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Bioinformatics Core

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As a central facility providing bioinformatics services to the on- and off-campus research community, the Bioinformatics Core has the expertise to manage and analyze various types of biological data. The Core staff provides assistance in analyzing Next Generation Sequencing data, including: (1) de novo assembly of genomes and transcriptomes, (2) gene prediction and annotation, (3) alignment to reference genomes/transcriptomes, (4) detection of SNPs and SSRs, and (5) analysis of CNV/SV, small RNA, RNA-Seq, ChIP-Seq, metagenomic, metatranscriptomic and phylogenomic data.

The core partners with the Rosen Center for Advanced Computing (RCAC) to provide a robust, redundant, accessible, and distributed hardware computational platform. The system includes the following.

- High-performance computing clusters for computationally intensive tasks. The Bioinformatics Cores has eight 256 GB RAM nodes, two 128 GB RAM nodes and two 64 GB RAM nodes, each with two 2.60 GHz processor per node and 20 cores per node. Additional computational resources are available through RCAC of Information Technology at Purdue.
- The Bioinformatics Core currently has 250 TB of storage and will continue to add more disk space as needed. Data storage is secure and redundant, and tiered storage options are available for varying levels of data integrity (high performance and redundancy, moderate cost, no backup, offline, etc.), to provide the flexibility to define data retention policies that balance the needs of researchers. The Bioinformatics Core also has access to a large, long-term, multi-tiered file caching archival storage system through RCAC.

The Core has internal system administration support and leverages Information Technology at Purdue (ITaP) for broader computational support. The Bioinformatics Core personnel have experience in bioinformatics, programming, and database and system administration. The Bioinformatics Core is uniquely positioned to handle various ‘-omics’ data analyses and to develop various workflows that are required for project specific analyses.