

tappAS Installation

Application Overview and Requirements

TappAS is a Graphical User Interface (GUI) application written in Java. It uses SQLite for its database management and R, along with some statistical packages, for data analysis. Like most applications dealing with large datasets, the more computational power and memory available, the faster the application will run. Be aware that insufficient resources, - CPU, memory, and disk space - will make the application sluggish or unusable.

Listed below are the requirements for running tappAS:

Computer Hardware

Minimum of 4 cores (multi-core CPU or single core CPUs)

Minimum of 8 GBs of memory

Minimum of 20 GBs of available, unused, disk space

Operating System

Linux Ubuntu recent version, or

Mac OS X recent version, or

Other Linux/Unix desktop environments may work but HAVE NOT BEEN TESTED

Client Java

Java (Oracle JRE or JDK) version 8 update 40 or later - version 9 has not been officially released yet and tappAS HAS NOT BEEN TESTED on it

Application will not work with OpenJDK

Software

Rscript version 3.2.2 or later

R packages

You can install automatically all of packages entering the following in R console:

```
source("http://tappas.org/resources/downloads/tappas_packages.R")
```

Or you can install each packages manually:

[DEXSeq recent version \(Bioconductor\)](#)

[maSigPro recent version \(Bioconductor\)](#)

[edgeR recent version \(Bioconductor\)](#)

[NoiSeq recent version \(Bioconductor\)](#)

[goseq recent version \(Bioconductor\)](#)

[mdgsa recent version \(Bioconductor\)](#)

[ggplot2 recent version \(CRAN\)](#)

[MASS recent version \(CRAN\)](#)

[plyr recent version \(CRAN\)](#)

[VennDiagram recent version \(CRAN\)](#)

[GOglm version 0.4.2. or later](#)

Miscellaneous software and package installation notes:

- Make sure to check to see if you already have some of the software and packages installed before trying to install them.
- Also, if you have R on your computer, you may already have some of the packages installed.
- Most statistical R packages are from <https://www.bioconductor.org/>
- If you are using Ubuntu, it's a lot simpler to use the Ubuntu Software Center application or Advanced Packaging Tool (APT) command line tool to install software.
- To install GOglm you can enter the following in R console:

```
install.packages("devtools")  
library(devtools)  
install_github("gu-mi/GOglm")
```

Application Installation

To install TAPPAS:

1. Download the application file, tappas.VER.zip, from <http://tappas.org/downloads/> to your computer. Where VER is the downloaded TAPPAS file's version number, e.g. tappas.0.99.05.zip
2. Uncompress tappas.VER.zip. A tappas folder, including the application version number, will be extracted containing the application files. You may move the folder anywhere you like or just leave it where it's at. A common place would be your home directory, ~/tappas.VER

WARNING: Make sure to uncompress the file. It is possible to look at the compressed file contents without uncompressing the file but you will likely get an error if you try to run the application.

3. To run the application, double click on the tappas.jar file located in the uncompressed tappas folder. Java must be installed and associated with JAR files for this to work.

Note: The first time you run the application, you will be asked to select a location for the application's data folder, tappasWorkspace. This is where the application will store all the application data files including you data analysis results. A common place would be your home directory, ~/tappasWorkspace.

Installation Notes

- Make sure to uncompress the tappas zip file. It is possible to look at the compressed file contents without uncompressing the file but you will likely get an error if you try to run the application by double clicking on the tappas.jar file.
- If you double click the tappas.jar file and nothing happens, you should try the following:

Open a command terminal, **cd** into the uncompressed tappas folder location and type **java -jar tappas.jar**

This may allow you to see what is preventing the application from running, in the form of an error or warning message. It will also allow you to confirm that you have Java JRE installed, not the OpenJDK implementation, and in your PATH.

- Windows OS - if you get the following message:

WARNING: Could not open/create prefs root node Software\JavaSoft\Prefs at root 0x80000002. Windows RegCreateKeyEx(...) returned error code 5.

It is a known Java bug and you may search for the solution on line using the message. A working solution is posted at <https://stackoverflow.com/questions/16428098/groovy-shell-warning-could-not-open-create-prefs-root-node>. It requires the creation of an entry in the Windows registry using the Windows Registry Editor, RegEdit.