FACILITIES AND OTHER RESOURCES
University of Idaho
Institute of Interdisciplinary Data Sciences (IIDS)

IIDS Genomics and Bioinformatics Resources Core Facility

Advances in DNA sequencing and transcriptome analysis have ushered in a new era of biological inquiry. To take advantage of these technologies, IIDS has developed a state-of-the-art core facility so researchers can study biological processes at the genome-scale. To enable the use of these technologies, the IIDS Genomics and Bioinformatics Resources Core not only provides access to technology, but access to staff with the experience and expertise in molecular biology methods and bioinformatics needed to acquire, analyze, and visualize data generated from high throughput technologies in genomic research.

Core Facility Infrastructure

The Genomics and Bioinformatics Resources Core Facility has equipment necessary to generate data for applications including DNA and RNA sequencing, high throughput sample preparation and quality assurance, and computational resources described below. In addition, there are thermocyclers, centrifuges, microcentrifuges, freezers, refrigerators, gel-imaging systems, vacuum/refrigerated-centrifuges, quantification instruments, and computational resources. The Core facility occupies approximately 780 sq. feet of laboratory space in the Integrated Research and Innovation Center (IRIC) room 210 for GBRC technicians, 620 sq. feet of laboratory space in IRIC 142 for users to access equipment, and approximately 300 sq. feet of office space in IRIC rooms 224 and 226 at the University of Idaho main campus in Moscow, Idaho. The GBRC has 616 sq. feet of space in the Gibb 241/A COVID sequencing lab. The Core facility infrastructure is described in more detail below.

DNA and RNA Sequencing

Sequencing has become an indispensable tool for basic biological research, biomedical research, diagnostics, and biological systematics. Current applications using sequencing include whole genome shotgun sequencing (including *de novo* sequencing of previously unknown genomes), RNA sequencing (transcriptome sequencing, mRNA sequencing, single-cell RNA sequencing), targeted re-sequencing, single nucleotide polymorphism (SNP) discovery, amplicon sequencing (e.g., 16S microbial community composition analysis, metabarcoding, population genetics, and phylogenetics), methylation identification, structural variant analysis, and many other applications. Equipment for sequence generation includes:

AVITI24 High-Throughput Sequencing

The Element AVITI24 delivers highly accurate short-read sequencing with exceptional cost efficiency. Its dual-flowcell design provides flexible run scheduling and output up to 720 Gb per run, supporting applications from whole-genome sequencing to RNA-seq, targeted panels, metagenomics, and degraded or low-input samples. AVITI's Avidity Sequencing chemistry produces Q30+ accuracy across the vast majority of bases, with low duplication rates and excellent GC balance. This platform offers a powerful combination of high data quality, fast turnaround, and significantly reduced per-Gb sequencing costs, enabling affordable large-scale or high-depth projects without

compromising performance. The AVITI24's 100, 250, 300, 500, and 1,000 million read kit offerings are desirably broad, and when considered in conjunction with its simple to use individually addressable lanes, the result is that the instrument delivers very flexible options to answer a variety of researcher's questions affordably and dynamically.

The AVITI24 integrates high-accuracy sequencing with advanced multiomic cytoprofiling, enabling simultaneous measurement of RNA, protein, morphology, and spatial features. The system supports sensitive transcript detection (up to thousands of transcripts per cell), comprehensive protein mapping of up to 138 targets, and visualization of six key cellular structures for integrated morphological context. High-throughput dynamic assays allow screening of compounds, doses, and gene perturbations across multiple well formats, with up to 96 samples processed in under 24 hours. Spatial resolution at single-cell precision captures intracellular localization of RNA and protein expression, providing a unified platform for functional genomics, drug discovery, and mechanistic cell biology.

Fluidigm Access Array and Juno Systems

The Access Array and Juno Systems provide PCR based, high-throughput, target-enrichment designed to work with all the major next-generation sequencing instruments. These systems enable the user to simultaneously enrich multiple unique targets (such as exons) from a large number of samples by using micro-fluidics and PCR. This results in quality sequence data while minimizing the time, cost, and labor required for targeted re-sequencing projects. The Access array can amplify up to 480 loci in 48 samples simultaneously, while the Juno can amplify as many as 2400 loci in 192 samples simultaneously.

Advanced Analytical Fragment Analyzer

The Fragment Analyzer is a 12-lane electrophoresis array that provides accurate fragment quantification and qualification. It can quantify and qualify genomic DNA, total or purified mRNA, and prepared libraries in a range of sensitivities.

High Throughput Sample Preparation and Quality Assurance

Access to equipment for high throughput sample preparation gives investigators abilities for increased throughput and reduction of sample-to-sample variability over manual methods. In addition to providing high-end equipment for generating sample data, the Core enables researchers to perform accurate assessment of sample quality before committing extensive financial resources to a project. Equipment for sample preparation and QA in the Core include:

Kingfisher Flex: The Kingfisher Flex is a bead-based sample preparation system that eliminates pipette steps and the resulting waste from its protocols. It is a fully automated, scalable, and customizable system that delivers rapid and consistent results for RNA and DNA. Accessible by clients in the user-core also.

Qiagen QIAxcel: The QIAxcel system is a multicapillary electrophoresis system designed to overcome the bottlenecks of gel electrophoresis. The fully automated system can process up to 96 samples per run. Accessible by clients in the user-core also.

Molecular Devices SpectraMax Paradigm and Gemini XPS: The SpectraMax Paradigm is a multimode microplate detection platform. It is the only user upgradeable microplate reader on the market that allows for real-time system configuration. Current cartridges include the absorbance (ABS) detection and the tunable wavelength (TUNE) detection cartridges. The Gemini performs nucleic-acid quantification, microbial growth assays, ELISAs, and reporter-gene assays to name a few. Also accessible by clients in the user-core.

Covaris Ultrasonicator M200: The ultrasonicator rapidly shears DNA to a specified size while maintaining a consistent size distribution and target for any number of samples. It is invaluable for protocols requiring precise and replicable DNA fragment sizes.

Sage Science BluePippin: The BluePippin allows selection of high molecular weight DNA for long-range genomic applications such as genome sequencing.

Fluorometry: The DNA or RNA in samples can be quantified using fluorescent assays. For multiple samples in a 96-well plate format these assays can be conducted using the Gemini XPS microplate reader from Molecular Devices. Smaller numbers of samples can be assayed using the Qubit 2 and 3 from Life Technologies. Accessible by clients in the user-core also.

Applied Biosystems StepOne Plus qPCR instrument: Accurate quantification of sequenceable library is essential for a successful sequence run. This instrument allows rapid and accurate quantification of Illumina libraries, thus improving cluster management on the flow cell and sequence quality. Also accessible by clients in the user-core.

Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument: The Applied Biosystems 7500 Fast Dx Real-Time PCR Instrument with SDS Software is a real-time nucleic acid amplification and five-color fluorescence detection system available for in vitro diagnostic use in addition to library quantification. Accessible by clients in the user-core.

Bio-Rad QX220 Droplet Digital PCR System: Bio-Rad's second-generation digital PCR system provides absolute quantification of target DNA or RNA molecules using EvaGreen or TaqMan Hydrolysis Probes. Unmatched sensitivity and precision for various applications including library quantification. Accessible by clients in the user-core.

Aurora System: A revolutionary platform for nucleic acid extraction based on a powerful electrophoretic purification technology from Boreal Genomics. The electrophoretic extraction technology is proven to purify DNA and RNA from extremely low abundance and heavily inhibited samples including soils from the Atacama Desert, Antarctic tundra, sea sediments, oil sands, and stool. Accessible by clients in the user-core.

Coastal Genomics LightBench MK II: Fast, easy, affordable, accurate, and precise automated agarose-based size-selection of DNA/library from 100bp to >20,000bp using real-time analysis and dual-colored fluorophores.

Bioinformatics Analysis Resources

The GBRC offers bioinformatics support through staff bioinformaticians and can perform a full range of analysis tasks to address biological questions in areas such as population genomics, functional genomics, genomic epidemiology, microbial community dynamics, and systems biology. GBRC bioinformaticians begin with raw data output from the instruments and proceed to quality assurance, data processing, and analysis. Results are shared with the collaborator through a dialog that includes data interpretation and visualization. Analyses are conducted using software tools available in the public domain or developed by the GBRC staff when custom project specific methods are needed. Core personnel have developed analysis techniques and pipelines for genome and transcriptome assembly, RNAseq differential expression analysis, amplicon sequence variant analysis, 16S microbial community analysis, population genetics, SNP/INDEL detection, speed congenics, and many other applications. These pipelines transform raw data into a form and format that can be mined by investigators. Throughout the data analysis process, a dialog is maintained with the investigator ensuring that the project meets its goals, figures are generated, and summary tables are provided in a form that answers the biological question is useful for publication. As needed, the Core staff provides investigators with detailed knowledge of the laboratory protocols and bioinformatics methods used so they can be included in reports and publications. The close collaboration between core staff and investigators often warrants inclusion of core staff as co-authors on publications.