pavlidis	Enhancing Genomic Research through National Collaboration: The Role of Canada's National Data Platform - Felipe Pérez-Jvostov
11:20 AM	11:40 AM		A Representation for Phylogenetic Trees and Networks - Louxin Zhang	MALAT1 expression consistently indicates cell quality in single-cell RNA and single-nucleus RNA sequencing - Zoe Clarke		Towards Equitable MHC Binding Predictions: Computational Strategies to Assess and Reduce Data Bias - Mona Singh					EASTR: Identifying and eliminating systematic alignment errors in multi-exon genes - Ida Shinder ROC Picker: propagating statistical and systematic uncertainties in biological analyses - Jeffrey Roskes Djerba: Sharing and Updating a Modular System for Clinical Report Generation - Iain Bancarz Q&A For Flash Talks	The Missense3D portal: Structure-based evaluation of missense variants including protein complexes and transmembrane regions - Alessia David
11:40 AM	12:00 PM	Deciphering High-order Structures in Spatial Transcriptomes with Graph-guided Tucker Decomposition - Charles Broadbent	Accurate, scalable, and fully automated inference of species trees from raw genome assemblies using ROADIES - Anshu Gupta	Combining DNA and protein alignments to improve genome annotation with LiftOn - Kuan-Hao Chao	Capturing biophysical and protein language model constraints for an improved assessment of the impact of mutations on protein function and stability - Wim Vranken	From CABANA to CABANAnet – Building bioinformatics and knowledge exchange capacity in Latin America - Selene L Fernandez-Valverde	EquiPNAS: improved protein–nucleic acid binding site prediction using protein-language-model-informed equivariant deep graph neural networks - Debswapna		Functional analysis of MS-based proteomics data: from protein groups to networks - Nadezhda T. Doncheva		Antimicrobial resistance prediction of nontuberculous mycobacteria from whole genome sequence data - Idowu Olawoye	Integrated Pathway/Genome/Omics Informatics in Pathway Tools and BioCyc - Suzanne Paley
12:00 PM	12:20 PM	CellPie: a fast spatial transcriptomics factor discovery method via joint factorization of gene expression and imaging data - Sokratia Georgaka Integrating patients in time series clinical transcriptomics data - Sachin Mathur	Generalized c/µ Ratio Test for Detecting Molecular Adaptation: Beyond the conventional Ka/Ks Ratio test without Assuming Synonymous Site Neutrality or Limitation to Translated Regions - Chun Wu AlphaHOGs, a protein structure-based reference classification to improve orthology inference - Christophe Dessimoz	Optimal Phylogenetic Reconstruction of Insertion and Deletion Events - Sanjana Tule	VespaG: Expert-guided protein Language Models enable accurate and blazingly fast fitness prediction - Burkhard Rost Addressing biases in large language models for variant impact prediction in macro proteins - Oriol Gracia I Carmona		Accurate High-throughput Cryptic Binding Site Prediction Using Protein Language Model - Shuo Zhang		Direct Contacts 2: identification of direct physical interactions from > 25,000 mass spectrometry experiments - Kevin Drew		Open2C: Advancing 3D and functional genomics research - Vedat Yilmaz A Framework for DNA Binding Motifs Prediction for Nontraditional Model Organism Transcription Factors - Stephanie Hao Bioinformatics tools for comparative genomics analysis of highly similar duplicate genes in eukaryotic genomes - Xi Zhang Q&A For Flash Talks	CATH and TED: Protein structure classification in the age of AI - Nicola Bordin
12:20 PM	2:20 PM	Poster Session with Lunch Bioinformatics Editorial Board meeting in 445 Education Committee meeting in 523b										

Start	End											
2:20 PM	2:40 PM	Learning the Language of Biology: Transforming Biomedical Discovery with Foundation Models and Causal Inference - TBD Deep Reinforcement Learning for Controlled Traversing of the Attractor Landscape of Boolean Models in the Context of Cellular Reprogramming - Jakub Zarzycki	Joint inference of cell lineage and mitochondrial evolution from single-cell sequencing data - Viola Chen	Approximating facial expression effects on diagnostic accuracy via generative AI - Tanviben Patel	Clinical classification of variation for disease causality - Heidi Rehm		Contrastive learning in protein language space predicts interactions between drugs and protein targets - Rohit Singh	The Gut Microbiome based Health Index Challenge - Introduction - Kinga Zielińska	Identifying new cancer genes based on the integration of annotated gene sets via hypergraph neural networks - Chao Deng	WEB 2024: Experiential Learning on How to Implement AI in Bioinformatics Training	The Data Shows We Need Better Data - Mélanie Courtot	GPCRVS – a machine learning system for GPCR drug discovery - Paulina Dragan
2:40 PM	3:00 PM		Tracking tumorigenesis and the transition state through copy number variation-based pseudotime - Jonghyun Lee	Using Relation Equivariant Graph Neural Networks to Explore the Mosaic-like Tissue Architecture of Kidney Diseases with Spatially Resolved Transcriptomics - Mauminah Raina			NRGDock: An open-source software for ultra-massive high-throughput virtual screening - Thomas Descoteaux		Are under-studied proteins under-represented? How to fairly evaluate link prediction algorithms in network biology - Mehmet Koyutürk			Modelling multi-omic, real-world data reveals immunogenomic drivers of resistance to cancer immunotherapy
3:00 PM	3:20 PM		SPICE: Probabilistic reconstruction of copy-number evolution in cancer - Abigail Bunkum	scResolve: Recovering single cell expression profiles from multi-cellular spatial transcriptomics - Young Je Lee	Ensemble Prediction of the Clinical Impact of Missense Variants Substantially Decreases VUS Rate in Genetic Testing - Robert Kueffner MAJIQ-CLIN: A novel tool for the identification of Mendelian disease-causing variants from RNA-seq data - Dina Issakova		Enhancing Generalizability and Performance in Drug-Target Interaction Identification by Integrating Pharmacophore and Pre-trained Models - Zuolong Zhang	Integrating Taxonomic and Functional Features for Gut Microbiome Health Indexing - Rafael Perez Estrada	Protein Large Language Models are Effective, Generalized Protein-Protein Interaction Predictors - Joseph Szymborski			Decoding the grammar of DNA using Natural Language Processing
3:20 PM	3:40 PM	AttentionPert: Accurately Modeling Multiplexed Genetic Perturbations with Multi-scale Effects -	Uncovering Cancer's Fitness Landscape - Meaghan Parks	Multiview factorization for joint modeling of spatial multi-omics and histology images via NMF - William Bowie	Reclassifying variants of uncertain significance with transcriptional profiling - Kivilcim Ozturk		DOCKGROUND: a new release of the long-standing resource for studying protein recognition - Petras Kundrotas	Using Gradient Boosting to Predict Health States from Composition and Function of the Gut Microbiome - Patrick Smyth	Addressing data scarcity in biomedical research using Multilayer Networks - Iker Núñez Carpintero		Creating an open-source data platform - Mitchell Shiell	Transform Healthcare and Life Science with Biomedical Foundation models and Quantum computing
3:40 PM	4:00 PM	Predicting single-cell cellular responses to perturbations using cycle consistency learning - Wei Huang	Measuring pseudogenes' kinship to unravel overlooked evolutionary patterns - Valeriia Vasylieva Pseudogenes in plasmid genomes reveal past transitions in plasmid mobility - Dustin Hanke	Predicting gene functional associations from coevolutionary signals with EvoWeaver - Erik Wright	Metacell burden: A method to quantify the effects on neurodevelopmental disorders of rare genomic variants aggregated across brain cells. - Thomas Renne		On finding the right match – a structural perspective - Marian Novotny	Microbiome time series data reveal predictable patterns of change - Karwowska Zuzanna	Target repositioning using multi-layer networks and machine learning: the case of prostate cancer - Milan Picard		Going Viral: The Development of the VirusSeq Data Portal - Justin Richardsson intermine.bio2rdf.org : A QLever SPARQL endpoint for InterMine databases - François Belleau Organizing community curation to create an Open database on Thermodynamics of Enzyme-Catalyzed Reactions (openTECR) - Robert T. Giessmann Q&A For Flash Talks	
4:00 PM	4:40 PM	Grab and Go Coffee										

Start	End										
4:40 PM	5:00 PM	The role of chromatin state in intron retention: a case study in leveraging large scale deep learning models - Asa Ben-Hur Predicting interchromosomal Hi-C contacts from DNA sequence with TwinC - Anupama Jha	Long range segmentation of prokaryotic genomes by gene age and functionality - Yuri Wolf	Efficient parameter estimation for ODE models of cellular processes using semi-quantitative data - Domagoj Doresic	Representing Mutations for Predicting Cancer Drug Response - Patrick Wall	Quality Assurance, Semantic Enrichment and Integration of Multimodal Health Data for Phenotype and Cohort Discovery with Deep Learning - Ian Overton	Explaining Conformational Diversity in Protein Families through Molecular Motion - Valentin Lombard Pathway of transition for HIV-1 envelope trimer from prefusion-closed to CD4-bound open through an occluded-intermediate state - Myungjin Lee	Prediction in microbiome science - Jesse Shapiro	Transfer Learning of Condition-Specific Perturbation in Gene Interactions Improves Drug Response Prediction - Dongmin Bang		Connecting Integrated Genome Browser to a huge genome database using its open API solves one problem and creates another - Ann Loraine	
5:00 PM	5:20 PM	MolPLA: A Molecular Pre-training Framework for Learning Cores, R-Groups and their Linker Joints - Mogan Gim	The evolution of antibiotic resistance islands occurs within the framework of plasmid lineages - Yiqing Wang Elucidating the Co-Evolution and Genetic Diversity of Acquired Phototrophy in Marine Worm Convolutriloba longifissura - Adena Collens	NCBI's RNA-seq analysis pipeline produces millions of pre-computed gene expression counts to accelerate data reuse and discovery - Emily Clough	Assessing lethal missense mutations and polymorphism in Drosophila melanogaster with an evolutionary-informed model - Marina Abakarova A phylogenetic mutation-selection model predicts fitness effects of mutations in extant mammals - Thibault Latrille	TA-RNN: an Attention-based Time-aware Recurrent Neural Network Architecture for Electronic Health Records - Serdar Bozdag	Analysis and prediction of RuBisCO kinetics using deep learning - Aleksey Porollo	The Elephant in the Room: Software and Hardware Security Vulnerabilities of Portable Sequencing Devices - Carson Stillman Improving genomic epidemiology of Giardia intestinalis with a core genome gene-by-gene subtyping schema - Miguel Prieto Analysis of Inverted Repeats in Viral Genomes at a Large Scale - Madhavi Ganapathiraju	Draphnet: Learning the drug and phenotype network linking drug effects to disease genetics - Rachel Melamed		Collaborating our way to optimal integration between Tripal 4 and JBrowse 2 - Carolyn T. Caron An integrated environment for browsing 3-D protein structures and multiple sequence alignments in JBrowse 2 - Colin Diesh iCn3D, a Platform to Integrate Structures with Functions and Genomics - Jiyao Wang Q&A For Flash Talks	
5:20 PM	5:40 PM	Deep generative models for RNA splicing predictions and design - Yoseph Barash NEAR: Neural Embeddings for Amino acid Relationships - Daniel Olson	Quality assessment of gene repertoires with OMArk - Yannis Nevers	Enabling Affordable Single-Cell Data in Large Cohort Studies via Deep Generative Neural Networks and Active Learning - Jingtao Wang	Functional variomics for decoding variant effects - Nidhi Sahni	Share genetics between breast cancer and its predisposing diseases identifies candidate drugs for repurposing for breast cancer - Panagiotis Nikolaos Lalagkas Prevalence and biological impact of clinically relevant gene fusions in head and neck cancer - Emily Hoskins	Understanding and predicting ligand efficacy in the mu-opioid receptor through quantitative dynamical analysis of complex structures - Gabriel Galdino	Intgration of Spatial Transcriptomics into Multimodal Imaging of Skin Aging - Christina Bauer	Blending Biology, Chemistry and AI through network embeddings - Patrick Aloy		Codefair: Make Biomedical Research Software FAIR Without Breaking a Sweat - Bhavesh Patel An Open-source Ecosystem For Scalable And Computationally Efficient Nanopore Data Processing - Hasindu Gamaarachchi GenomeKit, a Python library for fast and easy access to genomic resources - Avishai Weissberg Q&A For Flash Talks	
5:40 PM	6:00 PM	Machine learning-enabled highly multiplexed monitoring of subcellular protein localization in live cells - Jiri Reinis PTM-Mamba: A PTM-Aware Protein Language	Leveraging machine learning to predict antimicrobial resistance in ESKAPE pathogens - Ethan Wolfe Predicting pathogen preferences and host adaptation by leveraging microbial genomics and machine learning - Evan Brenner	HINN: A Novel Neural Network Architecture to Integrate Multi-Omics Data based on their Biological Relationships - Yashu Vashishath		PhiHER2: Phenotype-informed weakly supervised model for HER2 status prediction from pathological images - Jian Liu	Dynamic network analysis of protein structural change - Aydin Wells	CAMDA 1st Day Summary			Tataki: Enhancing the robustness of bioinformatics workflows with simple, tolerant file format detection - Masaki Fukui Arvados Project Update - Peter Amstutz BiocPy: Facilitate Bioconductor Workflows in Python - Jayaram Kancherla	
6:15 PM	7:15 PM	ISCB Town Hall in 518										
		COSI Dinners - RSVP in advance is required										

Tuesday, July 16											
Start Time	End Time	517d	518	519	521	522	520a	520b	520c	524ab	524c
7:30 AM	8:00 AM	Serene Stretch Symposium - Yoga in Level 2, Hall Viger									
		MLCSB	EvolCompGen	TransMed	SysMod	CSI	3D	CAMDA	Digital Agriculture	BOSC	
8:40 AM	9:00 AM	Domain adaptation for cell-free DNA fragmentomics - Natalie Davidson DeepROCK: Error-controlled	Maximum Likelihood Phylogeographic Inference of Cell Motility and Cell Division from Spatial Lineage Tracing Data - Gary Hu	Advancing Genomic Medicine through Clinical and Research Strategies - Heidi Rehm	Keynote Speaker Talk: Digital twins and longitudinal deep phenotyping for preventive medicine and precision health - Nathan Price		Metallic origins of life - Yana Bromberg	Computational dissection of complex human disease - Andrey Rzhetsky	Current and new development in Digital Agriculture – Implication of deep learning and robotics in this new data science - Etienne Lord	Enhancing Reproducibility in Immunogenetics: Leveraging Containerization Technology for Bioinformatics Workflows - Rayo Suseno	
9:00 AM	9:20 AM	CODEX: COunterfactual Deep learning for the in-silico EXploration of cancer cell line perturbations - Stefan Schrod	Interpretable variational encoding of genotypes identifies comprehensive clonality and lineages in single cells geometrically - Hoi Man Chung			Building models of CAR-T signal integration, using automatized/dynamic high-dimensional dynamic profiling - Gregoire Altan-Bonnet				Breaking the silo: composable bioinformatics through cross-disciplinary open standards - Nezar Abdennur	
9:20 AM	9:40 AM	A statistical method for migration history inference reveals alternative patterns of metastatic dissemination, clonality and phyleticity - Divya Koyyalagunta A deep learning model of tumor cell architecture elucidates response and resistance to CDK4/6 inhibitors - Sungjoon Park	PHALCON: Phylogeny-aware variant calling from large-scale single-cell panel sequencing datasets - Priya	Transcriptional modulation unique to vulnerable motor neurons predict ALS across species and SOD1 gene mutations - Irene Mei Multi-dimensional Integration of PPI Network with Genetic and Molecular Data to Decipher the Genetic Underpinnings of RA Endotypes - Javad Rahimikollu	Building high quality dynamical models of gene regulatory circuits driving cellular state transitions using scRNA-seq data - Mingyang Lu	Invited Speaker with titleTBD - Duygu Ucar	De Novo Atomic Protein Structure Modeling for Cryo-EM Density Maps Using 3D Transformer and Hidden Markov Model - Jianlin Cheng		Single-plant omics : profiling individual plants in a field to identify processes affecting yield - Steven Maere	For long-term sustainable software in bioinformatics: a manifesto - Luis Pedro Coelho BioCompute: A Descriptive Standard for Computable Metadata - Jonathon Keeney Breaking Down Research Silos and Fostering Radical Collaboration through Collective Intelligence - Alberto Pepe Q&A For Flash Talks	
9:40 AM	10:00 AM	oncotree2vec – A method for embedding and clustering of tumor mutation trees - Monica-Andreea Baciu-Dragan	Genome streamlining: effect of mutation rate and population size on genome size reduction - Juliette Luiselli Evolutionary dynamics of microRNAs pinpoint innovations in the gene regulatory network of vertebrates - Felix Langschied	AI Epilepsy: Software solution to aid in the diagnosis of epilepsy using machine learning algorithms - Juan Carvajal HTJ2K as a Default Storage Format for Medical Images - Utkarsh Rai	Deciphering epigenetic regulatory mechanisms of IFNg-induced Epithelial to Mesenchymal Transition in human breast cells using systems approach - Humza Hemani	Inferring B cell phylogenies from single cell and bulk BCR sequence data with Dowser - Kenneth Hoehn	RiboDiffusion: Tertiary Structure-based RNA Inverse Folding with Generative Diffusion Models - Han Huang		Biomarker-based learning for disease prediction in precision dairy farming - Hayda Almeida	Tripal: a community-driven framework supporting open science, sustainable data web portals - Lacey-Anne Sanderson	
10:00 AM	10:40 AM	Caffeinate and Connect with Exhibitors - Coffee Break									

10:40 AM	11:00 AM	Deep learning of personal genomes - Sara Mostafavi

ConfuseNN: Interpreting convolutional neural network inferences in population genomics with data shuffling - Linh Tran | A machine-learning based alternative to phylogenetic bootstrap - Tal Pupko | The challenges of clinical deployment of automated cancer type classification for routine use - Quaid Morris | Mathematical Modeling suggests that Monocyte Activity may drive Sex Disparities during Influenza Infection - Tatum Liparulo | Invited Speaker with titleTBD - Hatice Hatice | Positional Protein Bioinformatics: A universal residue numbering scheme for the Immunoglobulin (Ig) fold enables its systemic detection in the protein universe - Philippe Youkharibache

ImmunoMatch: Illuminating the design of antibody heavy and light chain pairs using deep learning approaches and structure analysis - Dongjun Guo

Exploring the biophysical boundaries of protein families with deep learning methods - Miriam Poley-Gil | The Synthetic Clinical Health Records Challenge - Introduction - Joaquin Dopazo

Predicting Diabetes Complications from Electronic Health Record Visits Using Machine Learning Algorithms - Daniel Voskergian

Cluster-based machine learning prediction of diabetes complications - Daniel Santana-Quinteros

Statistical Measures for the Evaluation of Clustering Methods on Single Cell Data - Owen Visser | Empowering Dairy Farmers: A Transformer-Based Framework for Informed Decision Making in Dairy Agriculture - Vahid Naghashi

Anomaly Detection for Smart Aquaculture: Predicting Water Color Changes in Grouper Ponds - Kuan Y. Chang

Extracting meaningful video segments using a movement detection algorithm applied to dairy cow behavior study and welfare monitoring - Thomas Gisiger | Open Data, Knowledge Graphs, and Large Language Models - Andrew Su | Publishing reproducibility, FAIR, and using best practices - Patricia Palagi

Use of LLMs in writing, plagiarism and text recycling - Alex Bateman

Open Access Publishing: pros and cons - David Landsman

Strategies for managing expectations for submission, review, and

Challenges with reviewers: reviewing fatigue, acknowledgement, and dealing with delays and rejections - Scott Edmunds

Emerging Trends in Publishing Computational Biology Research - Jason Papin |
| 11:00 AM | 11:20 AM | | Neutral variation in a protein interaction network limits predictability of protein evolution - Soham Dibyachintan | | Predictive Modeling and Experimental Control of Macrophage Pro-Inflammatory Dynamics - Jennifer Riccio | Learning multiomic velocities of dynamic germinal center B cells using single-cell multiome - Alireza Karbalayghareh | | | | | |
| 11:20 AM | 11:40 AM | | Simultaneously Building and Reconciling a Synteny Tree - Mathieu Gascon | CIViC - an open-access knowledgebase for community driven curation of clinical variants in cancer - Mariam Khanfar

Timing the development of chemoresistance in relapsed pediatric cancer - Sasha Blay | Deciphering Cellular Fate Decisions: A Boolean Network Approach to Stress Response Network Tipping Points - Imran Shah | Sliding Window INteraction Grammar (SWING): a generalized interaction language model for peptide and protein interactions - Jane Siwek | | | | | |
| 11:40 AM | 12:00 PM | Panel: Trustworthy AI in the life sciences | ntSynt: multi-genome synteny detection using minimizer graph mappings - Inanc Birol | PHENO-DEX: Phenotypic Mapping of Dexamethasone Response in Breast Cancer Cells using Single-cell Transcriptomics - Jiaqi Li

Spatial landscape of malignant pleural and peritoneal mesothelioma tumor immune microenvironment - Hatice Osmanbeyoglu | Integrative Systems and Synthetic Biology identifies a Yeast Minimal Cell Cycle network that coordinates cell proliferation dynamics - Matteo Barberis | Improved Peptide-MHC Interaction Predictions through Deep Generative Adversarial Networks and a Unified MHC Class I and Class II Representation - Michael Klausen

TSpred: a robust prediction framework for TCR-epitope interactions using paired chain TCR sequence data - Ha Young Kim

Comprehensive neoantigen identification and prioritization using pVACtools and pVACview - Susanna Kiwala

Immune checkpoint molecule Tim-3 regulates microglial function and the development of Alzheimer's disease pathology - Ayshwarya Subramanian

Single-cell multi-omics reveals similarity between progenitor stem-cell-like CD8+ T cells and CD4+ follicular helper T cells in viral infection - Sarah Walker

Optimizing CAR T cell design using quantum | SPfast: Highly efficient protein structure alignment with segment-level representations and block-sparse optimization - Thomas Litfin

STRPsearch: fast detection of structured tandem repeat proteins - Alexander Monzon | | Precision Farming for Profit: Leveraging Profitability Maps and ILPMZ to Optimize Return on Investment and Soil Conservation of Agricultural Fields - Amanda Ashley Boatswain Jacques | Gene Set Summarization Using Large Language Models - Marcin Joachimiak | Panel: Panel Discussion |
| 12:00 PM | 12:20 PM | | | Poster Flash Talks | Harnessing Agent-Based Modeling in CellAgentChat to Unravel Cell-Cell Interactions from Single-Cell Data - Vishvak Raghavan | | The Encyclopedia of Domains - Nicola Bordin | | Revolutionizing Livestock Monitoring: AI-Powered Cow Detection in Farm Environments - Voncarlos Marcelo De Araujo | FAIR, modular and reproducible image-based ML workflows for biologists: a template and case study from imageomics - Hilmar Lapp | |
| 12:20 PM | 2:20 PM | Poster Session with Lunch
LGBTQ+ Meetup in 523b | | | | | | | | | |

Start	End	Track 1	Track 2	Track 3	Track 4	Track 5	Track 6	Track 7	Track 8	Track 9
2:20 PM	2:40 PM	Towards spatiotemporal design principles in multicellular systems - Mor Nitzan	Automated clade-level detection of Incomplete lineage sorting Confirmed Presenter: Maureen Stolzer	Integrative transcriptomic analysis and predictive modeling for immunotherapy response in melanoma - Yamil Damian Mahmoud A computational approach for the high-throughput identification of cancer-specific antigens for immunotherapeutic development - Rawan Shraim	Metabolic Objectives and Trade-offs in Single-cells during Cellular Transitions - Da-Wei Lin	Invited Speaker with titleTBD - Joshua Welch	Unraveling SARS-CoV-2 Spike Protein Evolution: A Comprehensive Structural Analysis - Natalia Fagundes Borges Teruel Dynamic and Energetic Consequences of Disulfide Bonds in Proteins - Miguel Fernandez-Martin	The Anti-Microbial Resistance Prediction Challenge - Introduction - TBD The Antimicrobial Resistance Prediction Challenge - Alper Yurtseven	Temporal Synchronization of Multi-View Video for Cattle Movement Analysis in Dynamic Farm Settings - Houda Orchi	Trust and Transparency in Reporting Machine Learning: The DOME-GigaScience Press Trial - Chris Armit
2:40 PM	3:00 PM		Sparse Neighbor Joining: rapid phylogenetic inference using a sparse distance matrix - Semih Kurt	Leveraging a Single-Cell Language Model for Precise EMT Status Prediction and Gene Signature Identification in Cancer - Shi Pan Streamlining Clinical Trial Matching Using a Two-Stage Zero-Shot LLM with Advanced Prompting - Mozhgan Saeidi	Structural Systems Biology of Levan Biosynthesis in Bacillus subtilis - Ragothaman Yennamalli Simple rules of intercellular communication for modeling emergent multicellular organization - Melissa Kemp	sciCSR infers B cell state transition and predicts class-switch recombination dynamics using single-cell transcriptomic data - Joseph Ng	DDMut-PPI: predicting effects of mutations on protein-protein interactions using graph-based deep learning - Yunzhuo Zhou		TBD	Panel: Open Approaches to AI/ML in Bioinformatics
3:00 PM	3:20 PM	Probabilistic Pathway-based Multimodal Factor Analysis - Alexander Immer SLIDE:	Scalable distance-based phylogeny inference using divide-and-conquer - Lars Arvestad	Multi-Omics Integration with High-Resolution AI-Derived Retinal Thickness: Unraveling Spatial Patterns of Retinal Susceptibility to Systemic Influences - Roberto Bonelli		FineST: Super resolved ligand-receptor interaction discovery by fusing spatial RNA-seq and histology images - Lingyu Li	DDAffinity: Predicting the changes in binding affinity of multiple point mutations using protein three-dimensional structure - Qichang Zhao	Machine learning models for AMR prediction - Anton Pashkov		
3:20 PM	3:40 PM	Significant Latent Factor Interaction Discovery and Exploration across biological domains - Jishnu Das	Panel: Panel session	New methods to discover drug combinations impacting cancer incidence - Rachel Melamed Closing Remarks	Closing Words	Computational integration of cellular circuits and immune repertoires based on multilayer network community association - Chang Lu	A multiscale functional map of somatic mutations in cancer integrating protein structure and network topology - Yingying Zhang	Biomarker identification by interpretable Maximum Mean Discrepancy - Dexiong Chen CAMDA Trophy Ceremony & Closing Remarks	HaloClass: State-of-the-art salt tolerant protein classification with natural language models - Kush Narang	
3:40 PM	4:00 PM	Grab and Go - Quick Coffee Break								
4:00 PM	5:00 PM	Keynote - Su-In Lee in 517d								
5:00 PM	5:30 PM	Awards Presentation in 517d								