**Course: Advanced Bioinformatics**

**Module title: Bioinformatics Toolbox**

**Module no. : 209**

Bioinformatics Toolbox provides algorithms and apps for Next Generation Sequencing (NGS), microarray analysis, mass spectrometry, and gene ontology. Using toolbox functions, you can read genomic and proteomic data from standard file formats such as SAM, FASTA, CEL, and CDF, as well as from online databases such as the NCBI Gene Expression Omnibus and GenBank®. You can explore and visualize this data with sequence browsers, spatial heatmaps, and clustergrams. The toolbox also provides statistical techniques for detecting peaks, imputing values for missing data, and selecting features.

You can combine toolbox functions to support common bioinformatics workflows. You can use ChIP-Seq data to identify transcription factors; analyze RNA-Seq data to identify differentially expressed genes; identify copy number variants and SNPs in microarray data; and classify protein profiles using mass spectrometry data.

[**High-Throughput Sequencing**](http://www.mathworks.com/help/bioinfo/high-throughput-sequencing.html)

Gene expression, transcription factor, and methylation analysis of NGS data, including RNA-Seq and ChIP-Seq

[**Microarray Analysis**](http://www.mathworks.com/help/bioinfo/microarray-analysis.html)

Gene expression and genetic variant analysis of microarray data

[**Sequence Analysis**](http://www.mathworks.com/help/bioinfo/sequence-analysis.html)

Genomic and proteomic sequences, alignment, and phylogenetics

[**Structural Analysis**](http://www.mathworks.com/help/bioinfo/structural-analysis.html)

Visualize and manipulate 3-D chemical structure of proteins and other biomolecules; RNA secondary structure prediction and visualization

**Mass Spectrometry and Bioanalytics**

Data from separation techniques that produce traces with peaks, including MS, LC/MS, NMR, chromatography, and electrophoresis

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Key Features

• Next Generation Sequencing analysis and browser

• Sequence analysis and visualization, including pairwise and multiple sequence alignment and peak detection

• Microarray data analysis, including reading, filtering, normalizing, and visualization

• Mass spectrometry analysis, including preprocessing, classification, and marker identification

• Phylogenetic tree analysis

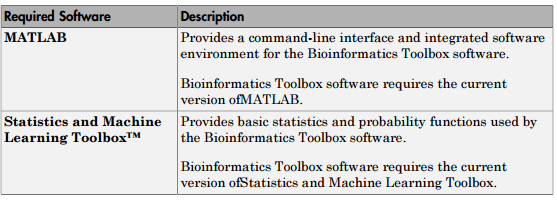
• Graph theory functions, including interaction maps, hierarchy plots, and pathways

• Data import from genomic, proteomic, and gene expression files, including SAM, FASTA, CEL, and CDF, and from databases such as NCBI and GenBank

**Installing**

Install the Bioinformatics Toolbox software from a DVD or Web release using the MathWorks Installer.

**Required Software:** The Bioinformatics Toolbox software requires the following MathWorks products to be installed on your computer.



**Optional Software:** Using the Bioinformatics Toolbox software with other MATLAB toolboxes and products will allow you to do advanced algorithm development and solve multidisciplinary problems. MATLAB and the Bioinformatics Toolbox software environment is open and extensible. In this environment you can interactively explore ideas, prototype new algorithms, and develop complete solutions to problems in bioinformatics. MATLAB facilitates computation, visualization, prototyping, and deployment.

