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.
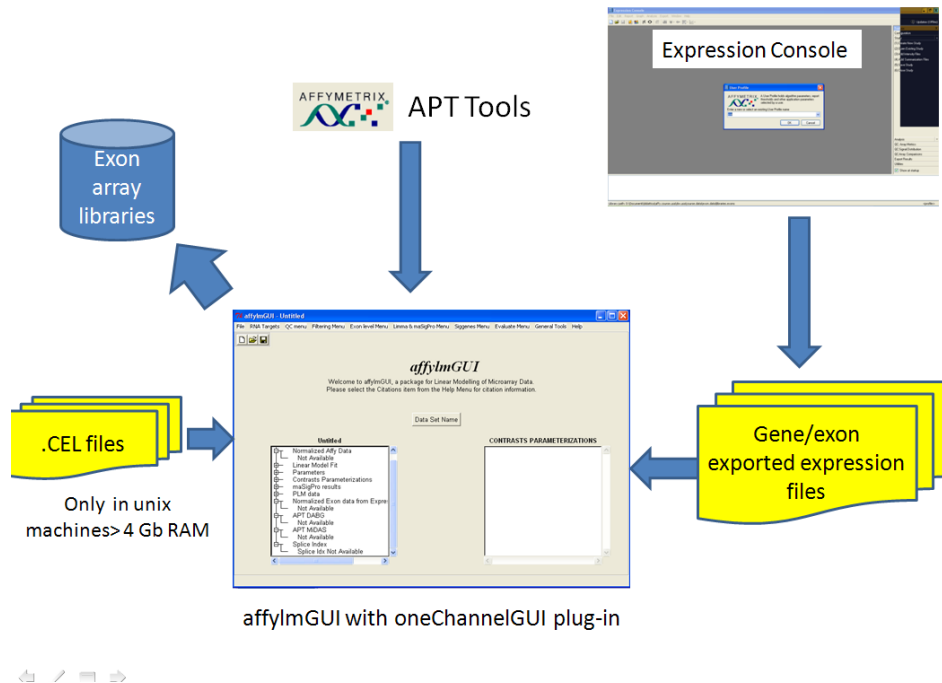

Figure 1: External tools needed for exon array analysis when oneChannelGUI add-on is loaded in affylmGUI.

1.1 Windows users

The lastest 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, affylmGUI, tkWidgets, IRanges, Rsamtools, Biostrings, siggenes"
```

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.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://bioconductor.org/biocLite.R")
biocLite(c("AnnotationDbi","affy","AffyCompatible","affylmGUI","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 affylmGUI. 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 Affymtrix 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 er
```

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 oneChanneGUI, affylmGUI 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 pckage "Bwidget" available on the Bioconductor mailing list.