



GenExAT

A Web Application for Analysis and Visualization of Gene Expression Data

- Homepage of GenExAT App



GenExAT: Gene Expression Analysis Tool



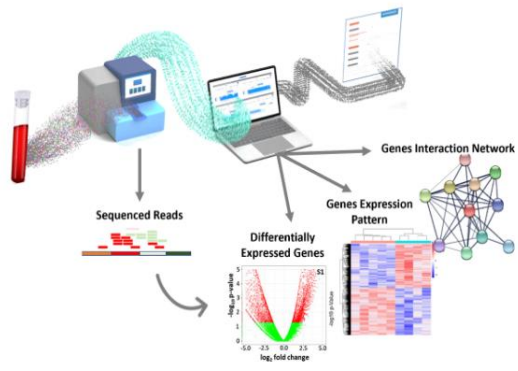
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GenExAT app is a gene expression analysis tool to analyze and interpret the insights from biological data. It primarily focuses on the genomics and transcriptomics data analysis. **But do not worry!** you will find alternatives to learn all these technical aspects independently.

GenExAT will enable to perform multiple NGS data analysis and visualization for microarray, RNA-seq (NGS-based transcriptome analysis) and Single cell (scRNA) data.

The NGS data analysis process includes six main steps:


1. library preparation
2. reads sequencing
3. reads mapping on reference genome
4. differential gene analysis
5. visualization
6. results interpretation.




For more information please contact the [developers](#) [Here](#)

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- Microarray description and analysis tab



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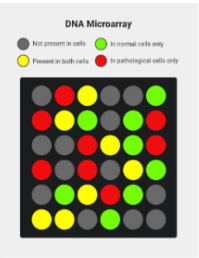
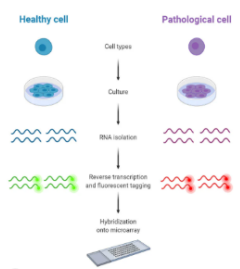
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Microarray Data Analysis

Microarrays can be used in many types of experiments including genotyping, epigenetics, translation profiling, and gene expression profiling. Gene expression profiling is by far the most common use of microarray technology. Both one- and two-color microarrays can be used for this type of experiment. The process of analyzing gene expression data is similar for both types of microarrays and involves feature extraction, quality control, normalization, differential expression analysis, and biological interpretation of the results.

Microarrays are used to measure the expression levels of large numbers of genes simultaneously or to genotype multiple regions of a genome. Each DNA spot contains picomoles (10–12 moles) of a specific DNA sequence, known as probes (or reporters or oligos). These can be a short section of a gene or other DNA element that are used to hybridize a cDNA or cRNA (also called anti-sense RNA) sample (called target) under high-stringency conditions. Probe-target hybridization is usually detected and quantified by detection of fluorophore-, silver-, or chemiluminescence-labeled targets to determine relative abundance of nucleic acid sequences in the target. The original nucleic acid arrays were macro arrays approximately 9 cm × 12 cm and the first computerized image based analysis was published in 1981 by Patrick O. Brown. [Read More](#)

[Start Analysis](#)



Healthy cell Pathological cell

Cell types

Culture

RNA isolation

Reverse transcription and fluorescent tagging


Hybridization onto microarray

DNA Microarray


● Not present in cells ● In normal cells only
● Present in both cells ● In pathological cells only

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- **RNA-seq description and analysis tab**



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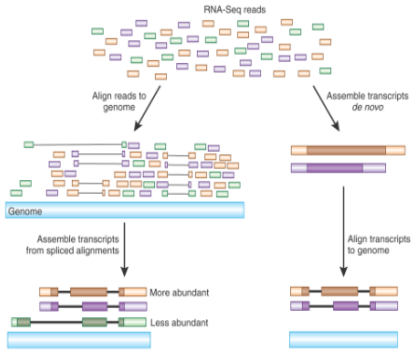
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RNA sequence(s)

RNA-seqs can be used in many types of experiments including genotyping, epigenetics, translation profiling, and gene expression profiling. Gene expression profiling is by far the most common use of RNA-seq technology. Both one- and two-color RNA-seqs can be used for this type of experiment. The process of analyzing gene expression data is similar for both types of RNA-seqs and involves feature extraction, quality control, normalization, differential expression analysis, and biological interpretation of the results.

RNA-seq over Microarrays


Prior to RNA-Seq, gene expression studies were done with hybridization-based microarrays. Issues with microarrays include cross-hybridization artifacts, poor quantification of lowly and highly expressed genes, and needing to know the sequence a priori. Due to these technical issues, transcriptomics transitioned to sequencing-based methods. These progressed from Sanger sequencing of Expressed sequence tag libraries, to chemical tag-based methods (e.g., serial analysis of gene expression), and finally to the current technology, next-gen sequencing of complementary DNA (cDNA), notably RNA-Seq. [Read More](#)



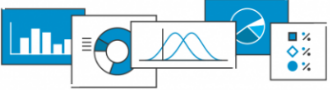
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- **Single-cell RNA-seq description and analysis tab.**



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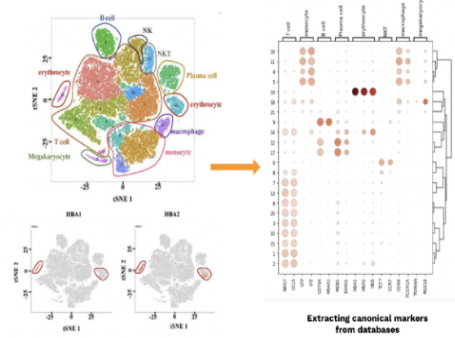


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Single cell RNA-Sequencing

Single-cell sequencing examines the nucleic acid sequence information from individual cells with optimized next-generation sequencing technologies, providing a higher resolution of cellular differences and a better understanding of the function of an individual cell in the context of its microenvironment. In cancer, sequencing the DNA of individual cells can give information about mutations carried by small populations of cells. In development, sequencing the RNAs expressed by individual cells can give insight into the existence and behavior of different cell types. In microbial systems, a population of the same species can appear genetically clonal. Still, single-cell sequencing of RNA or epigenetic modifications can reveal cell-to-cell variability that may help populations rapidly adapt to survive in changing environments.


A typical human cell consists of about 2 x 3.3 billion base pairs of DNA and 600 million mRNA bases. Usually, a mix of millions of cells is used in sequencing the DNA or RNA using traditional methods like Sanger sequencing or next generation sequencing. By deep sequencing of DNA and RNA from a single cell, cellular functions can be investigated extensively. Like typical next-generation sequencing experiments, single-cell sequencing protocols generally contain the following steps: isolation of a single cell, nucleic acid extraction and amplification, sequencing library preparation, sequencing, and bioinformatic data analysis. It is more challenging to perform single-cell sequencing than sequencing from cells in bulk. [Read More](#)




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- Exome-seq description and analysis tab.



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Exome-Sequencing

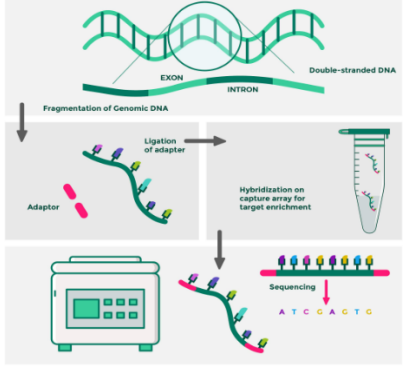
Exome sequencing, also known as whole exome sequencing (WES), is a genomic technique for sequencing all of the protein-coding regions of genes in a genome (known as the exome). It consists of two steps: the first step is to select only the subset of DNA that encodes proteins. These regions are known as exons—humans have about 180,000 exons, constituting about 1% of the human genome, or approximately 30 million base pairs. The second step is to sequence the exonic DNA using any high-throughput DNA sequencing technology.

While many more genetic changes can be identified with whole exome and whole genome sequencing than with select gene sequencing, the significance of much of this information is unknown. Because not all genetic changes affect health, it is difficult to know whether identified variants are involved in the condition of interest. Sometimes, an identified variant is associated with a different genetic disorder that has not yet been diagnosed.

Exome-seq vs. RNA-seq

WES sequencing refers to genomic DNA sequencing that is enriched for exonic regions. RNA sequencing, on the other hand, may or may not be enriched (for example for polyadenylated transcripts). [Read More](#)


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The diagram illustrates the exome sequencing workflow. It begins with 'Double-stranded DNA' containing 'EXON' and 'INTRON' regions. This is followed by 'Fragmentation of Genomic DNA'. The next step is 'Ligation of adaptor', where 'Adaptor' sequences are attached to the DNA fragments. This is followed by 'Hybridization on capture array for target enrichment', where the fragments bind to a specific array. Finally, the process moves to 'Sequencing', represented by a sequencing machine and a sequence read 'A T C C A G T C'.

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- The tabular view of the pre-loaded data as example data.



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Input Data
DEG Result
Data Filter
Box Plot
Volcano Plot
Heatmap
PCA (Principal Component Analysis)

Use example file or upload your own data

☐ Upload Data
☒ Example Data

[Start Analysis](#)

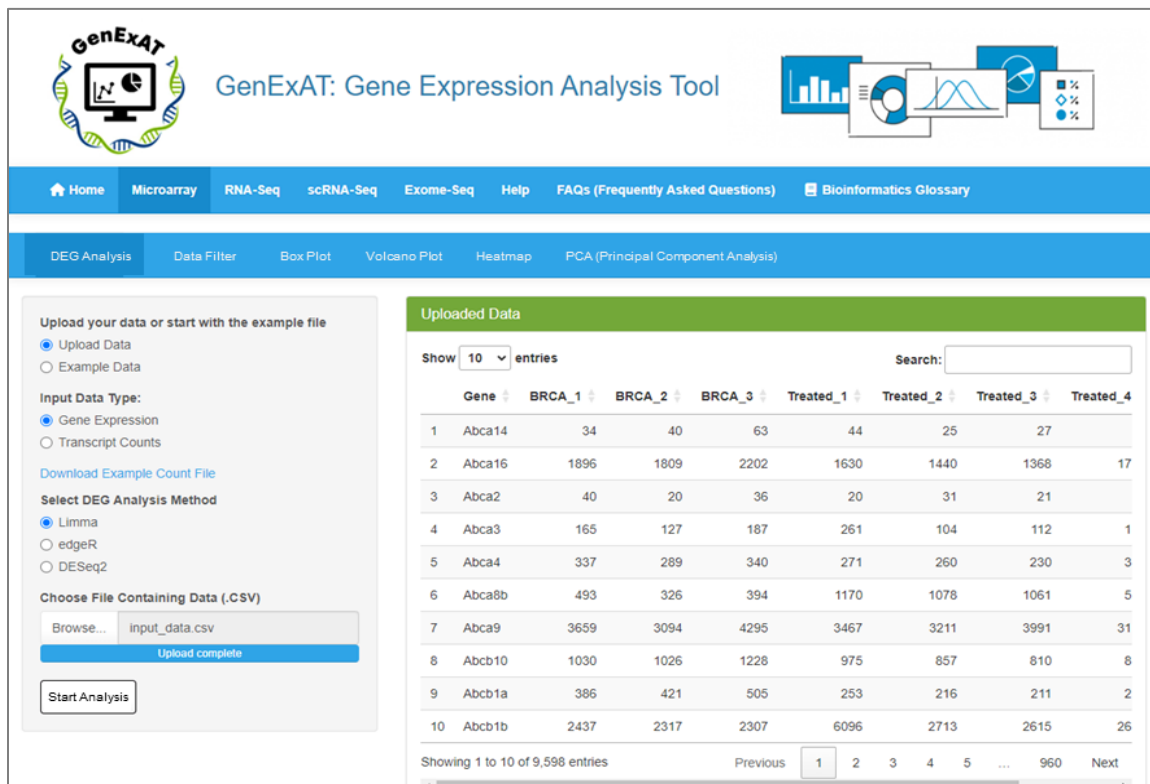
Uploaded Data

Show entries Search:

	Gene	Healthy_1	Healthy_2	Healthy_3	Healthy_4	Tumor_1	Tumor_2	Tum
1	UBC	5934	5940	6747	4874	4798	4796	
2	EEF1G	444	404	519	80	115	90	
3	RPL5	2003	5036	4405	2393	1663	3429	
4	TXNIP	72	48	58	26	12	19	
5	MTND1P23	1234	1416	1441	1177	1259	1137	
6	RPS27	25650	21816	25463	28817	26772	28241	
7	GAPDH	12814	13958	15515	11359	13073	14312	
8	RPS3A	1518	1356	1492	1565	1720	1587	
9	RPL4	1141	975	1179	1049	1015	1128	
10	RPS3A	1049	946	1327	914	948	902	

Showing 1 to 10 of 100 entries Previous 2 3 4 5 ... 10 Next

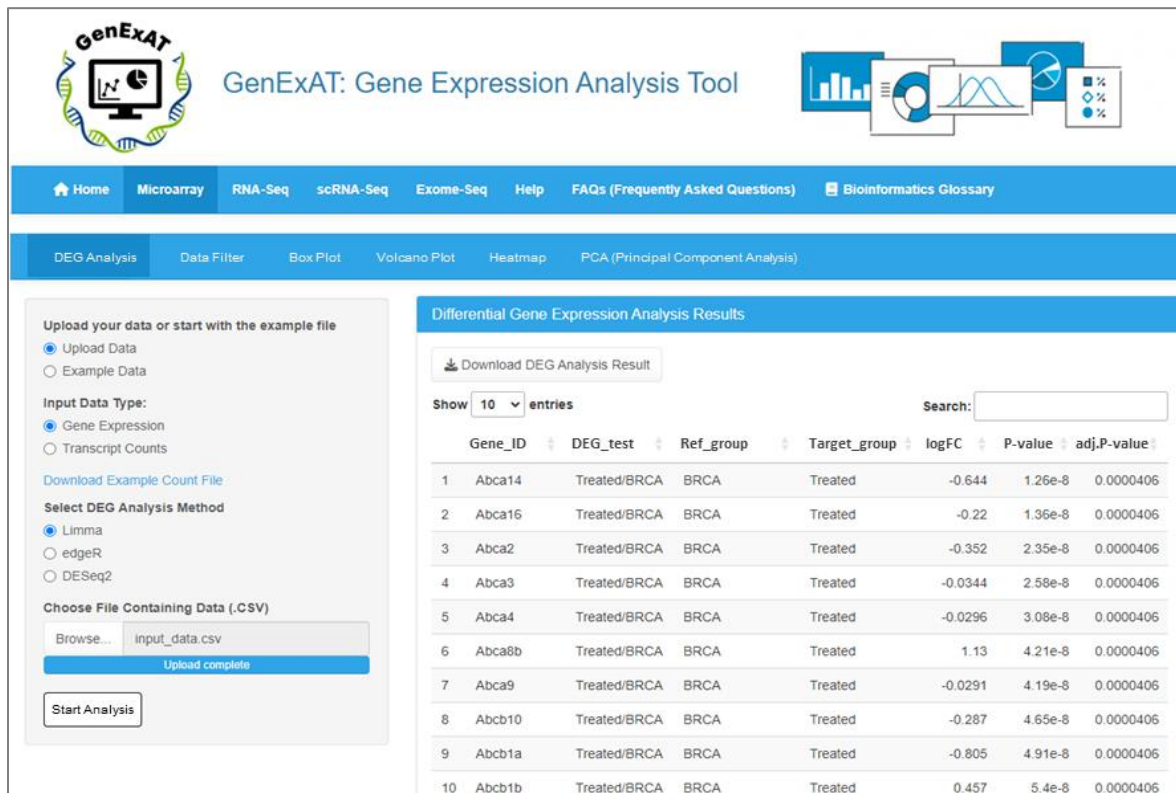
- The tabular view of data uploaded by user for microarray analysis.



The screenshot displays the GenExAT web application interface. The top navigation bar includes links for Home, Microarray, RNA-Seq, scRNA-Seq, Exome-Seq, Help, FAQs, and Bioinformatics Glossary. The main navigation bar highlights 'DEG Analysis' and includes sub-links for Data Filter, Box Plot, Volcano Plot, Heatmap, and PCA. The left sidebar contains options for uploading data, selecting input data type (Gene Expression or Transcript Counts), choosing a DEG analysis method (Limma, edgeR, or DESeq2), and uploading a CSV file. The main content area shows the 'Uploaded Data' table with 10 entries displayed. The table columns are Gene, BRCA_1, BRCA_2, BRCA_3, Treated_1, Treated_2, Treated_3, and Treated_4. The data rows show gene expression values for various genes across different conditions.

	Gene	BRCA_1	BRCA_2	BRCA_3	Treated_1	Treated_2	Treated_3	Treated_4
1	Abca14	34	40	63	44	25	27	
2	Abca16	1896	1809	2202	1630	1440	1368	17
3	Abca2	40	20	36	20	31	21	
4	Abca3	165	127	187	261	104	112	1
5	Abca4	337	289	340	271	260	230	3
6	Abca8b	493	326	394	1170	1078	1061	5
7	Abca9	3659	3094	4295	3467	3211	3991	31
8	Abcb10	1030	1026	1228	975	857	810	8
9	Abcb1a	386	421	505	253	216	211	2
10	Abcb1b	2437	2317	2307	6096	2713	2615	26

- DEG analysis result, where Gene_ID represents input genes, DEG_test shows the group level test, the Reference group is secondary group and Target group



The screenshot displays the GenExAT web application interface showing the 'Differential Gene Expression Analysis Results' tabular view. The left sidebar is identical to the previous screenshot. The main content area shows the 'Differential Gene Expression Analysis Results' table with 10 entries displayed. The table columns are Gene_ID, DEG_test, Ref_group, Target_group, logFC, P-value, and adj.P-value. The data rows show the results of the differential expression analysis for the same genes as in the 'Uploaded Data' table.

	Gene_ID	DEG_test	Ref_group	Target_group	logFC	P-value	adj.P-value
1	Abca14	Treated/BRCA	BRCA	Treated	-0.644	1.26e-8	0.0000406
2	Abca16	Treated/BRCA	BRCA	Treated	-0.22	1.36e-8	0.0000406
3	Abca2	Treated/BRCA	BRCA	Treated	-0.352	2.35e-8	0.0000406
4	Abca3	Treated/BRCA	BRCA	Treated	-0.0344	2.58e-8	0.0000406
5	Abca4	Treated/BRCA	BRCA	Treated	-0.0296	3.08e-8	0.0000406
6	Abca8b	Treated/BRCA	BRCA	Treated	1.13	4.21e-8	0.0000406
7	Abca9	Treated/BRCA	BRCA	Treated	-0.0291	4.19e-8	0.0000406
8	Abcb10	Treated/BRCA	BRCA	Treated	-0.287	4.65e-8	0.0000406
9	Abcb1a	Treated/BRCA	BRCA	Treated	-0.805	4.91e-8	0.0000406
10	Abcb1b	Treated/BRCA	BRCA	Treated	0.457	5.4e-8	0.0000406

- Plots generated from GenExAT after DEG analysis.

