Transcriptome Analysis Console (TAC) Software

Powerful and intuitive software for deciphering the complexity of the transcriptome

Data to insight in minutes
Detailed analysis is now at the fingertips of every researcher. Transcriptome Analysis Console (TAC) Software from Affymetrix takes differential expression profiles to a new level with the ability to develop meaningful insights from the visualization of miRNA regulatory networks and biological pathways.

Researchers now have a cost-free solution to quickly analyze their data, enabling discovery and understanding of the biological diversity underpinning their research. These tools were designed with the end user in mind and enable investigators to analyze and explore data at their own pace. Combined with the comprehensive coverage of high-density microarray solutions and Expression Console™ Software from Affymetrix, TAC Software provides an easy-to-use, integrated solution to go from raw data to biological results in just a few clicks.

Designed for the biologist
- Perform statistical tests for differential expression.
- Generate lists of differentially expressed genes.
- Explore interactions between coding and non-coding RNA.
- 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 validation experiments.

You decide — gene-level, exon-level, or alternative splicing analysis
TAC Software supports three types of differential expression analysis for microarrays from Affymetrix, depending upon array type:

<table>
<thead>
<tr>
<th>Array type</th>
<th>Analysis type</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Gene</td>
</tr>
<tr>
<td>Transcriptome view</td>
<td>X</td>
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<tr>
<td>Exon ST</td>
<td>X</td>
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<tr>
<td>Gene ST</td>
<td>X</td>
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<td>3’ IVT</td>
<td>X</td>
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<tr>
<td>miRNA</td>
<td>X</td>
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Data workflow
1. Select analysis
2. Create conditions
3. Import data
4. Run analysis

Visualize results
Exon | Gene | Alt. splice

Visualize expression changes in pathways

Visualize mRNA and miRNA interactions

Link out to public databases such as Ensembl or NCBI
Map expression changes between miRNA and target genes
Decipher the diverse network of interactions between miRNA and long coding and non-coding transcripts.

Gene expression changes in pathways
Identify more differentially expressed genes relevant to your research with pathway visualizations.

Download TAC Software today
To access TAC Software and a complete list of supported arrays, please visit www.affymetrix.com.

System requirements

<table>
<thead>
<tr>
<th>Microsoft Windows® 7 professional (SP1)</th>
<th>Microsoft Windows® 10 professional</th>
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<tbody>
<tr>
<td>Operating system (bits)</td>
<td>64-bit</td>
</tr>
<tr>
<td>Processor</td>
<td>2.83 GHz Intel® Pentium® Quad Core</td>
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<tr>
<td>Memory (RAM)</td>
<td>8 GB (minimum)</td>
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<tr>
<td></td>
<td>16 GB (recommended)</td>
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<tr>
<td>Web browser</td>
<td>Internet Explorer® 8.0 and above</td>
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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**
  Visualize significant fold changes along each chromosome (human only).

- **Alternative splicing**
  Utilize intuitive visualizations of alternatively spliced exons to identify transcript isoforms.

Alternative splicing
Utilize intuitive visualizations of alternatively spliced exons to identify transcript isoforms.