

Working with DNA strings and ranges

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Introduction

Genomic Intervals with Data

Coverage and Other Piecewise Constant Measures

Long Biological Strings

Developer's Notes

Resources

Outline

Introduction

Genomic Intervals with Data

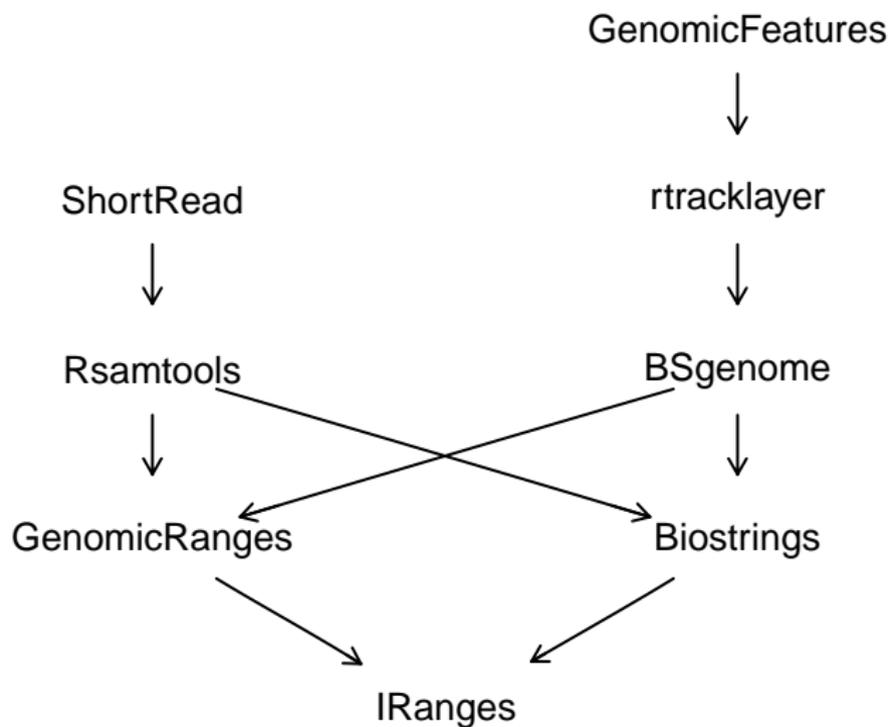
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Bioconductor Sequence Packages



Bioconductor Sequence Infrastructure Packages

IRanges

- ▶ Long sequences (compressed & pointer referenced)
- ▶ Views on long sequences
- ▶ Integer interval tools (e.g. interval overlap)

GenomicRanges

- ▶ Genomic intervals (*GRanges*)
- ▶ Discontiguous genomic interval sets (*GRangesList*)

Biostrings

- ▶ Long DNA/RNA/amino acids sequences
- ▶ Sequence & PWM matching and pairwise alignment tools

Bioconductor Sequence Infrastructure Classes

Long piecewise constant sequences

Rle, *RleList*

Ranges (as sequences & intervals)

IRanges

Genomic intervals with data

GRanges

Genomic interval sets (e.g. spliced transcripts)

GRangesList

Long DNA sequences

DNASTring, *DNASTringSet*, ...

Views on long sequences

RleViews, *RleListViews*, *XStringViews*, ...

Concept I: Run-Length Encoding (RLE)

Issue

- ▶ Chromosomes can be hundreds of million of base pairs long, making them hard to manage in computer memory.
- ▶ Fortunately, coverage vectors tend to follow an integer step function.

Solution

- ▶ Run-length encoding (RLE) is a common compression technique for storing long sequences with lengthy repeats.
- ▶ An RLE couples values with run lengths, e.g. the vector 0, 0, 0, 1, 1, 2 would be represented as (3) 0's, (2) 1's, and (1) 2.
- ▶ The *IRanges* package uses the *Rle* and *RleList* classes to house coverage vectors.

Concept II: Sequence Views

Issue

- ▶ Chromosomes can be hundreds of million of base pairs long, making subsequence selection inefficient.

Solution

- ▶ Store the original sequence using a pass-by-reference semantic.
- ▶ Associate ranges with the sequence to select subsequence.
- ▶ Example:
 - ▶ 7007-letter sequence: <<SNIP-3000>>AGATTCA<<SNIP-4000>>
 - ▶ View range: [3001, 3007]
 - ▶ => 7-letter subsequence: AGATTCA

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Introduction

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Developer's Notes

Resources

Naive representation for intervals with data

Data characteristics

- ▶ Genomic coordinates consist of chromosome, position, and potentially strand information
- ▶ May have additional values, such as GC content or alignment coverage

data.frame approach

```
> chr <- c("chr1", "chr2", "chr1")
> strand <- c("+", "+", "-")
> start <- c(3L, 4L, 1L)
> end <- c(7L, 5L, 3L)
> naive <- data.frame(chr = chr, strand = strand,
+                     start = start, end = end)
```

Genomic intervals with data

GRanges

- ▶ Used by *GenomicFeatures*, a transcript annotation generator
- ▶ Intervals not required to be grouped by chromosome/contig
- ▶ Methods strand aware
- ▶ *GRangesList* class can hold exons within spliced transcripts

GRanges construction

GRanges constructor

- ▶ Instances are created using the `GRanges` constructor.
- ▶ Starts and ends are wrapped in an `IRanges` constructor.
- ▶ Chromosome/contig supplied to `seqnames` argument.
- ▶ Underlying sequence lengths can be supplied to `seqlengths` argument.

GRanges example

```
> bioc <- GRanges(seqnames = chr,  
+                 ranges = IRanges(start = start, end = end),  
+                 strand = strand,  
+                 seqlengths = c("chr1" = 24, "chr2" = 18))
```

GRanges display

GRanges show method

```
> bioc
```

```
GRanges with 3 ranges and 0 elementMetadata values
```

	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
[1]	chr1	[3, 7]	+	
[2]	chr2	[4, 5]	+	
[3]	chr1	[1, 3]	-	

```
seqlengths  
chr1 chr2  
24 18
```

Note

- ▶ Optional interval data would appear to the right of | divider.

GRanges class decomposition

GRanges slots

```
> getSlots("GRanges")
```

seqnames	ranges	strand	seqinfo
"Rle"	"IRanges"	"Rle"	"Seqinfo"
elementMetadata	elementType	metadata	
"ANY"	"character"	"list"	

Notes

- ▶ If (mostly) sorted, *Rle* vectors reduce memory usage and provide faster group selection
- ▶ `elementMetadata` holds optional interval data
- ▶ `metadata` holds optional whole object info

Interval operations

Intra-interval

flank, resize, shift

Inter-interval I

disjoin, gaps, reduce, range

Inter-interval II

coverage

Between two interval sets I

union, intersect, setdiff

Between two interval sets II

punion, pintersect, psetdiff

Between two interval sets III

findOverlaps, countOverlaps, %in%, match

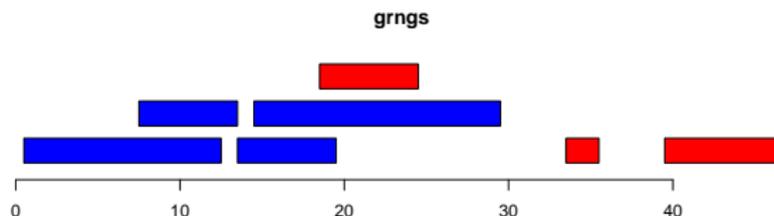
Low level

start, end, width

Creating a new *GRanges* object

New object to use in interval operations

```
> ir <- IRanges(c(1, 8, 14, 15, 19, 34, 40),  
+             width=c(12, 6, 6, 15, 6, 2, 7))  
> strand <- rep(c("+", "-"), c(4,3))  
> grngs <- GRanges(seqnames = "chr1", ranges = ir,  
+                 strand = strand,  
+                 seqlengths = c("chr1" = 50))
```



blue = positive strand, red = negative strand

GRanges subsetting

seqselect

```
> seqselect(grngs, strand(grngs) == "-")
```

GRanges with 3 ranges and 0 elementMetadata values

	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
[1]	chr1	[19, 24]	-	
[2]	chr1	[34, 35]	-	
[3]	chr1	[40, 46]	-	

```
seqlengths
```

```
chr1  
50
```

Other functions

[, head, tail, window, subset, subsetByOverlaps

Intra-interval (1/2)

Shifting intervals

If your interval bounds are off by 1, you can shift them.

```
> shift(grngs, 1)
```

GRanges with 7 ranges and 0 elementMetadata values

	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
[1]	chr1	[2, 13]	+	
[2]	chr1	[9, 14]	+	
[3]	chr1	[15, 20]	+	
[4]	chr1	[16, 30]	+	
[5]	chr1	[20, 25]	-	
[6]	chr1	[35, 36]	-	
[7]	chr1	[41, 47]	-	

```
seqlengths
```

```
chr1
```

```
50
```

Intra-interval (2/2)

Resizing intervals

“Growing” alignment intervals to an estimated fragment length.

```
> resize(grngs, 10)
```

```
GRanges with 7 ranges and 0 elementMetadata values
```

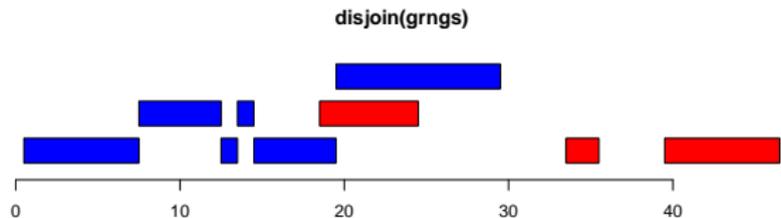
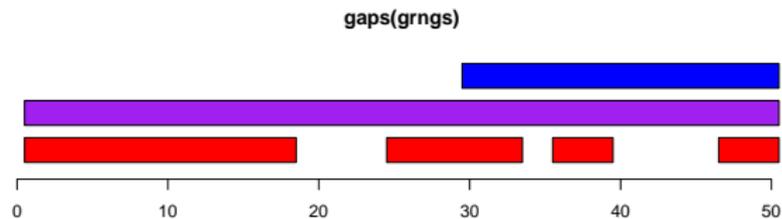
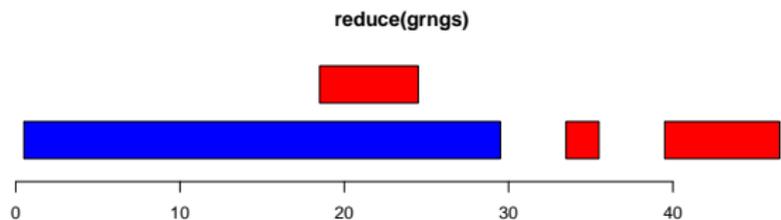
	seqnames	ranges	strand	
	<Rle>	<IRanges>	<Rle>	
[1]	chr1	[1, 10]	+	
[2]	chr1	[8, 17]	+	
[3]	chr1	[14, 23]	+	
[4]	chr1	[15, 24]	+	
[5]	chr1	[15, 24]	-	
[6]	chr1	[26, 35]	-	
[7]	chr1	[37, 46]	-	

```
seqlengths
```

```
chr1
```

```
50
```

Inter-interval I



Overlap detection

Finding interval overlaps

`findOverlaps` and `countOverlaps` produce a mapping and a tabulation of interval overlaps, respectively

```
> ol <- findOverlaps(grngs, reduce(grngs))  
> as.matrix(ol)
```

	query	subject
[1,]	1	1
[2,]	2	1
[3,]	3	1
[4,]	4	1
[5,]	5	2
[6,]	6	3
[7,]	7	4

```
> countOverlaps(reduce(grngs), grngs)
```

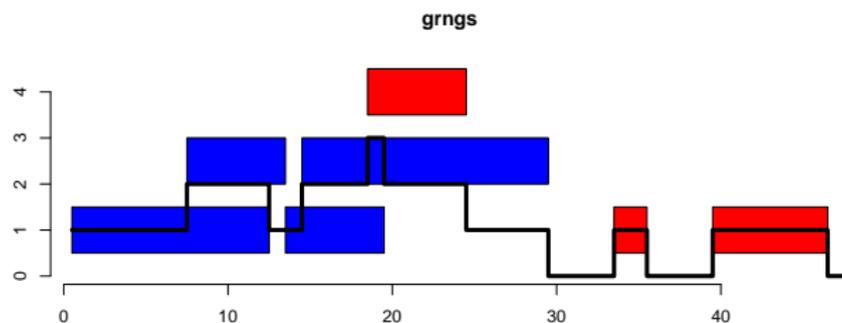
```
[1] 4 1 1 1
```

Elementwise counts of overlapping intervals

Coverage

- ▶ coverage counts number of ranges over each position
- ▶ Subset by strand to get stranded coverage

```
> cover <- coverage(grngs)
```



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Piecewise constant measures

Issue restated

- ▶ The number of genomic positions in a genome is often in the billions for higher organisms, making it challenging to represent in memory.
- ▶ Some data across a genome tend to be sparse (i.e. large stretches of “no information”)

Rle and *RleList* classes

- ▶ Solve the set of problems for positional measures that tend to have consecutively repeating values.
- ▶ *Do not* address the more general problem of positional measures that constantly fluxuate, such as conservation scores.

Numerous *R*/*e* methods (1/2)

[1] "!"	"["	"[<-"	"%in%"
[5] "aggregate"	"as.character"	"as.complex"	"as.data.frame"
[9] "as.factor"	"as.integer"	"as.logical"	"as.numeric"
[13] "as.raw"	"as.vector"	"c"	"chartr"
[17] "coerce"	"Complex"	"cor"	"cov"
[21] "diff"	"end"	"findRange"	"findRun"
[25] "gsub"	"IQR"	"is.na"	"is.unsorted"
[29] "length"	"levels"	"levels<-"	"mad"
[33] "match"	"Math"	"Math2"	"mean"
[37] "median"	"nchar"	"nrun"	"Ops"
[41] "paste"	"pmax"	"pmax.int"	"pmin"
[45] "pmin.int"	"quantile"	"rep"	"rep.int"
[49] "rev"	"runLength"	"runLength<-"	"runmean"
[53] "runmed"	"runq"	"runsum"	"runValue"
[57] "runValue<-"	"runwsum"	"sd"	"seqselect"
[61] "seqselect<-"	"shiftApply"	"show"	"slice"
[65] "smoothEnds"	"sort"	"split"	"splitRanges"
[69] "start"	"sub"	"substr"	"substring"
[73] "summary"	"Summary"	"table"	"tolower"
[77] "toupper"	"unique"	"var"	"Views"
[81] "which"	"width"	"window"	

Numerous R/e methods (2/2)

Arith

+, -, *, ^, %%, %/%, /

Compare

==, >, <, !=, <=, >=

Logic

&, |

Math

abs, sign, sqrt, ceiling, floor, trunc, cummax, cummin, cumprod, cumsum, log, log10, log2, log1p, acos, acosh, asin, asinh, ...

Math2

round, signif

Summary

max, min, range, prod, sum, any, all

Complex

Arg, Conj, Im, Mod, Re

Coverage example

Coverage from a *Saccharomyces cerevisiae* (Yeast) RNA-seq experiment contained in two objects `SRR002051.pluscvg` & `SRR002051.minuscvg`

```
> c(class(SRR002051.pluscvg), class(SRR002051.minuscvg))
[1] "SimpleRleList" "SimpleRleList"
> SRR002051.pluscvg[["chrI"]]
'integer' Rle of length 230208 with 10746 runs
  Lengths: 1061  33 271  33 2937 ...  33 237  33 679
  Values :   0   1   0   1   0 ...   2   0   1   0
> SRR002051.minuscvg[["chrI"]]
'integer' Rle of length 230208 with 10966 runs
  Lengths:  10  33 1070  33 4050 ...  29 104  33 808
  Values :   0   1   0   1   0 ...   2   0   1   0
> SRR002051.pluscvg[["chrI"]] + SRR002051.minuscvg[["chrI"]]
'integer' Rle of length 230208 with 18155 runs
  Lengths:  10  33 1018  33  19 ...  33  96  33 679
  Values :   0   1   0   1   0 ...   1   0   1   0
```

Plotting coverage

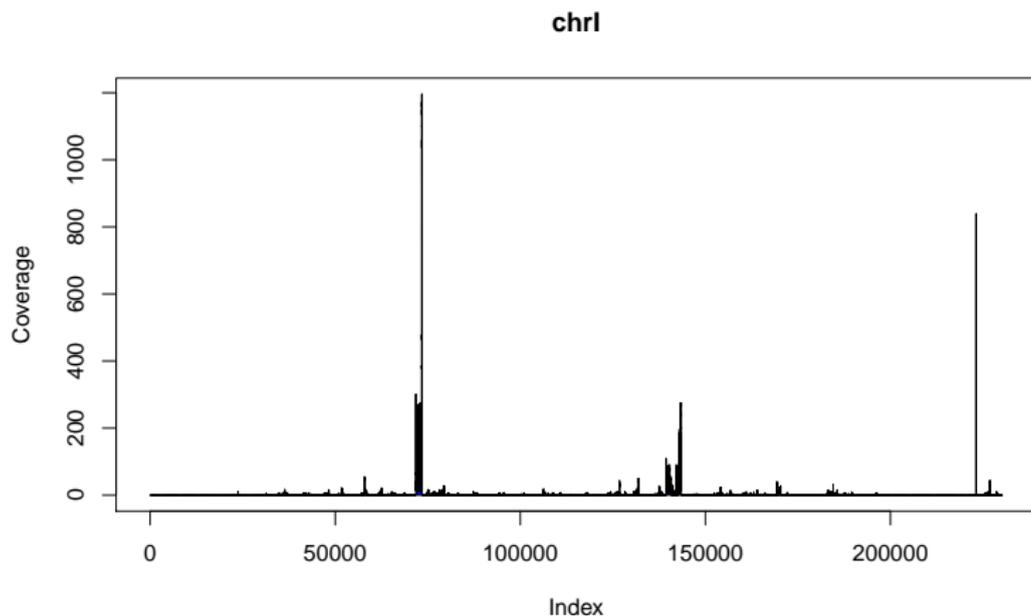
Custom function

```
> plotCoverage <-  
+ function(x, chrom, start=1, end=length(x[[chrom]]), col="blue",  
+         xlab="Index", ylab="Coverage", main=chrom)  
+ {  
+   xWindow <- as.vector(window(x[[chrom]], start, end))  
+   x <- start:end  
+   xlim <- c(start, end)  
+   ylim <- c(0, max(xWindow))  
+   plot(x = start, y = 0, xlim = xlim, ylim = ylim,  
+        xlab = xlab, ylab = ylab, main = main, type = "n")  
+   polygon(c(start, x, end), c(0, xWindow, 0), col = col)  
+ }
```

Plotting coverage on one strand

Plotting chr1+ coverage

```
> plotCoverage(SRR002051.pluscvg, "chr1")
```



Plotting stranded coverage

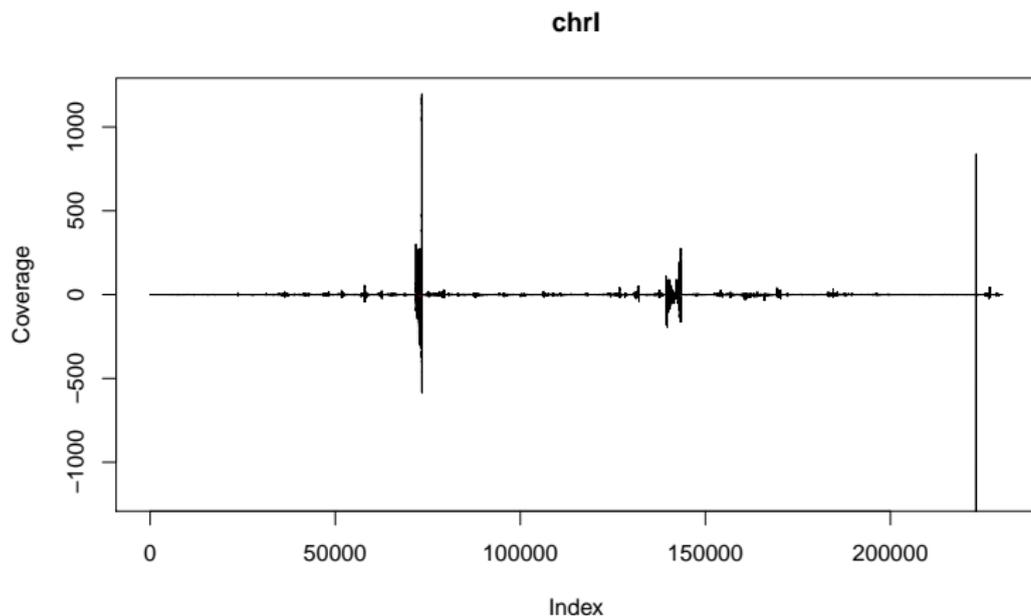
Custom function

```
> plotCoverageStrands <-  
+ function(pos, neg, chrom, start=1,  
+         end=max(length(pos[[chrom]]), length(neg[[chrom]])),  
+         pos.col="blue", neg.col="red", xlab="Index",  
+         ylab="Coverage", main=chrom)  
+ {  
+   pos1 <- pos[[chrom]]  
+   neg1 <- neg[[chrom]]  
+   if (length(pos1) < end)  
+     pos1 <- c(pos1, Rle(0L, end - length(pos1)))  
+   if (length(neg1) < end)  
+     neg1 <- c(neg1, Rle(0L, end - length(neg1)))  
+   posWindow <- as.vector(window(pos1, start, end))  
+   negWindow <- as.vector(window(neg1, start, end))  
+   x <- start:end  
+   xlim <- c(start, end)  
+   ylim <- c(-1, 1) * min(max(posWindow), max(negWindow))  
+   plot(x = start, y = 0, xlim = xlim, ylim = ylim,  
+       xlab = xlab, ylab = ylab, main = main, type = "n")  
+   polygon(c(start, x, end), c(0, posWindow, 0), col = pos.col)  
+   polygon(c(start, x, end), c(0, -negWindow, 0), col = neg.col)  
+ }
```

Plotting coverage on both strands

Plotting chr1 coverage, both strands

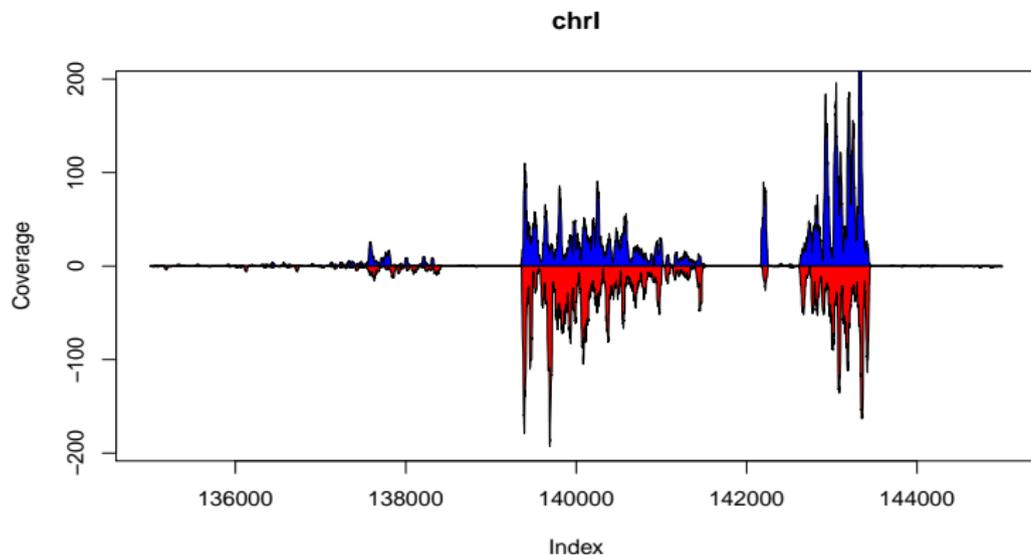
```
> plotCoverageStrands(SRR002051.pluscvg, SRR002051.minuscvg, "chr1")
```



Plotting Coverage on both strands

Plotting chr1 coverage, both strands

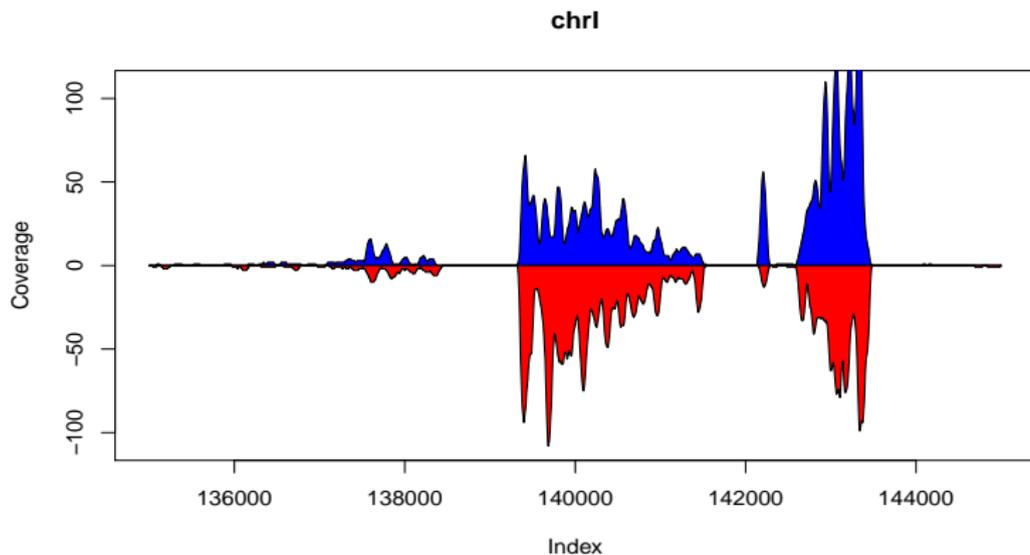
```
> plotCoverageStrands(SRR002051.pluscvg, SRR002051.minuscvg, "chr1", 135000, 145000)
```



Smoothing coverage

Running window mean

```
> posSmoothCover <- round(runmean(SRR002051.pluscvg, 75, endrule = "constant"))  
> negSmoothCover <- round(runmean(SRR002051.minuscvg, 75, endrule = "constant"))  
> plotCoverageStrands(posSmoothCover, negSmoothCover, "chrI", 135000, 145000)
```



Combining coverage

Combining coverage using "parallel" minimums

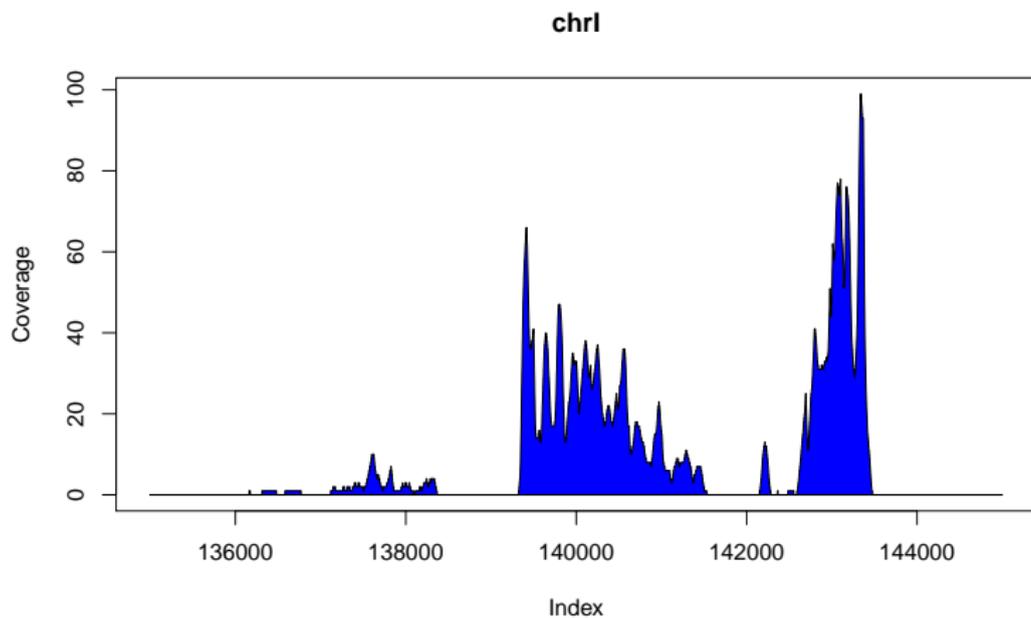
```
> combSmoothCover <- mendoapply(pmin,  
+                               posSmoothCover,  
+                               negSmoothCover)  
> identical(class(posSmoothCover), class(combSmoothCover))  
[1] TRUE
```

- ▶ The `mendoapply` function defined in *IRanges* packages as a member of the `apply` family.
 - ▶ Performs elementwise operations across multiple inputs of the same type.
 - ▶ Returns an object of the same type as the inputs.
- ▶ The minimum coverage value on either strand can be computed using `pmin`.

Plotting combined coverage

Plotting chr1, combined strands

```
> plotCoverage(combSmoothCover, "chr1", 135000, 145000)
```



Island selection

```
> islands <- slice(combsmoothCover, lower=1)
> islandsWithWidePeaks <- islands[viewMaxs(islands) >= 8L &
+                               width(islands) >= 500L]
> islandsWithWidePeaks
```

SimpleRleViewsList of length 18

\$chrI

Views on a 230208-length Rle subject

views:

	start	end	width	
[1]	35842	36437	596	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[2]	51702	52348	647	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 2 2 2 ...]
[3]	57739	58468	730	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[4]	71710	73489	1780	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[5]	78565	79577	1013	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[6]	125982	126891	910	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[7]	131073	132113	1041	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[8]	137117	138090	974	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[9]	139324	141532	2209	[1 1 1 1 1 1 2 2 2 2 3 ...]
[10]	142591	143476	886	[1 1 1 1 1 1 1 1 1 2 2 2 2 2 2 3 3 ...]
[11]	169320	170437	1118	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]
[12]	225804	226924	1121	[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 ...]

...

<17 more elements>

Common methods for *Views* objects

- ▶ Subset via `[]`, `[[[]]`, etc.
- ▶ Manage edge cases via `trim` & `restrict`
- ▶ *Ranges* operations such as `start`, `end`, `width`, etc.
- ▶ Perform within view calculations via `viewSums`, `viewMins`, `viewMaxs`, `viewWhichMins`, `viewWhichMaxs`, `viewApply`

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Developer's Notes

Resources

Long biological string framework

Biostrings string types

```
> library(Biostrings)
> names(completeSubclasses(getClass("XString")))

[1] "BString" "DNAStrng" "RNAStrng" "AAString"
```

DNA

```
> data(yeastSEQCHR1)
> c(class(yeastSEQCHR1), nchar(yeastSEQCHR1))

[1] "character" "230208"

> yeast1 <- DNAStrng(yeastSEQCHR1)
> yeast1

230208-letter "DNAStrng" instance
seq: CCACACCACCCACACACCCACACACC...GGTGTGGTGTGGGTGTGGTGTGTGGG

> IUPAC_CODE_MAP

  A      C      G      T      M      R      W      S      Y
"A"   "C"   "G"   "T"   "AC"  "AG"  "AT"  "CG"  "CT"
  K      V      H      D      B      N
"GT"  "ACG"  "ACT"  "AGT"  "CGT"  "ACGT"
```

List of strings

Biostrings string list types

```
> head(names(completeSubclasses(getClass("XStringSet"))), 4)
[1] "BStringSet" "DNAStringSet" "RNAStringSet" "AAStringSet"
```

DNA strings

```
> data(srPhiX174)
> length(srPhiX174)
[1] 1113
> head(srPhiX174, 3)
  A DNAStringSet instance of length 3
  width seq
[1] 35 GTTATTATACCGTCAAGGACTGTGTGACTATTGAC
[2] 35 GGTGGTTATTATACCGTCAAGGACTGTGTGACTAT
[3] 35 TACCGTCAAGGACTGTGTGACTATTGACGTCCTC
```

XString class decomposition

XString slots

```
> getSlots("XString")
```

shared	offset	length	elementMetadata
"SharedRaw"	"integer"	"integer"	"ANY"
elementType	metadata		
"character"	"list"		

```
> getSlots("XStringSet")
```

pool	ranges	elementMetadata
"SharedRaw_Pool"	"GroupedIRanges"	"ANY"
elementType	metadata	
"character"	"list"	

Notes

- ▶ shared, offset, length, pool, and ranges slots regulate pass-by-reference semantic.
- ▶ metadata slot can be used to hold annotation information.

Basic string utilities

Subsequence selection

`subseq`, `Views`

Letter frequencies

`alphabetFrequency`, `dinucleotideFrequency`, `trinucleotideFrequency`,
`oligonucleotideFrequency`, `letterFrequencyInSlidingView`, `uniqueLetters`

Letter consensus

`consensusMatrix`, `consensusString`

Letter transformation

`reverse`, `complement`, `reverseComplement`, `translate`, `chartr`

I/O

`read.DNAStringSet`, `read.RNAStringSet`, `read.AAStringSet`, `read.BStringSet`,
`write.XStringSet`, `save.XStringSet`

String matching/alignment utilities

matchPDict

matchPDict, countPDict, whichPDict, vmatchPDict, vcountPDict, vwhichPDict

vmatchPattern

matchPattern, countPattern, vmatchPattern, vcountPattern, neditStartingAt,
neditEndingAt, isMatchingStartingAt, isMatchingEndingAt,
which.isMatchingStartingAt, which.isMatchingEndingAt

pairwiseAlignment

pairwiseAlignment, stringDist

matchPWM

matchPWM, countPWM

OTHER

matchLRPatterns, trimLRPatterns, matchProbePair, findPalindromes,
findComplementedPalindromes

Letter frequencies

Single-letter frequencies

```
> alphabetFrequency(yeast1, baseOnly=TRUE)
```

A	C	G	T	other
69830	44643	45765	69970	0

Multi-letter frequencies

```
> dinucleotideFrequency(yeast1)
```

AA	AC	AG	AT	CA	CC	CG	CT	GA	GC
23947	12493	13621	19769	15224	9218	7089	13112	14478	8910
GG	GT	TA	TC	TG	TT				
9438	12938	16181	14021	15617	24151				

```
> head(trinucleotideFrequency(yeast1), 12)
```

AAA	AAC	AAG	AAT	ACA	ACC	ACG	ACT	AGA	AGC	AGG	AGT
8576	4105	4960	6306	3924	2849	2186	3534	4537	2680	2707	3697

Basic transformations

Standard transformations

```
> x
 21-letter "DNAString" instance
seq: TCAACGTTGAATAGCGTACCG
> reverseComplement(x)
 21-letter "DNAString" instance
seq: CGGTACGCTATTCAACGTTGA
> translate(x)
 7-letter "AAString" instance
seq: STLNSVP
```

Bisulfite transformation

```
> library(BSgenome.Celegans.UCSC.ce2)
> alphabetFrequency(Celegans$chrII, baseOnly=TRUE)
  A      C      G      T  other
4878194 2769208 2762193 4869710      3
> chrIIbis <- chartr("C", "T", Celegans$chrII)
> alphabetFrequency(chrIIbis, baseOnly=TRUE)
  A      C      G      T  other
4878194      0 2762193 7638918      3
```

Letter consensus

Consensus matrix

```
> snippet <- subseq(head(sort(srPhiX174), 5), 1, 10)
> consensusMatrix(snippet, baseOnly=TRUE)
```

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
A	5	5	1	0	4	2	1	0	1	0
C	0	0	1	0	0	2	0	0	0	0
G	0	0	3	4	0	0	0	4	0	3
T	0	0	0	1	1	1	4	1	4	2
other	0	0	0	0	0	0	0	0	0	0

Consensus string

```
> consensusString(snippet)
[1] "AAGGAMTGTK"
> consensusString(snippet, ambiguityMap = "N", threshold = 0.5)
[1] "AAGGANTGTG"
```

String matching

Match counting

```
> data(phiX174Phage)
> genome <- phiX174Phage[["NEB03"]]
> negPhiX174 <- reverseComplement(srPhiX174)
> posCounts <- countPDict(PDict(srPhiX174), genome)
> negCounts <- countPDict(PDict(negPhiX174), genome)
> table(posCounts, negCounts)
```

	negCounts
posCounts 0	0
0	1030
1	83

Match locations

```
> matchPDict(PDict(srPhiX174[posCounts > 0]), genome)
```

MIndex object of length 83

Pairwise alignments

Alignment scores

```
> data(phiX174Phage)
> posScore <- pairwiseAlignment(srPhiX174, genome,
+                               type = "global-local", scoreOnly = TRUE)
> negScore <- pairwiseAlignment(negPhiX174, genome,
+                               type = "global-local", scoreOnly = TRUE)
> cutoff <- max(pmin.int(posScore, negScore))
```

Alignments

```
> pairwiseAlignment(srPhiX174[posScore > cutoff], genome,
+                   type = "global-local")
```

```
Global-Local PairwiseAlignedFixedSubject (1 of 1112)
pattern:  [1] GTTATTATACCGTCAAGGACTGTGTGACTATTGAC
subject:  [2750] GTTATTATACCGTCAAGGACTGTGTGACTATTGAC
score: 69.36144
```

Outline

Introduction

Genomic Intervals with Data

Coverage and Other Piecewise Constant Measures

Long Biological Strings

Developer's Notes

Resources

Long compressed sequence classes (*IRanges*)

Rle

- ▶ Compressed atomic vectors
- ▶ Methods for standard *R atomic vector* functions
- ▶ Concrete class with sub-typing at the slot level

CompressedList

- ▶ Compressed list of S4 objects
- ▶ Methods for standard *R list* functions
- ▶ Virtual class with sub-typing at the subclass level

IRanges (as Sequences)

- ▶ `as.integer` coercion
- ▶ Subscripting via `seqselect`, `window`, and `[`

Pointer referenced sequence classes

XVector (IRanges)

- ▶ External pointer-based atomic vectors
- ▶ Virtual class
- ▶ Concrete subclasses:
 - ▶ *XRaw* – Underlies *Biostrings* infrastructure
 - ▶ *XInteger* – Experimental integer vector class
 - ▶ *XDouble* – Experimental real number vector class

XString (Biostrings)

- ▶ Virtual class
- ▶ Concrete subclasses:
 - ▶ *BString* – Any “biological” sequence
 - ▶ *DNAStrng* – DNA sequence
 - ▶ *RNAStrng* – RNA sequence
 - ▶ *AAString* – Amino acid sequence

Outline

Introduction

Genomic Intervals with Data

Coverage and Other Piecewise Constant Measures

Long Biological Strings

Developer's Notes

Resources

Resources

Bioconductor Web site

- ▶ '*IRanges*', '*GenomicRanges*', and '*Biostrings*' links.
- ▶ <http://bioconductor.org>
- ▶ 'Installation', 'Software', and 'Mailing lists' links.

Help in *R*

- ▶ `help.start()` to view a help browser.
- ▶ `help(package = "Biostrings")`
- ▶ `?findOverlaps`
- ▶ `browseVignettes("GenomicRanges")`