

# Genex: CyberT - Statistical Analysis for Large Scale Gene Expression Data

**Data File to Upload:** (Format expected, Data Coding)  
If your file won't upload, or Cyber-T won't process it, [check these possible reasons](#).  
wt-noirp(4x4)(4290).csv   
Data fields delimited by:  \* whitespace = TABS & spaces  
☒ Delete lines with NULL Labels.

Please enter any text that you would like to have as a header for the analysis output.

Columns start at 0, not 1; leading / lagging spaces are bad.

Label Columns (as # # #...):

Control Data Replicate Columns (as # # #...):

Experimental Data Replicate Columns (as # # #...):

Minimum non-zero Replicates Required (#):  
 If left blank, the number of values of Experimental Data will be used.

- Low Value Handling

- ☒ Values less than  will be set to 0 and ignored in calculations. (Including negative values will cause the app to die. If you need to correct for negatives, use the option below)
  - ☐ Offset the values by the lowest value in the dataset, effectively right-shifting the entire dataset. Useful if you want to include negative values. This value will be noted in the output

In the Analytical selections below, this LIGHT GREEN SECTION refers to the Bayesian analysis and is OPTIONAL (it will not be done unless there is a value in the "Confidence Value" space).		101
Choose a sliding window size for approximating the variance of your values (ie. How many total samples around the point of interest will give you a satisfactory estimate of the local variance?)		
Enter a confidence value here that applies to the Bayesian Variance Estimate that you set immediately above. A decent default would be '10' or about 3 times the number of replicates per treatment		
If left blank, the whole Bayesian Estimate Analysis (light green) will be skipped.		
Bonferroni Correction - Experiment-wide false positive rate (the probability of a single gene scoring significant by chance alone)		0.25
Repeat Label Line every ~50 lines to tell you what the columns are		
In the Graphics Output, this many plots should be placed on 1 page		1
Convert default postscript output to PDF (can view the results with Acrobat)		
How many decimal places would you like in the numeric results? (Max' is the maximum precision that R generates)		
Convert plaintext output to Excel format?		Max
The bottom two options require a Pre-Existing Arrangement with the Hosting Institution to allow X Windows or VNC protocol to be sent to your location.		
View input/output from top N results (by 'p' value) in 2/3D using xgobi interactively. If you know your X DISPLAY value, you can type it in the following window. Otherwise, we'll assume that it's the same machine that your Netscape is running on (usually a good bet) Your X DISPLAY: [machine.net.domain.edu:0.0 or 128.200.34.145:0.0]		
Leave entries blank to skip (Requires a running X Window Server allowing X access from this server, or use of the VNC client below)		View top results by 'p'
Use Virtual Network Computing client to view xgobi? If your sysadmin has installed the VNC server AND you want to view the xgobi output in your browser or using the VNC client THEN fill in the # of results you want to see in the row above (right column) AND replace NO with the SCREEN NUMBER to the right as described in the lead URL. The server will generate a URL that you can click that will start the VNC viewer in your browser. No other software required. OR, for better performance, you can start the VNC client and connect to the GeneX server on that DISPLAY number.		

Be Patient. This analysis can take SEVERAL MINUTES to run, depending on the server speed and load.  
(~5 min for ~6400 genes, 3 sets of ratios, on a 200MHz PPro/Linux).

Reset to Defaults

Submit Data

Figure D.1. The CyberT interface at the UCI genomics web site.