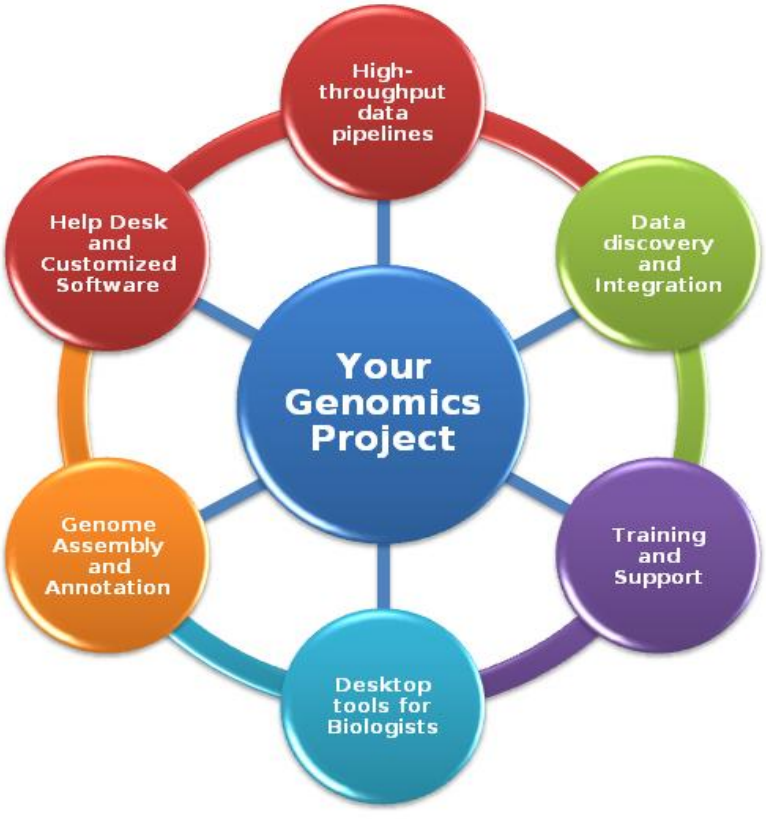

Don't re-invent the wheel!

www.gcbioinformatics.ca

The Bioinformatics Innovation Centre (BIC) is a distributed bioinformatics service facility that has been supported by Genome Canada since 2002. It has currently 4 nodes, based in Calgary, Edmonton, Vancouver and Winnipeg. The BIC continues to provide services to Genome Canada funded initiatives through the Applied Genomics and Proteomic Research in Human Health Competition, Competition III projects and Applied Genomics Research in Bioproducts or Crops (ABC) projects, as well as other research initiatives around the world.

The BIC team, which includes Drs. Christoph Sensen (BIC Director, U of C), David Wishart (U of A), Mark Wilkinson (UBC) and Brian Fristensky (U of M), continues to explore leading edge research and develop new approaches to the understanding of genomic data. To accomplish this, the BIC focuses effort on these major components:

- High-throughput database search engines, data storage, generic login accounts, and access to software tools and databases. Accessible COE infrastructure includes the state-of-the-art CAVE Automated Virtual Environment, a Java 3D middleware layer (JABIRU) that enhances portability of Java 3D visualization tools, and related computational infrastructure.
- Bioinformatics data and tools in the Center, and worldwide, are made interoperable and easily accessible through our own semantic integration platform, based on the BioMoby and SADI technologies.
- Pathway and plant/animal metabolomic data analysis: BIC offers web servers and databases for metabolite identification, pathway reconstruction, multivariate statistical analysis, disease identification and pathway interpretation. These resources include DrugBank, SMPDB, T3DB, FooDB, MSEA, MetPA and Metaboanalyst.
- Sequence analysis & annotation: automated functional analysis of DNA and protein sequences through the MAGPIE system. MAGPIE provides a Web-based graphical analysis of genomic, EST, protein and other types of sequences that can facilitate data sharing, searching, and GenBank submissions.
- Microarray analysis: the COE's Bluejay software integrates TIGR's microarray statistical analysis software into a genomic context. The COE has also developed the Merlin software for the automated analysis of a few to hundreds of Affymetrix microarrays. The Osprey software can also be used to design primers and probes of all sorts, including custom microarrays.
- Comparative genomics: Bluejay can be used to view explore genomic data from whole eukaryotic chromosomes down to individual genes. Key Bluejay features include -Ability to compare multiple genomes in a single display -Easy navigation and searching through genome features -Highly customizable display of genetic features -Publication quality export of graphical DNA representation
- Analysis automation: Seahawk provides an easy-to-use interface for chaining together bioinformatics tools, reducing headaches caused by data format incompatibilities. The resulting analytical workflows are compatible with the Taverna high-throughput analysis environment, and can be automatically re-run at regular intervals as the underlying data is updated.
- Generic and customized programming capability (fee for service).
- Training courses to create power users and introduce BIC services.
- BioLegato graphic interface designed to make it easier for biologists to utilize bioinformatics software

The goal is to continue all aspects of the BIC while working with Genome Canada funded projects and others, as well as expand the service base, through provision of excellence in bioinformatics.

For additional information on the Bioinformatics Innovation Centre and its services or to discuss how we can be of service to you, please contact:

Christoph W. Sensen at csensen@ucalgary.ca
David Wishart at david.wishart@ualberta.ca
Mark Wilkinson at markw@illuminae.com
Brian Fristensky at frist@cc.umanitoba.ca

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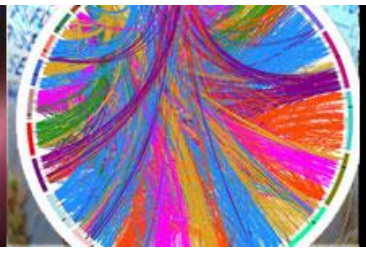
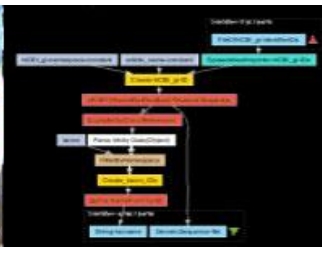
Genome Canada
BIOINFORMATICS
Innovation Centre





Services focus on the areas of:

BioMOBY/SADI Web Services (Mark Wilkinson)

SADI
Find. Integrate. Analyze.

BioMOBY/SADI The Bioinformatics Innovation Center is a world-leader in the creation of data integration and interoperability technologies, including being the source of the BioMoby and SADI semantic web service frameworks.
These "invisible" technologies allow Innovation Center data and analysis services to run seamlessly together with third-party data and analytical tools worldwide, requiring no custom programming or data manipulation by our end-users. Thus, Innovation Center users can create and run their own complex analytical pipelines, involving the full spectrum of global bioinformatics data and analytical tools, in minutes, and with only minimal software training.

Help Desk/Tools for Proteomics (David Wishart)

The Help Desk offers access to: Phytochemical and food component databases * Biostatistical support and programming * Metabolomic data interpretation * Proteomic data analysis * Microarray data analysis *Automated and semi-automated plant, animal and microbial genome annotation * Text mining and text extraction * Data mining * Machinelearning * Custom programming and custom tool development * Support for~40 general-use databases and webservers * Laboratory Information Management System (LIMS) development * Scientific Database ManagementSystem (SDMS) development * Freely available software (from the HelpDesk's Software Repository) * Web site development * Software advice and assistance * Learning how to program * Monthly Newsletters * a Bioinformatics Researcher Directory.

The Help Desk offers many software tools and databases to the research community, including * BASys (Bacterial Annotation System) * ThePlasMapper server * BacMap * CGView * DrugBank * T3DB * HMDB * PROSESS *VADAR * GelScape * MetaboAnalyst * MSEA * SMPDB and many other tools .

Large Scale Genome Analysis and Hardware Provision (C. Sensen)

The Sun Centre of Excellence for Visual Genomics (COE) is the lead site for the BIC located at the University of Calgary's Faculty of Medicine, providing computational infrastructure support through a unique and extremely powerful combination of hardware and database resources. The COE offers:

- Genome and transcript assembly for traditional and next-gen sequencing
- In-depth sequence annotation, controlled access Web presentation, and public database submission
- Metagenomics/environmental sample analysis
- Taxonomy, comparative genomics, phylogenetics, clustering and visualization
- Gene expression and microarray analysis of all kinds
- Oligonucleotide design, biomarker development
- Advanced 2D and 3D medical image analysis, model construction
- Web portal development
- Command-line access to high-performance computing resources
- Large-scale, archival quality data storage

Training (Brian Fristensky & Christoph Sensen)

The Applied Computational Genomics Course (ACGC) The ACGC provides researchers with entry-level skills an opportunity to become empowered and increase their problem-solving skills through provision of a hands-on course, with lectures and tutorials presented by a panel of experts. The course uses tools and services available through the Bioinformatics Innovation Centre. Most tools used are open-source and can be freely downloaded for use at one's home institution. Topics include (subject to change): Becoming a power user * Perl Programming * Creating automated data pipelines * High throughput genome annotation * Help Desk Services * Secure use of remote bioinformatics systems.

BIRCH - Desktop bioinformatics tools (Brian Fristensky)

Birch – a comprehensive desktop bioinformatics system which comes with many of the commonly-used bioinformatics programs pre-installed (e.g. NCBI, FASTA, PHYLIP, TIGR, TCOFFE, Jalview). It is also a framework of tools, files, and documentation for organizing and managing a bioinformatics core facility and an expandable system that allows you to merge 3rd party programs and documentation seamlessly into the standard BIRCH distribution

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