

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.

1.3 ncScaffold

This function builds scaffold for ncRNA using bioMart this function create a scaffold used to load ncRNA-seq data and the corresponding set fasta sequence on which mapping should be done.

```
> ncScaffold(genome = c("hg19", "mm9", "rn4"), fasta = TRUE)
```

The function produces ncHs.data.rda, ncMm.data.rda, ncRn.data.rda which are the scaffolds present in the data dir in oneChannelGUI. The function produces also hs.fa, mm.fa and rn.fa which can be extracted from the oneChannelGUI data dir using the General Tool function: Export non-coding RNA fasta reference file for ncRNA-seq quantitative analysis.

1.4 makeGeneScaffold

This function builds a GRange object at chromosome level on UCSC genome data. It builds a gene level scaffold to associate reads derived from bowtie mapping. The function is embedded in bowtieGenome function that build, at chromosome level, the reference genome for primary mapping. Built scaffolds are available as precompiled at sourceforge oneChannelGUI.extras project. The function also calculates gene-level GC content to be used for GC based normalization of counts data.