Canada’s national platform for genome sequencing and analysis
VISION

To serve as Canada’s engine for genomics-enabled research and discovery.

MISSION

- To fuel the discovery of next-generation scientific solutions by producing, bringing access to and analyzing massive genomic datasets with national and international impact.
- To enable Canadian genomics research by building and operating an unprecedented genomic technologies platform that enhances our national capacity for genome sequencing and informatics analysis.
1. Participate in large-scale human genomic data generation programs and catalyze the development of a national cohort study that would seek to characterize the vast diversity of Canada’s population.

2. Create and assemble clinically relevant data, algorithms, technologies and methodologies in medically relevant areas, such as rare diseases, paediatric cancer, autism and other neurodevelopmental disorders, health and disease in ageing, bringing shared ideas and datasets to enhance applications in medicine across Canada.

3. Advance projects, develop and improve methodologies for sequencing non-human species that are of critical relevance to the ecology, health and wealth of Canada.

4. Develop powerful and efficient solutions for big data storage and high-speed data exchange, and standardize tools and workflows to fuel genomics science across the country.

5. Lead technology development through innovation, validation and integration of new genomic methodologies and platforms and establish best practices in key application areas.

6. Educate and train users, enrich the Canadian genomics talent pool and cultivate internal knowledge and personnel by fostering user groups, vendor programming and partnerships with academic educational institutions and programs.
IMPACT – 2018-19 Snapshot

- Over $41 million invoiced for service work
- 1879 Principal Investigator laboratories from all 10 provinces and multiple sectors supported.
- 214 HQP trained at 3 CGEn nodes.
- Over 1684 Tb generated
- 150 peer-reviewed publications by CGEn staff
- 279 peer-reviewed publications cited CGEn nodes
- Data generated by CGEn help train; 69 under-graduates, 324 master students, 525 PhDs, 736 Post-doc fellows and 1858 Technical & professional staff.
Current Technologies & Capacity

<table>
<thead>
<tr>
<th>CGEn-Vancouver</th>
<th>CGEn- Toronto</th>
<th>CGEn-Montreal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Illumina HiSeq X</td>
<td>Illumina HiSeq X</td>
<td>Illumina HiSeq X</td>
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<tr>
<td>Illumina HiSeq 2500</td>
<td>Illumina HiSeq 2500</td>
<td>Illumina HiSeq 4000</td>
</tr>
<tr>
<td>Illumina NextSeq 500</td>
<td>Illumina NovaSeq 6000</td>
<td>Illumina NovaSeq 6000</td>
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<tr>
<td>Illumina MiSeq</td>
<td>Illumina NextSeq 500</td>
<td>Illumina MiSeq</td>
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<tr>
<td>ABI 3730XL</td>
<td>Illumina MiSeq</td>
<td>PacBio RSII</td>
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<td>PacBio Sequel</td>
<td>PacBio Sequel</td>
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<tr>
<td></td>
<td>ABI 3730XL</td>
<td>Oxford Nanopore MinION</td>
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</tbody>
</table>

**OUTPUT**

<table>
<thead>
<tr>
<th>Sequencing Capacity - 30X Human genomes per year</th>
<th>&gt;40,000</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data generation Capacity (Optimal Use max); Gigabases / year</td>
<td>4,646,505</td>
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</tbody>
</table>

**High Performance Computing (HPC)**

<table>
<thead>
<tr>
<th>Hyper-threaded cores</th>
<th>50,000+</th>
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<tbody>
<tr>
<td>On-line Disk Storage</td>
<td>26+ petabytes</td>
</tr>
<tr>
<td>Network Connectivity</td>
<td>Upto 40 Gb/s</td>
</tr>
<tr>
<td>Desktop computers</td>
<td>800+</td>
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</tbody>
</table>
Our Partners & Users

Federal Government Departments

International projects & consortia

Non-Profit Research Organizations

Provincial Government Departments

Industry

Academia
IMPACT – 6 publication examples from hundreds of output metrics

**RESOURCE**

Whole genome sequencing resource identifies 18 new candidate genes for autism spectrum disorder

The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis
By Gregory A. Taylor 1, 2, Heather Kohl 3, Lauren Ceccante, Brian D. Jackson 7, Jina Lee 8, Kasey T. Tye 3, David Cheng 9, Eric Chau 10, Pauline Poulin 11, Rebecca Carson 12, Yangjun Zhai 13, Andrew J. Mangel 14, Richard Moore 1, Burke Barr 15, Blackstone 16, Jenny I. F. Chen 17, et al.

Spatial heterogeneity in medulloblastoma
Aparna Sukumar, Flora L. Carney, Marc L. Letourneau, Christopher P. Wainer, Zhengyong He, Michael Sheehy, Elizabeth M. Chubukov, et al.

Dissecting features of epigenetic variants underlying cardiometabolic risk using full-resolution epigenome profiling in regulatory elements

Systems Genetics of Hepatic Metabolome Reveals Octopamine as a Target for Non-Alcoholic Fatty Liver Disease Treatment

The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 96 participants

**SCIENTIFIC REPORTS**

**Article** | **Open Access** | **Published**
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The Personal Genome Project Canada: findings from whole genome sequences of the inaugural 96 participants
New De Novo assembly methodologies
Developed in the academic domain and made widely available through publication and deposition of relevant materials in public-access software repositories (e.g. GitHub).

Advanced Bioinformatics
New methods for interpretation and annotation of human whole genome sequence data.

10X Genomics Chromium long-read protocol improvements
Results published and used to obtain further grant funding; this technology is now available to CGEn clients.

DNA extraction and library prep FFPE tissues
This has already been validated and implemented in production at the CGEn-Vancouver node and is now available to all CGEn clients.

TECHNOLOGY DEVELOPMENT
Further Information

Web: http://cgen.ca

Twitter: @CGEnSeq