

Transcriptome Analysis Console (TAC) Software 4.0.1 Release Notes

(For research use only. Not for use in diagnostic procedures.)

Transcriptome Analysis Console Software 4.0.1 addresses the following defect fixes:

1. TAC will not be installed on systems with lower than 8GB of memory.
2. TAC will now handle the Turkish operating system that contains i/l character.
3. TAC now recognizes operating systems that use commas as decimal separator. The default p-value filter has been correctly set as 0.05..
4. TAC will be able to analyze CEL files that have space in the file names.
5. TAC will now find the correct R version required for analysis even if there is another version of R installed in the system.
6. TAC will no longer crash even if the splicing viewer window is too small.
7. TAC will now appropriately display the interaction table contents when there are ≥ 2 factor values in ≥ 2 factors.
8. TAC will now handle RMA background failure due to low signal distribution.
9. TAC will no longer crash if there are non-ASCII characters in the result output path. TAC will not support non-ASCII characters in the library path.

Transcriptome Analysis Console Software 4.0 and 4.0.1 includes the following:

1. Integration of Expression Console (EC) and Transcriptome Analysis Console (TAC)
2. Incorporation of LIMMA Tools, including batch effect adjustment
3. Support for large datasets in recommended systems
4. Exploratory Grouping Analysis (EGA)
5. Improved Alt-splicing analysis including individual sample visualization
6. Most of the CHP data from previous versions will be supported (not including exon CHP files and alt-splice CHP files), but not all data will be available. It is recommended to re-analyze data with TAC 4.0 to take advantage of the new functionalities
7. TAC 4.0 does not directly support all GCOS file formats. GCOS files from some of the arrays must be converted to AGCC file format before using in TAC 4.0.

Software and Hardware Requirements:

Transcriptome Analysis 4.0 is only supported on 64-bit systems with the following operating systems:

- Windows 7 Professional SP1 (64-bit)
- Windows 10 Professional (64-bit)

Memory and CPU Recommended Requirements

- Quad Core System, 2.83 GHz or above
- Minimum 8GB RAM, recommended 16GB RAM

The following are the known issues/differences that exist in Transcriptome Analysis Console Software 4.0.1:

1. When installing TAC 4.0.1, please ensure the correct operating system(s) is installed prior to installing the application.
2. For the Volcano Plot, it only displays up to 4 decimal places.
3. In some cases, clicking on Wikipathways may display an error message "Failed to load pathways". If this occurs, close the results and then reopen it.
4. In the Interactive miRNA and mRNA graph, if the nodes have been moved to new locations in the graph, using the navigational "back" and "forward" buttons will not preserve the new node locations. The nodes will appear in their original location when navigating.
5. Some of the QC metrics are not generated in TAC 4.0.1 anymore. For more information, please contact support.
6. When exporting histogram in wikipathway, save the image and then print to get the histogram in the current view.
7. When running close to 1000 samples, some select samples may be overlapped and to see them, resize the viewer window.