Package ‘BSgenome’

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Title  Software infrastructure for efficient representation of full genomes and their SNPs

Description Infrastructure shared by all the Biostrings-based genome data packages.

biocViews Genetics, Infrastructure, DataRepresentation, SequenceMatching, Annotation, SNP

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BugReports https://github.com/Bioconductor/BSgenome/issues

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LazyLoad yes

available.genomes.R injectSNPs.R getSeq-methods.R
extractAt-methods.R bsapply.R BSgenomeViews-class.R
BSgenome-utils.R export-methods.R BSgenomeForge.R

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### R topics documented:

available.genomes .................................................. 2
bsapply ................................................................. 5
BSgenome-class ....................................................... 7
BSgenome-utils ......................................................... 11
BSgenomeForge ........................................................ 13
BSgenomeViews-class ................................................ 16
BSParams-class ........................................................ 20
export-methods .......................................................... 21
getSeq-methods .......................................................... 22
injectSNPs ............................................................... 28
SNPlocs-class ........................................................... 30
XtraSNPlocs-class .................................................... 34

---

### Index

available.genomes ........................................................... 38

Find available/installed genomes

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### Description

available.genomes gets the list of BSgenome data packages that are available in the Bioconductor repositories for your version of R/Bioconductor.

installed.genomes gets the list of BSgenome data packages that are currently installed on your system.

getBSgenome searches the installed BSgenome data packages for the specified genome and returns it as a BSgenome object.
available.genomes

Usage

available.genomes(splitNameParts=FALSE, type=getOption("pkgType"))

installed.genomes(splitNameParts=FALSE)

getBSgenome(genome, masked=FALSE, load.only=FALSE)

Arguments

splitNameParts  Whether to split or not the package names in parts. In that case the result is returned in a data frame with 5 columns.

type          Character string indicating the type of package ("source", "mac.binary" or "win.binary") to look for.

genome        A BSgenome object, or the full name of an installed BSgenome data package, or a short string specifying the name of an NCBI assembly (e.g. "GRCh38", "TAIR10.1", etc...) or UCSC genome (e.g. "hg38", "bosTau9", "galGal6", "ce11", etc...). The supplied short string must refer unambiguously to an installed BSgenome data package.

masked        TRUE or FALSE. Whether to search for the masked BSgenome object (i.e. the object that contains the masked sequences) or not (the default).

load.only     TRUE or FALSE. By default getBSgenome loads and attaches the BSgenome data package containing the requested genome, resulting in its addition to the search path. Use load.only=TRUE to prevent this, in which case the BSgenome data package is loaded but not attached.

Details

A BSgenome data package contains the full genome sequences for a given organism.

Its name typically has 4 parts (5 parts if it's a masked BSgenome data package i.e. if it contains masked sequences) separated by a dot e.g. BSgenome.Mmusculus.UCSC.mm10 or BSgenome.Mmusculus.UCSC.mm10.masked.

1. The 1st part is always BSgenome.

2. The 2nd part is the name of the organism in abbreviated form e.g. Mmusculus, Hsapiens, Celegans, Scerevisiae, Ecoli, etc...

3. The 3rd part is the name of the organisation who provided the genome sequences. We formally refer to it as the provider of the genome. E.g. UCSC, NCBI, TAIR, etc...

4. The 4th part is a short string specifying the name of an NCBI assembly (e.g. GRCh38, TAIR10.1, etc...) or UCSC genome (e.g. hg38, mm10, susScr11, bosTau9, galGal6, ce11, etc...).

5. If the package contains masked sequences, its name has the .masked suffix added to it, which is typically the 5th part.

A BSgenome data package contains a single top-level object (a BSgenome object) named like the package itself that can be used to access the genome sequences.
available.genomes

Value

For available.genomes and installed.genomes: by default (i.e. if splitNameParts=FALSE), a character vector containing the names of the BSgenome data packages that are available (for available.genomes) or currently installed (for installed.genomes). If splitNameParts=TRUE, the list of packages is returned in a data frame with one row per package and the following columns: pkgname (character), organism (factor), provider (factor), genome (character), and masked (logical).

For getBSgenome: the BSgenome object containing the sequences for the specified genome. Or an error if the object cannot be found in the BSgenome data packages currently installed.

Author(s)

H. Pagès

See Also

• BSgenome objects.
• available.packages.

Examples

```r
## available.genomes() and installed.genomes()
library(BSgenome.Scerevisiae.UCSC.sacCer1)
Scerevisiae # same as BSgenome.Scerevisiae.UCSC.sacCer1
```

bsapply

## getBSgenome()
## Specify the full name of an installed BSgenome data package:
genome <- getBSgenome("BSgenome.Celegans.UCSC.ce2")
genome

## Specify a UCSC genome:
genome <- getBSgenome("hg38")
class(genome) # BSgenome object
seqinfo(genome)
genome$chrM

genome <- getBSgenome("hg38", masked=TRUE)
class(genome) # MaskedBSgenome object
seqinfo(genome)
genome$chr22

---

bsapply  bsapply

Description

Apply a function to each chromosome in a genome.

Usage

bsapply(BSParams, ...)

Arguments

BSParams a BSParams object that holds the various parameters needed to configure the
bsapply function

... optional arguments to 'FUN'.

Details

The exclude parameter of the BSParams object must be a character vector containing regular expressions. By default it's empty so nothing gets excluded. A popular option will probably be to set this to "rand" so that random bits of unassigned contigs are filtered out.

Value

If BSParams sets simplify=FALSE, an ordinary list is returned containing the results generated using the remaining BSParams specifications. If BSParams sets simplify=TRUE, an sapply-like simplification is performed on the results.

Author(s)

Marc Carlson
See Also

BSParams-class, BSgenome-class, BSgenome-utils

Examples

## Load the Worm genome:
library("BSgenome.Celegans.UCSC.ce2")

## Count the alphabet frequencies for every chromosome but exclude
## mitochondrial and scaffold ones:
params <- new("BSParams", X = Celegans, FUN = alphabetFrequency,
             exclude = c("M", ","))
bsapply(params)

## Or we can do this same function with simplify = TRUE:
params <- new("BSParams", X = Celegans, FUN = alphabetFrequency,
             exclude = c("M", ","), simplify = TRUE)
bsapply(params)

## Examples to show how we might look for a string (in this case an
## ebox motif) across the whole genome.
Ebox <- DNAStringSet("CACGTG")
pdict0 <- PDict(Ebox)

params <- new("BSParams", X = Celegans, FUN = countPDict, simplify = TRUE)
bsapply(params, pdict = pdict0)

params@FUN <- matchPDict
bsapply(params, pdict = pdict0)

## And since its really overkill to use matchPDict to find a single pattern:
params@FUN <- matchPattern
bsapply(params, pattern = "CACGTG")

## Examples on how to use the masks
library(BSgenome.Hsapiens.UCSC.hg38.masked)
genome <- BSgenome.Hsapiens.UCSC.hg38.masked

## I can make things verbose if I want to see the chromosomes getting processed.
options(verbose=TRUE)

## For the 1st example, lets use default masks
params <- new("BSParams", X = genome, FUN = alphabetFrequency,
             exclude = c(1:8,"M","X","_"), simplify = TRUE)
bsapply(params)

if (interactive()) {
  ## Set up the motifList to filter out all double T's and all double C's
  params@motifList <-c("TT","CC")
  bsapply(params)

  ## Get rid of the motifList
params$motifList=as.character()
}

##Enable all standard masks
params$maskList <- c(RM=TRUE,TRF=TRUE)
bsapply(params)

##Disable all standard masks
params$maskList <- c(AGAPS=FALSE,AMB=FALSE)
bsapply(params)

options(verbose=FALSE)

---

BSgenome-class

BSgenome objects

Description

The BSgenome class is a container for storing the full genome sequences of a given organism. BSgenome objects are usually made in advance by a volunteer and made available to the Bioconductor community as "BSgenome data packages". See ?available.genomes for how to get the list of "BSgenome data packages" currently available.

Accessor methods

In the code snippets below, x is a BSgenome object.

metadata(x) Returns a named list containing metadata associated with the BSgenome object. The components of the list are:

- organism: The scientific name of the organism that this BSgenome object is for. E.g. "Homo sapiens", "Mus musculus", "Caenorhabditis elegans", etc...
- common_name: The common name of the organism that this BSgenome object is for. E.g. "Human", "Mouse", "Worm", etc...
- provider: The provider of this genome. E.g. "UCSC", "BDGP", "FlyBase", etc...
- genome: The name of the genome. Typically the name of an NCBI assembly (e.g. "GRCh38.p12", "WBcel1235", "TAIR10.1", "ARS-UCD1.2", etc...) or UCSC genome (e.g. "hg38", "bosTau9", "galGal6", "ce11", etc...).
- release_date: The release date of this genome e.g. "Mar. 2006".
- source_url: The permanent URL to the place where the FASTA files used to produce the sequences contained in x can be found (and downloaded).

seqnames(x), seqnames(x) <- value Gets or sets the names of the single sequences contained in x. Each single sequence is stored in a DNAString or MaskedDNAString object and typically comes from a source file (FASTA) with a single record. The names returned by seqnames(x) usually reflect the names of those source files but a common prefix or suffix was eventually removed in order to keep them as short as possible.
seqlengths(x) Returns the lengths of the single sequences contained in x.

See ?'length,DNAString-method' and ?'length,MaskedDNAString-method' for the definition of the length of a DNAString or MaskedDNAString object. Note that the length of a masked sequence (MaskedDNAString object) is not affected by the current set of active masks but the nchar method for MaskedDNAString objects is.

names(seqlengths(x)) is guaranteed to be identical to seqnames(x).

mseqnames(x) Returns the index of the multiple sequences contained in x. Each multiple sequence is stored in a DNAStringSet object and typically comes from a source file (FASTA) with multiple records. The names returned by mseqnames(x) usually reflect the names of those source files but a common prefix or suffix was eventually removed in order to keep them as short as possible.

names(x) Returns the index of all sequences contained in x. This is the same as c(seqnames(x), mseqnames(x)).

length(x) Returns the length of x, i.e., the total number of sequences in it (single and multiple sequences). This is the same as length(names(x)).

x[[name]] Returns the sequence (single or multiple) in x named name (name must be a single string). No sequence is actually loaded into memory until this is explicitly requested with a call to x[[name]] or x$name. When loaded, a sequence is kept in a cache. It will be automatically removed from the cache at garbage collection if it’s not in use anymore i.e. if there are no reference to it (other than the reference stored in the cache). With options(verbose=TRUE), a message is printed each time a sequence is removed from the cache.

x$name Same as x[[name]] but name is not evaluated and therefore must be a literal character string or a name (possibly backtick quoted).

masknames(x) The names of the built-in masks that are defined for all the single sequences. There can be up to 4 built-in masks per sequence. These will always be (in this order): (1) the mask of assembly gaps, aka "the AGAPS mask";
(2) the mask of intra-contig ambiguities, aka "the AMB mask";
(3) the mask of repeat regions that were determined by the RepeatMasker software, aka "the RM mask";
(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), aka "the TRF mask".
All the single sequences in a given package are guaranteed to have the same collection of built-in masks (same number of masks and in the same order).

masknames(x) gives the names of the masks in this collection. Therefore the value returned by masknames(x) is a character vector made of the first N elements of c("AGAPS", "AMB", "RM", "TRF"), where N depends only on the BSgenome data package being looked at (0 <= N <= 4). The man page for most BSgenome data packages should provide the exact list and permanent URLs of the source data files that were used to extract the built-in masks. For example, if you’ve installed the BSgenome.Hsapiens.UCSC.hg38 package, load it and see the Note section in ?'BSgenome.Hsapiens.UCSC.hg38'.

Author(s)

H. Pagès
BSgenome-class

See Also

available.genomes, GenomeDescription-class, BSgenome-utils, DNAString-class, DNAStringSet-class, MaskedDNAString-class, getSeq, BSgenome-method, injectSNPs, subseq, XVector-method, rm, gc

Examples

## Loading a BSgenome data package doesn't load its sequences into memory:
library(BSgenome.Celegans.UCSC.ce2)

metadata(Celegans)

## Number of sequences in this genome:
length(Celegans)

## Display a summary of the sequences:
Celegans

## Index of single sequences:
seqnames(Celegans)

## Lengths (i.e. number of nucleotides) of the single sequences:
seqlengths(Celegans)

## Load chromosome I from disk to memory (hence takes some time)
## and keep a reference to it:
chrI <- Celegans[["chrI"]]
# equivalent to Celegans$chrI

chrI

class(chrI) # a DNAString instance
length(chrI) # with 15080483 nucleotides

## Single sequence can be renamed:
seqnames(Celegans) <- sub("chr", "", seqnames(Celegans))
seqlengths(Celegans)
Celegans$I
seqnames(Celegans) <- paste0("chr", seqnames(Celegans))

## Multiple sequences:
library(BSgenome.Rnorvegicus.UCSC.rn5)
rn5 <- BSgenome.Rnorvegicus.UCSC.rn5
rn5
sequences(rn5)
rn5$chr1 <- rn5$chr1
mseqnames(rn5)
rn5_random <- Rnorvegicus$random
rn5_random
class(rn5_random) # a DNAStringSet instance
## Character vector containing the description lines of the first
## 4 sequences in the original FASTA file:
## PASS-BY-ADDRESS SEMANTIC, CACHING AND MEMORY USAGE

## We want a message to be printed each time a sequence is removed from the cache:

```r
options( verbose = TRUE )

gc() # nothing seems to be removed from the cache

rm( rn5_chr1, rn5_random )
gc() # rn5_chr1 and rn5_random are removed from the cache (they are # not in use anymore)

options( verbose = FALSE )
```

## Get the current amount of data in memory (in Mb):

```r
mem0 <- gc()[ "Vcells", "(Mb)" ]

system.time( rn5_chr2 <- rn5$chr2 ) # read from disk

gc()[ "Vcells", "(Mb)" ] - mem0 # 'rn5_chr2' occupies 20Mb in memory

system.time( tmp <- rn5$chr2 ) # much faster! (sequence # is in the cache)

gc()[ "Vcells", "(Mb)" ] - mem0 # we're still using 20Mb (sequences # have a pass-by-address semantic # i.e. the sequence data are not # duplicated)
```

## subseq() doesn't copy the sequence data either, hence it is very # fast and memory efficient (but the returned object will hold a # reference to 'rn5_chr2'):

```r
y <- subseq( rn5_chr2, 10, 8000000 )
gc()[ "Vcells", "(Mb)" ] - mem0
```

## We must remove all references to 'rn5_chr2' before it can be # removed from the cache (so the 20Mb of memory used by this # sequence are freed):

```r
options( verbose = TRUE )

rm( rn5_chr2, tmp )
gc()
```

## Remember that 'y' holds a reference to 'rn5_chr2' too:

```r
rm( y )
gc()
```

```r
options( verbose = FALSE )
gc()[ "Vcells", "(Mb)" ] - mem0
```
BSgenome-utils

Description

Utilities for BSgenome objects.

Usage

```r
## S4 method for signature 'BSgenome'
vmatchPattern(pattern, subject, max.mismatch=0, min.mismatch=0,
              with.indels=FALSE, fixed=TRUE, algorithm="auto",
              exclude="", maskList=logical(0), userMask=IRangesList(),
              invertUserMask=FALSE)
```

```r
## S4 method for signature 'BSgenome'
vcountPattern(pattern, subject, max.mismatch=0, min.mismatch=0,
               with.indels=FALSE, fixed=TRUE, algorithm="auto",
               exclude="", maskList=logical(0), userMask=IRangesList(),
               invertUserMask=FALSE)
```

```r
## S4 method for signature 'BSgenome'
vmatchPDict(pdict, subject, max.mismatch=0, min.mismatch=0,
             fixed=TRUE, algorithm="auto", verbose=FALSE,
             exclude="", maskList=logical(0))
```

```r
## S4 method for signature 'BSgenome'
vcountPDict(pdict, subject, max.mismatch=0, min.mismatch=0,
            fixed=TRUE, algorithm="auto", collapse=FALSE,
            weight=1L, verbose=FALSE, exclude="", maskList=logical(0))
```

```r
## S4 method for signature 'BSgenome'
macthPWM(pwm, subject, min.score="80%", exclude="", maskList=logical(0))
```

```r
## S4 method for signature 'BSgenome'
countPWM(pwm, subject, min.score="80%", exclude="", maskList=logical(0))
```

Arguments

- **pattern**: A DNAString object containing the pattern sequence.
- **subject**: A BSgenome object containing the subject sequences.
- **max.mismatch, min.mismatch**: The maximum and minimum number of mismatching letters allowed (see ?'lowlevel-matching` for the details). If non-zero, an inexact matching algorithm is used.
- **with.indels**: If TRUE then indels are allowed. In that case, min.mismatch must be 0 and max.mismatch is interpreted as the maximum "edit distance" allowed between any pattern and any of its matches (see ?'matchPattern` for the details).
- **fixed**: If FALSE then IUPAC extended letters are interpreted as ambiguities (see ?'lowlevel-matching` for the details).
algorithm  For \texttt{vmatchPattern} and \texttt{vcountPattern} one of the following: "auto", "naive-exact", "naive-inexact", "boyer-moore", "shift-or", or "indels".
For \texttt{vmatchPDict} and \texttt{vcountPDict} one of the following: "auto", "naive-exact", "naive-inexact", "boyer-moore", or "shift-or".

exclude  A character vector with strings that will be used to filter out chromosomes whose names match these strings.

maskList  A named logical vector of maskStates preferred when used with a BSGenome object. When using the \texttt{bsapply} function, the masks will be set to the states in this vector.

userMask  An \texttt{IntegerRangesList}, containing a mask to be applied to each chromosome. See \texttt{bsapply}.

invertUserMask  Whether the userMask should be inverted.

collapse, weight  ignored arguments.

\texttt{pdict}  A \texttt{PDict} or \texttt{DNAStringSet} object containing the pattern sequences.

\texttt{verbose}  TRUE or FALSE.

\texttt{pwm}  A numeric matrix with row names A, C, G and T representing a Position Weight Matrix.

\texttt{min.score}  The minimum score for counting a match. Can be given as a character string containing a percentage (e.g. "85\%") of the highest possible score or as a single number.

Value

A \texttt{GRanges} object for \texttt{vmatchPattern}. genome and seqinfo information from "subject" are propagated to the return object.

A data.frame object for \texttt{vcountPattern} and \texttt{countPWM} with three columns: "seqname" (factor), "strand" (factor), and "count" (integer).

A \texttt{GRanges} object for \texttt{vmatchPDict} with one metadata column: "index", which represents a mapping to a position in the original pattern dictionary. genome and seqinfo information from "subject" are propagated.

A \texttt{DataFrame} object for \texttt{vcountPDict} with four columns: "seqname" ('factor' Rle), "strand" ('factor' Rle), "index" (integer) and "count" ('integer' Rle). As with \texttt{vmatchPDict} the index column represents a mapping to a position in the original pattern dictionary.

A \texttt{GRanges} object for \texttt{matchPWM} with two metadata columns: "score" (numeric), and "string" (DNAStringSet). genome and seqinfo information from "subject" are included.

Author(s)

P. Aboyoun

See Also

\texttt{matchPattern, matchPDict, matchPWM, bsapply}
Examples

```r
library(BSgenome.Celegans.UCSC.ce2)
data(HNF4alpha)

pattern <- consensusString(HNF4alpha)
vmatchPattern(pattern, Celegans, fixed="subject")
vcountPattern(pattern, Celegans, fixed="subject")

pdict <- PDict(HNF4alpha)
vmatchPDict(pdict, Celegans)
vcountPDict(pdict, Celegans)

pwm <- PWM(HNF4alpha)
matchPWM(pwm, Celegans)
countPWM(pwm, Celegans)
```

BSgenomeForge

The BSgenomeForge functions

Description

A set of functions for making a BSgenome data package.

IMPORTANT NOTE: A new package, the BSgenomeForge package, provides more user-friendly tools for creating a BSgenome data package from an NCBI assembly or UCSC genome. However, if your assembly or genome is not from NCBI or UCSC, you should still use the tools documented below.

Usage

```r
## Top-level BSgenomeForge function:
forgeBSgenomeDataPkg(x, seqs_srcdir=".", destdir=".", replace=FALSE, verbose=TRUE)

## Low-level BSgenomeForge functions:
forgeSeqlengthsRdsFile(seqnames, prefix="", suffix=".fa",
  seqs_srcdir=".", seqs_destdir=".",
  genome=NA_character_, verbose=TRUE)

forgeSeqlengthsRdaFile(seqnames, prefix="", suffix=".fa",
  seqs_srcdir=".", seqs_destdir=".",
  genome=NA_character_, verbose=TRUE)

forgeSeqFiles(provider, genome,
  seqnames, mseqnames=NULL,
  seqfile_name=NA, prefix="", suffix=".fa",
  seqs_srcdir=".", seqs_destdir=".",
```
onDisk_seq_format=c("2bit", "rds", "rda", "fa.rz", "fa"),
verbose=TRUE)

forgeMasksFiles(seqnames, nmask_per_seq,
   seqs_destdir=".",
   onDisk_seq_format=c("2bit", "rda", "fa.rz", "fa"),
   masks_srcdir=".", masks_destdir=".",
   AGAPSfiles_type="gap", AGAPSfiles_name=NA,
   AGAPSfiles_prefix="", AGAPSfiles_suffix="_gap.txt",
   RMfiles_name=NA, RMfiles_prefix="", RMfiles_suffix=".fa.out",
   TRFfiles_name=NA, TRFfiles_prefix="", TRFfiles_suffix=".bed",
   verbose=TRUE)

Arguments

x
A BSgenomeDataPkgSeed object or the name of a BSgenome data package seed file. See the BSgenomeForge vignette in this package for more information.

seqs_srcdir, masks_srcdir
Single strings indicating the path to the source directories i.e. to the directories containing the source data files. Only read access to these directories is needed. See the BSgenomeForge vignette in this package for more information.

destdir
A single string indicating the path to the directory where the source tree of the target package should be created. This directory must already exist. See the BSgenomeForge vignette in this package for more information.

replace
TRUE or FALSE. When set to TRUE, replace replaces the package directory if it already exists.

verbose
TRUE or FALSE.

provider
The provider of the sequence data files e.g. "UCSC", "NCBI", "BDGP", "FlyBase", etc...

gene
The name of the genome. Typically the name of an NCBI assembly (e.g. "GRCh38.p12", "WBcel235", "TAIR10.1", "ARS-UCD1.2", etc...) or UCSC genome (e.g. "hg38", "bosTau9", "galGal6", "ce11", etc...).

seqnames, mseqnames
A character vector containing the names of the single (for seqnames) and multiple (for mseqnames) sequences to forge. See the BSgenomeForge vignette in this package for more information.

seqfile_name, prefix, suffix
See the BSgenomeForge vignette in this package for more information, in particular the description of the seqfile_name, seqfiles_prefix and seqfiles_suffix fields of a BSgenome data package seed file.

seqs_destdir, masks_destdir
During the forging process the source data files are converted into serialized Biostrings objects. seqs_destdir and masks_destdir must be single strings indicating the path to the directories where these serialized objects should be saved. These directories must already exist. Both forgeSeqlengthsRdsFile and forgeSeqlengthsRdaFile will produce a single .rds or .rda file. Both forgeSeqFiles and forgeMasksFiles will produce one file per sequence (all files being either .rds or .rda files).
Specifying how the single sequences should be stored in the forged package. Can be "2bit", "rds", "rda", "fa.rz", or "fa". If "2bit" (the default), then all the single sequences are stored in a single twoBit file. If "rds" or "rda", then each single sequence is stored in a separated serialized XString derivative (one per single sequence). If "fa.rz" or "fa", then all the single sequences are stored in a single FASTA file (compressed in the RAZip format if "fa.rz").

A single integer indicating the desired number of masks per sequence. See the BSgenomeForge vignette in this package for more information.

These arguments are named accordingly to the corresponding fields of a BSgenome data package seed file. See the BSgenomeForge vignette in this package for more information.

These functions are intended for Bioconductor users who want to make a new BSgenome data package, not for regular users of these packages. See the BSgenomeForge vignette in this package (vignette("BSgenomeForge")) for an extensive coverage of this topic.

H. Pagès

See Also
- `forgeBSgenomeDataPkgFromNCBI` and `forgeBSgenomeDataPkgFromUCSC` in the BSgenomeForge package.
- `available.genomes` to find BSgenome data packages available in Bioconductor.
- BSgenome objects.

Examples

```r
seqs_sourcedir <- system.file("extdata", package="BSgenome")
seqnames <- c("chrX", "chrM")

## Forge .2bit sequence files:
forgeSeqFiles("UCSC", "ce2",
              seqnames, prefix="ce2", suffix=".fa.gz",
              seqs_sourcedir=seqs_sourcedir,
              seqs_destdir=tempdir(), ondisk_seq_format="2bit")

## Forge .rds sequence files:
forgeSeqFiles("UCSC", "ce2",
              seqnames, prefix="ce2", suffix=".fa.gz",
              seqs_sourcedir=seqs_sourcedir,
              seqs_destdir=tempdir(), ondisk_seq_format="rds")

## Sanity checks:
library(BSgenome.Celegans.UCSC.ce2)
```
BSgenomeViews-class

BSgenomeViews objects

Description

The BSgenomeViews class is a container for storing a set of genomic positions on a BSgenome object, called the "subject" in this context.

Usage

```r
## Constructor
## ------------
BSgenomeViews(subject, granges)
```

```r
## Accessors
## ---------
subject(x)
```

```r
## S4 method for signature 'BSgenomeViews'
```

```r
## S4 method for signature 'BSgenomeViews'
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## S4 method for signature 'BSgenomeViews'
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## S4 method for signature 'BSgenomeViews'
```
```r
strand(x)
## S4 method for signature 'BSgenomeViews'
ranges(x, use.mcols=FALSE)
## S4 method for signature 'BSgenomeViews'
elementNROWS(x)
## S4 method for signature 'BSgenomeViews'
seqinfo(x)

## DNAStringSet methods
## -------------------
## S4 method for signature 'BSgenomeViews'
seqtype(x)

## S4 method for signature 'BSgenomeViews'
nchar(x, type="chars", allowNA=FALSE)

## S4 method for signature 'BSgenomeViews'
unlist(x, recursive=TRUE, use.names=TRUE)

## S4 method for signature 'BSgenomeViews'
alphabetFrequency(x, as.prob=FALSE, collapse=FALSE, baseOnly=FALSE)

## S4 method for signature 'BSgenomeViews'
hasOnlyBaseLetters(x)

## S4 method for signature 'BSgenomeViews'
uniqueLetters(x)

## S4 method for signature 'BSgenomeViews'
letterFrequency(x, letters, OR="|", as.prob=FALSE, collapse=FALSE)

## S4 method for signature 'BSgenomeViews'
oligonucleotideFrequency(x, width, step=1,
                        as.prob=FALSE, as.array=FALSE,
                        fast.moving.side="right", with.labels=TRUE, simplify.as="matrix")

## S4 method for signature 'BSgenomeViews'
nucleotideFrequencyAt(x, at, as.prob=FALSE, as.array=TRUE,
                       fast.moving.side="right", with.labels=TRUE)

## S4 method for signature 'BSgenomeViews'
consensusMatrix(x, as.prob=FALSE, shift=0L, width=NULL, baseOnly=FALSE)

## S4 method for signature 'BSgenomeViews'
consensusString(x, ambiguityMap=IUPAC_CODE_MAP, threshold=0.25,
                shift=0L, width=NULL)
```
Arguments

subject
A BSgenome object or the name of a reference genome specified in a way that is accepted by the getBSgenome function. In that case the corresponding BSGenome data package needs to be already installed (see ?getBSgenome for the details).

granges
A GRanges object containing ranges relative to the genomic sequences stored in subject.

x
A BSgenomeViews object.

use.mcols
TRUE or FALSE (the default). Whether the metadata columns on x (accessible with mcols(x)) should be propagated to the returned object or not.

type, allowNA, recursive, use.names
Ignored.

as.prob, letters, OR, width

collapse, baseOnly
See ?alphabetFrequency in the Biostrings package.

step, as.array, fast.moving.side, with.labels, simplify.as, at
See ?oligonucleotideFrequency in the Biostrings package.

shift, ambiguityMap, threshold
See ?consensusMatrix in the Biostrings package.

Constructors

BSgenomeViews(subject, granges): Make a BSgenomeViews object by putting the views specified by granges on top of the genomic sequences stored in subject. See above for how argument subject and granges should be specified.

Views(subject, granges): Equivalent to BSgenomeViews(subject, granges). Provided for convenience.

Accessors

In the code snippets below, x is a BSgenomeViews object.

subject(x): Return the BSgenome object containing the full genomic sequences on top of which the views in x are defined.

granges(x, use.mcols=FALSE): Return the genomic ranges of the views as a GRanges object. These ranges are relative to the genomic sequences stored in subject(x).

length(x): The number of views in x.

names(x): The names of the views in x.

seqnames(x), start(x), end(x), width(x), strand(x): Equivalent to seqnames(granges(x)), start(granges(x)), end(granges(x)), width(granges(x)), strand(granges(x)), respectively.

ranges(x, use.mcols=FALSE): Equivalent to ranges(granges(x), use.mcols), use.mcols).

elementNROWS(x): Equivalent to width(x).

seqinfo(x): Equivalent to seqinfo(subject(x)) and to seqinfo(granges(x)) (both are guaranteed to be the same). See ?seqinfo in the GenomeInfoDb package for more information.
Coercion

In the code snippets below, `x` is a BSgenomeViews object.

- `as(x, "DNAStringSet")`: Turn `x` into a DNAStringSet object by extracting the DNA sequence corresponding to each view. Alternatively `as(x, "XStringSet")` can be used for this, and is equivalent to `as(x, "DNAStringSet")`.
- `as.character(x)`: Equivalent to `as.character(as(x, "DNAStringSet"))`.
- `as.data.frame(x)`: Turn `x` into a data.frame.

Subsetting

- `x[i]`: Select the views specified by `i`.
- `x[[i]]`: Extract the one view specified by `i`.

DNAStringSet methods

For convenience, some methods defined for DNAStringSet objects in the Biostrings package can be used directly on a BSgenomeViews object. In that case, everything happens like if the BSgenomeViews object `x` was turned into a DNAStringSet object (with `as(x, "DNAStringSet")`) before it’s passed to the method for DNAStringSet objects.

At the moment, the list of such methods is: seqtype, nchar, XStringSet-method, unlist, XStringSet-method, alphabetFrequency, hasOnlyBaseLetters, uniqueLetters, letterFrequency, oligonucleotideFrequency, nucleotideFrequencyAt, consensusMatrix, and consensusString.

See the corresponding man page in the Biostrings package for a description of these methods.

Author(s)

H. Pagès

See Also

- The BSgenome class.
- The GRanges class in the GenomicRanges package.
- The DNAStringSet class in the Biostrings package.
- The seqinfo and related getters in the GenomeInfoDb package for getting the sequence information stored in an object.
- TxDb objects in the GenomicFeatures package.

Examples

```r
library(BSgenome.Mmusculus.UCSC.mm10)
genome <- BSgenome.Mmusculus.UCSC.mm10
library(TxDb.Mmusculus.UCSC.mm10.knownGene)
txdb <- TxDb.Mmusculus.UCSC.mm10.knownGene
ex <- exons(txdb, columns=c("exon_id", "tx_name", "gene_id"))
v <- Views(genome, ex)
v
```
subject(v)
granges(v)
seqinfo(v)
as(v, "DNAStringSet")

v10 <- v[1:10] # select the first 10 views
subject(v10)  # same as subject(v)
granges(v10)
seqinfo(v10)  # same as seqinfo(v)
as(v10, "DNAStringSet")
alphabetFrequency(v10)
alphabetFrequency(v10, collapse=TRUE)

v12 <- v[width(v) <= 12] # select the views of 12 nucleotides or less
head(as.data.frame(v12))
trinucleotideFrequency(v12, simplify.as="collapsed")

## BSgenomeViews objects are list-like objects. That is, the
## BSgenomeViews class derives from List and typical list/List
## operations (e.g. [[, elementNROWS(), unlist(), elementType(),
## etc...) work on these objects:
is(v12, "List") # TRUE
v12[[2]]
head(elementNROWS(v12)) # elementNROWS(v) is the same as width(v)
unlist(v12)
elementType(v12)

BSParams-class  Class "BSParams"

Description

A parameter class for representing all parameters needed for running the bsapply method.

Objects from the Class

Objects can be created by calls of the form new("BSParams", ...).

Slots

X: a BSgenome object that contains chromosomes that you wish to apply FUN on
FUN: the function to apply to each chromosome in the BSgenome object ’X’
exclude: this is a character vector with strings that will be treated as regular expressions to filter out chromosomes whose names match these strings.
simplify: TRUE/FALSE value to indicate whether or not the function should try to simplify the output for you.
maskList: A named logical vector of maskStates preferred when used with a BSGenome object.
   When using the bsapply function, the masks will be set to the states in this vector.
motifList: A character vector which should contain motifs that the user wishes to mask from the sequence.

userMask: A IntegerRangesList object, where each element masks the corresponding chromosome in X. This allows the user to conveniently apply masks besides those included in X.

invertUserMask: A logical indicating whether to invert each mask in userMask.

Methods

bsapply(p) Performs the function FUN using the parameters contained within BSPrams.

Author(s)

Marc Carlson

See Also

bsapply

Description

export methods for BSgenome objects.

NOTE: The export generic function and most of its methods are defined and documented in the BiocIO package. This man page only documents the 2 export methods defined in the BSgenome package.

Usage

## S4 method for signature 'BSgenome,FastaFile,ANY'
export(object, con, format, compress=FALSE, compression_level=NA, verbose=TRUE)

## S4 method for signature 'BSgenome,TwoBitFile,ANY'
export(object, con, format, ...)

Arguments

object The BSgenome object to export.

con A FastaFile or TwoBitFile object. Alternatively con can be a single string containing the path to a FASTA or twoBit file, in which case either the file extension or the format argument needs to be "fasta", "twoBit", or "2bit". Also note that in this case, the export method that is called is either the method with signature c("ANY", "character", "missing") or the method with signature c("ANY", "character", "character"), both defined in the BiocIO package. If object is a BSgenome object and the file extension or the format argument is "fasta", "twoBit", or "2bit", then the flow eventually reaches one of 2 methods documented here.
getSeq-methods

getSeq methods for BSgenome and XStringSet objects

Description

getSeq methods for extracting a set of sequences (or subsequences) from a BSgenome or XStringSet object. For XStringSets, there are also convenience methods on [ that delegate to getSeq.

format
If not missing, should be "fasta", "twoBit", or "2bit" (case insensitive for "twoBit" and "2bit").

compress, compression_level
Forwarded to writeXStringSet. See ?writeXStringSet for the details.

verbose
Whether or not the function should display progress. TRUE by default.

... Extra arguments. The method for TwoBitFile objects forwards them to bsapply.

Author(s)

Michael Lawrence

See Also

• BSgenome objects.
• The export generic function in the BioCIO package.
• FastaFile and TwoBitFile objects in the rtracklayer package.

Examples

```r
library(BSgenome.Celegans.UCSC.ce2)
genome <- BSgenome.Celegans.UCSC.ce2

## Export as FASTA file.
out1_file <- file.path(tempdir(), "Celegans.fasta")
export(genome, out1_file)

## Export as twoBit file.
out2_file <- file.path(tempdir(), "Celegans.2bit")
export(genome, out2_file)

## Sanity checks:
dna0 <- DNAStringSet(as.list(genome))

system.time(dna1 <- import(out1_file))
stopifnot(identical(names(dna0), names(dna1)) && all(dna0 == dna1))

system.time(dna2 <- import(out2_file)) # importing twoBit is 10-20x faster than importing non-compressed FASTA
stopifnot(identical(names(dna0), names(dna2)) && all(dna0 == dna2))
```


Usage

```r
## S4 method for signature 'BSgenome'
getSeq(x, names, start=NA, end=NA, width=NA,
      strand="+", as.character=FALSE)
## S4 method for signature 'XStringSet'
getSeq(x, names)
```

Arguments

- **x**: A BSgenome or XStringSet object. See the available.genomes function for how to install a genome.

- **names**: When x is a BSgenome, names must be a character vector containing the names of the sequences in x where to get the subsequences from, or a GRanges object, or a GRangesList object, or a named IntegerRangesList object, or a named IntegerRanges object. The IntegerRangesList or IntegerRanges object must be named according to the sequences in x where to get the subsequences from. If names is missing, then seqnames(x) is used. See ?'BSgenome-class' for details on how to get the lists of single sequences and multiple sequences (respectively) contained in a BSgenome object. When x is a XStringSet object, names must be a character vector, GRanges or GRangesList object.

- **start, end, width**: Vector of integers (eventually with NAs) specifying the locations of the subsequences to extract. These are not needed (and it’s an error to supply them) when names is a GRanges, GRangesList, IntegerRangesList, or IntegerRanges object.

- **strand**: A vector containing "+"s or/and "-"s. This is not needed (and it’s an error to supply it) when names is a GRanges or GRangesList object.

- **as.character**: TRUE or FALSE. Should the extracted sequences be returned in a standard character vector?

Details

L, the number of sequences to extract, is determined as follow:

- If names is a GRanges or IntegerRanges object then \( L = \text{length}(\text{names}) \).
- If names is a GRangesList or IntegerRangesList object then \( L = \text{length}(\text{unlist}(\text{names})) \).
- Otherwise, L is the length of the longest of names, start, end and width and all these arguments are recycled to this length. NAs and negative values in these 3 arguments are solved according to the rules of the SEW (Start/End/Width) interface (see ?solveUserSEW for the details).

If names is neither a GRanges or GRangesList object, then the strand argument is also recycled to length L.

Here is how the names passed to the names argument are matched to the names of the sequences in BSgenome object x. For each name in names:

- (1): If x contains a single sequence with that name then this sequence is used for extraction;
• (2): Otherwise the names of all the elements in all the multiple sequences are searched. If the names argument is a character vector then name is treated as a regular expression and `grep` is used for this search, otherwise (i.e. when the names are supplied via a higher level object like `GRanges` or `GRangesList`) then name must match exactly the name of the sequence. If exactly 1 sequence is found, then it is used for extraction, otherwise (i.e. if no sequence or more than 1 sequence is found) then an error is raised.

There are convenience methods for extracting sequences from `XStringSet` objects using a `GenomicRanges` or `GRangesList` subscript (character subscripts are implicitly supported). Both methods are simple wrappers around `getSeq`, although the `GRangesList` method differs from the `getSeq` behavior in that the within-element results are concatenated and returned as an `XStringSet`, rather than an `XStringSetList`. See the examples.

Value

Normally a `DNAStringSet` object (or character vector if `as.character=TRUE`).

With the 2 following exceptions:

1. A `DNAStringSetList` object (or `CharacterList` object if `as.character=TRUE`) of the same shape as names if names is a `GRangesList` object.
2. A `DNAString` object (or single character string if `as.character=TRUE`) if L = 1 and names is not a `GRanges`, `GRangesList`, `IntegerRangesList`, or `IntegerRanges` object.

Note

Be aware that using `as.character=TRUE` can be very inefficient when extracting a "big" amount of DNA sequences (e.g. millions of short sequences or a small number of very long sequences).

Note that the masks in x, if any, are always ignored. In other words, masked regions in the genome are extracted in the same way as unmasked regions (this is achieved by dropping the masks before extraction). See `?MaskedDNAString-class` for more information about masked DNA sequences.

Author(s)

H. Pagès; improvements suggested by Matt Settles and others

See Also

`getSeq`, `available.genomes`, `BSgenome-class`, `DNAString-class`, `DNAStringSet-class`, `MaskedDNAString-class`, `GRanges-class`, `GRangesList-class`, `IntegerRangesList-class`, `IntegerRanges-class`, `grep`

Examples

```
## A. SIMPLE EXAMPLES

## Load the Caenorhabditis elegans genome (UCSC Release ce2):
library(BSgenome.Celegans.UCSC.ce2)

## Look at the index of sequences:
```
Celegans

## Get chromosome V as a DNAString object:
getSeq(Celegans, "chrV")
## which is in fact the same as doing:
Celegans$chrV

## Not run:
## Never try this:
getSeq(Celegans, "chrV", as.character=TRUE)
## or this (even worse):
getSeq(Celegans, as.character=TRUE)

## End(Not run)

## Get the first 20 bases of each chromosome:
getSeq(Celegans, end=20)

## Get the last 20 bases of each chromosome:
getSeq(Celegans, start=-20)

# B. EXTRACTING SMALL SEQUENCES FROM DIFFERENT CHROMOSOMES

myseqs <- data.frame(
  chr=c("chrI", "chrX", "chrM", "chrX", "chrI", "chrM", "chrI"),
  start=c(NA, -40, 8510, 301, 30001, 9220500, -2804, -30),
  end=c(50, NA, 8522, 324, 30011, 9220555, -2801, -11),
  strand=c("+", "+", "+", "+", "+", "+", "+"))

getSeq(Celegans, myseqs$chr,
       start=myseqs$start, end=myseqs$end)

getSeq(Celegans, myseqs$chr,
       start=myseqs$start, end=myseqs$end, strand=myseqs$strand)

# C. USING A GRanges OBJECT

gr1 <- GRanges( seqnames=c("chrI", "chrI", "chrM"),
                ranges=IRanges(start=101:103, width=9))
gr1 # all strand values are "*"
getSeq(Celegans, gr1) # treats strand values as if they were "+"

strand(gr1)[1] <- "-"
getSeq(Celegans, gr1)

strand(gr1)[1] <- "*"
getSeq(Celegans, gr1)

strand(gr1)[2] <- "*"
if (interactive())
getSeq(Celegans, gr1) # Error: cannot mix "*" with other strand values

gr2 <- GRanges(seqnames=c("chrM", "NM_058280_up_1000"),
               ranges=IRanges(start=103:102, width=9))
gr2

if (interactive()) {
  ## Because the sequence names are supplied via a GRanges object, they
  ## are not treated as regular expressions:
  getSeq(Celegans, gr2) # Error: sequence NM_058280_up_1000 not found
}

# D. USING A GRangesList OBJECT
# ---------------------------------------------------------------------
gr1 <- GRanges(seqnames=c("chrI", "chrII", "chrM", "chrII"),
               ranges=IRanges(start=101:104, width=12),
               strand="+")
gr2 <- shift(gr1, 5)
gr3 <- gr2
strand(gr3) <- "-"
gr1 <- GRangesList(gr1, gr2, gr3)
getSeq(Celegans, gr1)

# E. EXTRACTING A HIGH NUMBER OF RANDOM 40-MERS FROM A GENOME
# ---------------------------------------------------------------------
extractRandomReads <- function(x, density, readlength)
{
  if (!is.integer(readlength))
    readlength <- as.integer(readlength)
  start <- lapply(seqnames(x),
                   function(name)
                   {
                     seqlength <- seqlengths(x)[name]
                     sample(seqlength - readlength + 1L, seqlength * density, repl=TRUE)
                   })
  names <- rep.int(seqnames(x), elementNROW(start))
  ranges <- IRanges(start=unlist(start), width=readlength)
  strand <- strand(sample(c("+", "-"), length(names), repl=TRUE))
  gr <- GRanges(seqnames=names, ranges=ranges, strand=strand)
  getSeq(x, gr)
}

## With a density of 1 read every 100 genome bases, the total number of
## extracted 40-mers is about 1 million:
rndreads <- extractRandomReads(Celegans, 0.01, 40)

## Notes:
- The short sequences in 'rndreads' can be seen as the result of a simulated high-throughput sequencing experiment. A non-realistic one though because:
  (a) It assumes that the underlying technology is perfect (the generated reads have no technology induced errors).
  (b) It assumes that the sequenced genome is exactly the same as the reference genome.
  (c) The simulated reads can contain IUPAC ambiguity letters only because the reference genome contains them. In a real high-throughput sequencing experiment, the sequenced genome of course doesn't contain those letters, but the sequencer can introduce them in the generated reads to indicate ambiguous base-calling.
- Those reads are coming from the plus and minus strands of the chromosomes.
- With a density of 0.01 and the reads being only 40-base long, the average coverage of the genome is only 0.4 which is low. The total number of reads is about 1 million and it takes less than 10 sec. to generate them.
- A higher coverage can be achieved by using a higher density and/or longer reads. For example, with a density of 0.1 and 100-base reads the average coverage is 10. The total number of reads is about 10 millions and it takes less than 1 minute to generate them.
- Those reads could easily be mapped back to the reference by using an efficient matching tool like matchPDict() for performing exact matching (see ?matchPDict for more information). Typically, a small percentage of the reads (4 to 5% in our case) will hit the reference at multiple locations. This is especially true for such short reads, and, in a lower proportion, is still true for longer reads, even for reads as long as 300 bases.

options(verboset=TRUE)
first20 <- getSeq(Celegans, end=20)
first20
gc()
stopifnot(length(ls(Celegans@.seqs_cache)) == 0L)
# One more gc() call is needed in order to see the amount of memory in
# used after all the chromosomes have been removed from the cache:
gc()

# G. USING '[' FOR CONVENIENT EXTRACTION
seqs <- getSeq(Celegans)
seqs[gr1]
seqs[gr1]
**Description**

Inject SNPs from a SNPlocs data package into a genome.

**Usage**

```r
injectSNPs(x, snps)
SNPlocs_pkgname(x)
## S4 method for signature 'BSgenome'
snpcount(x)
## S4 method for signature 'BSgenome'
snplocs(x, seqname, ...)
```

**Related utilities**

```r
available.SNPs(type=getOption("pkgType"))
installed.SNPs()
```

**Arguments**

- **x**  
  A BSgenome object.
- **snps**  
  A SNPlocs object or the name of a SNPlocs data package. This object or package must contain SNP information for the single sequences contained in x. If a package, it must be already installed (injectSNPs won’t try to install it).
- **seqname**  
  The name of a single sequence in x.
- **type**  
  Character string indicating the type of package ("source", "mac.binary" or "win.binary") to look for.
- **...**  
  Further arguments to be passed to snplocs method for SNPlocs objects.

**Value**

injectSNPs returns a copy of the original genome x where some or all of the single sequences from x are altered by injecting the SNPs stored in snps. The SNPs in the altered genome are represented by an IUPAC ambiguity code at each SNP location.

SNPlocs_pkgname, snpcount and snplocs return NULL if no SNPs were injected in x (i.e. if x is not a BSgenome object returned by a previous call to injectSNPs). Otherwise SNPlocs_pkgname returns the name of the package from which the SNPs were injected, snpcount the number of SNPs for each altered sequence in x, and snplocs their locations in the sequence whose name is specified by seqname.

available.SNPs returns a character vector containing the names of the SNPlocs and XtraSNPlocs data packages that are currently available on the Bioconductor repositories for your version of
R/Bioconductor. A SNPlocs data package contains basic information (location and alleles) about the known molecular variations of class `snp` for a given organism. A XtraSNPlocs data package contains information about the known molecular variations of other classes (in-del, heterozygous, microsatellite, named-locus, no-variation, mixed, multinucleotide-polymorphism) for a given organism. Only SNPlocs data packages can be used for SNP injection for now.

`installed.SNPs` returns a character vector containing the names of the SNPlocs and XtraSNPlocs data packages that are already installed.

**Note**

`injectSNPs`, `SNPlocs_pkgname`, `snpcount` and `snplocs` have the side effect to try to load the SNPlocs data package that was specified thru the `snps` argument if it’s not already loaded.

**Author(s)**

H. Pagès

**See Also**

`BSgenome-class`, `IUPAC_CODE_MAP`, `injectHardMask`, `letterFrequencyInSlidingView`, `.inplaceReplaceLetterAt`

**Examples**

```r
## What SNPlocs data packages are already installed:
installed.SNPs()

## What SNPlocs data packages are available:
available.SNPs()

if (interactive()) {
  ## Make your choice and install with:
  if (!require("BiocManager"))
    install.packages("BiocManager")
  BiocManager::install("SNPlocs.Hsapiens.dbSNP144.GRCh38")
}

## Inject SNPs from dbSNP into the Human genome:
library(BSgenome.Hsapiens.UCSC.hg38.masked)
genome <- BSgenome.Hsapiens.UCSC.hg38.masked
SNPlocs_pkgname(genome)

genome2 <- injectSNPs(genome, "SNPlocs.Hsapiens.dbSNP144.GRCh38")
genome2 # note the extra "with SNPs injected from ..." line
SNPlocs_pkgname(genome2)
snpcount(genome2)
head(snplocs(genome2, "chr1"))
alphabetFrequency(genome$chr1)
alphabetFrequency(genome2$chr1)

## Find runs of SNPs of length at least 25 in chr1. Might require
```


## Description

The SNPlocs class is a container for storing known SNP locations (of class `snp`) for a given organism.

SNPlocs objects are usually made in advance by a volunteer and made available to the Bioconductor community as SNPlocs data packages. See `?available.SNPs` for how to get the list of SNPlocs and XtraSNPlocs data packages currently available.

The main focus of this man page is on how to extract SNPs from an SNPlocs object.

### Usage

```r
snpcount(x)
```

```r
snpsBySeqname(x, seqnames, ...)
```

## S4 method for signature 'SNPlocs'

```r
snpsBySeqname(x, seqnames, drop.rs.prefix=FALSE, genome=NULL)
```

```r
snpsByOverlaps(x, ranges, ...)
```

## S4 method for signature 'SNPlocs'

```r
snpsByOverlaps(x, ranges, drop.rs.prefix=FALSE, ..., genome=NULL)
```

```r
snpsById(x, ids, ...)
```

## S4 method for signature 'SNPlocs'

```r
snpsById(x, ids, ifnotfound=c("error", "warning", "drop"), genome=NULL)
```

```r
inferRefAndAltAlleles(gpos, genome)
```
Arguments

- **x**: A SNPlocs object.
- **seqnames**: The names of the sequences for which to get SNPs. Must be a subset of `seqlevels(x)`. NAs and duplicates are not allowed.
- **...**: Additional arguments, for use in specific methods.

Arguments passed to the `snpsByOverlaps` method for SNPloc objects thru ... are used internally in the call to `subsetByOverlaps()`. See `IRanges::subsetByOverlaps` in the **IRanges** package and `GenomicRanges::subsetByOverlaps` in the **GenomicRanges** package for more information about the `subsetByOverlaps()` generic and its method for `GenomicRanges` objects.

- **drop.rs.prefix**: Should the rs prefix be dropped from the returned RefSNP ids? (RefSNP ids are stored in the `RefSNP_id` metadata column of the returned object.)
- **genome**: For `snpsBySeqname`, `snpsByOverlaps`, and `snpsById`:
  - `NULL` (the default), or a **BSgenome** object containing the sequences of the reference genome that corresponds to the SNP positions. See `inferRefAndAltAlleles` below for an alternative way to specify genome.
  - If genome is supplied, then `inferRefAndAltAlleles` is called internally by `snpsBySeqname`, `snpsByOverlaps`, or `snpsById` to infer the reference allele (a.k.a. `ref` allele) and alternate allele(s) (a.k.a. `alt` allele(s)) for each SNP in the returned **GPos** object. The inferred `ref` allele and `alt` allele(s) are returned in additional metadata columns `ref_allele` (character) and `alt_alleles` (CharacterList).

  For `inferRefAndAltAlleles`:
  - A **BSgenome** object containing the sequences of the reference genome that corresponds to the SNP positions in `gpos`. Alternatively genome can be a single string containing the name of the reference genome, in which case it must be specified in a way that is accepted by the `getBSgenome` function (e.g. "GRCh38") and the corresponding BSgenome data package needs to be already installed (see `?getBSgenome` for the details).
- **ranges**: One or more genomic regions of interest specified as a **GRanges** or **GPos** object. A single region of interest can be specified as a character string of the form "ch14:5201-5300".
- **ids**: The RefSNP ids to look up (a.k.a. rs ids). Can be integer or character vector, with or without the "rs" prefix. NAs are not allowed.
- **ifnotfound**: What to do if SNP ids are not found.
- **gpos**: A **GPos** object containing SNPs. It must have a metadata column `alleles_as_ambig` like obtained when using any of the SNP extractor `snpsBySeqname`, `snpsByOverlaps`, or `snpsById` on a SNPloc object.

Details

When the reference genome is specified via the `genome` argument, SNP extractors `snpsBySeqname`, `snpsByOverlaps`, and `snpsById` call `inferRefAndAltAlleles` internally to infer the reference allele (a.k.a. `ref` allele) and alternate allele(s) (a.k.a. `alt` allele(s)) for each SNP.
For each SNP the ref allele is inferred from the actual nucleotide found in the reference genome at the SNP position. The alt alleles are inferred from metadata column alleles_as_ambig and the ref allele. More precisely for each SNP the alt alleles are considered to be the alleles in alleles_as_ambig minus the ref allele.

Value

snpcount returns a named integer vector containing the number of SNPs for each sequence in the reference genome.

snpsBySeqname, snpsByOverlaps, and snpsById return an unstranded GPos object with one element (genomic position) per SNP and the following metadata columns:

- RefSNP_id: RefSNP ID (aka "rs id"). Character vector with no NAs and no duplicates.
- alleles_as_ambig: A character vector with no NAs containing the alleles for each SNP represented by an IUPAC nucleotide ambiguity code. See ?IUPAC_CODE_MAP in the Biostrings package for more information.

If the reference genome was specified (via the genome argument), the additional metadata columns are returned:

- genome_compat: A logical vector indicating whether the alleles in alleles_as_ambig are consistent with the reference genome.
- ref_allele: A character vector containing the inferred reference allele for each SNP.
- alt_alleles: A CharacterList object where each list element is a character vector containing the inferred alternate allele(s) for the corresponding SNP.

Note that this GPos object is unstranded i.e. all the SNPs in it have their strand set to "*". Alleles are always reported with respect to the positive strand.

If ifnotfound="error", the object returned by snpsById is guaranteed to be parallel to ids, that is, the i-th element in the GPos object corresponds to the i-th element in ids.

inferRefAndAlt Alleles returns a DataFrame with one row per SNP in gpos and with columns genome_compat (logical), ref_allele (character), and alt_alleles (CharacterList).

Author(s)

H. Pagès

See Also

- available.SNPs
- GPos and GRanges objects in the GenomicRanges package.
- XtraSNPlocs packages and objects for molecular variations of class other than snp e.g. of class in-del, heterozygous, microsatellite, etc...
- IRanges::subsetByOverlaps in the IRanges package and GenomicRanges::subsetByOverlaps in the GenomicRanges package for more information about the subsetByOverlaps() generic and its method for GenomicRanges objects.
- injectSNPs
- IUPAC_CODE_MAP in the Biostrings package.
Examples

```r
library(SNPlocs.Hsapiens.dbSNP144.GRCh38)
snps <- SNPlocs.Hsapiens.dbSNP144.GRCh38
snpcount(snps)
```

```r
# snpsBySeqname()
# Get all SNPs located on chromosome 22 or MT:
snpsBySeqname(snps, c("22", "MT"))
```

```r
# snpsByOverlaps()
# Get all SNPs overlapping some genomic region of interest:
snpsByOverlaps(snps, "X:3e6-33e6")
```

```r
# With the regions of interest being all the known CDS for hg38
# located on chromosome 22 or MT (except for the chromosome naming
# convention, hg38 is the same as GRCh38):
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg38.knownGene
my_cds <- cds(txdb)
seqlevels(my_cds, pruning.mode="coarse") <- c("chr22", "chrM")
seqlevelsStyle(my_cds) # UCSC
seqlevelsStyle(snps) # NCBI
seqlevelsStyle(my_cds) <- seqlevelsStyle(snps)
genome(my_cds) <- genome(snps)
my_snps <- snpsByOverlaps(snps, my_cds)
my_snps
table(my_snps %within% my_cds)
```

```r
# snpsById()
# Lookup some RefSNP ids:
my_rsids <- c("rs10458597", "rs12565286", "rs7553394")
# Not run:
  snpsById(snps, my_rsids) # error, rs7553394 not found
```

```r
# End(Not run)
# The following example uses more than 2GB of memory, which is more
# than what 32-bit Windows can handle:
is_32bit_windows <- .Platform$OS.type == "windows" &&
  .Platform$r_arch == "i386"
if (!is_32bit_windows) {
  snpsById(snps, my_rsids, ifnotfound="drop")
}
```
## Obtain the ref allele and alt allele(s)

When the reference genome is specified (via the 'genome' argument),
SNP extractors `snpsBySeqname()`, `snpsByOverlaps()`, and `snpsById()`
call `inferRefAndAltAlleles()` internally to **infer** the ref allele
and alt allele(s) for each SNP.

```r
my_snps <- snpsByOverlaps(snps, "X:3e6-8e6", genome="GRCh38")
my_snps
```

```
## Most SNPs have only 1 alternate allele:
table(lengths(mcols(my_snps)$alt_alleles))

## SNPs with 2 alternate alleles:
my_snps[lengths(mcols(my_snps)$alt_alleles) == 2]

## SNPs with 3 alternate alleles:
my_snps[lengths(mcols(my_snps)$alt_alleles) == 3]

## Note that a small percentage of SNPs in dbSNP have alleles that
## are inconsistent with the reference genome (don't ask me why):
table(mcols(my_snps)$genome_compat)

## For the inconsistent SNPs, all the alleles reported by dbSNP have alleles that
## are considered alternate alleles i.e. for each inconsistent SNP
## metadata columns "alleles_as_ambig" and "alt_alleles" represent
## the same set of nucleotides (the latter being just an expanded
## representation of the IUPAC ambiguity letter in the former):
my_snps[!mcols(my_snps)$genome_compat]
```

---

**Description**

The XtraSNPlocs class is a container for storing extra SNP locations and alleles for a given organism. While a `SNPlocs` object can store only molecular variations of class `snp`, an XtraSNPlocs object contains molecular variations of other classes (`in-del`, `heterozygous`, `microsatellite`, `named-locus`, `no-variation`, `mixed`, `multinucleotide-polymorphism`).

XtraSNPlocs objects are usually made in advance by a volunteer and made available to the Bioconductor community as `XtraSNPlocs data packages`. See `?available.SNPs` for how to get the list of `SNPlocs` and `XtraSNPlocs data packages` currently available.

The main focus of this man page is on how to extract SNPs from an XtraSNPlocs object.

**Usage**

```r
## S4 method for signature 'XtraSNPlocs'
snpcount(x)
```
XtraSNPlocs-class

## S4 method for signature 'XtraSNPlocs'

```r
snpsBySeqname(x, seqnames,  
columns=c("seqnames", "start", "end", "strand", "RefSNP_id"),  
drop.rs.prefix=FALSE, as.DataFrame=FALSE)
```

## S4 method for signature 'XtraSNPlocs'

```r
snpsByOverlaps(x, ranges,  
columns=c("seqnames", "start", "end", "strand", "RefSNP_id"),  
drop.rs.prefix=FALSE, as.DataFrame=FALSE, ...)
```

## S4 method for signature 'XtraSNPlocs'

```r
snpsById(x, ids,  
columns=c("seqnames", "start", "end", "strand", "RefSNP_id"),  
ifnotfound=c("error", "warning", "drop"), as.DataFrame=FALSE)
```

## S4 method for signature 'XtraSNPlocs'

colnames(x, do.NULL=TRUE, prefix="col")

### Arguments

- **x**  
  An XtraSNPlocs object.

- **seqnames**  
  The names of the sequences for which to get SNPs. NAs and duplicates are not allowed. The supplied seqnames must be a subset of seqlevels(x).

- **columns**  
  The names of the columns to return. Valid column names are: seqnames, start, end, width, strand, RefSNP_id, alleles, snpClass, loctype. See Details section below for a description of these columns.

- **drop.rs.prefix**  
  Should the rs prefix be dropped from the returned RefSNP ids? (RefSNP ids are stored in the RefSNP_id metadata column of the returned object.)

- **as.DataFrame**  
  Should the result be returned in a DataFrame instead of a GRanges object?

- **ranges**  
  One or more regions of interest specified as a GRanges object. A single region of interest can be specified as a character string of the form "chr1:5201-5300".

- **...**  
  Additional arguments, for use in specific methods.

  Arguments passed to the snpsByOverlaps method for XtraSNPlocs objects thru ... are used internally in the call to subsetByOverlaps(). See ?IRanges::subsetByOverlaps in the IRanges package and ?GenomicRanges::subsetByOverlaps in the GenomicRanges package for more information about the subsetByOverlaps() generic and its method for GenomicRanges objects.

- **ids**  
  The RefSNP ids to look up (a.k.a. rs ids). Can be integer or character vector, with or without the "rs" prefix. NAs are not allowed.

- **ifnotfound**  
  What to do if SNP ids are not found.

- **do.NULL, prefix**  
  These arguments are ignored.
Value

snpcount returns a named integer vector containing the number of SNPs for each chromosome in the reference genome.

snpsBySeqname and snpsById both return a GRanges object with 1 element per SNP, unless as.DataFrame is set to TRUE in which case they return a DataFrame with 1 row per SNP. When a GRanges object is returned, the columns requested via the columns argument are stored as meta data columns of the object, except for the following columns: seqnames, start, end, width, and strand. These "spatial columns" (in the sense that they describe the genomic locations of the SNPs) can be accessed by calling the corresponding getter on the GRanges object.

Summary of available columns (my_snps being the returned object):

- seqnames: The name of the chromosome where each SNP is located. Access with seqnames(my_snps) when my_snps is a GRanges object.
- start and end: The starting and ending coordinates of each SNP with respect to the chromosome indicated in seqnames. Coordinated are 1-based and with respect to the 5' end of the plus strand of the chromosome in the reference genome. Access with start(my_snps), end(my_snps), or ranges(my_snps) when my_snps is a GRanges object.
- width: The number of nucleotides spanned by each SNP on the reference genome (e.g. a width of 0 means the SNP is an insertion). Access with width(my_snps) when my_snps is a GRanges object.
- strand: The strand that the alleles of each SNP was reported to. Access with strand(my_snps) when my_snps is a GRanges object.
- RefSNP_id: The RefSNP id (a.k.a. rs id) of each SNP. Access with mcols(my_snps)$RefSNP_id when my_snps is a GRanges object.
- alleles: The alleles of each SNP in the format used by dbSNP. Access with mcols(my_snps)$alleles when my_snps is a GRanges object.
- snpClass: Class of each SNP. Possible values are in-del, heterozygous, microsatellite, named-locus, no-variation, mixed, and multinucleotide-polymorphism. Access with mcols(my_snps)$snpClass when my_snps is a GRanges object.
- loctype: See ftp://ftp.ncbi.nih.gov/snp/00readme.txt for the 6 loctype codes used by dbSNP, and their meanings. WARNING: The code assigned to each SNP doesn't seem to be reliable. For example, loctype codes 1 and 3 officially stand for insertion and deletion, respectively. However, when looking at the SNP ranges it actually seems to be the other way around. Access with mcols(my_snps)$loctype when my_snps is a GRanges object.

colnames(x) returns the names of the available columns.

Author(s)

H. Pagès

See Also

- available.SNPs
- GRanges objects in the GenomicRanges package.
- SNPlocs packages and objects for molecular variations of class snp.
Examples

library(XtraSNPlocs.Hsapiens.dbSNP144.GRCh38)
snps <- XtraSNPlocs.Hsapiens.dbSNP144.GRCh38
snpcount(snps)
colnames(snps)

## ---------------------------------------------------------------------
## snpsBySeqname()
## ---------------------------------------------------------------------

## Get the location, RefSNP id, and alleles for all "extra SNPs"
## located on chromosome 22 or MT:
snpsBySeqname(snps, c("ch22", "chMT"), columns=c("RefSNP_id", "alleles"))

## ---------------------------------------------------------------------
## snpsByOverlaps()
## ---------------------------------------------------------------------

## Get the location, RefSNP id, and alleles for all "extra SNPs"
## overlapping some regions of interest:
snpsByOverlaps(snps, "ch22:33.63e6-33.64e6",
    columns=c("RefSNP_id", "alleles"))

## With the regions of interest being all the known CDS for hg38
## (except for the chromosome naming convention, hg38 is the same
## as GRCh38):
library(TxDB.Hsapiens.UCSC.hg38.knownGene)
txdb <- TxDB.Hsapiens.UCSC.hg38.knownGene
hg38_cds <- cds(txdb)
seqlevelsStyle(hg38_cds) # UCSC
seqlevelsStyle(snps) # dbSNP
seqlevelsStyle(hg38_cds) <- seqlevelsStyle(snps)
genome(hg38_cds) <- genome(snps)

snpsByOverlaps(snps, hg38_cds, columns=c("RefSNP_id", "alleles"))

## ---------------------------------------------------------------------
## snpsById()
## ---------------------------------------------------------------------

## Get the location and alleles for some RefSNP ids:
my_rsids <- c("rs367617508", "rs398104919", "rs3831697", "rs372470289",
    "rs141568169", "rs34628976", "rs67551854")

snpsById(snps, my_rsids, c("RefSNP_id", "alleles"))

## See ?XtraSNPlocs.Hsapiens.dbSNP144.GRCh38 for more examples of using
## snpsBySeqname() and snpsById().
Index

* classes
  BSgenome-class, 7
  BSgenomeViews-class, 16
  BSParams-class, 20
  SNPlocs-class, 30
  XtraSNPlocs-class, 34

* manip
  available.genomes, 2
  bsapply, 5
  BSgenomeForge, 13
  getSeq-methods, 22
  injectSNPs, 28

* methods
  BSgenome-class, 7
  BSgenome-utils, 11
  BSgenomeViews-class, 16
  export-methods, 21
  SNPlocs-class, 30
  XtraSNPlocs-class, 34

* utilities
  BSgenome-utils, 11
  export-methods, 21
  .inplaceReplaceLetterAt, 29
  [,XStringSet,GRangesList-method
  (getSeq-methods), 22
  [,XStringSet,GenomicRanges-method
  (getSeq-methods), 22
  [[,BSgenome-method (BSgenome-class), 7
  $,BSgenome-method (BSgenome-class), 7
  alphabetFrequency, 18, 19
  alphabetFrequency,BSgenomeViews-method
  (BSgenomeViews-class), 16
  as.character,BSgenomeViews-method
  (BSgenomeViews-class), 16
  as.data.frame,BSgenomeViews-method
  (BSgenomeViews-class), 16
  as.list,BSgenome-method
  (BSgenome-class), 7
  available.genomes, 2, 7, 9, 15, 23, 24
  available.packages, 4
  available.SNPs, 30, 32, 34, 36
  available.SNPs (injectSNPs), 28
  bsapply, 5, 12, 21, 22
  BSgenome, 2–4, 11, 15, 16, 18, 19, 21–23, 28, 31
  BSgenome (BSgenome-class), 7
  BSgenome-class, 6, 7, 24, 29
  BSgenome-utils, 6, 9, 11
  BSgenome.Hsapiens.UCSC.hg38, 8
  BSgenomeDataPkgSeed (BSgenomeForge), 13
  BSgenomeDataPkgSeed-class
  (BSgenomeForge), 13
  BSgenomeForge, 13
  bsgenomeName,BSgenome-method
  (BSgenome-class), 7
  BSgenomeViews (BSgenomeViews-class), 16
  BSgenomeViews-class, 16
  BSParams (BSParams-class), 20
  BSParams-class, 6, 20
  CharacterList, 24, 32
  class:BSgenome (BSgenome-class), 7
  class:BSgenomeDataPkgSeed
  (BSgenomeForge), 13
  class:BSgenomeViews
  (BSgenomeViews-class), 16
  class:BSParams (BSParams-class), 20
  class:InjectSNPsHandler (injectSNPs), 28
  class:ODLT_SNPlocs (SNPlocs-class), 30
  class:OldFashionSNPlocs
  (SNPlocs-class), 30
  class:SNPlocs (SNPlocs-class), 30
  class:XtraSNPlocs (XtraSNPlocs-class), 34
  coerce,BSgenome,GenomeDescription-method
  (BSgenome-class), 7
  coerce,BSgenomeViews,DNAStringSet-method
  (BSgenomeViews-class), 16
INDEX

coerce, BSgenomeViews, XStringSet-method
  (BSgenomeViews-class), 16
coename, XStringSet-method
  (BSgenomeViews-class), 16
commonName, BSgenome-method
  (BSgenome-class), 7
commonName, SNPloc-method
  (SNPloc-class), 30
commonName, XtraSNPloc-method
  (XtraSNPloc-class), 34
compatibleGenomes (SNPloc-class), 30
compatibleGenomes, SNPloc-method
  (SNPloc-class), 30
consensusMatrix, 18, 19
consensusMatrix, BSgenomeViews-method
  (BSgenomeViews-class), 16
consensusString, 19
consensusString, BSgenomeViews-method
  (BSgenomeViews-class), 16
countPWM, BSgenome-method
  (BSgenome-utils), 11
data, 12, 32, 35, 36
dim, XtraSNPloc-method
  (XtraSNPloc-class), 34
DNAString, 7, 8, 11, 24
DNAString-class, 9, 24
DNAStringSet, 8, 12, 19, 24
DNAStringSet-class, 9, 24
dnaStringSetList, 24
elementNROWS, BSgenomeViews-method
  (BSgenomeViews-class), 16
end, BSgenomeViews-method
  (BSgenomeViews-class), 16
export, 21, 22
export, BSgenome, FastaFile, ANY-method
  (export-methods), 21
export, BSgenome, TwoBitFile, ANY-method
  (export-methods), 21
export-methods, 21
extractROWS, BSgenomeViews-method
  (BSgenomeViews-class), 16
FastaFile, 21, 22
forgeBSgenomeDataPkg (BSgenomeForge), 13
forgeBSgenomeDataPkg, character-method
  (BSgenomeForge), 13
forgeBSgenomeDataPkg, list-method
  (BSgenomeForge), 13
forgeBSgenomeDataPkgFromNCBI, 15
forgeBSgenomeDataPkgFromUCSC, 15
forgeMasksFiles (BSgenomeForge), 13
forgeSeqFiles (BSgenomeForge), 13
forgeSeqlengthsRdaFile (BSgenomeForge), 13
forgeSeqlengthsRdsFile (BSgenomeForge), 13
gc, 9
GenomeDescription-class, 9
GenomicRanges, 24, 31, 32, 35
getBSgenome, 18, 31
getBSgenome (available.genomes), 2
getElement, BSgenomeViews-method
  (BSgenomeViews-class), 16
getSeq, 22, 24
getSeq (getSeq-methods), 22
getSeq, BSgenome-method
  (getSeq-methods), 22
getSeq, XStringSet-method
  (getSeq-methods), 22
grep-methods, 22
GPos, 31, 32
GRanges, 12, 18, 19, 23, 24, 31, 32, 35, 36
granges, BSgenomeViews-method
  (BSgenomeViews-class), 16
GRanges-class, 24
GRangesList, 23, 24
GRangesList-class, 24
grep, 24
hasOnlyBaseLetters, 19
hasOnlyBaseLetters, BSgenomeViews-method
  (BSgenomeViews-class), 16
inferRefAndAltAlleles (SNPloc-class), 30
injectHardMask, 29
injectSNPs, 9, 28, 32
injectSNPs, BSgenome-method
  (injectSNPs), 28
InjectSNPsHandler (injectSNPs), 28
InjectSNPsHandler-class (injectSNPs), 28
installed.genomes (available.genomes), 2
INDEX

installed.SNPs (injectSNPs), 28
IntegerRanges, 23, 24
IntegerRanges-class, 24
IntegerRangesList, 12, 21, 23, 24
IntegerRangesList-class, 24
IUPAC_CODE_MAP, 29, 32

length, BSgenome-method
   (BSgenome-class), 7
length, BSgenomeViews-method
   (BSgenomeViews-class), 16
letterFrequency, 19
letterFrequency, BSgenomeViews-method
   (BSgenomeViews-class), 16
letterFrequencyInSlidingView, 29

MaskedDNAString, 7, 8
MaskedDNAString-class, 9, 24
MaskedXString, 8
masknames (BSgenome-class), 7
masknames, BSgenome-method
   (BSgenome-class), 7
masknames, MaskedBSgenome-method
   (BSgenome-class), 7
matchPattern, 11, 12
matchPDict, 12
matchPWM, 12
matchPWM, BSgenome-method
   (BSgenome-utils), 11
mseqnames (BSgenome-class), 7
mseqnames, BSgenome-method
   (BSgenome-class), 7

names, BSgenome-method (BSgenome-class), 7
names, BSgenomeViews-method
   (BSgenomeViews-class), 16
nchar, BSgenomeViews-method
   (BSgenomeViews-class), 16
new_ODLT_SNPlocs (SNPlocs-class), 30
newSNPlocs (SNPlocs-class), 30
newXtraSNPlocs (XtraSNPlocs-class), 34
nucleotideFrequencyAt, 19
nucleotideFrequencyAt, BSgenomeViews-method
   (BSgenomeViews-class), 16

ODLT_SNPlocs (SNPlocs-class), 30
ODLT_SNPlocs-class (SNPlocs-class), 30
OldFashionSNPlocs (SNPlocs-class), 30

OldFashionSNPlocs-class
   (SNPlocs-class), 30
oligonucleotideFrequency, 18, 19
oligonucleotideFrequency, BSgenomeViews-method
   (BSgenomeViews-class), 16
organism, BSgenome-method
   (BSgenome-class), 7
organism, SNPlocs-method
   (SNPlocs-class), 30
organism, XtraSNPlocs-method
   (XtraSNPlocs-class), 34

PDict, 12
provider, BSgenome-method
   (BSgenome-class), 7
provider, SNPlocs-method
   (SNPlocs-class), 30
provider, XtraSNPlocs-method
   (XtraSNPlocs-class), 34
providerVersion, BSgenome-method
   (BSgenome-class), 7
providerVersion, SNPlocs-method
   (SNPlocs-class), 30
providerVersion, XtraSNPlocs-method
   (XtraSNPlocs-class), 34
ranges, BSgenomeViews-method
   (BSgenomeViews-class), 16
referenceGenome (SNPlocs-class), 30
referenceGenome, SNPlocs-method
   (SNPlocs-class), 30
referenceGenome, XtraSNPlocs-method
   (XtraSNPlocs-class), 34
releaseDate, BSgenome-method
   (BSgenome-class), 7
releaseDate, SNPlocs-method
   (SNPlocs-class), 30
releaseDate, XtraSNPlocs-method
   (XtraSNPlocs-class), 34
releaseName (SNPlocs-class), 30
releaseName, SNPlocs-method
   (SNPlocs-class), 30
releaseName, XtraSNPlocs-method
   (XtraSNPlocs-class), 34
rm, 9

seqinfo, 18, 19
seqinfo, BSgenome-method
   (BSgenome-class), 7
subject, BSgenomeViews-method
  (BSgenomeViews-class), 16
subseq, XVector-method, 9
subsetByOverlaps, 31, 32, 35

TwoBitFile, 21, 22
TxDb, 19

uniqueLetters, 19
uniqueLetters, BSgenomeViews-method
  (BSgenomeViews-class), 16
unlist, BSgenomeViews-method
  (BSgenomeViews-class), 16

vcountPattern, BSgenome-method
  (BSgenome-utils), 11
vcountPDict, BSgenome-method
  (BSgenome-utils), 11
Views, BSgenome-method
  (BSgenomeViews-class), 16
vmatchPattern, BSgenome-method
  (BSgenome-utils), 11
vmatchPDict, BSgenome-method
  (BSgenome-utils), 11

width, BSgenomeViews-method
  (BSgenomeViews-class), 16
writeBSgenomeToFasta (export-methods), 21
writeBSgenomeToTwobit (export-methods), 21
writeXStringSet, 22

XString, 15
XStringSet, 22–24
XtraSNPlocs, 30, 32
XtraSNPlocs (XtraSNPlocs-class), 34
XtraSNPlocs-class, 34