TheCenter for Bioinformatics (bioinformatics.unc.edu) at UNC-CH was established in 1999 to provide resources to help bench scientists take advantage of computational tools in biology. Since then, the Center has grown and diversified to address various information technology based needs of researchers at UNC-Chapel Hill. The Center for Bioinformatics manages UNC-CH site licenses for several commercial software packages (Vector NTI Suite, Partek Genomics Suite, Lasergene DNASTAR, Ingenuity Pathway Analysis) and provides support and training for all UNC-CH site-licensed software and most freeware applications that are related to bioinformatics. The Center’s staff are responsible for data processing, data management, initial analysis and distribution of all data generated at UNC High Throughput Sequencing Facility (HTSF). They have worked with a number of open-source software tools (including but not limited to SAMTOOLS, Bowtie, TOPHAT, BWA, SOAP2, MAQ etc.) that are used for analysis of deep-sequencing data. Hardware support for the facility includes four Dell Poweredge 2950 servers running Redhat enterprise Linux (EL4) (each with 2 x 2.66 GHz Quad core Xeon CPU’s, 32 GB RAM, 6 TB of disk storage) available for management/analysis of data from the next-gen sequencers within the Center, and a 30TB iSCSI SAN for next-gen sequence data analysis and storage. A small Linux cluster (20 node) was recently installed shortly to help facilitate large-scale analysis of sequence data. In addition to open source software programs meant for analysis of next-gen sequence data (maq, ChIP-seq, mosaik, phred/phrap/consed) there are two network licenses for CLC Genomics Workbench.

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