INSTITUTE FOR
COMPUTATIONAL
BIOLOGY

Computational Biology Core

The Computational Biology Core is a collaborative and fee for service facility within the Institute for Computational Biology (ICB) aimed at providing computational and analytical support for a variety of research questions. Modern high-throughput experiments generate massive amounts of data that most labs are not equipped to handle. The ICB Computational Biology Core supports these experiments with standardized and custom pipelines for data processing and analysis of next-generation sequencing data.

What kinds of experiments does the core support?
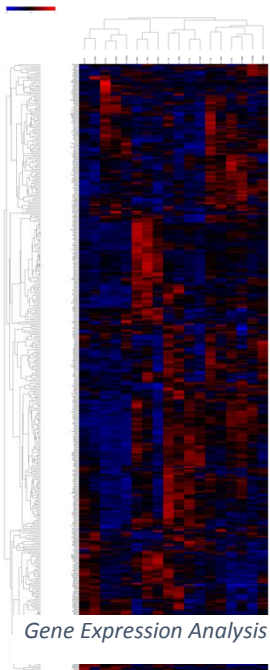
The Computational Biology Core supports a variety of experimental designs and analyses, both for ICB-based projects and for research across the Cleveland area. These include:

- RNA-seq expression analysis
- DNA sequencing for genomic variant identification
- *De novo* assembly of genomes
- ChIP-seq and other functional genomics experiments

In addition to these basic study designs, we also support various analysis approaches for extracting new biological insights from large-scale 'omics data, including:

- Microbiome analysis
- Transcriptional Isoform analysis including
- *De novo* transcriptome assembly
- Allele-specific expression
- Pathway or Function based enrichment analyses
- Gene and Variant annotation

Gene Expression Analysis
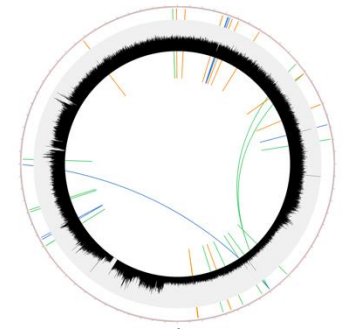
Genomic rearrangement detection
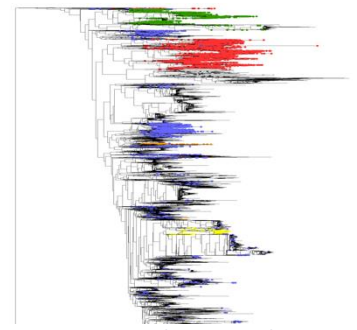
16s Microbiome Analysis

How do I get started!

Experiments should start with experimental design and we are happy to assist you from the very beginning. Feel free to contact Ricky Chan (erc6@case.edu) for a consultation appointment.

We work closely with the sequencing cores of Case Western Reserve University and the Cleveland Clinic and can help determine your sequencing and analysis needs as well as provide you with a cost estimate.

Who are the Core's Primary Faculty?

- Ricky Chan, PhD (Core Director)
- Chun Li, PhD
- William Bush, PhD, MS

CASE WESTERN RESERVE UNIVERSITY   Cleveland Clinic   UH University Hospitals

www.icompbio.net