Overview
The Canadian Centre for Computational Genomics (C3G) acts as the bioinformatics platform at the McGill Genome Centre. As such, it offers users the following services:

- Support for **collaborative grant applications**
- For-fee analysis of omics data
- Assistance in the **planning** of sequencing experiments
- A **help desk** and **training** events
- Development and maintenance bioinformatics **software**
- Organization and distribution of **data** generated by large projects

Visit our website at [www.c3g.ca](http://www.c3g.ca) to learn more.

Contact

C3G Services Team  
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To inquire about our services, please email us at [services.mtl@c3g.ca](mailto:services.mtl@c3g.ca). Providing a short description of the following is often helpful:

- The experiment (technology, number of samples, conditions, etc.)
- Any existing or future data (type, location, ETA)
- Scientific goals
- Expected deliverables
- Ideal timeline

For any questions or requests regarding raw data delivered to you by other McGill Genome Centre platforms, please contact your project manager directly or email [pm.genome@mcgill.ca](mailto:pm.genome@mcgill.ca).

Pricing

Charges for services are calculated based on an hourly rate of $80.00 (CAD) for academic and nonprofit organizations and $100.00 (CAD) for the private sector.

Total cost for C3G services will vary from project to project depending on the amount of work necessary to help users achieve their research goals. Please [contact us](mailto:contact@mcgill.ca) to discuss the project and obtain an estimate.
Analysis Services Portfolio

Below are brief descriptions of what analysis work typically involves. In each case, our platform can support the project from planning up to the public repository submission and publication stages. Visit c3g.ca/services for more information.

**RNA-Seq**
- Preprocessing: alignment, assembly, quantification of expression
- Expert QC and EDA (e.g. PCA)
- Testing for simple or complex differential expression using linear models
- Customized visualisations
- Testing pathways & gene sets
- Other: eSNV calling, gene fusion detection, deconvolution, PDX, decontamination, alternative splicing analysis.

**Whole Genome Sequencing & Exome-Seq**
- Processing raw sequencing data to variant calls following the GATK best practices
- Detecting structural variants and CNVs
- Annotating and filtering variants according to specific needs of the project to help with variant prioritization (e.g. de novo, compound het. in trios using the GEMINI framework.)
- For cancer WGS, somatic variants detection, mutation signature analysis, subclonal analysis and tumour phylogenies.

**Single-cell RNA-seq**
- Preprocessing of fastq files with cellranger
- Project specific QC using Seurat
- Identification and labeling of sub-populations
- Differential gene and pathway expression
- Trajectory inference, RNA-velocity

**Microbiome & Metagenomics**
- Processing of raw amplicon data (16S, 18S, ITS, COI, etc.) to ASVs using dada2
- Taxonomic assignments
- Diversity calculations and ordinations (e.g. PcOA)
- Differential abundance and differential diversity analysis
- Machine learning approaches for classification
- Assembly & annotation of metagenomes from shotgun sequencing data

**Genome Assembly & Annotation**
- Assembly of small and large novel genomes using both long and short read technologies
- Detection, polishing and circularization of bacterial chromosome/s or other circular molecules (plasmid, mitochondria)
- Refinement of de novo assembly using data from supporting technologies (ex.: Hi-C)
- Complete annotation processes (eg. PGAP, Augustus/MAKER)
- Reference based variant detection (INDEL, SNP, large structural rearrangements, phased alleles) and multi genome comparison
- Full-length RNA transcript isoform identification and detection of novel isoforms
- Epigenetic base modification detection (ie. microbial/eukaryotic DNA modifications)
De novo Transcriptome Assembly
- Read normalization and assembly of short reads using Trinity
- Gene and transcript expression quantification
- Annotation by homology against UniProt, protein domains, functional annotations using Trinotate
- Exploratory and differential expression analysis

ChIP-Seq / ATAC-seq
- Trimming and alignment of short reads
- Broad or narrow peak calling & genomic context annotation
- Motif enrichment analysis
- Differential binding or differential accessibility analysis
- Functional enrichment analysis
- Visualizations

Methyl-seq
- Aligning of bisulfite-converted DNA reads from WGBS, RRBS or Methyl-capture to a reference genome
- 5mC or 5hmC levels quantification
- Quality control metrics
- SNP calling
- Differential methylation at the loci or region level
- Functional enrichment analysis
- Visualizations

Hi-C
- To interrogate the genome’s 3D structure
- Preprocessing: Alignment, filtering pairs
- ENCODE QC standards
- Contact maps, TAD domain annotation
- Others: Visualization, integration with other genomics data (ChIPseq), etc.

Structural Bioinformatics
- Structure visualization
- Mutation mapping
- MD simulation, binding energy
- Contact maps
- Integrate with genomic studies

Other Applications
- Single-Cell Assays (snATAC-seq, snDNA-seq, snRNA-seq)
- Expression & methylation microarrays
- Ribo-seq (ribosome footprinting)
- Omics integrative analyses
- Custom Databases & Portals
- miRNA-seq and other small RNAs
- DRIPc-seq
- RIP-seq
- Pool-seq
Bioinformatics

- GBS, RAD-Seq
- CyTOF
- Metabolomics and Proteomics Data Integration
- Network Visualization and Analysis
- Image analysis

Resources for Analysis
C3G recommends the following resources to users looking for ways to analyze data by themselves. The goal here is not to provide a comprehensive guide to all bioinformatics tools, so please email help@c3g.ca to obtain specific guidance.

Compute Canada
Compute Canada puts high performance computing systems (e.g. Beluga, Cedar, Graham) at the disposal of all Canadian researchers, free of charge. We strongly encourage PIs to apply for an account and others to seek sponsorship with their PI.

Benefits of Applying for an Account at Compute Canada
- Terabytes of disk space, often necessary to store genomic data sets
- Systems with the most common bioinformatics software and data sets readily available
- Compute nodes with many CPUs to speed up processing through parallelization
- Expert support (support@computecanada.ca) and training events
- Easier sharing of large datasets with other Compute Canada users
- Access to GenAP web applications such as Galaxy or track hubs

IPA
C3G manages a single concurrency institutional license for QIAGEN’s Ingenuity Pathway Analysis (IPA). Visit c3g.ca/ipa to learn more about accessing this license.

GenPipes
GenPipes is a C3G developed pipeline workflow for processing NGS data from a wide range of applications (WGS, RNA-seq, Hi-C, etc.). It is aimed at users already familiar with Compute Canada systems. Visit c3g.ca/genpipes to learn more.

Other Frequently Recommended Tools
- Galaxy, a platform hosting a myriad of tools (e.g. BUSCO, Kraken) and workflows executable from an intuitive graphical interface.
- DEBrowser, for quick and user-friendly RNA-seq differential expression analysis.
- EnrichR, gene set enrichment analysis web server.
- nf-core, a set of readymade NextFlow bioinformatics pipelines.
Getting Help & Training Events

Users looking for punctual guidance on data analysis or planning an experiment are invited to consider the following (no fees involved):

- **C3G Open Doors** ([c3g.ca/open-door](http://c3g.ca/open-door)), consultation with a bioinformatician
- **C3G Help Desk**, for bioinformatics-related questions ([help@c3g.ca](mailto:help@c3g.ca))
- **Compute Canada Bioinformatics Help Desk** ([bioinformatics@computecanada.ca](mailto:bioinformatics@computecanada.ca)) for Compute Canada related questions.

Users looking for comprehensive training could consider these:

- **CBW - Canadian Bioinformatics Workshops** ([bioinformatics.ca/workshops](http://bioinformatics.ca/workshops))
- **MiCM Workshops** ([mcgill.ca/micm/training](http://mcgill.ca/micm/training))
- **Calcul Québec Training Offer** ([calculquebec.ca/en/business-services/training](http://calculquebec.ca/en/business-services/training))
- **For-fee C3G Services** ([services.mtl@c3g.ca](mailto:services.mtl@c3g.ca)) for personalized training events

FAQs

About our Services

- **Q:** _Can C3G analyze data from providers other than the MGC?_
  A: Yes, the platform can analyze data from any provider as well as publicly deposited data (e.g. NCBI GEO, TCGA).

- **Q:** _How much do C3G services cost?_
  A: See [Pricing](#) above.

- **Q:** _How long does it take for C3G to perform an analysis? Can you fast-track requests?_
  A: This depends on the work to be performed and the availability of staff, the size of our team being finite. Contact us at [services.mtl@c3g.ca](mailto:services.mtl@c3g.ca) to inquire. In general, it is better to order the service well in advance to secure a high priority. We consider fast-track requests for scientific reasons (e.g. grant, publication). We do not expedite analysis work to meet financial or other administrative requirements alone such as end of fiscal year deadlines, although some arrangements can be made on the invoicing side.

- **Q:** _Do you require authorship on papers?_
  A: The Canadian Center for Computational Genomics (C3G) requires its contributions to peer-reviewed publications to be communicated ([services@c3g.ca](mailto:services@c3g.ca)) and acknowledged in the corresponding acknowledgements section. The following statement should also appear in the said section:

  “The Canadian Center for Computational Genomics (C3G) is a Genomics Technology Platform (GTP) supported by the Canadian Government through Genome Canada.”

  Where applicable, C3G kindly requests platform users to cite GenPipes, our NGS data processing framework:

  _GenPipes: an open-source framework for distributed and scalable genomic analyses (PMID:31185495)_

- **Q:** _How secure is my data and results at the C3G platform?_
  A: C3G will not share nor make use of platform users data for purposes other than for providing the agreed upon service. Data from each project will be stored on its internal servers or on Compute Canada systems and will generally be read-accessible by all staff at C3G. Users with
strict data confidentiality needs should clarify this at the project planning stage.

• **Q: How long will C3G keep my raw data and analysis results?**
  A: C3G will keep all data related to a given project for at least six months after results delivery. In the longer term, C3G will delete raw and intermediary data files and send only the most critical files and scripts to a data archival server. C3G does not, however, provide any data retention guarantee, as files may become accidentally erased, corrupt or lost. Platform users are therefore advised to maintain their own copy of results and raw data files. This will avoid the need of requesting additional services to regenerate lost data or perform additional analysis.

• **Q: I am trying to perform analysis myself but it has been challenging. Can you help?**
  A: Yes, see [Getting Help](#) above. Please note that our help desk and open doors are meant to help users solve specific issues or provide general guidance. Users looking for step-by-step support through entire complex workflows should instead consider our for-fee analysis services.

• **Q: Do you offer customized workshops as a service?**
  A: Yes, this is entirely possible and we have done this in the past for RNA-seq, microarrays and microbiome analysis, so do not hesitate to inquire at [services.mtl@c3g.ca](mailto:services.mtl@c3g.ca). It should be noted, however, that creating a personalized training event is in many cases a time-consuming task. Delays might therefore be long and total cost might exceed that of getting a team member doing the analysis for you as a service instead.

• **Q: Do you have IPA?**
  A: Yes, see [c3g.ca/ipa](http://c3g.ca/ipa). Other options for (free) pathway-functional analysis include [Enrichr](http://www.enrichr.com), [Reactome](http://www.reactome.org).

• **Q: How will data be transferred from and to the platform?**
  A: There are many options for this. Most common ones include setting up an sftp account for you at the MGC, Globus, GenAP data hubs, Google Drive and shipping physical hard drives.

• **Q: What sort of reporting does C3G provide?**
  A: We are currently working on a results delivery portal. For the time being, our analysts will most often prepare HTML documents describing methods and results, share an archive of larger files and provide many important details by email. Clients with very specific reporting needs should request this upfront.