

Template Facilities and Other Resources Document for the Michigan State University Bioinformatics Core

The Bioinformatics Core integrates expertise in compute systems, software, data management and analysis, with background in genetics and genomics research to provide a full spectrum of bioinformatics and computational biology support to researchers. The Core's bioinformatics consultants are PhD scientists with extensive experience in genomic sequencing data analysis including bulk- and single-cell RNA-seq and ATAC-seq, ChIP-seq, genome assembly, annotation, and variant calling. They provide one-on-one consultations on experimental design to individuals and research groups and utilize current best practices when analyzing sequencing data.

Bioinformatics Core consultants use MSU's High Performance Computing Center (HPCC) which maintains four clusters comprised of a total of 1,047 nodes, which collectively have 56,236 CPU cores, 614 GPUs, and 317 TB of memory. These resources allow the Bioinformatics Core to process and analyze large amounts of sequencing data and accommodate projects of almost any scale.