

Installation Guide

Affymetrix® Transcriptome Analysis Console (TAC) Software

A NEW analysis solution that transforms data to insight

Detailed analysis is now at the fingertips of every researcher—regardless of access to bioinformatics resources. The new Affymetrix® Transcriptome Analysis Console (TAC) Software takes the normalized and summarized data from Affymetrix Expression Console™ (EC) Software to the next level, providing differential expression analysis and visualization for easy interpretation.

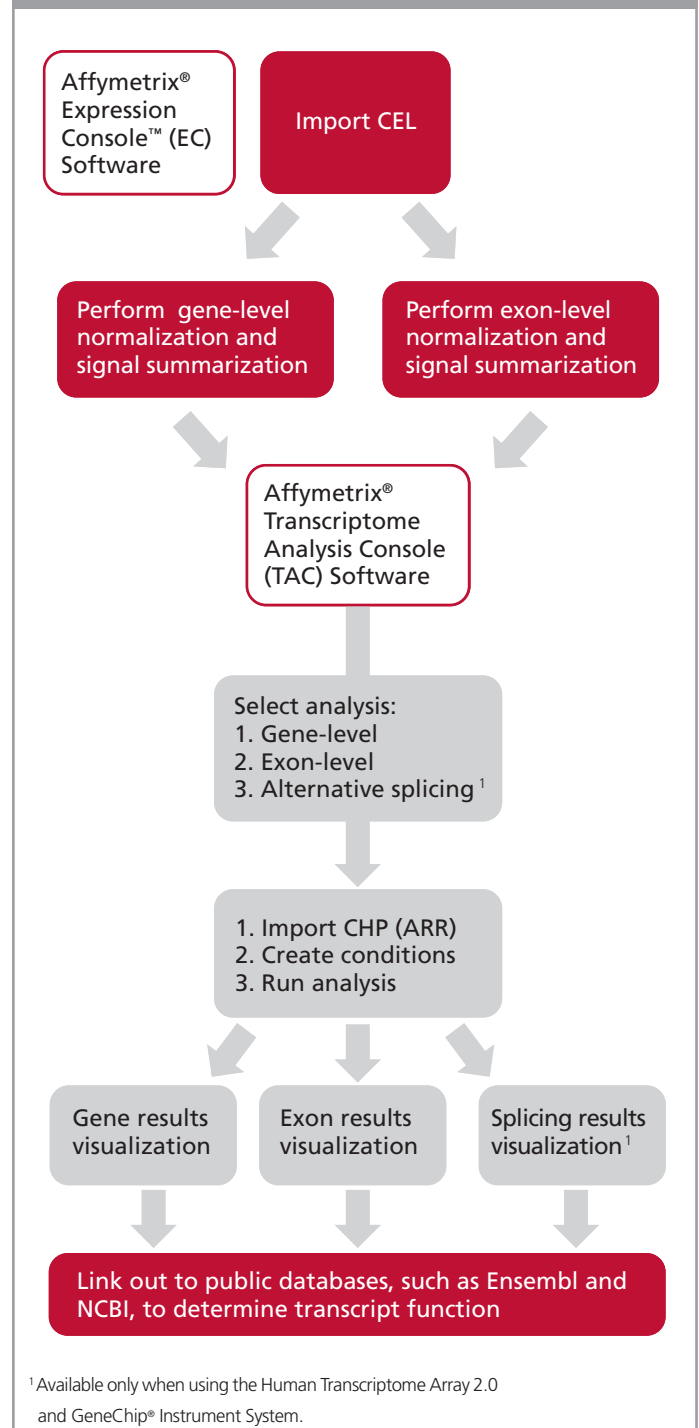
Easy-to-use TAC Software provides:

- Sample grouping and cluster visualization
- Statistical tests for differential expression
- Detailed summary view of comparisons
- Direct links to available public annotations

Software installation instructions

1. Install the EC software
 - Go to www.affymetrix.com/install_ec
 - Locate and download the EC software package
 - Unzip the file
 - Double-click EC64bit.exe to install the software
2. Install the TAC software
 - Go to www.affymetrix.com/install_tac
 - Locate and download the TAC software package
 - Unzip the file
 - Double-click TAC64bit.exe to install the software

Figure 1: Data workflow.

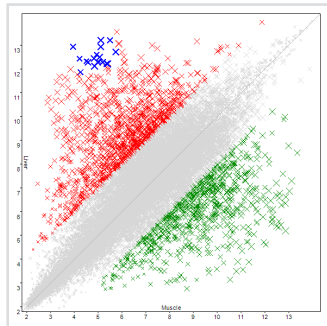


Powerful visualization tools

TAC Software provides powerful visualization tools that allow easy interpretation of significant expression changes. Some of the visualization tools in TAC include:

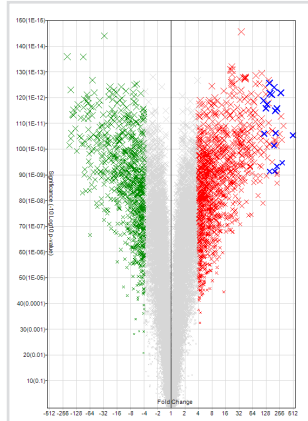
Scatter plot

Visualize significant changes in signal between conditions.



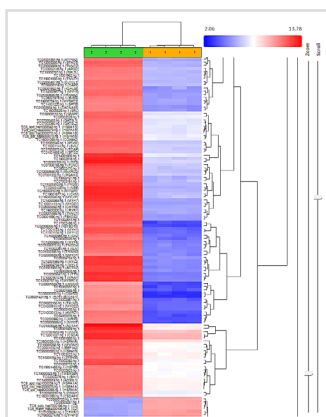
Volcano plot

Visualize significant fold-changes between conditions.



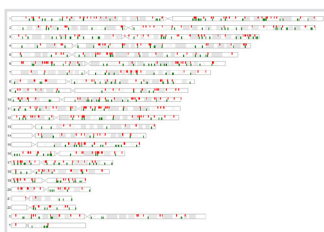
Hierarchical clustering

Arrange samples and genes into groups based on their expression levels.



Chromosome view

Significant fold-changes visualized along each chromosome (human only).



Export your results and link to external databases

- Table contents can be exported as tab-delimited text files
- Genes, transcript isoforms, and exons can be linked out to public databases
- Experimental data seamlessly imports into pathway analysis tools

Recommended system requirements for GeneAtlas System compatible arrays²

Microsoft Windows[®] 7 Professional operating system with Service Pack 1

Operating system (bits) 64-bit

Processor 2.8 GHz Intel[®] Pentium[®] Core 2 Duo

Memory (RAM) 4 GB (recommended) 8 GB

Web browser Internet Explorer[®] 7.0 and above

²Higher system requirements published elsewhere are intended for splice-junction analysis using the Human Transcriptome Array 2.0.

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