m6A-seq Data Analysis (exomePeak2)

Here we are going to use exomePeak2 for peak calling and differential methylation analysis. The BED file as output will be used for further analysis.

```r
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)

f1 = file.path(root, "SRR5179446_sorted.bam")
f2 = file.path(root, "SRR5179447_sorted.bam")
f3 = file.path(root, "SRR5179448_sorted.bam")
TREATED_INPUT_BAM = c(f1,f2,f3)

f1 = file.path(root, "SRR5978869_sorted.bam")
f2 = file.path(root, "SRR5978870_sorted.bam")
f3 = file.path(root, "SRR5978871_sorted.bam")
TREATED_IP_BAM = c(f1,f2,f3)

exomePeak2(bam_ip = IP_BAM,
           bam_input = INPUT_BAM,
           bam_treated_input = TREATED_INPUT_BAM,
           bam_treated_ip = TREATED_IP_BAM,
           genome = "hg19",
           library_type = "1st_strand",
           paired_end = FALSE)
```

```r
library(exomePeak2)
set.seed(1)
root = "/path/to/mm10_result"
setwd(root)

f1 = file.path(root, "SRR866997_sorted.bam")
f2 = file.path(root, "SRR866999_sorted.bam")
f3 = file.path(root, "SRR867001_sorted.bam")
IP_BAM = c(f1,f2,f3)

f1 = file.path(root, "SRR866998_sorted.bam")
f2 = file.path(root, "SRR867000_sorted.bam")
f3 = file.path(root, "SRR867002_sorted.bam")
INPUT_BAM = c(f1,f2,f3)
```

```
f1 = file.path(root, "SRR866992_sorted.bam")
f2 = file.path(root, "SRR866994_sorted.bam")
f3 = file.path(root, "SRR866996_sorted.bam")
TREATED_INPUT_BAM = c(f1,f2,f3)

f1 = file.path(root, "SRR866991_sorted.bam")
f2 = file.path(root, "SRR866993_sorted.bam")
f3 = file.path(root, "SRR866995_sorted.bam")
TREATED_IP_BAM = c(f1,f2,f3)

exomePeak2(bam_ip = IP_BAM,
           bam_input = INPUT_BAM,
           bam_treated_input = TREATED_INPUT_BAM,
           bam_treated_ip = TREATED_IP_BAM,
           genome = "mm10",
           library_type = "1st_strand",
           paired_end = FALSE)
```

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

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