exomePeak2

Here we use exomePeak2 to conduct reference based quantification and differential analysis.

1. Download and Convert Basic Site Information

Download single base RNA modification annotation of m6A on human genome from [m6A-Atlas database](), which should be tabular data in a txt file. Convert tabular data to genomic ranges by:

```
library(readr)
library(GenomicRanges)
# Downloaded from m6A-Atlas database
my.file="/path/to/home/tangyujiao/big/download/m6A_H.sapiens_basical_information
.txt"

# Load txt file
m6A_basic_info <- read_table2(my.file, col_names = FALSE)
m6A_basic_info <- m6A_basic_info[, c(1:11)]
colNames<- c("ID","chr","start","end", "num1","strand", "LOC", "ENS","RNA",
"Gene", "seq")
colnames(m6A_basic_info) <- colNames

# Concert to Grange object
mod_annot <- makeGRangesFromDataFrame(m6A_basic_info,
                          keep.extra.columns=FALSE,
                          ignore.strand=FALSE,
                          seqinfo=NULL,
                          seqnames.field="chr",
                          start.field="start",
                          end.field="end",
                          strand.field="strand",
                          starts.in.df.are.0based=FALSE)

# Save Grange to rds
saveRDS(mod_annot, "/path/to/mod_annot.rds")
```

2. Reference-based Analysis

```
library(exomePeak2)
set.seed(1)
root = "/path/to/homo_result"
setwd(root)

f1 = file.path(root, "SRR5978834_sorted.bam")
f2 = file.path(root, "SRR5978835_sorted.bam")
f3 = file.path(root, "SRR5978836_sorted.bam")
IP_BAM = c(f1,f2,f3)

f1 = file.path(root, "SRR5978827_sorted.bam")
f2 = file.path(root, "SRR5978828_sorted.bam")
f3 = file.path(root, "SRR5978829_sorted.bam")
```

```
INPUT_BAM = c(f1,f2,f3)

f2 = "/path/to/mod_annot.rds"
MOD_ANNO_GRANGE <- readRDS(f2)
exomePeak2(bam_ip = IP_BAM,
           bam_input = INPUT_BAM,
           genome = "hg19",
           library_type = "1st_strand",
           paired_end = FALSE,
           mod_annot = MOD_ANNO_GRANGE)
```

An output folder named `exomePeak2_output` will be created in the working directory containing:

```
- exomePeak2_output
    - LfcGC.pdf
    - RunInfo.txt
    - Mod.bed
    - Mod.csv
    - Mod.rds
    - ADDInfo
        - ADDInfo_SizeFactors.csv
        - ADDInfo_GLM_allDesigns.csv
        - ADDInfo_ReadsCount.csv
        - ADDInfo_RPKM.csv
```