Efficient genome searching with Biostrings and the BSgenome data packages

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1 The Biostrings-based genome data packages

The Bioconductor project provides data packages that contain the full genome sequences of a given organism. These packages are called Biostrings-based genome data packages because the sequences they contain are stored in some of the basic containers defined in the Biostrings package, like the DNAString, the DNAStringSet or the MaskedDNAString containers. Regardless of the particular sequence data that they contain, all the Biostrings-based genome data packages are very similar and can be manipulated in a consistent and easy way. They all require the BSgenome package in order to work properly. This package, unlike the Biostrings-based genome data packages, is a software package that provides the infrastructure needed to support them (this is why the Biostrings-based genome data packages are also called BSgenome data packages). The BSgenome package itself requires the Biostrings package.

See the man page for the available.genomes function (?available.genomes) for more information about how to get the list of all the BSgenome data packages currently available in your version of Bioconductor (you need an internet connection so that available.genomes can query the Bioconductor package repositories).

More genomes can be added if necessary. Note that the process of making a BSgenome data package is not yet documented but you are welcome to ask for help on the bioc-devel mailing list (http://bioconductor.org/docs/mailList.html) if you need a genome that is not yet available.
2 Finding an arbitrary nucleotide pattern in a chromosome

In this section we show how to find (or just count) the occurrences of some arbitrary nucleotide pattern in a chromosome. The basic tool for this is the matchPattern (or countPattern) function from the Biostrings package.

First we need to install and load the BSgenome data package for the organism that we want to look at. In our case, we want to search chromosome I of Caenorhabditis elegans.

UCSC provides several versions of the C. elegans genome: ce1, ce2 and ce4. These versions correspond to different releases from WormBase, which are the WS100, WS120 and WS170 releases, respectively. See http://genome.ucsc.edu/FAQ/FAQreleases#release1 for the list of all UCSC genome releases and for the correspondence between UCSC versions and release names.

The BSgenome data package for the ce2 genome is BSgenome.Celegans.UCSC.ce2. Note that ce1 and ce4 are not available in Bioconductor but they could be added if there is demand for them.

See ?available.genomes for how to install BSgenome.Celegans.UCSC.ce2. Then load the package and display the single object defined in it:

```r
> library(BSgenome.Celegans.UCSC.ce2)
> ls("package:BSgenome.Celegans.UCSC.ce2")
[1] "BSgenome.Celegans.UCSC.ce2" "Celegans"

> genome <- BSgenome.Celegans.UCSC.ce2
> genome

Worm genome:
# organism: Caenorhabditis elegans (Worm)
# provider: UCSC
# provider version: ce2
# release date: Mar. 2004
# release name: WormBase v. WS120
# 7 sequences:
# chrI chrII chrIII chrIV chrV chrX chrM
# (use 'seqnames()' to see all the sequence names, use the '$' or '[[]' operator
# to access a given sequence)

  genome is a BSgenome object:

> class(genome)
[1] "BSgenome"
attr("package")
[1] "BSgenome"
```

When displayed, some basic information about the origin of the genome is shown (organism, provider, provider version, etc...) followed by the index of single sequences and eventually an additional index of multiple sequences. Methods (adequately called accessor methods) are defined for individual access to this information:

```r
> organism(genome)
[1] "Caenorhabditis elegans"

> provider(genome)
[1] "UCSC"
```
> providerVersion(genome)
[1] "ce2"

> seqnames(genome)
[1] "chrI" "chrII" "chrIII" "chrIV" "chrV" "chrX" "chrM"

> mseqnames(genome)
NULL

See the man page for the `BSgenome` class (`?BSgenome`) for a complete list of accessor methods and their descriptions.

Now we are ready to display chromosome I:

> genome$chrI
15080483-letter "DNAString" instance
seq: GCCTAAGCCTAAGCCTAAGCCTAAGCCTAAGCCTAA...TTAGGCTTAGGCTTAGGCTTAGGTTTAGGCTTAGGC

Note that this chrI sequence corresponds to the forward strand (aka direct or sense or positive or plus strand) of chromosome I. UCSC, and genome providers in general, don’t provide files containing the nucleotide sequence of the reverse strand (aka indirect or antisense or negative or minus or opposite strand) of the chromosomes because these sequences can be deduced from the forward sequences by taking their reverse complements. The BSgenome data packages are no exceptions: they only provide the forward strand sequence of every chromosome. See `?reverseComplement` for more details about the reverse complement of a DNAString object. It is important to remember that, in practice, the forward strand sequence of every chromosome can be computed from the forward strand sequence. Therefore trying to compute the reverse strand sequence of an entire chromosome by applying `reverseComplement` to its forward strand sequence is almost always a bad idea. See the Finding an arbitrary nucleotide pattern in an entire genome section of this document for how to find arbitrary patterns in the reverse strand of a chromosome.

The number of bases in this sequence can be retrieved with:

> chrI <- genome$chrI
> length(chrI)
[1] 15080483

Some basic stats:

> afI <- alphabetFrequency(chrI)
> afI

<table>
<thead>
<tr>
<th></th>
<th>A</th>
<th>C</th>
<th>G</th>
<th>T</th>
<th>M</th>
<th>R</th>
<th>W</th>
<th>S</th>
<th>Y</th>
<th>K</th>
</tr>
</thead>
<tbody>
<tr>
<td>V</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>H</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>D</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>B</td>
<td></td>
<td></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>-</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>+</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

> sum(afI) == length(chrI)
[1] TRUE

Count all exact matches of pattern "ACCCAGGGC":

3
Like most pattern matching functions in Biostrings, the countPattern and matchPattern functions support inexact matching. One form of inexact matching is to allow a few mismatching letters per match. Here we allow at most one:

```r
> countPattern(p1, chrI, max.mismatch=1)
[1] 235
```

With the matchPattern function, the locations of the matches are stored in an XStringViews object:

```r
> m1 <- matchPattern(p1, chrI, max.mismatch=1)
> m1[4:6]
```

Views on a 15080483-letter DNAString subject

```r
class(m1)
[1] "XStringViews"
attr(,"package")
[1] "Biostrings"
```

The mismatch function (new in Biostrings 2) returns the positions of the mismatching letters for each match:

```r
> mismatch(p1, m1[4:6])
```

Note: The mismatch method is in fact a particular case of a (vectorized) alignment function where only “replacements” are allowed. Current implementation is slow but this will be addressed.

It may happen that a match is out of limits like in this example:

```r
> p2 <- DNAString("AAGCCTAAGGCTAAGGCTAA")
> m2 <- matchPattern(p2, chrI, max.mismatch=2)
> m2[1:4]
```
Views on a 15080483-letter DNAString subject

subject: GCCTAAGCCTAAGCCTAAGCCTAAGCCTAAGCCTAAGCGT...AGGCTTAGGCTTAGGCTTAGGCTTAGGCT

views:

<table>
<thead>
<tr>
<th>start</th>
<th>end</th>
<th>width</th>
<th>pattern</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>-1</td>
<td>18</td>
<td>GCCTAAGCCTAAGCCTAAGCCTAA</td>
</tr>
<tr>
<td>5</td>
<td>24</td>
<td>20</td>
<td>AAGCCTAAGCCTAAGCCTAAGCCTAA</td>
</tr>
<tr>
<td>11</td>
<td>30</td>
<td>20</td>
<td>AAGCCTAAGCCTAAGCCTAAGCCTAA</td>
</tr>
<tr>
<td>17</td>
<td>36</td>
<td>20</td>
<td>AAGCCTAAGCCTAAGCCTAAGCCTAA</td>
</tr>
</tbody>
</table>

> p2 == m2[1:4]

1) FALSE TRUE TRUE TRUE

> mismatch(p2, m2[1:4])

[[1]]

1 2

[[2]]

integer(0)

[[3]]

integer(0)

[[4]]

integer(0)

The list of exact matches and the list of inexact matches can both be obtained with:

> m2[p2 == m2]

> m2[p2 != m2]

Note that the length of m2[p2 == m2] should be equal to countPattern(p2, chrI, max.mismatch=0).

3 Finding an arbitrary nucleotide pattern in an entire genome

Now we want to extend our analysis to the forward and reverse strands of all the C. elegans chromosomes. More precisely, here is the analysis we want to perform:

- The input dictionary: Our input is a dictionary of 50 patterns. Each pattern is a short nucleotide sequence of 15 to 25 bases (As, Cs, Gs and Ts only, no Ns). It is stored in a FASTA file called "ce2dict0.fa". See the Finding all the patterns of a constant width dictionary in an entire genome section of this document for a very efficient way to deal with the special case where all the patterns in the input dictionary have the same length.

- The target: Our target (or subject) is the forward and reverse strands of the seven C. elegans chromosomes (14 sequences in total). We want to find and report all occurrences (or hits) of every pattern in the target. Note that a given pattern can have 0, 1 or several hits in 0, 1 or several chromosomes.

- Exact or inexact matching? We are interested in exact matches only (for now).
• The output: We want to put the results of this analysis in a file so we can send it to our collaborators for some post analysis work. Our collaborators are not necessarily familiar with R or Bioconductor so dumping a high-level R object (like a list or a data frame) into an .rda file is not an option. For maximum portability (one of our collaborators wants to use Microsoft Excel for the post analysis) we choose to put our results in a tabulated file where one line describes one hit. The columns (or fields) of this file will be (in this order):
  - seqname: the name of the chromosome where the hit occurs.
  - start: an integer giving the starting position of the hit.
  - end: an integer giving the ending position of the hit.
  - strand: a plus (+) for a hit in the positive strand or a minus (−) for a hit in the negative strand.
  - patternID: we use the unique ID provided for every pattern in the "ce2dict0.fa" file.

Let’s start by loading the input dictionary with:

```r
> ce2dict0_file <- system.file("extdata", "ce2dict0.fa", package="BSgenome")
> ce2dict0 <- readDNAStringSet(ce2dict0_file, "fasta")
> ce2dict0
```

A DNAStringSet instance of length 50

<table>
<thead>
<tr>
<th>seq names</th>
<th>width</th>
</tr>
</thead>
<tbody>
<tr>
<td>18 GCGAACTAGGAGGCT pattern01</td>
<td></td>
</tr>
<tr>
<td>25 CTGTTAGCTAAATTTAAAAAAAT</td>
<td></td>
</tr>
<tr>
<td>24 ACTACCCACAAATTATATGATAT</td>
<td></td>
</tr>
<tr>
<td>24 AAATTTTTTTGTGTCAAAATTGA pattern04</td>
<td></td>
</tr>
<tr>
<td>25 TCTTCTGGCTTTGCTGTAACCTT</td>
<td></td>
</tr>
<tr>
<td>... ... ...</td>
<td></td>
</tr>
<tr>
<td>24 TTTTGAACAAACATGCTCTACTA pattern46</td>
<td></td>
</tr>
<tr>
<td>20 TAAACGAAATTTAGGATATAT pattern47</td>
<td></td>
</tr>
<tr>
<td>19 AAGGACAGATTGCACG pattern48</td>
<td></td>
</tr>
<tr>
<td>24 AAAATACTGCTAAAACAAAATA pattern49</td>
<td></td>
</tr>
<tr>
<td>22 AAAATGCCGGAGCATTTAAAAG pattern50</td>
<td></td>
</tr>
</tbody>
</table>

Here is how we can write the functions that will perform our analysis:

```r
> writeHits <- function(seqname, matches, strand, file="", append=FALSE) {
+   if (file.exists(file) && !append)
+     warning("existing file ", file, " will be overwritten with 'append=FALSE'")
+   if (!file.exists(file) && append)
+     warning("new file ", file, " will have no header with 'append=TRUE'")
+   hits <- data.frame(seqname=rep.int(seqname, length(matches)),
+     start=start(matches),
+     end=end(matches),
+     strand=rep.int(strand, length(matches)),
+     patternID=names(matches),
+     check.names=FALSE)
+   write.table(hits, file=file, append=append, quote=FALSE, sep="\t",
+     row.names=FALSE, col.names=!append)
+ }
> runAnalysis1 <- function(dict0, outfile="") {
  ```
library(BSgenome.Celegans.UCSC.ce2)
geno <- BSgenome.Celegans.UCSC.ce2
seqnames <- seqnames(geno)
seqnames_in1string <- paste(seqnames, collapse=", ")
cat("Target: ", providerVersion(geno), 
"chromosomes", seqnames_in1string, "\n")
append <- FALSE
for (seqname in seqnames) {
  subject <- geno[[seqname]]
cat(">>> Finding all hits in chromosome", seqname, "\n")
  for (i in seq_len(length(dict0))) {
    patternID <- names(dict0)[i]
    pattern <- dict0[[i]]
    plus_matches <- matchPattern(pattern, subject)
    names(plus_matches) <- rep.int(patternID, length(plus_matches))
    writeHits(seqname, plus_matches, "+", file=outfile, append=append)
    append <- TRUE
    rcpattern <- reverseComplement(pattern)
    minus_matches <- matchPattern(rcpattern, subject)
    names(minus_matches) <- rep.int(patternID, length(minus_matches))
    writeHits(seqname, minus_matches, "-", file=outfile, append=append)
  }
}
cat(">>> DONE\n")
}

Some important notes about the implementation of the runAnalysis1 function:

- subject <- geno[[seqname]] is the code that actually loads a chromosome sequence into memory. Using only one sequence at a time is a good practice to avoid memory allocation problems on a machine with a limited amount of memory. For example, loading all the human chromosome sequences in memory would require more than 3GB of memory!

- We have 2 nested for loops: the outer loop walks thru the target (7 chromosomes) and the inner loop walks thru the set of patterns. Doing the other way around would be very inefficient, especially with a bigger number of patterns because this would require to load each chromosome sequence into memory as many times as the number of patterns. runAnalysis1 loads each sequence only once.

- We find the matches in the minus strand (minus_matches) by first taking the reverse complement of the current pattern (with rcpattern <- reverseComplement(pattern)) and NOT by taking the reverse complement of the current subject.

Now we are ready to run the analysis and put the results in the "ce2dict0_ana1.txt" file:

> runAnalysis1(ce2dict0, outfile="ce2dict0_ana1.txt")

Target: ce2 chromosomes chrI, chrII, chrIII, chrIV, chrV, chrX, chrM
>>> Finding all hits in chromosome chrI ...
>>> DONE
>>> Finding all hits in chromosome chrII ...
>>> DONE
>>> Finding all hits in chromosome chrIII ...
>>> DONE
>>> Finding all hits in chromosome chrIV ...

Here is some very simple example of post analysis:

- Get the total number of hits:

  ```
  > hits1 <- read.table("ce2dict0_anal.txt", header=TRUE)
  > nrow(hits1)
  [1] 79
  ```

- Get the number of hits per chromosome:

  ```
  > table(hits1$seqname)
  chrI chrII chrIII chrIV chrM chrV chrX
  11  5  16  8  8  15  16
  ```

- Get the number of hits per pattern:

  ```
  > hits1_table <- table(hits1$patternID)
  > hits1_table
  pattern01 pattern02 pattern03 pattern04 pattern06 pattern07 pattern08 pattern09
  1  1  1  1  2  1  1  1
  pattern10 pattern11 pattern12 pattern13 pattern14 pattern15 pattern16 pattern17
  1  1  1  1  1  1  1  1
  pattern18 pattern19 pattern20 pattern21 pattern22 pattern23 pattern24 pattern25
  1  9  1 10  2  1  1  1
  pattern26 pattern27 pattern28 pattern29 pattern30 pattern31 pattern32 pattern33
  1  1  1  1  1  1  1  1
  pattern34 pattern35 pattern36 pattern37 pattern38 pattern39 pattern40 pattern41
  2  1  1  7  1  1  1  1
  pattern42 pattern43 pattern44 pattern45 pattern46 pattern47 pattern48 pattern49
  1  5  1  1  1  1  1  1
  pattern50
  1
  ```

- Get the pattern(s) with the higher number of hits:

  ```
  > hits1_table[hits1_table == max(hits1_table)] # pattern(s) with more hits
  pattern21
  10
  ```

- Get the pattern(s) with no hits:

  ```
  > setdiff(names(ce2dict0), hits1$patternID) # pattern(s) with no hits
  ```
And finally a function that can be used to plot the hits:

```r
plotGenomeHits <- function(bsgenome, seqnames, hits) {
  chrlengths <- seqlengths(bsgenome)[seqnames]
  XMAX <- max(chrlengths)
  YMAX <- length(seqnames)
  plot.new()
  plot.window(c(1, XMAX), c(0, YMAX))
  axis(1)
  axis(2, at=seq_len(length(seqnames)), labels=rev(seqnames), tick=FALSE, las=1)
  ## Plot the chromosomes
  for (i in seq_len(length(seqnames)))
    lines(c(1, chrlengths[i]), c(YMAX + 1 - i, YMAX + 1 - i), type="l")
  ## Plot the hits
  for (i in seq_len(nrow(hits))) {
    seqname <- hits$seqname[i]
    y0 <- YMAX + 1 - match(seqname, seqnames)
    if (hits$strand[i] == "+") {
      y <- y0 + 0.05
      col <- "red"
    } else {
      y <- y0 - 0.05
      col <- "blue"
    }
    lines(c(hits$start[i], hits$end[i]), c(y, y), type="l", col=col, lwd=3)
  }
}
```

Plot the hits found by `runAnalysis1` with:

```r
plotGenomeHits(genome, seqnames(genome), hits1)
```

4 Some precautions when using `matchPattern`

Improper use of `matchPattern` (or `countPattern`) can affect performance.

If needed, the `matchPattern` and `countPattern` methods convert their first argument (the pattern) to an object of the same class than their second argument (the subject) before they pass it to the subroutine that actually implements the fast search algorithm.

So if you need to reuse the same pattern a high number of times, it’s a good idea to convert it before to pass it to the `matchPattern` or `countPattern` method. This way the conversion is done only once:

```r
library(hgu95av2probe)
> tmpseq <- DNAStringSet(hgu95av2probe$sequence)
> someStats <- function(v) {
  GC <- DNAString("GC")
  CG <- DNAString("CG")
  sapply(seq_len(length(v)),
    function(i) {
```
5 Masking the chromosome sequences

Starting with Bioconductor 2.2, the chromosome sequences in a \textit{BSgenome data package} can have built-in masks. Starting with Bioconductor 2.3, there can be up to 4 built-in masks per sequence. These will always be (in this order): (1) the mask of assembly gaps, (2) the mask of intra-contig ambiguities, (3) the mask of repeat regions that were determined by the RepeatMasker software, and (4) the mask of repeat regions that were determined by the Tandem Repeats Finder software (where only repeats with period less than or equal to 12 were kept).

For a given package, all the sequences will always have the same number of masks.

```r
> library(BSgenome.Hsapiens.UCSC.hg38.masked)
> genome <- BSgenome.Hsapiens.UCSC.hg38.masked
> chrY <- genome$chrY
> chrY

57227415-letter "MaskedDNAString" instance (# for masking)

seq: ####################################...####################################
masks:

maskedwidth  maskedratio  active  names        desc
1  30812367 5.384197e-01  TRUE  AGAPS      assembly gaps
2   5 8.737071e-08  TRUE  AMB      intra-contig ambiguities
3  16525661 2.887718e-01 FALSE  RM       RepeatMasker
4   872171 1.524044e-02 FALSE  TRF      Tandem Repeats Finder [period<=12]

all masks together:

maskedwidth  maskedratio
47464316 0.8293982

all active masks together:

maskedwidth  maskedratio
30812372 0.5384198

> chrM <- genome$chrM
> chrM

16569-letter "MaskedDNAString" instance (# for masking)

seq: GATCAGCATCCTATCATCACCACTCTAGAAGACATCAGATG...AGCCACACGTCTCTCTTCATTAATAAAGACATCAGATG
masks:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
<th>active</th>
<th>names</th>
<th>desc</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>TRUE</td>
<td>AGAPS</td>
<td>assembly gaps (empty)</td>
</tr>
<tr>
<td>1 6.035367e-05</td>
<td>TRUE</td>
<td>AMB</td>
<td>intra-contig ambiguities</td>
<td></td>
</tr>
<tr>
<td>418 2.522784e-02</td>
<td>FALSE</td>
<td>RM</td>
<td>RepeatMasker</td>
<td></td>
</tr>
<tr>
<td>0 0.000000e+00</td>
<td>FALSE</td>
<td>TRF</td>
<td>Tandem Repeats Finder [period&lt;=12]</td>
<td></td>
</tr>
</tbody>
</table>

all masks together:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>419 0.02528819</td>
<td></td>
</tr>
</tbody>
</table>

all active masks together:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 6.035367e-05</td>
<td></td>
</tr>
</tbody>
</table>

The built-in masks are named consistently across all the BSgenome data packages available in Bioconductor:

<table>
<thead>
<tr>
<th>Name</th>
<th>Active by default</th>
<th>Short description</th>
<th>Long description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGAPS</td>
<td>yes</td>
<td>assembly gaps</td>
<td>Masks the big N-blocks that have been placed between the contigs.</td>
</tr>
<tr>
<td>AMB</td>
<td>yes</td>
<td>intra-contig ambiguities</td>
<td>Masks any IUPAC ambiguity letter that was found in the contig regions.</td>
</tr>
<tr>
<td>RM</td>
<td>no</td>
<td>RepeatMasker</td>
<td>Masks the repeat regions determined by the RepeatMasker software.</td>
</tr>
<tr>
<td>TRF</td>
<td>no</td>
<td>Tandem Repeats Finder</td>
<td>Masks the tandem repeat regions that were determined by the TRF software.</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Name</th>
<th>Active by default</th>
<th>Short description</th>
<th>Long description</th>
</tr>
</thead>
<tbody>
<tr>
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<td>assembly gaps</td>
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</tr>
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<td>AMB</td>
<td>yes</td>
<td>intra-contig ambiguities</td>
<td>Masks any IUPAC ambiguity letter that was found in the contig regions.</td>
</tr>
<tr>
<td>RM</td>
<td>no</td>
<td>RepeatMasker</td>
<td>Masks the repeat regions determined by the RepeatMasker software.</td>
</tr>
<tr>
<td>TRF</td>
<td>no</td>
<td>Tandem Repeats Finder</td>
<td>Masks the tandem repeat regions that were determined by the TRF software.</td>
</tr>
</tbody>
</table>

Table 1: The built-in masks provided by the BSgenome data packages.

When displaying a masked sequence (here a MaskedDNAString object), the masked width and masked ratio are reported for each individual mask, as well as for all the masks together, and for all the active masks together. The masked width is the total number of nucleotide positions that are masked and the masked ratio is the masked width divided by the length of the sequence.

To activate a mask, use the active replacement method in conjunction with the masks method. For example, to activate the RepeatMasker mask, do:

```r
> active(masks(chrY))[^"RM"^] <- TRUE
> chrY
```

57227415-letter "MaskedDNAString" instance (# for masking)

seq: #---------------------------------...#---------------------------------

masks:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
<th>active</th>
<th>names</th>
<th>desc</th>
</tr>
</thead>
<tbody>
<tr>
<td>30812367</td>
<td>5.384197e-01</td>
<td>TRUE</td>
<td>AGAPS</td>
<td>assembly gaps</td>
</tr>
<tr>
<td>5 8.737071e-08</td>
<td>TRUE</td>
<td>AMB</td>
<td>intra-contig ambiguities</td>
<td></td>
</tr>
<tr>
<td>16525661 2.887718e-01</td>
<td>TRUE</td>
<td>RM</td>
<td>RepeatMasker</td>
<td></td>
</tr>
<tr>
<td>872171 1.524044e-02</td>
<td>FALSE</td>
<td>TRF</td>
<td>Tandem Repeats Finder [period&lt;=12]</td>
<td></td>
</tr>
</tbody>
</table>

all masks together:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>47464316 0.8293982</td>
<td></td>
</tr>
</tbody>
</table>

all active masks together:

<table>
<thead>
<tr>
<th>maskedwidth</th>
<th>maskedratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>47337931 0.8271897</td>
<td></td>
</tr>
</tbody>
</table>

As you can see, the masked width for all the active masks together (i.e. the total number of nucleotide positions that are masked by at least one active mask) is now the same as for the first mask. This represents a masked ratio of about 83%.
Now when we use a function that is *mask aware*, like `alphabetFrequency`, the masked regions of the input sequence are ignored:

```r
> active(masks(chrY)) <- FALSE
> active(masks(chrY))['AGAPS'] <- TRUE
> alphabetFrequency(unmasked(chrY))
```

```
  A  C  G  T  M  R  W  S
7886192 5285789 5286894 7956168 0  0  0  0
   Y   K   V   H   D   B   N -
  0  0  0  0  0  0  30812372 0
   +  .
  0  0
```

```r
> alphabetFrequency(chrY)
```

```
  A  C  G  T  M  R  W  S   Y   K
7886192 5285789 5286894 7956168 0  0  0  0  0  0
   V   H   D   B   N   +  .
  0  0  0  5  0  0  0
```

This output indicates that, for this chromosome, the assembly gaps correspond exactly to the regions in the sequence that were filled with the letter N. Note that this is not always the case: sometimes Ns, and other IUPAC ambiguity letters, can be found inside the contigs.

When coercing a `MaskedXString` object to an `XStringViews` object, each non-masked region in the original sequence is converted into a view on the sequence:

```r
> as(chrY, "XStringViews")
```

```
Views on a 57227415-letter DNAString subject:
subject: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN...NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
views:
            start   end   width
[1] 10001  44821  34821 [CTAACCCTAAACCTAAACCTAA...TAGGTCTCATTGAGGACAGATA]
[2] 94822 133871  39050 [CCCTTCTGTGTCAGGGGCGGAGG...GGCTAATGGCAGACTCTAAAGG]
[3] 222347 226276  3930  [ACCCTTCTCTCTCTCTCTCTCTCT...GCTCCTTCCCTCCGTGGCGCATCC]
[4] 226352 1722994 1722994 [CCCGCTCCTCCCCCTCGGGGACCA...AGTCATAACAAACACAGATCG]
[5] 2132995 2137388  4394  [TGTCTGTGATGTATATATATATAT...ACCTCTCCCATCATCATCATCA]
[51] 21748372 21750013  1642 [GAAGTAAGCATCTCTGTATTAG...CTCCAGGCAAGGGAAGGGA]
[52] 21750315 21789281  38967 [CTGTACTTATCGTCTCTGTTG...AGGCGCCAAATCTCGACAGAT]
[53] 21805282 26673214 4867933 [AGAGTTTGCTATATATATCTCTCT...GAGGTGTCAGAGGTGAGATTC]
[54] 56673215 56771509  98295 [GATCTCCATTGAAATGGAGGGA...GGATTGAATGGAAATGGAAAT]
[55] 56821510 57217415 395906 [GAATTCAACATTATCTCTGTT...GGGTTGTTGTTGGTGTTGTT]
```

This can be used in conjunction with the `gaps` method to see the gaps between the views i.e. the masked regions themselves:

```r
> gaps(as(chrY, "XStringViews"))
```

To extract the sizes of the assembly gaps:

```r
> width(gaps(as(chrY, "XStringViews")))
```
Note that, if applied directly to chrY, `gaps` returns a `MaskedDNAString` object with a single mask masking the regions that are not masked in the original object:

```r
> gaps(chrY)
57227415-letter "MaskedDNAString" instance (# for masking)
seq: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN...NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
masks:
   maskedwidth maskedratio active
1    26415048  0.4615803 TRUE
```

In fact, for any `MaskedDNAString` object, the following should always be `TRUE`, whatever the masks are:

```r
> af0 <- alphabetFrequency(unmasked(chrY))
> af1 <- alphabetFrequency(chrY)
> af2 <- alphabetFrequency(gaps(chrY))
> all(af0 == af1 + af2)
[1] TRUE
```

With all chrY masks active:

```r
> active(masks(chrY)) <- TRUE
> af1 <- alphabetFrequency(chrY)
> af1

A   C   G   T   M   R   W   S   Y   K
2994088 1876822 1889305 3002884 0  0  0  0  0  0
V   H   D   B   N   -   +   .
   0  0  0  0  0  0    0   0

> gaps(chrY)
57227415-letter "MaskedDNAString" instance (# for masking)
seq: NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN...NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN
masks:
   maskedwidth maskedratio active
1     9763099  0.1706018 TRUE
```
> af2 <- alphabetFrequency(gaps(chrY))
> af2

<table>
<thead>
<tr>
<th>A</th>
<th>C</th>
<th>G</th>
<th>T</th>
<th>M</th>
<th>R</th>
<th>W</th>
<th>S</th>
</tr>
</thead>
<tbody>
<tr>
<td>4892104</td>
<td>3408967</td>
<td>3397589</td>
<td>4953284</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Y</td>
<td>K</td>
<td>V</td>
<td>H</td>
<td>D</td>
<td>B</td>
<td>N</td>
<td>-</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>30812372</td>
</tr>
<tr>
<td>+</td>
<td>.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

> all(af0 == af1 + af2)
[1] TRUE

Now let’s compare three different ways of finding all the occurrences of the "CANNTG" consensus sequence in chrY. The Ns in this pattern need to be treated as wildcards i.e. they must match any letter in the subject.

Without the mask feature, the first way to do it would be to use the fixed=FALSE option in the call to matchPattern (or countPattern):

> Ebox <- "CANNTG"
> active(masks(chrY)) <- FALSE
> countPattern(Ebox, chrY, fixed=FALSE)

[1] 30953762

The problem with this method is that the Ns in the subject are also treated as wildcards hence the abnormally high number of matches. A better method is to specify the side of the matching problem (i.e. pattern or subject) where the Ns should be treated as wildcards:

> countPattern(Ebox, chrY, fixed=c(pattern=FALSE,subject=TRUE))

[1] 141609

Finally, countPattern being mask aware, this can be achieved more efficiently by just masking the assembly gaps and ambiguities:

> active(masks(chrY))[c("AGAPS", "AMB")]<- TRUE
> alphabetFrequency(chrY, baseOnly=TRUE) # no ambiguities

<table>
<thead>
<tr>
<th>A</th>
<th>C</th>
<th>G</th>
<th>T</th>
<th>other</th>
</tr>
</thead>
<tbody>
<tr>
<td>7886192</td>
<td>5285789</td>
<td>5286894</td>
<td>7956168</td>
<td>0</td>
</tr>
</tbody>
</table>

> countPattern(Ebox, chrY, fixed=FALSE)

[1] 141609

Note that some chromosomes can have Ns outside the assembly gaps:

> chr2 <- genome$chr2
> active(masks(chr2))[-2]<- FALSE
> alphabetFrequency(gaps(chr2))

<table>
<thead>
<tr>
<th>A</th>
<th>C</th>
<th>G</th>
<th>T</th>
<th>M</th>
<th>R</th>
<th>W</th>
<th>S</th>
<th>Y</th>
<th>K</th>
<th>V</th>
<th>H</th>
<th>D</th>
<th>B</th>
<th>N</th>
<th>-</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2913</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>+</td>
<td>.</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
so it is recommended to always keep the AMB mask active (in addition to the AGAPS mask) whatever the sequence is.

Note that not all functions that work with an XString input are mask aware but more will be added in the near future. However, most of the times there is an alternate way to exclude some arbitrary regions from an analysis without having to use mask aware functions. This is described below in the Hard masking section.

6 Hard masking

coming soon...

7 Injecting known SNPs in the chromosome sequences

coming soon...

8 Finding all the patterns of a constant width dictionary in an entire genome

The `matchPDict` function can be used instead of `matchPattern` for the kind of analysis described in the Finding an arbitrary nucleotide pattern in an entire genome section but it will be much faster (between 100x and 10000x faster depending on the size of the input dictionary). Note that a current limitation of `matchPDict` is that it only works with a dictionary of DNA patterns where all the patterns have the same number of nucleotides (constant width dictionary). See `?matchPDict` for more information.

Here is how our `runAnalysis1` function can be modified in order to use `matchPDict` instead of `matchPattern`:

```r
> runOneStrandAnalysis <- function(dict0, bsgenome, seqnames, strand, outfile="", append=FALSE) {
+ cat("\nTarget: strand", strand, " of", providerVersion(bsgenome), " chromosomes", paste(seqnames, collapse="", ", "), 
+ if (strand == "-" 관서
+ dict0 <- reverseComplement(dict0)
+ pdict <- PDict(dict0)
+ for (seqname in seqnames) {
+ subject <- bsgenome[[seqname]]
+ cat(">>> Finding all hits in strand", strand, " of chromosome", seqname, "...
")
+ mindex <- matchPDict(pdict, subject)
+ matches <- extractAllMatches(subject, mindex)
+ writeHits(seqname, matches, strand, file=outfile, append=append)
+ append <- TRUE
+ cat(">>> DONE"
+ }
+ }
> runAnalysis2 <- function(dict0, outfile="") {
+ library(BSgenome.Celegans.UCSC.ce2)
+ genome <- BSgenome.Celegans.UCSC.ce2
+ seqnames <- seqnames(genome)
```

15
+ runOneStrandAnalysis(dict0, genome, seqnames, "+", outfile=outfile, append=FALSE)
+ runOneStrandAnalysis(dict0, genome, seqnames, "-", outfile=outfile, append=TRUE)
+
Remember that matchPDict only works if all the patterns in the input dictionary have the same length so for this 2nd analysis, we will truncate the patterns in ce2dict0 to 15 nucleotides:

```r
> ce2dict0cw15 <- DNAStringSet(ce2dict0, end=15)
```

Now we can run this 2nd analysis and put the results in the "ce2dict0cw15_ana2.txt" file:

```r
> runAnalysis2(ce2dict0cw15, outfile="ce2dict0cw15_ana2.txt")
```

Target: strand + of ce2 chromosomes chrI, chrII, chrIII, chrIV, chrV, chrX, chrM

```r
>>> Finding all hits in strand + of chromosome chrI ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrII ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrIII ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrIV ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrV ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrX ...
>>> DONE
>>> Finding all hits in strand + of chromosome chrM ...
>>> DONE
```

Target: strand - of ce2 chromosomes chrI, chrII, chrIII, chrIV, chrV, chrX, chrM

```r
>>> Finding all hits in strand - of chromosome chrI ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrII ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrIII ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrIV ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrV ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrX ...
>>> DONE
>>> Finding all hits in strand - of chromosome chrM ...
>>> DONE
```

9 Session info

```r
> sessionInfo()
```

R version 3.4.1 (2017-06-30)
Platform: x86_64-pc-linux-gnu (64-bit)
Running under: Ubuntu 16.04.3 LTS