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 affyImGUI.
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:

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

[1] "Biobase, affylmGUI, tkrplot, tkWidgets, IRanges, Rsamtools (>= 1.13.1),\n
Biostrings, siggenes, chimera"
```

oneChannelGUI suggests the installation of the following packages:

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

[1] "annotate, genefilter, maSigPro, pamr, pdmclass, ChIPpeakAnno,\n
nchipseq, 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/

To use it user needs to open an R session on a computer connected to internet and copy and paste the following code:

```r
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","illum
"inaHumanv2BeadID.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","Rgraphviz
"sizepower","ssize","tkrplot","tkWidgets","widgetTools","xtable","HuExExonProbesetLocation","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 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 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 package ”Bwidget” available on the Bioconductor mailing list.