Rsubread package: high-performance read alignment, quantification and mutation discovery

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1 Introduction

This vignette provides a brief description to the Rsubread package. For more details, please refer to the Users Guide which can brought up in your R session via the following commands:

```
> library(Rsubread)
> RsubreadUsersGuide()
```

The Rsubread package provides facilities for processing the read data generated by next-gen sequencing technologies. These facilities include quality assessment, read alignment, read summarization, exon-exon junction detection, absolute expression calling and SNP discovery. They can be used to analyze data generated from all major sequencing platforms including Illumina GA/HiSeq, Roche 454, ABI SOLiD and Ion Torrent.

The Subread aligner (`align` function) is a highly efficient and accurate aligner for mapping genomic DNA and RNA sequencing reads. It adopts a novel mapping paradigm called "seed-and-vote". Under this paradigm, a number of 16mers (called seeds or subreads) are extracted from each read and they were mapped to the reference genome to vote for the mapping location of the read. Read mapping performed under this paradigm has been found to be more efficient and accurate than that carried out under the conventional "seed-and-extend" paradigm (Liao et al. 2013). This package also includes a program for detecting exon-exon junctions, `subjunc`, that makes use of the powerful "seed-and-vote" paradigm too.

An important step in processing next-gen sequencing data is to assign mapped reads to genomic features such as genes, exons, and promoters. This package includes a general-purpose read summarization function `featureCounts` that takes mapped reads as input and assigns them to genomic features. In-built annotations are provided for users convenience.

Different from microarray technologies, the next-gen sequencing technologies do not provide Present/Absent calls for genomic features such as genes. We have developed

an algorithm to use the background noise measured from the RNA-seq data to call absolutely expressed genes. The function `detectionCall` returns a detection p value for each gene from the read mapping results.

We have also developed a new SNP calling algorithm which is being implemented in function `exactSNPs`. Our results showed that it compared favorably to competing methods, but was an order of magnitude faster.

This package also includes some other useful functions such as quality assessment (`qualityScores`, `atgcContent`), duplicate read removal (`removeDupReads`) and mapping percentage calculation (`propmapped`).

2 Read alignment

An index needs to be built first and then alignments can be carried out. Building the index is an one-off operation. The generated index can be re-used in subsequent read alignments.

Step 1: Index building

The Rsubread package includes a dummy reference sequence that was generated by concatenating 900 100bp reads that were taken from a pilot dataset generated from the SEquencing Quality Control (SEQC) project. We further extracted 100 reads from the same dataset and combine them with the 900 reads to make a read dataset for mapping. Below is the command for building an index for the reference sequence:

```
> library(Rsubread)
> ref <- system.file("extdata","reference.fa",package="Rsubread")
> buildindex(basename="reference_index",reference=ref)


        ==========     _____ _    _ ____  _____  _____           _____
        =====         / ____| |  | |  _ \|  __ \|  ____|   /\    |  __ \
          =====      | (___ | |  | | |_) | |__) | |__     /  \   | |  | |
            ====      \___ \| |  | |  _ <|  _  /|  __|   / /\ \  | |  | |
              ====    ____) | |__| | |_) | | \ \| |____ / ____ \ | |__| |
        ==========   |_____/ \____/|____/|_|  _____/_/    _____/
        Rsubread 1.22.3

//========================== indexBuilder setting ==========================\\
||                                                                          ||
||                Index name : reference_index                              ||
||               Index space : base-space                                  ||
||                    Memory : 8000 Mbytes                                  ||
||           Repeat threshold : 100 repeats                                 ||
||   Distance to next subread : 3                                          ||
||                                                                          ||
||                Input files : 1 file in total                            ||
||                             o /tmp/RtmpGOAk7V/Rinst7c5874e3f184/Rsubre ... ||
||                                                                          ||
\\==================== http://subread.sourceforge.net/ ====================//

//================================= Running =================================\\
||                                                                          ||
```

```
|| Check the integrity of provided reference sequences ...             ||
|| No format issues were found                                         ||
|| Scan uninformative subreads in reference sequences ...              ||
||    8%,    0 mins elapsed, rate=9.5k bps/s, total=0m                 ||
||   16%,    0 mins elapsed, rate=19.0k bps/s, total=0m                ||
||   24%,    0 mins elapsed, rate=27.9k bps/s, total=0m                ||
||   33%,    0 mins elapsed, rate=37.1k bps/s, total=0m                ||
||   41%,    0 mins elapsed, rate=46.3k bps/s, total=0m                ||
||   49%,    0 mins elapsed, rate=55.6k bps/s, total=0m                ||
||   58%,    0 mins elapsed, rate=64.8k bps/s, total=0m                ||
||   66%,    0 mins elapsed, rate=73.9k bps/s, total=0m                ||
||   74%,    0 mins elapsed, rate=83.2k bps/s, total=0m                ||
||   83%,    0 mins elapsed, rate=92.3k bps/s, total=0m                ||
||   91%,    0 mins elapsed, rate=101.4k bps/s, total=0m               ||
||   99%,    0 mins elapsed, rate=110.6k bps/s, total=0m               ||
|| 1 uninformative subreads were found.                                ||
|| These subreads were excluded from index building.                   ||
|| Build the index...                                                  ||
||    8%,    0 mins elapsed, rate=7454.8k bps/s, total=0m              ||
||   16%,    0 mins elapsed, rate=4970.6k bps/s, total=0m              ||
||   24%,    0 mins elapsed, rate=5592.1k bps/s, total=0m              ||
||   33%,    0 mins elapsed, rate=5964.7k bps/s, total=0m              ||
||   41%,    0 mins elapsed, rate=6213.3k bps/s, total=0m              ||
||   49%,    0 mins elapsed, rate=5591.9k bps/s, total=0m              ||
||   58%,    0 mins elapsed, rate=5799.1k bps/s, total=0m              ||
||   66%,    0 mins elapsed, rate=5964.8k bps/s, total=0m              ||
||   74%,    0 mins elapsed, rate=5592.0k bps/s, total=0m              ||
||   83%,    0 mins elapsed, rate=2982.4k bps/s, total=0m              ||
||   91%,    0 mins elapsed, rate=3154.5k bps/s, total=0m              ||
||   99%,    0 mins elapsed, rate=3195.4k bps/s, total=0m              ||
|| Save current index block...                                         ||
|| [ 0.0% finished ]                                                   ||
|| [ 10.0% finished ]                                                  ||
|| [ 20.0% finished ]                                                  ||
|| [ 30.0% finished ]                                                  ||
|| [ 40.0% finished ]                                                  ||
|| [ 50.0% finished ]                                                  ||
|| [ 60.0% finished ]                                                  ||
|| [ 70.0% finished ]                                                  ||
|| [ 80.0% finished ]                                                  ||
|| [ 90.0% finished ]                                                  ||
|| [ 100.0% finished ]                                                 ||
||                                                                     ||
||                    Total running time: 0.0 minutes.                ||
||              Index reference_index was successfully built!          ||
||                                                                     ||
\\==================== http://subread.sourceforge.net/ ====================//
```

The generated index files were saved to the current working directory. Rsubread creates a hash table for indexing the reference genome. Keys in the hash table are the 16bp sequences and hash values are their corresponding chromosomal locations. Color space index can be built by setting the `colorsapce` argument to `TRUE`.

A unique feature of Rsubread is that it allows users to control the computer memory usage in read mapping process. Users can do this by tuning the amount of memory (in MB) to be used in read mapping.

Step 2: read mapping

After the index was successfully built, we map the read dataset (including 1,000 reads) to the reference sequence:

```
> reads <- system.file("extdata","reads.txt.gz",package="Rsubread")
> align(index="reference_index",readfile1=reads,output_file="alignResults.BAM",phredOffset=64)


        ==========     _____ _    _ ____  _____  _____        _____
        =====         / ____| |  | |  _ \| __ \|  ____|   /\  | __ \
         =====       | (___ | |  | | |_) | |__) | |__     /  \ | |  | |
           ====       \___ \| |  | |  _ <|  _  /|  __|   / /\ \| |  | |
             ====      ____) | |__| | |_) | | \ \| |____ / ____ \| |__| |
        ==========    |_____/ \____/|____/|_|  _____/_/    _____/
        Rsubread 1.22.3

//========================== subread-align setting ===========================\\
||                                                                            ||
|| Function       : Read alignment (RNA-Seq)                                  ||
|| Input file     : /tmp/RtmpGOAk7V/Rinst7c5874e3f184/Rsubread/extdata/rea ... ||
|| Output file    : alignResults.BAM (BAM)                                    ||
|| Index name     : reference_index                                          ||
||                                                                            ||
||                        Threads : 1                                         ||
||                    Phred offset : 64                                       ||
||                      Min votes : 3 / 10                                    ||
||      Maximum allowed mismatches : 3                                        ||
||     Maximum allowed indel bases : 5                                        ||
|| # of best alignments reported : 1                                          ||
||                  Unique mapping : yes                                      ||
||                                                                            ||
\\===================== http://subread.sourceforge.net/ =====================//

//===================== Running (28-Jul-2016 19:51:55) ======================\\
||                                                                            ||
|| The input file contains base space reads.                                 ||
|| The range of Phred scores observed in the data is [2,34]                   ||
|| Load the 1-th index block...                                              ||
||                                                                            ||
||                       Completed successfully.                             ||
||                                                                            ||
\\===========================================================================//

//============================== Summary =====================================\\
||                                                                            ||
||            Processed : 1,000 reads                                        ||
||               Mapped : 904 reads (90.4%)                                  ||
||               Indels : 0                                                  ||
||                                                                            ||
||         Running time : 0.0 minutes                                        ||
||                                                                            ||
\\===================== http://subread.sourceforge.net/ =====================//
```

Map paired-end reads:

```
> reads1 <- system.file("extdata","reads1.txt.gz",package="Rsubread")
> reads2 <- system.file("extdata","reads2.txt.gz",package="Rsubread")
> align(index="reference_index",readfile1=reads1,readfile2=reads2,
+ output_file="alignResultsPE.BAM",phredOffset=64)


        ==========     _____ _    _ ____  _____  _____        _____
        =====         / ____| |  | |  _ \| __ \|  ____|   /\  | __ \
         =====       | (___ | |  | | |_) | |__) | |__     /  \ | |  | |
           ====       \___ \| |  | |  _ <|  _  /|  __|   / /\ \| |  | |
```

```
        ====    ____) | |__| | |_) | | \ \| |____ / ____ \| |__| |
   =========    |_____/ \____/|____/|_|  _____/_/    _____/
      Rsubread 1.22.3

//========================= subread-align setting ==========================\\
||                                                                          ||
|| Function      : Read alignment (RNA-Seq)                                 ||
|| Input file 1  : /tmp/RtmpGOAk7V/Rinst7c5874e3f184/Rsubread/extdata/rea ... ||
|| Input file 2  : /tmp/RtmpGOAk7V/Rinst7c5874e3f184/Rsubread/extdata/rea ... ||
|| Output file   : alignResultsPE.BAM (BAM)                                 ||
|| Index name    : reference_index                                         ||
||                                                                          ||
||                        Threads : 1                                       ||
||                   Phred offset : 64                                      ||
||        # of extracted subreads : 10                                      ||
||                 Min read1 vote : 3                                       ||
||                 Min read2 vote : 1                                       ||
||              Max fragment size : 600                                     ||
||              Min fragment size : 50                                      ||
||      Maximum allowed mismatches : 3                                      ||
||     Maximum allowed indel bases : 5                                      ||
|| # of best alignments reported : 1                                        ||
||                 Unique mapping : yes                                     ||
||                                                                          ||
\\==================== http://subread.sourceforge.net/ =====================//

//===================== Running (28-Jul-2016 19:51:57) =====================\\
||                                                                          ||
|| The input file contains base space reads.                               ||
|| The range of Phred scores observed in the data is [2,34]                 ||
|| Load the 1-th index block...                                            ||
||                                                                          ||
||                     Completed successfully.                             ||
||                                                                          ||
\\==========================================================================//

//============================== Summary ===================================\\
||                                                                          ||
||           Processed : 1,000 fragments                                   ||
||              Mapped : 909 fragments (90.9%)                             ||
||     Correctly paired : 899 fragments                                    ||
||              Indels : 0                                                 ||
||                                                                          ||
||        Running time : 0.0 minutes                                       ||
||                                                                          ||
\\==================== http://subread.sourceforge.net/ =====================//
```

3   Counting mapped reads for genomic features

The `featureCounts` function is a general-purpose read summarization function that assigns mapped reads (RNA-seq or gDNA-seq reads) to genomic features such as genes, exons, promoters, gene bodies and genomic bins.

This function takes as input a set of files that contain read mapping results and an annotation file that includes genomic features. It automatically detects the format of input read files (supported formats include SAM and BAM). For paired end reads, it automatically re-orders the reads if reads from the same pair were found not to be next to each other in the input.

In-built NCBI RefSeq gene annotations for genomes mm9, mm10 and hg19 are provided for convenience. These annotations include chromosomal coordinates of exons of each gene. When these annotations are used for summarization, only reads overlapping with exons will be counted by `featureCounts`. Users can use `getInBuiltAnnotation` function to retrieve these annotations.

Below gives the example code of assigning reads and fragments, generated in the last section, to two artificial genes. Assign single end reads to genes:

```
> ann <- data.frame(
+ GeneID=c("gene1","gene1","gene2","gene2"),
+ Chr="chr_dummy",
+ Start=c(100,1000,3000,5000),
+ End=c(500,1800,4000,5500),
+ Strand=c("+","+","-","-"),
+ stringsAsFactors=FALSE)
> ann

  GeneID       Chr Start  End Strand
1  gene1 chr_dummy   100  500      +
2  gene1 chr_dummy  1000 1800      +
3  gene2 chr_dummy  3000 4000      -
4  gene2 chr_dummy  5000 5500      -

> fc_SE <- featureCounts("alignResults.BAM",annot.ext=ann)


        ==========     _____ _    _ ____  _____  _____    _____
        =====         / ____| |  | |  _ \|  __ \|  ____|  /\    |  __ \
          =====      | (___ | |  | | |_) | |__) | |__    /  \   | |  | |
            ====      \___ \| |  | |  _ <|  _  /|  __|  / /\ \  | |  | |
            ====      ____) | |__| | |_) | | \ \| |____ / ____ \| |__| |
        ==========   |_____/ \____/|____/|_|  _____/_/    _____/
        Rsubread 1.22.3

//========================== featureCounts setting ===========================\\
||                                                                            ||
||             Input files : 1 BAM file                                       ||
||                           S alignResults.BAM                               ||
||                                                                            ||
||             Output file : ./.Rsubread_featureCounts_pid2185               ||
||                 Summary : ./.Rsubread_featureCounts_pid2185.summary       ||
||              Annotation : ./.Rsubread_UserProvidedAnnotation_pid2185 ( ... ||
||                                                                            ||
||                 Threads : 1                                                ||
||                   Level : meta-feature level                              ||
||              Paired-end : no                                              ||
||         Strand specific : no                                              ||
||      Multimapping reads : not counted                                     ||
|| Multi-overlapping reads : not counted                                     ||
||                                                                            ||
\\=================== http://subread.sourceforge.net/ ====================//

//================================= Running ==================================\\
||                                                                            ||
|| Load annotation file ./.Rsubread_UserProvidedAnnotation_pid2185 ...        ||
||    Features : 4                                                            ||
||    Meta-features : 2                                                       ||
||    Chromosomes/contigs : 1                                                 ||
||                                                                            ||
|| Process BAM file alignResults.BAM...                                       ||
||    Single-end reads are included.                                          ||
```

```
||    Assign reads to features...                                        ||
||    Total reads : 1000                                                 ||
||    Successfully assigned reads : 31 (3.1%)                            ||
||    Running time : 0.00 minutes                                        ||
||                                                                       ||
||                       Read assignment finished.                       ||
||                                                                       ||
\\==================== http://subread.sourceforge.net/ ===================//


> fc_SE


$counts
      alignResults.BAM
gene1            14
gene2            17


$annotation
  GeneID                Chr    Start        End Strand Length
1 gene1 chr_dummy;chr_dummy  100;1000   500;1800    +;+   1202
2 gene2 chr_dummy;chr_dummy 3000;5000  4000;5500    -;-   1502


$targets
[1] "alignResults.BAM"


$stat
                   Status alignResults.BAM
1                Assigned               31
2      Unassigned_Ambiguity              0
3   Unassigned_MultiMapping              0
4      Unassigned_NoFeatures            873
5        Unassigned_Unmapped             96
6  Unassigned_MappingQuality              0
7  Unassigned_FragmentLength              0
8         Unassigned_Chimera              0
9       Unassigned_Secondary              0
10      Unassigned_Nonjunction             0
11       Unassigned_Duplicate              0
```

Assign fragments (read pairs) to the two genes:

```
> fc_PE <- featureCounts("alignResultsPE.BAM",annot.ext=ann,isPairedEnd=TRUE)


        ==========     _____ _          _ ____  _____ _____      _____
        =====         / ____| |        | |  _ \|  __ \|  ____|    /\    |    __ \
         =====       | (___ | |  | | | |_) | |__) | |__      /  \  |  |  | |
          ====        \___ \| |  | |  | |  _ <|  _  /|  __|    / /\ \ | |  | |
           ====       ____) | |__| | |_) | | \ \| |____  / ____ \| |__| |
          ==========  |_____/ \____/|____/|_|  _____/_/    _____/
        Rsubread 1.22.3


//========================== featureCounts setting ===========================\\
||                                                                            ||
||             Input files : 1 BAM file                                        ||
||                           P alignResultsPE.BAM                              ||
||                                                                            ||
||             Output file : ./.Rsubread_featureCounts_pid2185                 ||
||                 Summary : ./.Rsubread_featureCounts_pid2185.summary         ||
||              Annotation : ./.Rsubread_UserProvidedAnnotation_pid2185 ( ... ||
||                                                                            ||
||                 Threads : 1                                                 ||
||                   Level : meta-feature level                               ||
||              Paired-end : yes                                              ||
```

```
||             Strand specific : no                                     ||
||           Multimapping reads : not counted                          ||
||     Multi-overlapping reads : not counted                           ||
||                                                                      ||
||                Chimeric reads : counted                             ||
||              Both ends mapped : not required                        ||
||                                                                      ||
\\==================== http://subread.sourceforge.net/ ====================//

//=============================== Running ===================================\\
||                                                                      ||
|| Load annotation file ././.Rsubread_UserProvidedAnnotation_pid2185 ...  ||
||     Features : 4                                                     ||
||     Meta-features : 2                                                ||
||     Chromosomes/contigs : 1                                         ||
||                                                                      ||
|| Process BAM file alignResultsPE.BAM...                              ||
||     Paired-end reads are included.                                  ||
||     Assign fragments (read pairs) to features...                    ||
||     Total fragments : 1000                                          ||
||     Successfully assigned fragments : 35 (3.5%)                     ||
||     Running time : 0.00 minutes                                     ||
||                                                                      ||
||                      Read assignment finished.                      ||
||                                                                      ||
\\==================== http://subread.sourceforge.net/ ====================//


> fc_PE


$counts
      alignResultsPE.BAM
gene1                 16
gene2                 19


$annotation
  GeneID                Chr      Start       End Strand Length
1  gene1 chr_dummy;chr_dummy  100;1000  500;1800    +;+   1202
2  gene2 chr_dummy;chr_dummy 3000;5000 4000;5500    -;-   1502


$targets
[1] "alignResultsPE.BAM"


$stat
                     Status alignResultsPE.BAM
1                  Assigned                 35
2       Unassigned_Ambiguity                  0
3    Unassigned_MultiMapping                  0
4       Unassigned_NoFeatures                874
5         Unassigned_Unmapped                 91
6   Unassigned_MappingQuality                  0
7   Unassigned_FragmentLength                  0
8          Unassigned_Chimera                  0
9        Unassigned_Secondary                  0
10     Unassigned_Nonjunction                  0
11       Unassigned_Duplicate                  0
```

4   Finding exon junctions

The RNA-seq technology provides a unique opportunity to identify the alternative splic-ing events that occur during the gene transcription process. The `subjunc` function can

be used to detect exon-exon junctions. It first extracts a number of subreads (16mers) from each read, maps them to the reference genome and identifies the two best mapping locations for each read (representing potential locations of exons spanned by the read). Then, it builds a junction table including all putative junctions. Finally, it carries out a verification step to remove false positives in junction detection by realigning all the reads. The donor ('GT') and receptor sites('AG'), are required to be present when calling exon-exon junctions. Output of this function includes the discovered exon-exon junctions and also read mapping results.

5   Base quality scores

Quality scores give the probabilities of read bases being incorrectly called, which is useful for examining the quality of sequencing data. The `qualityScores` function can be used to quickly retrieve and display the quality score data extracted from a read file.

```
> x <- qualityScores(filename=reads,offset=64,nreads=1000)

qualityScores Rsubread 1.22.3

Scan the input file...
Totally 1000 reads were scanned; the sampling interval is 1.
Now extract read quality information...

Completed successfully. Quality scores for 999 reads (equally spaced in the file) are returned.

> x[1:10,1:10]

        1  2  3  4  5  6  7  8  9 10
 [1,]  33 33 33 20 20 24 31 15 21 16
 [2,]  33 33 30 33 33 30 34 30 32 28
 [3,]  32 33 33 32 33 33 33 20 32 24
 [4,]  33 33 33 33 33 30 29 34 31 25
 [5,]  33 33 33 33 33 34 34 34 33 30
 [6,]  33 30 31 24 24 28 33 33 30 32
 [7,]  33 33 33 33 30 28 17 25 31 33
 [8,]  33 32  2  2  2  2  2  2  2  2
 [9,]  33 33 33 34 33 33 31 33 33 33
[10,]  33 33 33 33 28 24 33 33 33 28
```

6   GC content

The `atgcContent` function returns fractions of A, T, G and C bases at each base location of reads or in the entire dataset.

7   Mapping percentage

Function `propmapped` returns the proportion of mapped reads included in a SAM/BAM file. For paired end reads, it can return the proportion of mapped fragments (ie. read pairs).

```
> propmapped("alignResults.BAM")


The input file is opened as a BAM file.
The fragments in the input file are being counted.
Finished. All records: 1000; all fragments: 1000; mapped fragments: 904; the mappability is 90.40%
           Samples NumTotal NumMapped PropMapped
1 alignResults.BAM     1000       904      0.904
```

8   Citation

Yang Liao, Gordon K Smyth and Wei Shi (2013). The Subread aligner: fast, accurate and scalable read mapping by seed-and-vote. Nucleic Acids Research, 41(10):e108.

Yang Liao, Gordon K Smyth and Wei Shi (2014). featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics, 30(7):923-30

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Please post to Bioconductor mailing list (`http://bioconductor.org/`) if you find any bugs and have any inquires. Or, you may contact Wei Shi (shi at wehi dot edu dot au) directly.