An Introduction to the *REMP* Package

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Contents

1 Introduction

REMP predicts DNA methylation of locus-specific repetitive elements (RE) by learning surrounding genetic and epigenetic information. *REMP* provides genomewide single-base resolution of DNA methylation on RE that is difficult to measure directly using array-based or sequencing-based platforms, which enables epigenome-wide association study (EWAS) and differentially methylated region (DMR) analysis on RE. *REMP* also provides handy tool to extract methylation data of CpGs that are located within RE sequences.

REMP supports both Illumina methylation BeadChip array platforms (450k and EPIC) and sequencing platforms (e.g. TruSeq Methyl Capture EPIC). Both genome build hg19 and hg38 are supported.

2 Installation

Install *REMP* (release version):

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

To install devel version:

```
> library(devtools)
> install_github("YinanZheng/REMP")
```

Load *REMP* into the workspace:

```
> library(REMP)
```

3 REMP: Repetitive Element Methylation Prediction

Currently *REMP* supports Human (hg19/hg38) Alu, LINE-1 (L1), and Long Terminal Repeat (LTR) (including endogenous retroviruses, ERV) repetitive element (RE) methylation prediction using Illumina 450k/EPIC array or sequencing platform.

3.1 Groom methylation data

Appropriate data preprocessing including quality control and normalization of methylation data are recommended before running *REMP*. Many packages are available to carry out these data preprocessing steps, for example, *minfi*, *wateRmelon*, and *methylumi*.

REMP is trying to minimize the requirement of the methylation data format. Users can maintain the methylation data in *RatioSet* or *GenomicRatioSet* object offered by *minfi*, *data.table*, *data.frame*, *DataFrame*, or *matrix*. Users can input either beta value or M-value. There are only two basic requirements of the methylation array data (450k/EPIC):

1. Each row should represent CpG probe and each column should represent sample.
2. The row names should indicate Illumina probe ID (i.e. cg00000029).

However, there are some other common data issues that may prevent *REMP* from running correctly. For example, if the methylation data are in beta value and contain zero methylation values, logit transformation (to create M-value) will create negative infinite value; or the methylation data contain `NA`, `Inf`, or `NaN` data. To tackle these potential issues, *REMP* includes a handy function `grooMethy` which can help detect and fix these issues. We highly recommend to take advantage of this function:

```
> # Get GM12878 methylation data (450k array)
> GM12878_450k <- getGM12878('450k')
> GM12878_450k <- grooMethy(GM12878_450k)
> GM12878_450k

class: RatioSet
dim: 482421 1
metadata(0):
assays(2): Beta M
rownames(482421): cg00000029 cg00000108 ... cg27666046
  cg27666123
rowData names(0):
colnames(1): GM12878
colData names(0):
Annotation
  array: IlluminaHumanMethylation450k
  annotation: ilmn12.hg19
Preprocessing
  Method: NA
  minfi version: NA
  Manifest version: NA
```

For zero beta values, `grooMethy` will replace them with smallest non-zero beta value. For one beta values, `grooMethy` will replace them with largest non-one beta value. For `NA`/`NaN`/`Inf` values, `grooMethy` will treat them as missing values and then apply KNN-imputation to complete the dataset. If the imputed value is out of the original range (which is possible when `imputebyrow = FALSE`), mean value will be used instead. Warning: imputed values for multimodal distributed CpGs (across samples) may not be correct. Please check package *ENmix* to identify the CpGs with multimodal distribution.

For sequencing data, the users only need to prepare a methylation data matrix (row = CpGs, column = samples). The corresponding CpG location information (either in hg19 or hg38) should be prepared in a separate *GRanges* object and provide it to the `Seq.GR` argument in `grooMethy`. For an example of `Seq.GR`, please run:

```
> library(IlluminaHumanMethylation450kanno.ilmn12.hg19)
> getLocations(IlluminaHumanMethylation450kanno.ilmn12.hg19)

GRanges object with 485512 ranges and 0 metadata columns:
                  seqnames    ranges strand
                     <Rle> <IRanges>  <Rle>
       cg00050873     chrY   9363356      *
       cg00212031     chrY  21239348      *
       cg00213748     chrY   8148233      *
       cg00214611     chrY  15815688      *
       cg00455876     chrY   9385539      *
              ...      ...       ...    ...
    ch.22.909671F    chr22  46114168      *
  ch.22.46830341F    chr22  48451677      *
   ch.22.1008279F    chr22  48731367      *
  ch.22.47579720R    chr22  49193714      *
  ch.22.48274842R    chr22  49888838      *
  -------
  seqinfo: 24 sequences from hg19 genome; no seqlengths
```

Note that the row names of the CpGs in `Seq.GR` can be `NULL`.

3.2 Prepare annotation data

To run *REMP* for RE methylation prediction, users first need to prepare some annotation datasets. The function `initREMP` is designed to do the job.

Suppose users will predict Alu methylation using Illumina 450k array data:

```
> data(Alu.hg19.demo)
> remparcel <- initREMP(arrayType = "450k",
+                       REtype = "Alu",
+                       annotation.source = "AH",
+                       genome = "hg19",
+                       RE = Alu.hg19.demo,
+                       ncore = 1)
> remparcel

REMParcel object
RE type: Alu
Genome build: hg19
Illumina platform: 450k
Valid (max) Alu-CpG flanking window size: 1200
Number of RE: 500
Number of Alu-CpG: 5138
```

For demonstration, we only use 500 selected Alu sequence dataset which comes along with the package (`Alu.hg19.demo`). We specify `RE = Alu.hg19.demo`, so that the annotation dataset will be generated for the 500 selected Alu sequences. Most of the time, specifying `RE` is not necessary, as the function will fetch the complete RE sequence dataset from package *AnnotationHub* using `fetchRMSK`. Users can also use this argument `RE` to provide customized RE dataset.

`annotation.source` allows the users to switch the source of the annotation databases, including the RefSeq Gene annotation database and RepeatMasker annotation database. If `annotation.source = "AH"`, the database will be obtained from the AnnotationHub package. If `annotation.source = "UCSC"`, the database will be downloaded from the UCSC website http://hgdownload.cse.ucsc.edu/goldenpath. The corresponding build (`"hg19"` or `"hg38"`) can be specified in the argument `genome`. Most of the time `"hg19"` is used for array data. But if `"hg38"` is specified, the function will liftover the CpG probe location information to `"hg38"` and obtain annotation databases in `"hg38"`.

If `arrayType = "Sequencing"`, users should provide the genomic location information of the CpGs in a *GRanges* object to `Seq.GR`. Note that the genome build of `Seq.GR` provided should match the genome build specified in `genome`.

All data are stored in the *REMParcel* object:

```
> saveParcel(remparcel)
```

It is recommended to specify a working directory using argument `work.dir` in `initREMP` so that the annnotation data generated can be re-used. Without specifying working directory, the annotation dataset will be created under the temporal directory `tempdir()` by default. Users can also turn on the `export` argument in `initREMP` to save the data automatically.

3.3 Run prediction

Once the annotation data are ready, users can pass the annotation data parcel to `remp` for prediction:

```
> remp.res <- remp(GM12878_450k,
+                  REtype = 'Alu',
```

```
+                   parcel = remparcel,
+                   ncore = 1,
+                   seed = 777)
```

If `parcel` is missing, `remp` will then try to search the *REMParcel* data file in the directory indicated by `work.dir`. If `work.dir` is also missing, `remp` will try to search the REMParcel data file in the temporal directory `tempdir()`.

By default, `remp` uses Random Forest (`method = 'rf'`) model (package *ranger* for fast implementation) for prediction. Random Forest model is recommended because it offers more accurate prediction results and it automatically enables Quantile Regression Forest (Nicolai Meinshausen, 2006) for prediction reliability evaluation. `remp` constructs predictors to carry out the prediction. For Random Forest model, the tuning parameter `param = 6` (i.e. `mtry` in *ranger* or *randomForest*) indicates how many predictors will be randomly selected for building the individual trees. The performance of random forest model is often relatively insensitive to the choice of `mtry`. Therefore, auto-tune will be turned off using random forest and `mtry` will be set to one third of the total number of predictors. It is recommended to specify a seed for reproducible prediction results.

Besides random forest, `remp` provides other machine learning engines for users to explore, including Extreme Gradient Boosting, SVM with linear kernel, and SVM with radial kernel).

`remp` will return a *REMPset* object, which inherits Bioconductor's *RangedSummarizedExperiment* class:

```
> remp.res

class: REMProduct
dim: 4952 1
metadata(8): REannotation RECpG ... GeneStats Seed
assays(3): rempB rempM rempQC
rownames: NULL
rowData names(1): RE.Index
colnames(1): GM12878
colData names(1): mtry

> # Display more detailed information
> details(remp.res)

RE type: Alu
Genome build: hg19
Methylation profiling platform: 450k
Flanking window size: 1000
Prediction model: Random Forest
QC model: Quantile Regression Forest
Seed: 777
Covered 4952 CpG sites in 500 Alu

Number of Alu-CpGs by chromosome:
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8
 429  195  257  197  142  382  202  153

 chr9 chr10 chr11 chr12 chr13 chr14 chr15 chr16
   93   172   192   355    52   122   201   280

chr17 chr18 chr19 chr20 chr21 chr22
  361    65   803   107    56   136

Training information:
  500 profiled Alu are used for model training.
```

```
  490 Alu-CpGs that have at least 2 neighboring profiled CpGs are used for model training.

Coverage information:
  The data cover 500 Alu (4952 Alu-CpG).
  Gene coverage by Alu (out of total # of RefSeq genes):
    530 (2.13%) total genes;
    460 (2.4%) protein-coding genes;
    103 (1.43%) non-coding RNA genes.

Distribution of methylation value (beta value):
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.
0.01178818 0.43739915 0.64585305 0.57035834 0.75523415 0.90391551

Distribution of reliability score (lower score = higher reliability):
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
0.6405955 1.3005384 1.5831950 1.6681776 2.0136318 5.9084103
```

Prediction results can be obtained by accessors:

```
> # Predicted RE-CpG methylation value (Beta value)
> rempB(remp.res)

DataFrame with 4952 rows and 1 column
       GM12878
     <numeric>
1     0.658459
2     0.655791
3     0.658361
4     0.665226
5     0.664966
...        ...
4948  0.809959
4949  0.810494
4950  0.811938
4951  0.811706
4952  0.825812

> # Predicted RE-CpG methylation value (M value)
> rempM(remp.res)

DataFrame with 4952 rows and 1 column
       GM12878
     <numeric>
1     0.947032
2     0.929951
3     0.946409
4     0.990658
5     0.988975
...        ...
4948   2.09154
4949   2.09656
4950   2.11016
4951   2.10797
4952   2.24516
```

```
> # Genomic location information of the predicted RE-CpG
> # Function inherit from class 'RangedSummarizedExperiment'
> rowRanges(remp.res)

GRanges object with 4952 ranges and 1 metadata column:
         seqnames            ranges strand |    RE.Index
            <Rle>         <IRanges>  <Rle> |       <Rle>
     [1]     chr1   1149956-1149957      + | Alu_0000214
     [2]     chr1   1149966-1149967      + | Alu_0000214
     [3]     chr1   1149999-1150000      + | Alu_0000214
     [4]     chr1   1150049-1150050      + | Alu_0000214
     [5]     chr1   1150057-1150058      + | Alu_0000214
     ...      ...               ...    ... .         ...
  [4948]    chr22 50914839-50914840      - | Alu_1118131
  [4949]    chr22 50914853-50914854      - | Alu_1118131
  [4950]    chr22 50914860-50914861      - | Alu_1118131
  [4951]    chr22 50914869-50914870      - | Alu_1118131
  [4952]    chr22 50914907-50914908      - | Alu_1118131
  -------
  seqinfo: 24 sequences from an unspecified genome; no seqlengths

> # Standard error-scaled permutation importance of predictors
> rempImp(remp.res)

DataFrame with 18 rows and 1 column
                  GM12878
                <numeric>
RE.swScore        7.48388
RE.Length         3.42704
RE.CpG.density    6.81685
RE.InTSS          2.11638
RE.In5UTR         1.78648
...                   ...
Methy.mean.mov1  20.84179
Methy.mean.mov2  14.77652
Methy.mean.mov3   9.14708
Methy.mean.mov4  10.58181
Methy.std         7.29195

> # Retrive seed number used for the reesults
> metadata(remp.res)$Seed

[1] 777
```

Trim off less reliable predicted results:

```
> # Any predicted CpG values with quality score less than
> # threshold (default = 1.7) will be replaced with NA.
> # CpGs contain more than missingRate * 100% (default = 20%)
> # missing rate across samples will be discarded.
> remp.res <- rempTrim(remp.res, threshold = 1.7, missingRate = 0.2)
> details(remp.res)

RE type: Alu
Genome build: hg19
```

```
Methylation profiling platform: 450k
Flanking window size: 1000
Prediction model: Random Forest - trimmed (1.7)
QC model: Quantile Regression Forest
Seed: 777
Covered 2848 CpG sites in 397 Alu

Number of Alu-CpGs by chromosome:
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8
 295  145  155  138   88  134  102   93

 chr9 chr10 chr11 chr12 chr13 chr14 chr15 chr16
   39    89   117   223    31    63   107   168

chr17 chr18 chr19 chr20 chr21 chr22
  199    40   459    73    13    77

Coverage information:
  The data cover 397 Alu (2848 Alu-CpG).
  Gene coverage by Alu (out of total # of RefSeq genes):
    415 (1.67%) total genes;
    356 (1.86%) protein-coding genes;
    85 (1.18%) non-coding RNA genes.

Distribution of methylation value (beta value):
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.
0.03459213 0.62096126 0.72580862 0.66668785 0.79453724 0.90391551

Distribution of reliability score (lower score = higher reliability):
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
0.6405955 1.1777745 1.3414789 1.3299838 1.4916722 1.6996203
```

(Optional) Aggregate the predicted methylation of CpGs in RE by averaging them to obtain the RE-specific methylation level:

```
> remp.res <- rempAggregate(remp.res, NCpG = 2)
> details(remp.res)

RE type: Alu (aggregated by mean: min # of CpGs: 2)
Genome build: hg19
Methylation profiling platform: 450k
Flanking window size: 1000
Prediction model: Random Forest - trimmed (1.7)
QC model: Quantile Regression Forest
Seed: 777
Covered 339 Alu (aggregated by mean: min # of CpGs: 2)

Number of Alu (aggregated by mean: min # of CpGs: 2) by chromosome:
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8
  32   17   18   14    9   21   14   10

 chr9 chr10 chr11 chr12 chr13 chr14 chr15 chr16
    7    13    14    25     5     6    13    19
```

```
chr17 chr18 chr19 chr20 chr21 chr22
   24     4    55     8     2     9

Coverage information:
  The data cover 339 Alu (aggregated by mean: min # of CpGs: 2)
  Gene coverage by Alu (aggregated by mean: min # of CpGs: 2) (out of total # of RefSeq ge
    352 (1.41%) total genes;
    298 (1.56%) protein-coding genes;
    74 (1.03%) non-coding RNA genes.

Distribution of methylation value (beta value):
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.
0.04786608 0.59569784 0.70904833 0.64428356 0.78028163 0.85384885

Distribution of reliability score (lower score = higher reliability):
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
0.8250507 1.2487521 1.3836146 1.3658707 1.4913583 1.6902399
```

Aggregating CpGs in the same RE for RE-level methylation data is beneficial because 1) it greatly reduces the data dimension for downstream analysis and 2) it may produce more robust RE methylation estimation. Note that by default, RE with 2 or more predicted CpG sites will be aggregated. Therefore, the downside of doing this is the reduced coverage of RE. The assumption of doing this is the CpG methylation level within each RE are similar.

To add genomic regions annotation of the predicted REs:

```
> # By default gene symbol annotation will be added
> remp.res <- decodeAnnot(remp.res)
> rempAnnot(remp.res)

GRanges object with 339 ranges and 12 metadata columns:
        seqnames            ranges strand |   swScore     repName
           <Rle>         <IRanges>  <Rle> | <integer> <character>
    [1]     chr1   1149947-1150242      + |      2216      AluSx1
    [2]     chr1   1885941-1886230      + |      1962       AluJb
    [3]     chr1 14032197-14032500      + |      2768       AluSg
    [4]     chr1 22378622-22378926      + |      2142      AluSx1
    [5]     chr1 39408080-39408382      + |      2493       AluSp
    ...      ...                ...    ... .       ...         ...
  [335]    chr22 44964234-44964539      + |      2284      AluSq2
  [336]    chr22 50311037-50311333      + |      2251      AluSx1
  [337]    chr22 50493205-50493515      + |      2229       AluSx
  [338]    chr22 42078691-42078952      - |      1881      AluSx1
  [339]    chr22 50914608-50914917      - |      2526        AluY
           repClass   repFamily       Index  InNM.symbol InNR.symbol
        <character> <character>       <Rle>  <character> <character>
    [1]        SINE         Alu Alu_0000214      TNFRSF4        <NA>
    [2]        SINE         Alu Alu_0000634       CFAP74        <NA>
    [3]        SINE         Alu Alu_0004565        PRDM2        <NA>
    [4]        SINE         Alu Alu_0007535        CDC42        <NA>
    [5]        SINE         Alu Alu_0014170       RHBDL2        <NA>
    ...         ...         ...         ...          ...         ...
  [335]        SINE         Alu Alu_1104534         <NA>   LINC00207
  [336]        SINE         Alu Alu_1105703 CRELD2|ALG12      CRELD2
  [337]        SINE         Alu Alu_1105737         <NA>        <NA>
  [338]        SINE         Alu Alu_1115677        SNU13        <NA>
```

```
[339]        SINE         Alu Alu_1118131         SBF1        <NA>
      InTSS.symbol In5UTR.symbol InCDS.symbol InExon.symbol
       <character>   <character>  <character>   <character>
  [1]      TNFRSF4          <NA>         <NA>          <NA>
  [2]         <NA>          <NA>         <NA>        CFAP74
  [3]         <NA>         PRDM2         <NA>          <NA>
  [4]        CDC42          <NA>         <NA>          <NA>
  [5]       RHBDL2          <NA>         <NA>          <NA>
  ...          ...           ...          ...           ...
[335]    LINC00207          <NA>         <NA>          <NA>
[336]       CRELD2         ALG12         <NA>          <NA>
[337]         <NA>          <NA>         <NA>          <NA>
[338]         <NA>         SNU13        SNU13          <NA>
[339]         SBF1          <NA>         <NA>          <NA>
      In3UTR.symbol
        <character>
  [1]          <NA>
  [2]        CFAP74
  [3]          <NA>
  [4]          <NA>
  [5]          <NA>
  ...           ...
[335]          <NA>
[336]          <NA>
[337]          <NA>
[338]          <NA>
[339]          <NA>
-------
seqinfo: 24 sequences from hg19 genome
```

Seven genomic region indicators will be added to the annotation data in the input *REMProduct* object:

- InNM: in protein-coding genes (overlap with refSeq gene's "NM" transcripts + 2000 bp upstream of the transcription start site (TSS))
- InNR: in noncoding RNA genes (overlap with refSeq gene's "NR" transcripts + 2000 bp upstream of the TSS)
- InTSS: in flanking region of 2000 bp upstream of the TSS. Default upstream limit is 2000 bp, which can be modified globally using `remp_options`
- In5UTR: in 5'untranslated regions (UTRs)
- InCDS: in coding DNA sequence regions
- InExon: in exon regions
- In3UTR: in 3'UTRs

Note that intron region and intergenic region information can be derived from the above genomic region indicators: if "InNM" and/or "InNR" is not missing but "InTSS", "In5UTR", "InExon", and "In3UTR" are missing, then the RE is strictly located within intron region; if all indicators are missing, then the RE is strictly located in intergenic region.

3.4 Plot prediction

Make a density plot of the predicted methylation (beta values):

```
> remplot(remp.res, main = "Alu methylation (GM12878)", col = "blue")
```

4 Extract RE-CpG methylation profiled by Illumina BeadChip array

REMP offers a handy tool to extract methylation data of CpGs that are located in RE. Similar as `remp`, users can choose the source of annotation database (`AH`: AnnotationHub or `UCSC`: UCSC website) and genome build (`hg19` or `hg38`).

```
> # Use Alu.hg19.demo for demonstration
> remp.res <- remprofile(GM12878_450k,
+                        REtype = "Alu",
+                        annotation.source = "AH",
+                        genome = "hg19",
+                        RE = Alu.hg19.demo)
> details(remp.res)

RE type: Alu
Genome build: hg19
Methylation profiling platform: 450k
Flanking window size: N/A
Prediction model: Profiled
QC model: N/A
Covered 602 CpG sites in 500 Alu

Number of Alu-CpGs by chromosome:
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8
  58   22   33   23   17   59   26   18

 chr9 chr10 chr11 chr12 chr13 chr14 chr15 chr16
   12    27    20    42     8    11    20    30

chr17 chr18 chr19 chr20 chr21 chr22
   39     9    97    13     5    13

Coverage information:
  The data cover 500 Alu (602 Alu-CpG).
  Gene coverage by Alu (out of total # of RefSeq genes):
    530 (2.13%) total genes;
    460 (2.4%) protein-coding genes;
    103 (1.43%) non-coding RNA genes.

Distribution of methylation value (beta value):
    Min.  1st Qu.   Median     Mean  3rd Qu.     Max.
0.001000 0.344500 0.649500 0.567397 0.814000 0.959000

> # All accessors and utilites for REMProduct are applicable
> remp.res <- rempAggregate(remp.res)
> details(remp.res)

RE type: Alu (aggregated by mean: min # of CpGs: 2)
Genome build: hg19
Methylation profiling platform: 450k
Flanking window size: N/A
```

```
Prediction model: Profiled
QC model: N/A
Covered 86 Alu (aggregated by mean: min # of CpGs: 2)

Number of Alu (aggregated by mean: min # of CpGs: 2) by chromosome:
chr1 chr2 chr3 chr4 chr5 chr6 chr7 chr8
  13    2    6    2    1   14    3    2

chr10 chr11 chr12 chr14 chr15 chr16 chr17 chr18
    2     3     9     1     2     4     4     3

chr19 chr20 chr21 chr22
    9     3     1     2

Coverage information:
  The data cover 86 Alu (aggregated by mean: min # of CpGs: 2)
  Gene coverage by Alu (aggregated by mean: min # of CpGs: 2) (out of total # of RefSeq ge
    98 (0.39%) total genes;
    83 (0.43%) protein-coding genes;
    24 (0.33%) non-coding RNA genes.

Distribution of methylation value (beta value):
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
0.0408311 0.1983081 0.6649476 0.5265950 0.7829270 0.9288642
```