An Introduction to *Trumpet* Package

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1 Quick Start with Trumpet

This is a manual for Trumpet package. Trumpet is designed for visualization of quality assessment of methylated RNA immunoprecipitation sequencing data-**tr**anscriptome-guided q**u**ality assessment of **m**ethylated RNA immunopreci**p**itation sequencing da**t**a.

The Trumpet package takes the aligned BAM files from m6A-seq data together with the annotation information as the input to generate a quality assessment report in HTML format, which covers a number of metrics that are relevant to the m6A-seq technique.The following commands code will show how to use this package and generate the assessment report in HTML format.

Here is an examples to show how to use this package. Firstly, we need to import the RNA methylation sequencing data in `BAM` foramt for quality assessment.

```
> library(Trumpet)
> # Input all the bam files of MeRIP-Seq data
> f1 <- system.file("extdata", "IP1.bam", package="Trumpet")
> f2 <- system.file("extdata", "IP2.bam", package="Trumpet")
> f3 <- system.file("extdata", "IP3.bam", package="Trumpet")
> f4 <- system.file("extdata", "IP4.bam", package="Trumpet")
> f5 <- system.file("extdata", "Input1.bam", package="Trumpet")
> f6 <- system.file("extdata", "Input2.bam", package="Trumpet")
> f7 <- system.file("extdata", "Input3.bam", package="Trumpet")
> f8 <- system.file("extdata", "treated_IP1.bam", package="Trumpet")
> f9 <- system.file("extdata", "treated_Input1.bam", package="Trumpet")
> ip_bam <- c(f1,f2,f3,f4)
> input_bam <- c(f5,f6,f7)
> contrast_ip_bam <- c(f8)
> contrast_input_bam <- c(f9)
```

Then, we also need to give the reference genome and annotation information in `GTF` files or annotation database like `TXDB` or download from UCSC.

```
> # Input the annotation file
> gtf <- system.file("extdata", "hg19toy.gtf", package="Trumpet")
```

After importing the sequencing data and annotation inforamtion file, we can call the main function `Trumpet_report` to generate the assessment report in HTML format. The following command will show how to use the main function.

```
> # Call the main function to generate the HTML report
> trumpet_report <- Trumpet_report(IP_BAM = ip_bam,
+                                   Input_BAM = input_bam,
+                                   contrast_IP_BAM = contrast_ip_bam,
+                                   contrast_Input_BAM = contrast_input_bam,
+                                   condition1 = "untreated",
+                                   condition2 = "treated",
+                                   GENE_ANNO_GTF = gtf)
> # An HTML report will be generated under current working directory.
> # It can be opened with the following command.
> browseURL("Trumpet_report.html")
```

2 Session Information

```
> sessionInfo()

R version 3.3.0 (2016-05-03)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 7 x64 (build 7601) Service Pack 1

locale:
[1] LC_COLLATE=Chinese (Simplified)_People's Republic of China.936
[2] LC_CTYPE=Chinese (Simplified)_People's Republic of China.936
[3] LC_MONETARY=Chinese (Simplified)_People's Republic of China.936
[4] LC_NUMERIC=C
[5] LC_TIME=Chinese (Simplified)_People's Republic of China.936

attached base packages:
[1] stats     graphics  grDevices utils     datasets
[6] methods   base

loaded via a namespace (and not attached):
[1] tools_3.3.0
```