Administrative Centre	Co-lead Centre	Leader Last Name	Leader First Name	Lead Institution	Co-Leader(s)	Project Title	Stream	Research Keywords	Methods & Technologies Keywords
Genome Alberta	Ontario Genomics	Benseler	Susan	University of Calgary	Pascal Tyrell	Building the AI4Care Network: Enabling transformative AI solutions for clinical applications	Health	Arthritis, genomics, artificial intelligence, precision medicine, care transformation	machine learning, bioinformatics, computer science
Genome Alberta		de Koning	Jason	University of Calgary		A toolkit for quantitative experimental design when inferring the functional effects of natural genomic variation	Health	Sequence analysis; statistical experimental design; comparative genomics; asymptotic power calculation; population genetics	Probabilistic modelling; large-scale inference; Markov Chain Monte Carlo
Genome Alberta		Derda	Ratmir	University of Alberta	Russ Greiner	Computational tools and sequencing database to accelerate discovery of ligands that bind to diverse targets in human proteome	Health	protein-ligand interaction, druggability, specificity, machine learning, ligand discovery	Macrocyclic peptides, genetically-encoded library, machine learning, next generation sequencing, database
Genome Alberta		Long	Quan	University of Calgary		Analyzing huge genomic datasets by 'out-of-core' technologies	Health	Statistical Genomics, Precision Medicine, Precision Agriculture, Scalable Computing, Memory Virtualization	Association Mapping, Genotype-based Phenotype Prediction, Memory Map, HDF5
Genome Alberta		Long	Quan	University of Calgary		Characterizing within-host sub-types and evolution using bulk and single-cell sequencing data	Health	Single-cell sequencing, Bulk sequencing, Haplotype reconstruction, Pan-genome, Molecular evolution.	Markov-chain Monte Carlo, Haplotype reconstruction, Personalized pan-genome, Coalescence models, Neutrality test.
Genome Alberta		Noskov	Sergei	University of Calgary	Ian Lewis	Establishing the computational foundation for predicting tomorrow's antibiotic targets	Health	Antimicrobial resistance, precision medicine, infection management, genome-to-metabolome analysis	Metabolomics, proteomics, genomics, machine learning, high-performance computing
Genome Alberta		Nuin	Paulo	University of Alberta	Stacey Hume	A novel bioinformatics pipeline designed for mitochondrial disease detection	Health	Mitochondrial disease diagnostics, Haplotype determination, diagnostics, genotyping, Single Nucleotide Variants	Genome assembly, phylogeny-based haplotyping/genotyping, low-frequency variant detection, genotype-phenotype correlation
Genome Alberta	Genome Prairie	Stothard	Paul	University of Alberta	Gary Van Domselaar	A comprehensive analytical tool-kit and hihg-performance genome brwoser for rapid, reliable and in-depth characterization of bacterial genomes	Multi-sector	Genome assembly, genome analysis, data visualization, functional prediction	High-performance computing, high-throughput sequencing, comparative genomics, machine learning
Genome Alberta		Tieleman	Peter	University of Calgary	Justin MacCallum	Consolidated modelling of complex cellular assemblies for applications in nanobiotechnology	Health	Cell wall structure, rational design therapeutics, precision medicine, drug delivery	Structural proteomics, molecular modelling, cellular and tissue models
Genome Alberta		Wang	Edwin	University of Calgary		A network method integrating 3-D images and single-cell multi-omic data to identify key genes associated with quantitative traits	Health	Single-cell omics, genomic associations	Network tools, data integration
Genome Alberta		Wishart	David	Univeristy of Alberta	Russ Greiner	Integrative Bioinformatic Resources for Precision Medicine	Health	Precision medicine, biomarkers, omic data integration, disease, bioinformatics	Data mining, text mining, simulation, databases, risk prediction
Genome Alberta		Zimmerly	Stephen	University of Calgary		Automatic annotation of group II introns, their interrupted genes, and other retroelements in bacterial genomes	Multi-sector	bacteria, group II introns, diversity-generating retroelements, reverse transcriptase	genome annotation
Genome Alberta		Zovoilis	Athan	Univeristy of Lethbridge		Development of a transcriptomics platform for the analysis of non-coding RNAs in neurodegenerative diseases.	Health	Dementia, RNA genomics, non-coding RNAs	RNA bioinformatics, next-generation sequencing, RNA-sequencing, patient stratification models
Genome Atlantic	Genome BC	Beiko	Robert	Dalhousie	Fiona Brinkman	Antimicrobial Resistance: Emergence, Transmission, and Ecology (ARETE)	Multi-sector	Transmission of antimicrobial resistance; genomics; mobile genetic elements; microbial ecology; animal products and by-products	Genomic island / plasmid prediction; resistance-gene detection; phylogenetics; metacommunity models
Genome Atlantic		Bielawski	Joseph	Dalhousie	Toby Kenney	Novel analytical frameworks for microbial metagenomucs, complex human diseases, and the prediction of patient health outcomes	Health	Metagenomics, Human genetics, Inflammatory bowel disease, Predictive modeling, Personalized clinical care	Bayesian modeling, Network modeling, Time series, Supervised learning, Bioinformatics pipeline
Genome Atlantic		Hu	Ting	Memorial		Evolutionary Learning and Network Modeling Approach for Metabolic Marker Discovery	Health	Metabolomics, human diseases, osteoarthritis, biomarker discovery, drug targeting	Systems biology, evolutionary algorithms, network biology, bipartite network, attribute interactions
Genome BC		Birol	Inanc	British Columbia Cancer Agency		Arrow: Advanced data types and pipelines for targeted analysis of sequencing data	Health	Repeat expansion; Alternative polyadenylation; Transcriptome assembly; Fusion detection; Analysis turnaround time	Machine learning; Targeted sequence analysis; Chromium sequencing; scRNA-seq analysis; Novel data types
Genome BC		Birol	Inanc	British Columbia Cancer Agency		AnnoVis: Annotation and visualization of de novo genome and transcriptome assemblies	Multi-sector	Functional annotation; Comparative genomics; Assembly quality control; Assembly visualization; Characterization of genic space	Machine learning; De novo sequence assembly; Long reads; Linked reads; High dimensional data visualization
Genome BC		Borchers	Christoph	University of Victoria	Yassene Mohammed	Proteogenomic Improved Guided Quantification Pipeline (PIGQpipe): Toward Personalized Targeted Proteomics	Health	Automation, information integration, complete experimental workflows, targeted proteomics, absolute quantification	API software modules, R statistical language, Java, Apache Tomcat, Apache eXtensible Interaction System
Genome BC		Breden	Felix	Simon Fraser University	Jamie Scott	Providing Secure Analysis of Federated Data Across Multiple Large-Scale Immunogenetic Repositories through the iReceptor Gateway	Health	Immune Repertoires; Vaccines; Therapeutic Antibodies; Cancer Immunotherapy;	Scientific Gateway; Distributed Data Federation; Data Sharing;
Genome BC	Génome Québec	Chindelevitch	Leonid	Simon Fraser University	Maxwell Libbrecht Jesse Shapiro	Machine learning methods to predict drug resistance in pathogenic bacteria	Health	Genome-wide association studies, bacterial pathogen genomics, antimicrobial resistance, machine learning, predictive modelling	Supervised machine learning, statistical learning, convolutional neural networks, deep learning, linear mixed models
Genome BC		Daley	Denise	University of British Columbia		Software, tools and pipelines to analyze targeted whole genome bisulfate sequencing data in combination with the development of a genetic risk index for food allergies and atopic diseases	Health	Asthma, atopic disease, food allergy, risk index, epigenetics	Genome wide association analyses, statistical genetics, epidemiology
Genome BC		Emberly	Eldon	Simon Fraser University	Michael Kobor	Predicting social epigenetic traits from DNA methylation data using dense neural networks	Health	social epigenetics, DNA methylation, machine learning	DNA methylation arrays, dense neural networks, principal component analysis
Genome BC		Ester	Martin	Simon Fraser University	Faraz Hach Colin Collins Artem Cherkasov	Next Generation Computational Methods and Tools for Precision Oncology	Health	Precision Oncology, Patient Stratification, Driver Events, Biomarker Discovery, Drug Discovery	Machine learning, Deep learning, Single Cell, Next Generation Sequencing
Genome BC		Farrer	Matthew	University of British Columbia	Ioannis Stylianou	GENAA - a web-based GENomics Analysis and Annotation bioinformatic tool set to inform genetic diagnosis, enable discovery and accelerate therapeutic development	Health	Neurology, data analysis, clinical reporting, neurogenetics	High-throughput sequencing, human genetics, web application, database
Genome BC	Genome Alberta	Foster	Leonard	University of British Columbia	David Wishart	Illuminating the dark matter of the human metabolome with convolutional neural networks	Health	metabolomics, cheminformatics, mass spectrometry, big data	deep learning, convolutional neural networks, machine learning, chemical structures
Genome BC		Friedman	Jan	University of British Columbia	Inanc Birol	Expanding the clinical diagnostic utility of whole-genome sequencing with an advanced bioinformatics tool for the analysis of short-tandem repeat variability in disease-associated genes	Health	Clinical testing, short-tandem repeats, genetics	Bioinformatics, whole genome sequencing
Genome BC		Gardy	Jennifer	University of British Columbia	Caroline Colijin	TBTB (Tuberculosis Bioinformatics Tool Box)	Health	Tuberculosis, genomic epidemiology, clinical microbial genomics	Information visualization, phylogenetics, mathematical modelling
Genome BC		Gsponer	Joerg	Michael Smith Laboratories	Nawar Malhis	Cancer driver versus passenger mutations: finding needles in hay stacks by new means	Health	Cancer, high-throughput sequencing, driver and passenger mutations, phenotype predictions, allosteric protein regulation	Data mining, machine learning, statistical inference
Genome BC		Hallam	Steven	University of British Columbia		Global scale metabolic pathway reconstruction from environmental genomes	Multi-sector	Microbial ecology, environmental genomics, biological engineering, data platforms and analytics, cloud computing	Scalable high-performance assembly and annotation services, metabolic models, visual analytics, data exploration and discovery portal

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Genome BC		Hsiao	William	University of British Columbia	Gary Van Domselaar	Bioinformatics Tools to Enable Federated, Real Time Genomic Epidemiology Data Sharing and Analysis in a One Health Framework	Multi-sector	data sharing, data integration, genomic epidemiology, one health, infectious diseases	ontology, semantic web technologies, data warehousing, sequence analysis, implementation science
Genome BC		Jones	Steven	British Columbia Cancer Agency	Marco Marra	Automated assessment of cancer drug sensitivities from genomic analysis	Health	precision medicine, drug sensitivity, cancer, pharmacogenomics	natural language processing, graph database, web application
Genome BC		Joy	Jeffrey	University of British Columbia	Julio Montaner	Development and implementation of bioinformatics tools for HIV and HCV phylogenetic monitoring platforms	Health	Phylodynamics, Epidemic Monitoring, Bioinformatic Tools for Epidemiology, Human Immunodeficiency virus (HIV), Hepatitis C (HCV)	Phylogenetic clustering, Birth-Death models, Javascript, Python, Geographic information systems (GIS)
Genome BC		Marra	Marco	BC Cancer Agency	Robin Coope	Machine Learning at the interface of Genomics, Tissue Morphology, and Radiology	Health	Cancer Genomics, Pathology Image Analysis, Clinical Automation	Machine Learning, Convolutional Neural Network Digital Pathology, Whole Slide Imaging
Genome BC		Morin	Gregg	Genome Sciences Centre	Steven Jones	Computational integration of Genome, Transcriptome, and Proteome datasets (iGTP): The development of computational methodologies for analysis of homologous proteomic, transcriptomic, and genomic tumour profiling data.	Health	tumourigenesis, cancer pathogenesis, biomarkers, treatment prediction	proteomics, RNA-seq, proteogenomics
Genome BC		Obeidat	Ma'en	University of British Columbia	Xuekui Zhang Don Sin	Novel computational Biology and Bioinformatics Approaches to Uncover the Molecular Drivers of COPD	Health	Lung, genetics, eQTL, SNP, mRNA	Integrative genomics, Bayesian hierarchical model, machine learning, causal inference
Genome BC		Tawhid	Mohamed	Thompson Rivers University		Genomic data analysis using machine learning and soft computing approaches	Health	Computational intelligence, Data analytics and mining for genomic data, biological image analysis, various genomic data (image data), deep learning.	Swarm intelligent algorithms, data mining algorithms, optimization, image processing approaches.
Genome BC		Tebbutt	Scott	University of British Columbia	Raymond Ng	DIABLO - a multi-OMIC data integration platform for robust biomarker development and enhanced biological interpretation	Health	Data integration; Multi-omics; Systems biology	Tensors factorization; Higher-order partial least squares; R Shiny; Docker
Genome BC		Wasserman	Wyeth	BC Children's Hospital Research Institute		Noncoding Variant ToolKit: Applied Bioinformatics for Interpreting Patient Whole Genomes	Health	Whole-genome sequence analysis Clinical genome interpretation Noncoding alterations Transcription factors Genome structure	Genome analysis pipelines Predictive algorithms/machine learning Motif (transcription factor binding site) detection Data-to-knowledge Open-source software
Genome BC		Zandstra	Peter	University of British Columbia	Martin Hirst	From cells to tissues and organs: Multi-scale modeling of development and disease	Health	stem cells, gastrulation, gene regulatory networks (GRN), self-organization, hematopoietic development	multi-scale modeling, agent-based modeling, computational modeling, automation, media development
Genome Prairie		Alexander	David	Cadham Provincial Laboratory (CPL)	Natalie Knox	UTOPIAN: A Metagenomics Pipeline for Universal Typing Of PAthogeNs	Health	Public health, pathogen detection, subtyping	Culture-independent diagnostic testing, metagenomics
Genome Prairie		Bidinosti	Christopher	University of Winnipeg	Mann Danny	Enabling the next revolution in prairie crop farming through the development of large labeled data sets and machine learning techniques	Multi-sector	Advanced farming practices, automated identification of crop plants and weeds, robotics	Automated generation of large labeled data sets, image classification, machine learning, parallel computing
Genome Prairie		Links	Matthew	University of Saskatchewan		The Biolighthouse project	Multi-sector	Provisioning, Reproducibility, Agility	Ansible, Ansible-Galaxy, Docker, Bioconda
Genome Prairie		Wu	Fang-Xiang	University of Saskatchewan	Kusalik/Yang	Bionetwork Analysis Methodologies and Applications	Health	complex diseases, health-related complex dataset, drug repositioning, gene-disease association, miRNA-disease association	genomic data analytics, bionetwork analytics, manifold learning, deep learning, Cytoscape
Génome Québec		Blanchette	Mathieu	McGill University	Jacek Majewski; Jérôme Waldispühl	Bioinformatics tools for integrative 3D epigenomics	Health	Epigenomics, Chromosome Conformation, 3D genome structure, Cancer, Development	Probabilistic modeling, Comparative Statistical Analysis, Visualization, Chromosome conformation capture technologies, Data integration
Génome Québec		Bourque	Guillaume	McGill University		Epigenomics Secure Data Sharing Platform for Integrative Analyses (EpiShare)	Health	Genomics, Epigenomics, Integretaive Analysis, Privacy, eQTL	Web portal, Distributed computing, GA4GH API, High Performance Computing, Docker images
Génome Québec		Bourque	Guillaume	McGill University	Toby Dylan Hocking	PeakLearner, a machine learning genome browser for interactive epigenomic data analysis	Health	Genomics, epigenomics, genetic disease, genome browser	Machine learning, artificial intelligence, data visualization, statistics, web
Génome Québec		Butler	Gregory	Concordia University		TooT Suite: Prediction and classification of transmembrane transport proteins	Multi-sector	Bioinformatics software and tools, protein annotation, transport protein classification, transport in biological networks	Genomics, machine learning, network analysis, big data, data integration
Génome Québec		Corbeil	Jacques	Université Laval	François Laviolette	Machine learning algorithms for biomarker and drug discovery enabled by high throughput technologies	Health	Diagnostics and prognostic, drug discovery, mechanism of action, biomarker discovery	mass spectrometry, metabolomic, machine learning, sparse and interpretable algorithms
Génome Québec		Diallo	Abdoulaye Banire	UQAM	Steven Kembel	Bioinformatics and AI for monitoring of pathogens: application to agriculture and forestry	Multi-sector	pathogen outbreaks biodiversity monitoring microbiome	phylodynamic and spatiotemporal methods Artificial Intelligence
Génome Québec		Diallo	Abdoulaye Banire	UQAM	Marc-André Sirard	Bioinformatics and Artificial Intelligence to model dairy production	Multi-sector	Dairy production, genotype-phenotype integration	Pattern discovery, classification, Machine learning, integrative genomics
Génome Québec		Droit	Arnaud	Université Laval	Daniel Sinnett	High-performance data integration platform for exploration and visualization of massive clinical and research data	Health	clinical data integration, multi-omics profiling and biomarker signatures, massive data, valorization	ElasticSearch, data linking, data sharing, dynamic visualizations
Génome Québec		Droit	Arnaud	Université Laval	Serge-Étienne Parent	Bioinformatics initiative for Soil Agriculture Microbiome Interpretation (BIOSAMI)	Multi-sector	Soil Health / Agricultural indicators / Soil Microbiome / Plant-microbe ecology	Bioinformatic tools / Visualization / Compositional biostatistics
Génome Québec		Girard	Simon	UQAC		A genealogical-genetic platform for data-sharing and complex population structures analysis	Health	Population genetics, genomics, health, genealogy, data sharing	Sequencing, genotyping, genealogical research, open-access data sharing
Génome Québec		Gravel	Simon	McGill University		Multi-cohort imputation using anonymized genomic data	Health	Genetics, statistics, privacy, data sharing	Imputation, inference, coalescent theory
Génome Québec		Greenwood	Celia	McGill University	Karim Oualkacha	Precision Medicine in Cellular Epigenomics	Health	DNA methylation; epigenetic alterations in autoimmune disease; cell type specific epigenetic profiles; epigenetic profiles and treatment response; asthma	Whole genome bisulfite sequencing and custom capture bisulfite sequencing; local smoothing regression; statistical methods for correlated counts; copula models; imputation methods
Génome Québec		Hallett	Michael	Concordia University	Vanessa Dumeaux	Computational Approaches for Cancer Monitoring and Surveillance	Health	computational biology, surveillance cancer studies, immuno-monitoring, microbiome, surrogate tissue analysis	Probabilistic models, single cell RNA and DNA DROP-sequencing, time series analyses, network, co-variation and correlative analyses
Génome Québec		Hussin	Julie	Université de Montréal		Deep Learning Methods in Biomedical Research	Health	Genomics, Multi-omics, Precision medicine	Bioinformatics, Deep learning, Predictive Modelling

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Génome Québec		Jacques	Pierre-Étienne	Université de Sherbrooke		Quality control and labelling prediction of epigenomic data using thousands of publicly available data sets	Health	Quality control, Labelling prediction, Data analysis and interpretation, Bioinformatics tool development, Data sharing	Machine Learning, Application programming interface, High-Performance Computing, Python, C++
Génome Québec		Major	François	Université de Montréal		Tools to determine and analyze cell-type specific microRNA-mRNA interaction networks	Health	MicroRNA-mediated gene regulation, transcriptome-proteome relationships, genome-wide identification of microRNA targets, stoichiometric analysis of microRNA activity, gene regulation alteration in disease	Stable matching algorithm, next generation sequencing, graph theory, machine learning, RNA-seq metadata
Génome Québec		Najafabadi	Hamed S.	McGill University	Olivia Wilkins	NatRegs: a resource for tapping into natural variation in regulatory network diversity	Multi-sector	Crop production, climate change, regulatory network, evolutionary diversity, stress	Network component analysis, population genomics
Génome Québec		Najmanovich	Rafael	Université de Montréal		Next-generation molecular docking leveraging artificial intelligence techniques to understand large-scale kinase inhibitor datasets	Health	kinase-specific scoring; backbone flexibility; massive virtual screening; large-scale kinase-inhibitor binding affinity datasets;	Molecular docking; machine learning; normal mode analysis; data-mining
Génome Québec		Salavati	Reza	McGill University	Hamed S. Najafabadi	A universal framework for analysis of parasite genome sequences for drug discovery	Health	Computational biology, pathogenic parasite genomes, gene regulatory networks, essential genes, targets for chemotherapeutics	RNA profiling, proteomics, computational platform, pipelining, function prediction, drug targets from genomics
Génome Québec		Strömvik	Martina	McGill University		Integrative computational tools for assessing genome-environment effects on crop plants in a changing climate	Multi-sector	Genomics and phenomics, gene expression, crop improvement, crop management in a changing climate, sustainable agriculture	Genome and transcriptome sequencing, crop sensing, precision agriculture, plant breeding, algorithm development, image analysis
Génome Québec	Ontario Genomics	Tyers	Michael	Université de Montréal	Daniel Durocher	A database and toolset for unification, dissemination and integrative analysis of CRISPR/Cas9-based genetic screen data	Health	genotype-phenotype relationship, disease gene, tissue-specific phenotype, data normalization, data visualization	CRISPR/Cas9, genetic screens, human cell lines, scoring algorithms, open access data portal
Génome Québec	Genome BC	Waldispühl	Jérôme	McGill University	Ryan Brinkman	Human-centered computational methods for the analysis of flow cytometry data sets	Health	Flow cytometry, high dimensional data analysis, cancer, immunology, transplantation	Clustering, unsupervised learning, Human-in-the-loop, Virtual/Augmented reality, human-computer interaction
Génome Québec		Xia	Jianguo	McGill University	Niladri Basu	Development, validation and application of a web-based toxicogenomics platform to address environmental pollutants	Multi-sector	Toxicogenomics, Toxicometabolomics, Environmental Health, Risk assessment, Food safety	Web-based Applications, Cloud computing, Chemoinformatics, Machine learning, Networks, Big Data Mining, Visualizations
Génome Québec		Xia	Jianguo	McGill University	Guillaume Bourque; Pierre-Étienne Jacques	An integrative platform for metabolomics and microbiomics	Health	Metabolomics, Microbiome, Systems Biology, Biomarker, Infectious Diseases	Cloud computing, Browser-based computing, Statistics, Machine Learning, Web-based Platform
Génome Québec		Xia	Yu	McGill University	Edward Fon	Using multi-scale models of biomolecular networks to interpret genomic data in neurological disorders	Health	Protein structure and function, protein-protein interaction, genetic variation, alternative splicing, neurological disorders	Protein bioinformatics, structural modelling, network modelling, sequence analysis, data integration.
Ontario Genomics		Adamowicz	Sarah	University of Guelph	Paul Hebert	Extracting Signal from Noise: Big Biodiversity Analysis from High-Throughput Sequence Data	Multi-sector	Metagenomics, metabarcoding, biodiversity, genomic signatures, data mining	High-throughput DNA sequencing, machine learning, classification algorithms, data visualization, signal processing
Ontario Genomics		Bader	Gary	University of Toronto	Quaid Morris	Improving GeneMANIA machine learning technology for disease research	Health	Data integration; Gene function prediction; precision medicine; machine learning; tissue/disease genomics	Machine learning; deep learning; network integration; gene and patient similarity networks
Ontario Genomics		Boone	Charles	University of Toronto	Chad L. Myers	BridGE: A novel, network-based approach to discover genetic interactions underlying human disease	Health	Genetic interaction, networks, genetic modifiers, disease	Computational method to discover genetic interactions that modify disease risk
Ontario Genomics		Briollais	Laurent	Tanenbaum-Lunenfeld Research Institute	Rayjean Hung	Development and application of innovative computational and analytical tools for translational research in genomics and complex diseases	Health	Statistical genetics– Molecular epidemiology – Clinical studies – Translation – Personalized medicine	High-throughput technology – Genetic association – Reproducibility – Simulations - Risk prediction
Ontario Genomics		Brudno	Michael	University of Toronto	Rosanna Weksberg	EpigenDIG: distributed analysis of epigenetic datasets related to congenital, developmental and childhood disorders	Health	Bioinformatics, epigenetics, neurodevelopmental disorders, genetic mutations, DNA methylation	Machine learning, predictive models, DNA methylation analysis, high-performance computing, next generation sequencing
Ontario Genomics		Doxey	Andrew	University of Waterloo	Trevor Charles	Hydroponics Health Predictor: predicting and modelling healthy plant microbiomes through'omic datasets and machine learning	Multi-sector	Metagenomics, hydroponics, microbiome, precision agriculture	Next generation sequencing, machine learning, envirogenomics
Ontario Genomics		Farber	Jeff	University of Guelph	Emma Hartnett	Computational Tools to Harness WGS in Risk-Based Decision Making for Safe Food	Multi-sector	Genotype-phenotype link, microbial risk assessment, molecular epidemiology, food/hazard risk, preventative controls	in silico virulence gene mapping, Whole Genome Single Nucleotide Polymorphisms (wgSNP), stochastic simulation, FDA-iRISK
Ontario Genomics		Feilotter	Harriet	Queen's University	Mojib Javadi	Genomic Data Ingestion, Indexing and Federation System (GDIIFS) for an extended research informatics platform	Health	Data ingestion, Data integration, Query, Genomics, Quality Metrics	Pipeline development, Query API, Sequencing, visual analytics
Ontario Genomics		Ferretti	Vincent	Ontario Institute for Cancer Research	Ivan Borozan	A comprehensive software platform for metagenomic analysis and pathogen identification in human genomes	Health	Metagenomics, Virome, Cancer	Next generation sequencing data analysis, Scrum software development
Ontario Genomics		Ferretti	Vincent	Ontario Institute for Cancer Research	Junjun Zhang	JTracker - an open framework for scientific workflow authoring, sharing and execution	Health	big data; data provenance; reproducible analysis scaled for the cloud; enabling large-scale data analysis; compute environment agnostic workflow automation	cloud computing; standardized API; interoperability with existing workflow systems; Common Workflow Language
Ontario Genomics		Gingras	Anne-Claude	Tanenbaum-Lunenfeld Research Institute Mount Sinai Hospital	Hannes Röst	Computational tools for Data-Independent Acquisition (DIA) for quantitative proteomics and metabolomics	Health	Proteomics, metabolomics, post-translational modifications, systems biology, cellular perturbations	Quantitative mass spectrometry, data-independent acquisition, high-performance and cloud computing, data visualization, user training
Ontario Genomics		Gnaneshan	Saravanamuttu	Public Health Ontario/ University of Toronto	Samir Patel	A multi-functional metagenomics platform for the detection, characterization and transmission of public health pathogens.	Health	Infectious diseases; Rapid clinical testing; Identification, characterization and transmission of pathogens; Metagenomics; Outbreak and surveillance.	Unbiased taxon assignation; Machine learning; Tools development, validation and integration; Data Integration / federation; Web framework development.
Ontario Genomics		Haibe-Kains	Benjamin	Princess Margaret Cancer Centre	N/A	Open-source web-application for integrative drug taxonomy	Health	Drugs, Experimental Compounds, Cancer, Pharmacogenomics, Machine Learning	Machine Learning, Statistical Inference, Genomics, Benchmark, Web-Application
Ontario Genomics		Haibe-Kains	Benjamin	Princess Margaret Cancer Centre	N/A	SYNERGx: an open-source computational framework for drug combination synergy prediction	Health	Cancer, Pharmacogenomics, Biomarker Discovery, Machine Learning, Drug Combination Synergy	Machine Learning, Statistical Inference, Genomics, Benchmark, Web-Application

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Ontario Genomics		Haibe-Kains	Benjamin	Princess Margaret Cancer Centre	Trevor Pugh	Open-access framework for linkage of preclinical and clinical data to guide treatment decision in cancer	Health	Cancer, Pharmacogenomics, Biomarkers, Machine Learning, Translational Research	Genomics Profiling, Machine Learning Algorithms, Web-Applications
Ontario Genomics		Ioshikhes	Ilya	University of Ottawa	N/A	Cooperative mechanisms in Gene Regulation	Health	Gene regulation, chromatin, transcription factors, miRNA, algorithms	Sequence analyses, sequence alignment, target finding, in silico mapping
Ontario Genomics		Jorgensen	Lars	Ontario Institute for Cancer Research	Morgan Taschuk	Pantheon: Micro-services facilitating analysis of complex data sets using orchestration and automation	Health	Big data, reproducibility, workflows, FAIR, genomics	Software engineering, micro services, interoperability, scalability
Ontario Genomics		Jurisica	Igor	Krembil Research Institute Toronto Western Hospital	N/A	Tissue- and disease-specific knowledge repositories for integrative computational biology	Health	Protein interactions, microRNAs, tissue- and disease condition-specific modeling, arthritis, brain disorders, cancer	Machine learning, protein interactions, text mining, IBM Watson, high-performance computing
Ontario Genomics	Genome Quebec	Lavallée-Adam	Mathieu	University of Ottawa	Theodore Perkins Warren J. Gross	RealMetaPro: A reinforcement learning software package and supporting hardware for real-time analysis of mass spectrometry-based proteomics	Health	Proteomics, Proteogenomics, Microbiome, Analytical Chemistry, Inflammatory Bowel Disease	Mass Spectrometry, Reinforcement Learning, Field-Programmable Gate Array, RNA-Sequencing, Statistics
Ontario Genomics		Lerner-Ellis	Jordan	Sinai Health Systems	Marc Fiume Matthew Lebo	BasePair — a platform for crowdsourcing the interpretation of genetic variants	Health	variant prioritization, interpretation, sharing, discovery, reporting	soFware engineering, open standards, databases, search interfaces
Ontario Genomics		Ma	Bin	University of Waterloo	Michael Moran	Software for Peptide Identification and Quantification from Large Mass Spectrometry Data using Data Independent Acquisition	Health	Proteomics, quantification, biomarker, mass spectrometry, software	Data independent acquisition, machine learning, spectrum library, de novo sequencing, peptide-centric quantification
Ontario Genomics		Magarvey	Nathan	McMaster University	N/A	Mining Agricultural Microbiomes using Genomics and Metabolomics Tools	Multi-sector	Plant microbiomes, secondary metabolism, antibiotics, beneficial microbes	Machine and deep learning, comparative genomics and metabolomics, relational databasing, metabolite identification
Ontario Genomics		Mazalek	Alexandra	Ryerson University	Sarah Sabatinos	Tangible Heterogeneity: Interactive Visualization Tools to Track and Assess Heterogeneity in Cell Populations and Genomes	Health	Genomics, computational biology, cellular heterogeneity, fate mapping	Human computer interaction, data visualization, web technologies, single cell analysis, whole genome sequencing
Ontario Genomics		McConkey	Brendan	University of Waterloo	N/A	CASTOR--- Error tolerant metagenome and polyploid genome assembly using long reads	Multi-sector	genome assembly methods, long---read sequencing, polyploid genomes, metagenomics	nanopore sequencing, PacBio Sequencing, Illumina sequencing, long---read assembly, genome assembly
Ontario Genomics		McPherson	Ruth	University of Ottawa Heart Institute	Majid Nikpay	A Biomarker Knowledgebase of Coronary Artery Disease for use in Precision Medicine and Research	Health	Coronary Artery Disease, Biomarker, Knowledgebase	Multi-Omic Data, Quantitative Genetics, Semantic Web, Analytical Tools
Ontario Genomics		Moffat	Jason	University of Toronto	N/A	Analytical tools for functional annotation of the human genome with CRISPR/Cas genetic screening data	Health	CRISPR, functional genomics, high throughput screening, computational biology	Exploratory data analysis, data modelling, machine learning, algorithm development, network analysis
Ontario Genomics		Morris	Quaid	University of Toronto	Philip Awadalla	Bringing cancer evolution into the clinic	Health	Tumour evolution, somatic mutations, population and phylogenomics, deep learning, Bayesian inference	Neural networks, variational autoencoders, approximate Bayesian computation, non-parametric models
Ontario Genomics		Pare	Guillaume	McMaster University	N/A	Development of a machine learning-based bioinformatics platform that integrates genomic and proteomic data for disease prediction	Health	Biomarkers, risk stratification, early disease detection, cardiometabolic diseases	Machine learning, genome-wide meta-analyses, -omics technology and bioinformatics, Mendelian randomization, genome-wide associations
Ontario Genomics		Parkinson	John	The Hospital for Sick Children	Radhakrishnan Mahadevan	Defining microbial communities for maintaining gut health in livestock	Multi-sector	Microbiome; Livestock gut health; Community metabolism; Probiotic consortia; Pathogen resistance	Metabolic reconstruction; Flux balance analysis; Community network analysis; Metatranscriptomics; Genomics
Ontario Genomics		Perkins	Theodore	Ottawa Hospital Research Institute & University of Ottawa	Steffany A. L. Bennett	Scaling Up Lipidomic Profiling Through Machine Learning and Probabilistic Inference	Health	Lipidomics, Metabolomics, Neurodegenerative Disease, Biomarkers, Aging	Mass Spectrometry, High Performance Liquid Chromatography, Machine Learning, Probabilistic Modeling, Probabilistic Inference
Ontario Genomics	Genome BC	Provart	Nicholas	University of Toronto	Jörg Bohlmann	From ePlants to eEcosystems: New Frameworks and Tools for Sharing, Accessing, Exploring and Integrating Genomic Data from Plants	Multi-sector	systems biology, agriculture	data visualization, data integration, plant cyberinfrastructure, functional 'omics
Ontario Genomics		Pugh	Trevor	Princess Margaret Cancer Centre	Michael Brudno	Integration and federation of single cell genomics data to inform patient care	Health	Cell biology, data-sharing, gene regulation	Single cell sequencing, genomics, transcriptomics and epigenomics, web technologies, databases, machine learning
Ontario Genomics		Reimand	Juri	Ontario Institute for Cancer Research	N/A	Deep learning models for integrative analysis of -omics data	Health	biomarker discovery, survival analysis, cancer genomics, genome-wideassociation studies, disease genes	machine learning, data integration, convolutional neural networks, -omics data analysis
Ontario Genomics		Röst	Hannes	University of Toronto	Denina Simmons	Establishing a platform to create and share robust workflows for transcriptomic and proteomic analysis of non-model organisms	Multi-sector	Sequence database, Non-model organisms, Proteomics, Transcriptomics, Canadian Wildlife	RNAseq data, spectral peptide data, data analysis pipeline, quantitation, open-source
Ontario Genomics		Shlien	Adam	The Hospital for Sick Children	N/A	Making advanced transcriptome analysis of cancer broadly available	Health	Cancer, transcriptomics, therapeutics	RNA-seq, gene expression, fusion detection, cloud computing
Ontario Genomics		Stein	Lincoln	Ontario Institute for Cancer Research	N/A	Computational Prediction of Pathway Activity with MP-BioPath	Health	Pathway activity modelling, druggability prediction, cancer biomarkers	machine learning, biological network analysis, CRISPR
Ontario Genomics		Stein	Lincoln	Ontario Institute for Cancer Research	N/A	Reactome cancer portal: A hallmarks-based pathway visualization platform for cancer research	Health	cancer hallmarks, somatic mutation, protein structure, biological pathway and network, drug	pathway and network analysis, data visualization, mathematical modeling, web application, RESTful API
Ontario Genomics		Stein	Lincoln	Ontario Institute for Cancer Research	N/A	Automated determination of tissue of origin in cancers	Health	genomics, cancer, tumour types, molecular pathology	machine learning, whole genome sequencing, liquid biopsies
Ontario Genomics		Stein	Lincoln	Ontario Institute for Cancer Research	Marc Fiume	Dockstore 2.0: Enhancing a community platform for sharing cloud-agnostic research tools	Health	genomics, bioinformatics, computational biology, data science	big data, cloud computing, docker, workflows, GA4GH
Ontario Genomics		Stein	Lincoln	Ontario Institute for Cancer Research	Vincent Ferretti	The Turnkey Genome: Cancer Genome Analysis without Tears	Health	genomics, bioinformatics, computational biology, data science	big data, cloud computing, workflows, GA4GH
Ontario Genomics	Genome Prairie	Xu	Wei	University of Toronto	Pingzhao Hu	Bioinformatics tools for modeling host genetic variation and longitudinal human microbiome for precision medicine	Health	Precision health, biomarker-based stratification tools, risk prediction models, modeling longitudinal data, artificial intelligence	Data integration, machine learning, statistical modeling, bioinformatics, sequencing, metagenomics, genome-wide association analysis
Ontario Genomics		Yuen	Ryan	The Hospital for Sick Children	Marc Fiume	Developing software platforms for Canadian's Genomics Cloud Commons	Health	genomics, bioinformatics, networks, sharing, collaboration	software engineering, open standards, cloud computing, virtualization