

oneChannelGUI Package Installation

Raffaele A Calogero, Francesca Cordero, Remo Sanges

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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.

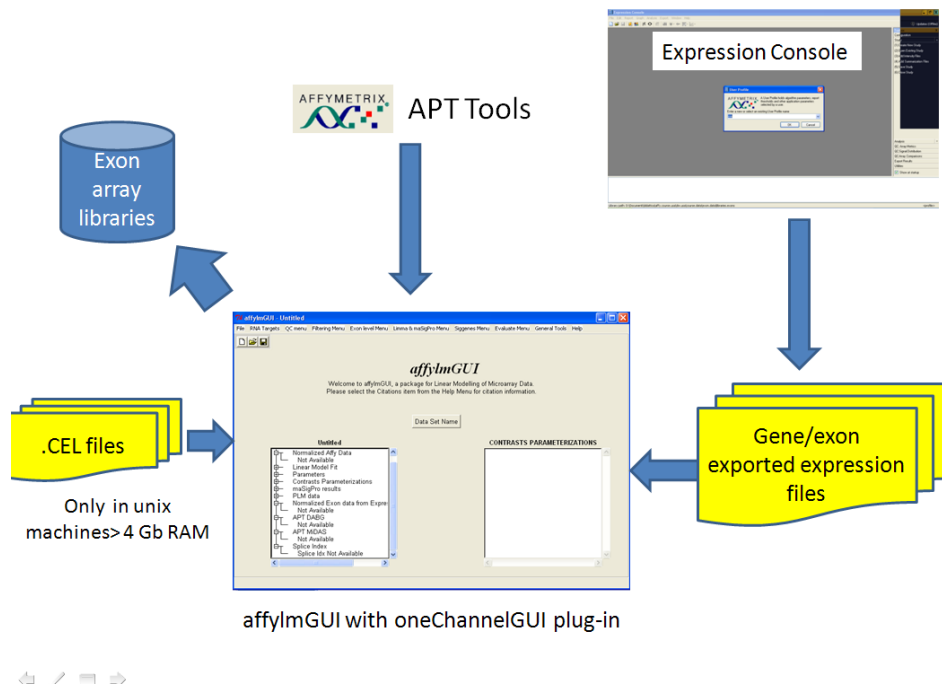


Figure 1: External tools needed for exon array analysis when oneChannelGUI add-on is loaded in affyGUI.

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, affyilmGUI, tkWidgets, IRanges, Rsamtools, Biostrings, siggenes, chimera"
```

oneChannelGUI suggests the installation of the following packages:

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

```
[1] "annotate, genefilter, maSigPro, pamr, pdmclass, ChIPpeakAnno, chipseq, BSgenome,"
```

In order to install all the Bioconductor packages needed to run oneChannelGUI a specific R function can be downloaded from <http://www.bioinformatics.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://bioconductor.org/biocLite.R")
biocLite(c("AnnotationDbi", "affy", "AffyCompatible", "affyilmGUI", "affyPLM", "annaffy",
          "beadarray", "Biobase", "biomaRt", "Biostrings", "IRanges", "DynDoc", "ge
          "GO.db", "GOstats", "graph", "hugene10sttranscriptcluster.db", "hgu133a.
          "hgu133a2probe", "hgu133acdf", "hgu133aprobe", "hgu133plus2.db", "hgu133
          "hgu95av2cdf", "hgu95av2probe", "hugene10sttranscriptcluster.db", "illu
          "illuminaHumanv2BeadID.db", "illuminaHumanv3BeadID.db", "IRanges", "lim
          "MergeMaid", "metaArray", "MiPP", "mogene10sttranscriptcluster.db", "mul
          "org.Hs.eg.db", "org.Mm.eg.db", "org.Rn.eg.db", "pamr", "pdmclass", "prep
          "ragene10sttranscriptcluster.db", "RankProd", "RColorBrewer", "Rgraphvi
          "sizepower", "ssize", "tkrplot", "tkWidgets", "widgetTools", "xtable", "H
          "MoExExonProbesetLocation", "RaExExonProbesetLocation", "edgeR", "b
          "BSgenome", "snow", "RmiR", "RmiR.Hs.miRNA", "oneChannelGUI"))
```

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

To load Hs/Mm/Rn exon 1.0 ST Affymatrix arrays users need to install APT tools 1.12.0. The windows binaries can be downloaded from: <http://www.affymetrix.com/support/developer/powertools/index.affx> In addition library files for gene/exon arrays are directly downloaded and installed locally from oneChannelGUI interface, the first time an Exon 1.0 ST or Gene 1.0 ST analysis is started. Or using the function *oneChannelGUI: Set library folder and install Affy gene/Exon library files* present in the General tools Menu.

*IMPORTANT APT TOOLS AND EXON LIBRARY FILES NEED TO BE LOCATED
IN A FOLDER CHARACTERIZED BY A PATH WITHOUT SPACES*

C:/apt.1.8.0 THIS IS OK

C:/PROGRAM FILES/APT.1.8.0 STARTING APT TOOLS FROM oneChannelGUI will produce an error

If you are interested to run RNA-seq secondary analysis it is also required the installation of perl. The easy way is to install the active perl: <http://www.activestate.com/activeperl>

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, affyImGUI 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.