Peak Calling (exomePeak2)

exomePeak2 is an R/Bioconductor package which provides bias-aware quantification and peak detection for Methylated RNA immunoprecipitation sequencing data (MeRIP-Seq) [10]. We are going to use this package for peak calling to predict significant methylation sites.

Installation

```
if(!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install("exomePeak2")
```

Peak Calling

```
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)

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

```
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)

exomePeak2(bam_ip = IP_BAM,
           bam_input = INPUT_BAM,
           genome = "mm10",
           paired_end = FALSE)
```

An output folder named `exomePeak2_output` will be created in the working directory containing. The most important two files "Mod.bed" and "Mod.csv" will be used in further analysis.

```
- 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
```