The REDseq user’s guide

Lihua Julie Zhu*

May 1, 2024

Contents

1 Introduction 1

2 Examples of using REDseq 2

  2.1 Task 1: Build a RE map for a genome 2

  2.2 Task 2: Assign mapped sequence tags to RE site 3

  2.3 Task 3: Visualize the distribution of cut frequency in selected genomic regions

  and the distance distribution of sequence tags to corresponding RE sites 4

  2.4 Task 4: Generating count table for identifying statistically significant RE sites 7

  2.5 Task 5: Identifying differential cut RE sites for experiment with one experiment condition 7

  2.6 Task 6: Identifying differential cut RE sites for early stage experiment without replicates 7

3 References 8

4 Session Info 8

1 Introduction

Restriction Enzyme digestion (RED) followed by high throughput sequencing (REDseq) enables genome wide differentiation of highly accessible regions and inaccessible regions. Comparing the profiles of restriction enzyme (RE) digestion among different cell types, developmental stages, disease stages, or different tissues facilitates deciphering of complex regulation network of cell differentiation, developmental control, and disease etiology and progression. We have developed a Bioconductor package called REDSeq to address the fundamental upstream analysis tasks of REDseq dataset. We have implemented functions for building genomic map of restriction enzyme sites (buildREmap), assigning sequencing tags to

* julie.zhu@umassmed.edu
RE sites (assignSeq2REsite), visualizing genome-wide distribution of differentially cut regions (distanceHistSeq2RE) and the distance distribution of sequence tags to corresponding RE sites (distanceHistSeq2RE), generating count table for identifying statistically significant RE sites (summarizeByRE). We have leveraged BSgenome on implementing function buildREmap for building genome-wide RE maps. The input data for assignSeq2REsite are represented as GRanges, for efficiently associating sequences with RE sites. It first identifies RE sites that have mapped sequence tags around the cut position taking consideration of user-defined offset, sequence length and strand in the aligned sequences. The user-defined offset guards against imperfect sticky end repair and primer addition process. These RE sites are used as seeds for assigning the remaining tags depending on which of five strategies the users select for partitioning sequences associated with multiple RE sites, i.e., unique, average, estimate, best and random. For experiment with at least two conditions with biological replicates, count summary generated from summarizeByRE can be easily used for identifying differentially cut RE sites using either DESeq or edgeR. Differentially cut RE sites can be annotated to the nearest gene using ChIPpeakAnno. In addition, for early stage experiments without replicates, compareREDseq outputs differentially cut RE sites between two experimental conditions using Fisher’s Exact Test. For experiment with one experimental condition, binom.test.REDseq outputs differentially cut RE sites in the genome. Multiplicity adjustment functions from multtest package were integrated in both functions.

2 Examples of using REDseq

2.1 Task 1: Build a RE map for a genome

Given a fasta/fastq file containing the restriction enzyme recognition site and a BSgenome object, the function buildREmap builds a genome-wide RE map.

```r
library(REDseq)
REpatternFilePath = system.file("extdata", "examplePattern.fa", package="REDseq")
library(BSgenome.Celegans.UCSC.ce2)
myMap = buildREmap( REpatternFilePath, BSgenomeName=Celegans, outfile="example.REmap")
```

```bash
>>> Finding all hits in sequences chrI ...
>>> DONE searching
>>> Finding all hits in sequences chrII ...
>>> DONE searching
>>> Finding all hits in sequences chrIII ...
>>> DONE searching
>>> Finding all hits in sequences chrIV ...
>>> DONE searching
>>> Finding all hits in sequences chrV ...
>>> DONE searching
>>> Finding all hits in sequences chrX ...
>>> DONE searching
>>> Finding all hits in sequences chrM ...
>>> DONE searching
```
2.2 Task 2: Assign mapped sequence tags to RE site

Given a mapped sequence tags as a GRanges and REMap as a Granges, assignSeq2REsite function assigns mapped sequence tags to RE site depending on the strategy users select. There are five strategies implemented, i.e., unique, average, estimate, best and random. For details, type help(assignSeq2REsite) in a R session.

```R
> data(example.REDseq)
> data(example.map)
> r.unique = assignSeq2REsite(example.REDseq, example.map, cut.offset = 1,
  + seq.length = 36, allowed.offset = 5, min.FragmentLength = 60,
  + max.FragmentLength = 300, partitionMultipleRE = "unique")
> r.best = assignSeq2REsite(example.REDseq, example.map,
  + cut.offset = 1, seq.length = 36, allowed.offset = 5,
  + min.FragmentLength = 60, max.FragmentLength = 300, partitionMultipleRE = "best")
> r.random = assignSeq2REsite(example.REDseq, example.map, cut.offset = 1,
  + seq.length = 36, allowed.offset = 5, min.FragmentLength = 60,
  + max.FragmentLength = 300, partitionMultipleRE = "random")
> r.average = assignSeq2REsite(example.REDseq, example.map, cut.offset = 1,
  + seq.length = 36, allowed.offset = 5, min.FragmentLength = 60,
  + max.FragmentLength = 300, partitionMultipleRE = "average")
> r.estimate = assignSeq2REsite(example.REDseq, example.map, cut.offset = 1,
  + seq.length = 36, allowed.offset = 5, min.FragmentLength = 60,
  + max.FragmentLength = 300, partitionMultipleRE = "estimate")
```
Wed May 1 01:34:22 2024 Validating input ...
Wed May 1 01:34:22 2024 Prepare map data ...
Wed May 1 01:34:22 2024 Align to chromosome 2 ...
Wed May 1 01:34:22 2024 Finished 1st round of aligning! Start the 2nd round of aligning ...
Wed May 1 01:34:22 2024 Align to chromosome 2 ...
Wed May 1 01:34:22 2024 Start filtering ...
Wed May 1 01:34:22 2024 Partitioning reads over RE sites within 300 ...
Wed May 1 01:34:22 2024 get count for each RE ...

> head(r.estimate$passed.filter)

<table>
<thead>
<tr>
<th>SeqId</th>
<th>REId</th>
<th>Chr</th>
<th>Strand</th>
<th>SeqStart</th>
<th>SeqEnd</th>
<th>REStart</th>
<th>REEnd</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>00000037</td>
<td>Sau96I.chr10.29</td>
<td>+</td>
<td>3012091</td>
<td>3012126</td>
<td>3012090</td>
<td>3012094</td>
</tr>
<tr>
<td>3</td>
<td>00000038</td>
<td>Sau96I.chr10.29</td>
<td>+</td>
<td>3012096</td>
<td>3012131</td>
<td>3012090</td>
<td>3012094</td>
</tr>
<tr>
<td>5</td>
<td>00000040</td>
<td>Sau96I.chr10.30</td>
<td>+</td>
<td>3012300</td>
<td>3012335</td>
<td>3012299</td>
<td>3012303</td>
</tr>
<tr>
<td>8</td>
<td>00000056</td>
<td>Sau96I.chr10.42</td>
<td>+</td>
<td>3018315</td>
<td>3018350</td>
<td>3018314</td>
<td>3018318</td>
</tr>
<tr>
<td>9</td>
<td>00000066</td>
<td>Sau96I.chr10.42</td>
<td>+</td>
<td>3018315</td>
<td>3018350</td>
<td>3018314</td>
<td>3018318</td>
</tr>
<tr>
<td>10</td>
<td>00000067</td>
<td>Sau96I.chr10.42</td>
<td>+</td>
<td>3018315</td>
<td>3018350</td>
<td>3018314</td>
<td>3018318</td>
</tr>
</tbody>
</table>

> data(example.assignedREDseq)

The above examples are for single-end sequencing data. For paired-end sequencing data, please create inputS.RD and inputE.RD from input.RD first with start(input.RD) and end(input.RD), where inputS.RD contains the start of the input.RD and inputE.RD contains the end of the input.RD. Then call assignSeq2REsite twice with inputS.RD and inputE.RD respectively. Please set min.FragmentLength = 0, max.FragmentLength = 1, seq.length = 1 with both calls.

2.3 Task 3: Visualize the distribution of cut frequency in selected genomic regions and the distance distribution of sequence tags to corresponding RE sites

> data(example.assignedREDseq)
Figure 1: Plot to show the distribution of cut frequency in the selected genomic-regions with the function `plotCutDistribution`. The red triangle is the expected cut frequency for each RE site.
> distanceHistSeq2RE(example.assignedREDseq, ylim=c(0, 25))

Figure 2: Plot to show the distribution of distance of sequence tags to associated RE sites with the function distanceHistSeq2RE.
2.4 Task 4: Generating count table for identifying statistically significant RE sites

Once you have obtained the assigned RE sites, you can use the function `summarizeByRE` to obtain a count table for identifying statistically significant RE sites using `DEseq` or `edgeR`.

```r
> REsummary = summarizeByRE(example.assignedREDseq, by="Weight")
```

2.5 Task 5: Identifying differential cut RE sites for experiment with one experiment condition

```r
> binom.test.REDseq(REsummary)
```

<table>
<thead>
<tr>
<th>p.value total.weight.count</th>
<th>REid</th>
<th>cut.frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>2.804822e-47</td>
<td>Sau96I.chr10.42</td>
<td>0.28125</td>
</tr>
<tr>
<td>9.061718e-31</td>
<td>Sau96I.chr10.43</td>
<td>0.16750</td>
</tr>
<tr>
<td>3.599987e-20</td>
<td>Sau96I.chr10.29</td>
<td>0.18660</td>
</tr>
<tr>
<td>4.969992e-15</td>
<td>Sau96I.chr10.50</td>
<td>0.09375</td>
</tr>
<tr>
<td>4.969991e-15</td>
<td>Sau96I.chr10.45</td>
<td>0.09375</td>
</tr>
<tr>
<td>3.199950e-05</td>
<td>Sau96I.chr10.40</td>
<td>0.03125</td>
</tr>
<tr>
<td>3.199950e-05</td>
<td>Sau96I.chr10.49</td>
<td>0.03125</td>
</tr>
<tr>
<td>3.199950e-05</td>
<td>Sau96I.chr10.47</td>
<td>0.03125</td>
</tr>
</tbody>
</table>

BH.adjusted.p.value

1 2.804822e-46
2 4.530859e-30
3 1.198640e-19
4 9.919784e-15
5 9.919784e-15
6 7.085573e-10
7 7.085573e-10
8 3.199950e-05
9 3.199950e-05
10 3.199950e-05

2.6 Task 6: Identifying differential cut RE sites for early stage experiment without replicates

```r
> x = cbind(c("RE1", "RE2", "RE3", "RE4"), c(10,1,100, 0),c(5,5,50, 40))
> colnames(x) = c("REid", "control", "treated")
> compareREDseq(x)
```

<table>
<thead>
<tr>
<th>p.value control.count treated.count</th>
<th>REid</th>
<th>control.total</th>
<th>treated.total</th>
</tr>
</thead>
<tbody>
<tr>
<td>6.233642e-16</td>
<td>0</td>
<td>40 RE4</td>
<td>111 100</td>
</tr>
<tr>
<td>1.199369e-10</td>
<td>100</td>
<td>80 RE3</td>
<td>111 100</td>
</tr>
<tr>
<td>1.036603e-01</td>
<td>1</td>
<td>5 RE2</td>
<td>111 100</td>
</tr>
<tr>
<td>2.943364e-01</td>
<td>10</td>
<td>5 RE1</td>
<td>111 100</td>
</tr>
</tbody>
</table>

odds.ratio BH.adjusted.p.value

1 Inf 2.493457e-15
2 0.1112945 2.318777e-10
3 5.7478720 1.380671e-01
4 0.5331227 2.943364e-01
3 References


4 Session Info

```R
> sessionInfo()
```

R version 4.4.0 beta (2024-04-15 r86425)
Platform: x86_64-pc-linux-gnu
Running under: Ubuntu 22.04.4 LTS

Matrix products: default
BLAS: /home/biocbuild/bbs-3.19-bioc/R/lib/libRblas.so
 LAPACK: /usr/lib/x86_64-linux-gnu/lapack/liblapack.so.3.10.0

locale:
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8 LC_COLLATE=en_US.UTF-8
[5] LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8 LC_NAME=C
[9] LC_ADDRESS=C LC_TELEPHONE=C
time zone: America/New_York
tzcode source: system (glibc)

attached base packages:
[1] stats4     stats     graphics   grDevices   utils     datasets   methods
[8] base

other attached packages:
[1] REDseq_1.50.0 ChIPpeakAnno_3.38.0
[3] multtest_2.60.0 Biobase_2.64.0
[5] BSgenome.Celegans.UCSC.ce2_1.4.0 BSgenome_1.72.0
[7] rtracklayer_1.64.0 BiocIO_1.14.0
[9] Biostrings_2.72.0 XVector_0.44.0
[11] GenomicRanges_1.56.0 GenomeInfoDb_1.40.0
[13] IRanges_2.38.0 S4Vectors_0.42.0
[15] BiocGenerics_0.50.0

loaded via a namespace (and not attached):
[ 1] DBI_1.2.2         bitops_1.0-7
[ 3] RBGL_1.80.0       httr2_1.0.1
[ 5] formatR_1.14      biomaRt_2.60.0
[ 7] rlang_1.1.3        magrittr_2.0.3
[ 9] matrixStats_1.3.0  compiler_4.4.0
[11] RSQLite_2.3.6      GenomicFeatures_1.56.0
[13] png_0.1-8          vctrs_0.6.5
[15] stringr_1.5.1      ProtGenerics_1.36.0
[17] pwalign_1.0.0      pkgconfig_2.0.3
[19] crayon_1.5.2       fastmap_1.1.1
[21] dbplyr_2.5.0       utf8_1.2.4
[23] Rsamtools_2.20.0   graph_1.82.0
[25] UCSC.utils_1.0.0   purrr_1.0.2
[27] bit_4.0.5          zlibbioc_1.50.0
[29] cachem_1.0.8       jsonlite_1.8.8
[31] progress_1.2.3     blob_1.2.4
[33] DelayedArray_0.30.0 BiocParallel_1.38.0
[35] parallel_4.4.0     prettyunits_1.2.0
[37] R6_2.5.1            stringi_1.8.3
[39] Rcpp_1.0.12         SummarizedExperiment_1.34.0
[41] VennDiagram_1.7.3   Matrix_1.7-0
[43] splines_4.4.0       tidyselect_1.2.1
<table>
<thead>
<tr>
<th>Package</th>
<th>Version</th>
</tr>
</thead>
<tbody>
<tr>
<td>abind</td>
<td>1.4-5</td>
</tr>
<tr>
<td>codetools</td>
<td>0.2-20</td>
</tr>
<tr>
<td>lattice</td>
<td>0.22-6</td>
</tr>
<tr>
<td>regioneR</td>
<td>1.36.0</td>
</tr>
<tr>
<td>KEGGREST</td>
<td>1.44.0</td>
</tr>
<tr>
<td>survival</td>
<td>3.6-4</td>
</tr>
<tr>
<td>BioCFileCache</td>
<td>2.12.0</td>
</tr>
<tr>
<td>universalmotif</td>
<td>1.22.0</td>
</tr>
<tr>
<td>filelock</td>
<td>1.0.3</td>
</tr>
<tr>
<td>generics</td>
<td>0.1.3</td>
</tr>
<tr>
<td>ensemblldb</td>
<td>2.28.0</td>
</tr>
<tr>
<td>ggplot2</td>
<td>3.5.1</td>
</tr>
<tr>
<td>scales</td>
<td>1.3.0</td>
</tr>
<tr>
<td>lazyeval</td>
<td>0.2.2</td>
</tr>
<tr>
<td>data.table</td>
<td>1.15.4</td>
</tr>
<tr>
<td>XML</td>
<td>3.99-0.16.1</td>
</tr>
<tr>
<td>tidyr</td>
<td>1.3.1</td>
</tr>
<tr>
<td>colorspace</td>
<td>2.1-0</td>
</tr>
<tr>
<td>restfulr</td>
<td>0.0.15</td>
</tr>
<tr>
<td>rappdirs</td>
<td>0.3.3</td>
</tr>
<tr>
<td>fansi</td>
<td>1.0.6</td>
</tr>
<tr>
<td>dplyr</td>
<td>1.1.4</td>
</tr>
<tr>
<td>gtable</td>
<td>0.3.5</td>
</tr>
<tr>
<td>SparseArray</td>
<td>1.4.0</td>
</tr>
<tr>
<td>memoise</td>
<td>2.0.1</td>
</tr>
<tr>
<td>httr</td>
<td>1.4.7</td>
</tr>
<tr>
<td>MASS</td>
<td>7.3-60.2</td>
</tr>
</tbody>
</table>