

## About the Bioinformatics Core Facility

The Bioinformatics Core Facility provides customized data analysis services and consultation to scientist and students, with the aim of advancing the research using cutting-edge bioinformatics methodologies. The service is available to scientists from all faculties, whose research is related to biology, bioinformatics, biomedicine, biotechnology and agriculture. In addition, the Core Facility staff can help in designing genomic experiments and in writing the relevant sections in grant proposals.

The Core Facility main areas of expertise include experiments that use genomic technologies, such as Next-Generation Sequencing, Mass Spectrometry proteomics profiling, metabolomics profiling, microarrays and more. In addition, we have extensive experience in sequence analysis, database development, statistical analysis and bioinformatics programming.

For each project, the facility Core Facility carefully selects and tests relevant software and parameters, performs the analysis and finally provides users with context-specific data and knowledge that they can use. Facility staff members work hand-in-hand with scientists in interpreting the results, and in exploring options for further research. Platforms for automated data analysis pipelines (NeatSeq-Flow, Microbe-Flow), developed by the Core Facility, are also available for students wishing to conduct bioinformatics analyses by themselves.

You are warmly welcome to contact Dr. Vered Caspi, head of the Bioinformatics Core Facility:  
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## Main services:

- Next Generation Sequencing (NGS) data analysis:
  - *de novo* sequence assembly and annotation of novel genomes and transcriptomes
  - Gene expression profiling (RNA-Seq)
  - Single cell RNA-Seq
  - Protein-DNA interaction analysis (Chip-Seq)
  - Micro-RNA discovery and profiling (miRNA-Seq)
  - SNP discovery and genotyping from exome sequencing, RAD-Seq, GBS and whole-genome sequencing.
  - Human, plant and livestock genetic analyses
  - Microbial genomics
  - Comparative genomics
  - Development of genomic markers
- Expression profiling using additional methods:
  - Mass Spectrometry Proteomics & Metabolomics Profiling
  - MiRNA expression profiling using Nanostring technology
  - DNA microarray analyses
  - Antibody microarray analyses
  - Downstream functional, pathway and biological network analyses
- Genomic analyses and molecular epidemiology of microbial pathogens:
  - Use of whole genome data for determination of microbial taxonomy, molecular subtype, virulence determinants and antimicrobial resistance
  - Outbreak investigation and strain tracking
  - Metagenomic studies of bacterial populations (microbiota) using 16S, 18S and shotgun metagenomics sequencing.
  - Detection of diagnostic and therapeutic targets
  - Marker development

## Infrastructure:

- Computers:
  - 14 servers in the BGU HPC cluster with up to 550 Giga RAM each + Elastic Storage Server
  - Access to the entire BGU HPC cluster
  - 2 Web servers
  - 2 Extremely strong PC workstations
  - 1 long-term storage server
  - Personal computers
- Programming environments:
  - Python
  - Perl
  - R/BioConductor
  - Other, as needed
- Databases
  - MySQL
  - FileMaker Pro
  - Other
- Software
  - Cutting edge commercial and publicly available software
  - NeatSeq-Flow – our in-house developed platform for designing and executing complex workflows on computer clusters. The platform allows automatic, efficient and well-documented execution of the workflows. It is easy to use through command line as well as a graphical user interface.

## Team:

Our team includes Ph.D. level bioinformaticians with strong backgrounds in biology, bioinformatics, and statistics, and with long experience in analyzing high-throughput genomic datasets.

## Web site:

<http://bioinfo.bgu.ac.il>