

Bioinformatics and Biomathematics Lab (Bistro Lab)

The Bistro lab has housed several collaborations with faculty at the Medical College of Wisconsin since 2001. These include projects analyzing microarray data, analyzing documents curated by the Rat Genome Database, and analyzing full-text biomedical articles. Recently, new collaborations with faculty at the Department of Biological Sciences at Marquette University have been established to analyze the regulation and surveillance of non-coding RNAs.

Lab resources were also used in 2009 for drug candidate screening in collaboration with Dr. Daniel Sem at Marquette University and Dr. Brian Volkman at the Medical College of Wisconsin.

Currently, the lab is involved in analyzing high throughput genomic, genetic, and epigenetic datasets to model the gene regulatory networks in various organisms. The lab is also developing pipelines to analyze next-generation sequencing datasets from prostate cancer cell lines through collaboration with Dr. Bekir Cinar at UCLA. The lab is also developing techniques for analyzing large-scale copy number variant (CNV) data sets associated with congenital heart disease in collaboration with Dr. Aoy Mitchell at the Children's Research Institute.

Technology & Resources

Technical library

8 computer workstations

15 node cluster

Mac OS X based computers and configured for distributed and parallel processing tasks with Condor, providing 50 cores for computation

Over 5 terabytes (TB) of collective storage in the lab, which is used for storing major genomic data, a copy of MEDLINE for biomedical data mining, and other bioinformatics related data and tools

Bioinformatics software (e.g., EMBOSS, NCBI Tools, CLUSTALW, etc.)

Database software (MySQL, PostgreSQL)

Machine learning tools (e.g., Weka)

Statistical and mathematical software (R, MATLAB)

Document preparation software (LaTeX, OpenOffice, MS Office)

Contact

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