

oneChannelGUI Package: Stand Alone Functions

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1 oneChannelGUI Stand Alone Functions

This section describes stand alone functions associated to oneChannelGUI package. The stand alone package can be used outside oneChannelGUI.

1.1 standAloneBuildingLocalAnnotation

The function `standAloneBuildingLocalAnnotation` creates gene-level annotation data using netaffx database:

```
> tmp <- standAloneBuildingLocalAnnotation(libDirLocation = getwd(), netaffxUser = "  
+                                         netaffxUserPw = "yourpassword", whichA
```

The function requires the folder where to save the annotation object, the email registered to Affymetrix netaffx web site, the password to access to netaffx, the annotation table (HuEx, human or MoEx, mouse or RaEx, rat)

1.2 standAloneAddingAnnotation

The function `standAloneAddingAnnotation` attaches gene-level annotation to a data frame:

```
> data(file="huex.annotation", package="oneChannelGUI")  
> mydf <- read.table("tmpTopTable.txt", sep="\t", header=T)  
> annotated.df <- standAloneAddingAnnotation(huex.annotation, mydf, ids.column = 1)
```

The function requires an annotation data frame generated with `standAloneBuildingLocalAnnotation` function, a data frame containing a gene-level data of any type (it is mandatory that one of the columns contains gene-level ids) and the column of the data frame to be annotated containing gene-level ids

This function can be used to attach to any data frame generated, for example with `limma`, to attach annotation data derived from the latest annotation available on netaffx.