

oneChannelGUI Package Installation

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1 Installation

It is important to install additional software other than R and Bioconductor libraries, for the complete functionality of oneChannelGUI.

The external tools and data needed to run exon array analysis in oneChannelGUI are shown in figure 1.

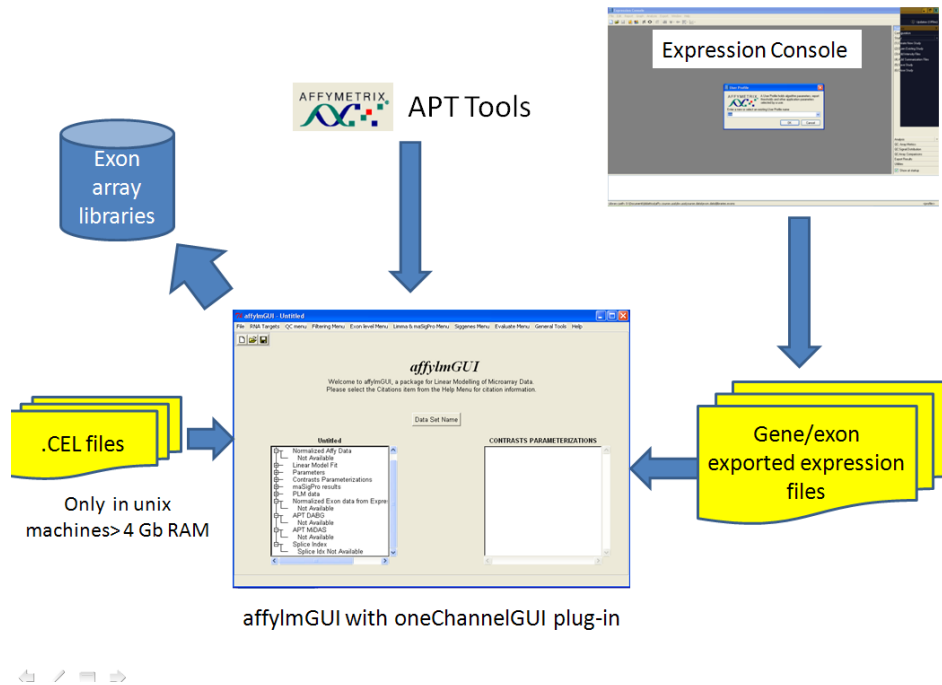


Figure 1: External tools needed for exon array analysis when oneChannelGUI add-on is loaded in affyGUI.

1.1 Windows users

The latest version of R need to be installed. It can be downloaded at: <http://www.r-project.org/> oneChannelGUI needs the installation of the following packages:

```
> packageDescription("oneChannelGUI")$Depends
```

```
[1] "Biobase, affyIbmGUI, tkWidgets"
```

oneChannelGUI suggests the installation of the following packages:

```
> packageDescription("oneChannelGUI")$Suggests
```

```
[1] "annotate, GOstats, genefilter, maSigPro, pamr, pdmclass,\nRgraphviz, affy ,annaffy"
```

In order to install all the Bioconductor packages needed to run oneChannelGUI a specific R function can be downloaded from <http://www.bioinformatica.unito.it/oneChannelGUI/> To use it user needs to open an R session on a computer connected to internet and copy and paste the following code:

```
> source("http://www.bioinformatica.unito.it/downloads/dwbioC.txt")  
> dwbioC()
```

oneChannelGUI inherits the core graphical interface of affyIbmGUI. This interface need, under windows, the installation of TCL/TK libraries that can be download from: <http://www.activestate.com/Products/ActiveTcl/>

Furthermore, to load Hs/Mm/Rn exon 1.0 ST Affymatrix arrays users need to install APT tools 1.6.0. The windows binaries can be downloaded from: <http://www.affymetrix.com/support/developer/powertools/index.affx> In addition library files for exon arrays should also be downloaded from: <http://www.affymetrix.com/support/technical/libraryfilesmain.affx> and located in a user defined directory, e.g. exon.library.files.

1.2 Unix users

The packages to be downloaded for unix users are those indicated for windows users unless for the TCL/TK libraries.

To use Tcl/Tk then the interface package tcltk must be installed into R. If an R package uses Tcl/Tk then Tcl/Tk must be installed on the OS before the R package can be installed into R. Furthermore, these two Tcl/Tk packages are needed by oneChannelGUI, affyIbmGUI and limmaGUI for their functionality:

1. BWidget, this is a package written entirely in the tcl scripting language and hence is not compiled. Consequently it is the same on any platform and should be in the Tcl/Tk path.

2. Tktable, this package has some code written in C and hence is a compiled package. It therefore is different for each type of CPU and OS.

It is possible to encounter problems in installing those libraries on x64 machines. For this reason I found quite useful the suggestions of Keith Satterley (24 Apr 2007) subject: Re: [Bioc-devel] Tcl/TK package "Bwidget" available on the Bioconductor mailing list.