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Transcriptome Analysis Console (TAC) Software

Fast, intuitive software for deciphering the complexity of the transcriptome

Detailed expression analysis is now at the fingertips of every researcher

Applied Biosystems™ Transcriptome Analysis Console (TAC) Software, designed for the end user, allows you to quickly develop meaningful insights from transcriptomic microarray (array) data using a variety of statistical, visualization, and quality control (QC) tools. With version 4.0 (and subsequent releases), TAC Software includes all of the functionality of previous versions as well as the added features of Applied Biosystems™ Expression Console (EC) Software. By combining EC Software and TAC Software into a single tool, we have reduced the number of workflow steps for QC through data analysis (Figure 1) so that you can focus on getting answers.

You now have an easy-to-use software at no additional cost to analyze and explore your data at your own pace. When combined with our comprehensive, high-density arrays and reagents, compatible with challenging and precious samples, you can go from sample to insight in just three days.

Import .cel file → Select comparison → Run analysis → View results
- QC
- Gene level
- Exon level

Figure 1. TAC Software offers a streamlined workflow for transcriptome-wide expression array analysis.

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Whole transcriptome data analysis made easy

TAC Software supports Applied Biosystems™ expression arrays for gene-level and exon-level analysis.

- Perform array QC and data normalization

- Perform statistical tests for differential expression analysis

- Generate lists of differentially expressed genes

- Explore interactions between coding RNA and noncoding RNA (ncRNA)

- Simplify the interpretation of complex alternative splicing events

- Easily focus on genes or pathways of interest

- Link to publicly available annotations

- Obtain sequence information to design verification experiments

New features and benefits in TAC Software version 4.0 (and subsequent releases)

- Streamlined QC and data analysis with the combination of EC Software and TAC Software into a single tool

- Capability to analyze large data sets of 1,000 or more samples

- Integration of established LIMMA (linear modeling for microarrays) package

- Improved alternative splicing analysis with enhanced visualization tools and additional algorithms for statistical analysis

Streamlined workflow and analysis of large data sets

TAC Software now includes upstream tools from EC Software, such as signal summarization, sample normalization, and QC, as well as state-of-the-art analysis methods for a single, more streamlined analysis workflow. TAC Software has also been upgraded to support analysis of larger data sets for 1,000 or more arrays, making it easier to analyze complex cohort or longitudinal studies.

LIMMA integration

Advanced LIMMA capabilities from Bioconductor [1], which has been cited by over 8,000 peer-reviewed publications and is one of the most popular, statistically rigorous analysis frameworks for differential expression analysis, is now included within TAC Software. A graphical user interface (GUI) for LIMMA is incorporated, making it easier to use than command-line versions. The LIMMA statistical methods help improve inference at both the gene and gene set level in small experiments. LIMMA offers flexible analysis that can handle complex experimental designs, batch effects, and empirical Bayesian analysis to increase the number of significant differential expression hits when analyzing small numbers of samples.

Improved alternative splicing analysis

TAC Software has been updated to include EventPointer, developed by Juan Romero and Angel Rubio at Ceit-IK4 [2]. EventPointer searches database-described splice events and statistically models them in expression data. Combining EventPointer with existing algorithms in TAC Software for alternative splicing analysis offers two independent algorithms for better statistical measurement of splicing results. Users of Applied Biosystems™ Clariom™ D arrays and earlier generations of transcriptome-view arrays can now see individual sample variation in the splicing viewer and identify previously undiscovered events detectable by the array but previously algorithmically hidden.

Powerful, interactive visualizations

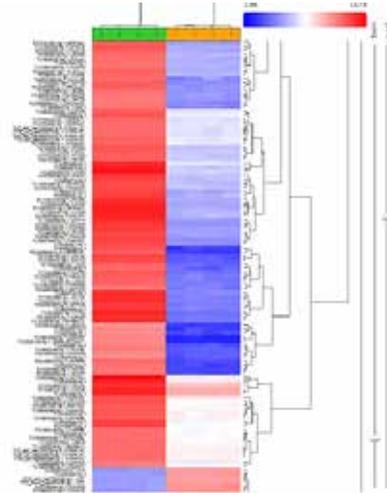TAC Software provides interactive visualizations for easy interpretation of significant expression changes.

Scatter and volcano plots

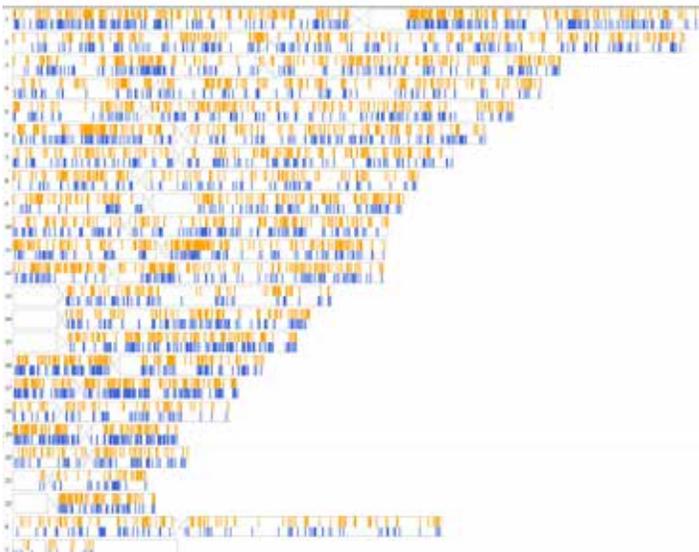Visualize significant changes in genes between conditions.
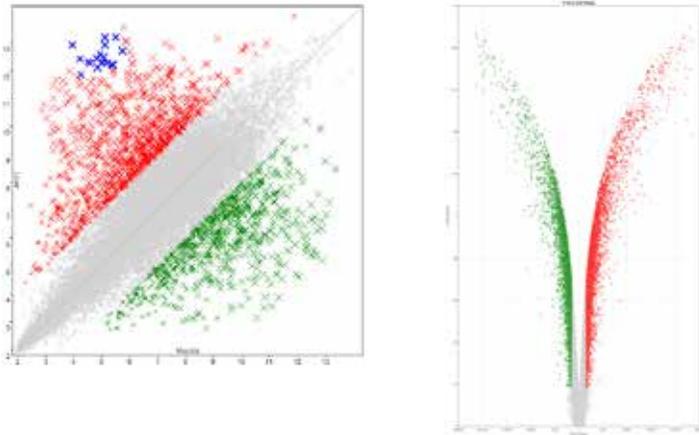
Hierarchical clustering

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

Chromosome view

Visualize significant fold changes on each chromosome.

Alternative splicing view

Identify and understand complex splicing events in multiple samples with a new statistical reporting chart and graphical representation combination view.

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System requirements	
Operating system (64-bit)	Windows™ 7 Professional (SP1) or Windows™ 10 Professional
Processor	2.83 GHz Intel™ Pentium™ Quad Core
Memory (RAM)	8 GB (minimum) 16 GB (recommended)
Web browser	Internet Explorer™ 11 and above (Windows 7) Microsoft™ Edge (Windows 10)

References

1. Ritchie ME et al. (2015) *limma* powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research* 43(7):e47.

2. Romero JP et al. (2016) EventPointer: an effective identification of alternative splicing events using junction arrays. *BMC Genomics* 17:467.

Find out more at **thermofisher.com/microarrays**

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