

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.

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available.genomes	<i>Find available/installed genomes</i>
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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.

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 a genome assembly (a.k.a. provider version) that refers unambiguously to an installed BSgenome data package.
masked	TRUE or FALSE. Whether to search for the <i>masked</i> 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 the release string or number used by this organisation for this particular genome assembly. We formally refer to it as the *provider version* of the genome. E.g. hg38, GRCh38, hg19, mm10, susScr11, 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.

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), `provider_version` (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

```
## -----
## available.genomes() and installed.genomes()
## -----

# What genomes are currently installed:
installed.genomes()

# What genomes are available:
available.genomes()

# Split the package names in parts:
av_gen <- available.genomes(splitNameParts=TRUE)
table(av_gen$organism)
table(av_gen$provider)

# Make your choice and install with:
if (interactive()) {
  if (!require("BiocManager"))
    install.packages("BiocManager")
  BiocManager::install("BSgenome.Scerevisiae.UCSC.sacCer1")
}

# Have a coffee 8-)

# Load the package and display the index of sequences for this genome:
library(BSgenome.Scerevisiae.UCSC.sacCer1)
Scerevisiae # same as BSgenome.Scerevisiae.UCSC.sacCer1

## -----
## getBSgenome()
## -----

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

## Specify a genome assembly (a.k.a. provider version):
genome <- getBSgenome("hg38")
class(genome) # BSgenome object
providerVersion(genome)
genome$chrM

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

bsapply	<i>bsapply</i>
---------	----------------

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("BSPParams", 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("BSPParams", 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" curenly available.

Accessor methods

In the code snippets below, `x` is a `BSgenome` object. Note that, because the `BSgenome` class contains the `GenomeDescription` class, then all the accessor methods for `GenomeDescription` objects can also be used on `x`.

`sourceUrl(x)` Returns the source URL i.e. 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,XVector-method`` and `?length,MaskedXString-method`` for the definition of the length of a `DNAString` or `MaskedDNAString` object. Note that the length of a masked sequence (`MaskedXString` object) is not affected by the current set of active masks but the `nchar` method for `MaskedXString` 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 ($0 \leq N \leq 4$). 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

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)

## 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
seqnames(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:
names(rn5_random)[1:4]

## -----
## PASS-BY-ADDRESS SEMANTIC, CACHING AND MEMORY USAGE
## -----

## We want a message to be printed each time a sequence is removed
## from the cache:
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):
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'):
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):
options(verbose=TRUE)
rm(rn5_chr2, tmp)
gc()

## Remember that 'y' holds a reference to 'rn5_chr2' too:
rm(y)
gc()

options(verbose=FALSE)
gc()["Vcells", "(Mb)"] - mem0

```

Description

Utilities for BSgenome objects.

Usage

```
## 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)
## 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)

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

## S4 method for signature 'BSgenome'
matchPWM(pwm, subject, min.score="80%", exclude="", maskList=logical(0))
## 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 ? <code>lowlevel-matching</code> 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 ? <code>matchPattern</code> for the details).
fixed	If FALSE then IUPAC extended letters are interpreted as ambiguities (see ? <code>lowlevel-matching</code> for the details).
algorithm	For vmatchPattern and vcountPattern one of the following: "auto", "naive-exact", "naive-inexact", "boyer-moore", "shift-or", or "indels". For vmatchPDict and 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 bsapply function, the masks will be set to the states in this vector.

userMask	An IntegerRangesList , containing a mask to be applied to each chromosome. See bsapply .
invertUserMask	Whether the userMask should be inverted.
collapse, weight	ignored arguments.
pdict	A PDict or DNAStringSet object containing the pattern sequences.
verbose	TRUE or FALSE.
pwm	A numeric matrix with row names A, C, G and T representing a Position Weight Matrix.
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 [GRanges](#) object for `vmatchPattern`.

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

A [GRanges](#) object for `vmatchPDict` with one metadata column: "index", which represents a mapping to a position in the original pattern dictionary.

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

A [GRanges](#) object for `matchPWM` with two metadata columns: "score" (numeric), and "string" ([DNAStringSet](#)).

Author(s)

P. Aboyoun

See Also

[matchPattern](#), [matchPDict](#), [matchPWM](#), [bsapply](#)

Examples

```
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)
```

Description

A set of functions for making a BSgenome data package.

Usage

```
## Top-level BSgenomeForge function:
```

```
forgeBSgenomeDataPkg(x, seqs_srcdir=".", destdir=".", verbose=TRUE)
```

```
## Low-level BSgenomeForge functions:
```

```
forgeSeqlengthsFile(seqnames, prefix="", suffix=".fa",
                    seqs_srcdir=".", seqs_destdir=".", verbose=TRUE)
```

```
forgeSeqFiles(provider, provider_version,
              seqnames, mseqnames=NULL,
              seqfile_name=NA, prefix="", suffix=".fa",
              seqs_srcdir=".", seqs_destdir=".",
              ondisk_seq_format=c("2bit", "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.
verbose	TRUE or FALSE.
provider	The provider of the <i>sequence data files</i> e.g. "UCSC", "NCBI", "BDGP", "FlyBase", etc...

provider_version

The provider-side version of the genome e.g. "hg38" or "bosTau9" if the genome is provided by UCSC, or "GRCh38.p12" or "ARS-UCD1.2" if it's provided by NCBI.

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.

forgeSeqLengthsFile will produce a single .rda file. Both forgeSeqFiles and forgeMasksFiles will produce one .rda file per sequence.

ondisk_seq_format

Specifies how the single sequences should be stored in the forged package. Can be "2bit", "rda", "fa.rz", or "fa". If "2bit" (the default), then all the single sequences are stored in a single twoBit file. If "rda", then each single sequence is stored in a separated serialized XString object (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").

nmask_per_seq

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

AGAPSfiles_type, AGAPSfiles_name, AGAPSfiles_prefix, AGAPSfiles_suffix, RMfiles_name, RMfiles_prefix

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.

Details

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.

Author(s)

H. Pagès

Examples

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

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

```

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

## Sanity checks:
library(BSgenome.Celegans.UCSC.ce2)
genome <- BSgenome.Celegans.UCSC.ce2

load(file.path(tempdir(), "chrX.rda"))
stopifnot(genome$chrX == chrX)
load(file.path(tempdir(), "chrM.rda"))
stopifnot(genome$chrM == chrM)

ce2_sequences <- import(file.path(tempdir(), "single_sequences.2bit"))
ce2_sequences0 <- DNASTringSet(list(chrX=genome$chrX, chrM=genome$chrM))
stopifnot(identical(names(ce2_sequences0), names(ce2_sequences)) &&
           all(ce2_sequences0 == ce2_sequences))

```

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

```

## Constructor
## -----

BSgenomeViews(subject, granges)

## Accessors
## -----

## S4 method for signature 'BSgenomeViews'
subject(x)
## S4 method for signature 'BSgenomeViews'
granges(x, use.mcols=FALSE)

## S4 method for signature 'BSgenomeViews'
length(x)
## S4 method for signature 'BSgenomeViews'
names(x)
## S4 method for signature 'BSgenomeViews'
seqnames(x)
## S4 method for signature 'BSgenomeViews'
start(x)
## S4 method for signature 'BSgenomeViews'

```

```
end(x)
## S4 method for signature 'BSgenomeViews'
width(x)
## S4 method for signature 'BSgenomeViews'
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 <code>mcols(x)</code>) should be propagated to the returned object or not.
type, allowNA, recursive, use.names	Ignored.
as.prob, letters, OR, width	See ?alphabetFrequency and ?oligonucleotideFrequency in the Biostrings package.
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

```
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, "DNAStrngSet")
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)

```

BSPParams-class

Class "BSPParams"

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("BSPParams", ...)`.

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 BParams.

Author(s)

Marc Carlson

See Also

[bsapply](#)

 export-methods

Export a BSgenome object as a FASTA or twoBit file

Description

`export` methods for [BSgenome](#) objects.

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

<code>object</code>	The BSgenome object to export.
<code>con</code>	A FastaFile or TwoBitFile object. Alternatively <code>con</code> can be a single string containing the path to a FASTA or twoBit file, in which case either the file extension or the <code>format</code> argument needs to be "fasta", "twoBit", or "2bit". Also note that in this case, the <code>export</code> method that is called is either the method with signature <code>c("ANY", "character", "missing")</code> or the method with signature <code>c("ANY", "character", "character")</code> , both defined in the <code>rtracklayer</code> package. If <code>object</code> is a BSgenome object and the file extension or the <code>format</code> argument is "fasta", "twoBit", or "2bit", then the flow eventually reaches one of 2 methods documented here.
<code>format</code>	If not missing, should be "fasta", "twoBit", or "2bit" (case insensitive for "twoBit" and "2bit").
<code>compress, compression_level</code>	Forwarded to writeXStringSet . See ?writeXStringSet for the details.
<code>verbose</code>	Whether or not the function should display progress. TRUE by default.
<code>...</code>	Extra arguments. The method for TwoBitFile objects forwards them to bsapply .

Author(s)

Michael Lawrence

See Also

- [BSgenome](#) objects.
- The [export](#) generic, and [FastaFile](#) and [TwoBitFile](#) objects in the [rtracklayer](#) package.

Examples

```
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))
```

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 [XStringSet](#)s, there are also convenience methods on `[]` that delegate to `getSeq`.

Usage

```
## 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.

<code>start, end, width</code>	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 <code>names</code> is a <code>GRanges</code> , <code>GRangesList</code> , <code>IntegerRangesList</code> , or <code>IntegerRanges</code> object.
<code>strand</code>	A vector containing "+"s or/and "-"s. This is not needed (and it's an error to supply it) when <code>names</code> is a <code>GRanges</code> or <code>GRangesList</code> object.
<code>as.character</code>	TRUE or FALSE. Should the extracted sequences be returned in a standard character vector?
<code>...</code>	Additional arguments. (Currently ignored.)

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", "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,
                         replace=TRUE)
                 })
  names <- rep.int(seqnames(x), elementNROWS(start))
  ranges <- IRanges(start=unlist(start), width=readlength)
  strand <- strand(sample(c("+", "-"), length(names), replace=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.

```



```

## -----
## F. SEE THE BSgenome CACHE IN ACTION
## -----

options(verbose=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]

```

injectSNPs

SNP injection

Description

Inject SNPs from a SNPlocs data package into a genome.

Usage

```

injectSNPs(x, snps)

SNPlocs_pkgname(x)

## S4 method for signature 'BSgenome'
snpcount(x)
## S4 method for signature 'BSgenome'
snplocs(x, seqname, ...)

## Related utilities
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 `snp`s. 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 `snp`s argument if it's not already loaded.

Author(s)

H. Pagès

See Also

[BSgenome-class](#), [IUPAC_CODE_MAP](#), [injectHardMask](#), [letterFrequencyInSlidingView](#), [.inplaceReplaceLetterAt](#)

Examples

```
## 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
## more memory than some platforms can handle (e.g. 32-bit Windows
## and maybe some Mac OS X machines with little memory):
is_32bit_windows <- .Platform$OS.type == "windows" &&
  .Platform$r_arch == "i386"
is_macosx <- substr(R.version$os, start=1, stop=6) == "darwin"
if (!is_32bit_windows && !is_macosx) {
  chr1 <- injectHardMask(genome2$chr1)
  ambiguous_letters <- paste(DNA_ALPHABET[5:15], collapse="")
  lf <- letterFrequencyInSlidingView(chr1, 25, ambiguous_letters)
  sl <- slice(as.integer(lf), lower=25)
  v1 <- Views(chr1, start(sl), end(sl)+24)
  v1
  max(width(v1)) # length of longest SNP run
}

```

SNPlocs-class

SNPlocs objects

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

```
snpcount(x)
```

```
snpBySeqname(x, seqnames, ...)
```

```
## S4 method for signature 'SNPlocs'
```

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

```
snpByOverlaps(x, ranges, ...)
```

```
## S4 method for signature 'SNPlocs'
```

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

```
snpById(x, ids, ...)
```

```
## S4 method for signature 'SNPlocs'
snpsById(x, ids, ifnotfound=c("error", "warning", "drop"), genome=NULL)

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 SNPlocs objects thru ... are used internally in the call to <code>subsetByOverlaps()</code> . See <code>?IRanges::subsetByOverlaps</code> in the IRanges package and <code>?GenomicRanges::subsetByOverlaps</code> in the GenomicRanges package for more information about the <code>subsetByOverlaps()</code> 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 <code>inferRefAndAltAlleles</code> below for an alternative way to specify genome. If genome is supplied, then <code>inferRefAndAltAlleles</code> is called internally by <code>snpsBySeqname</code> , <code>snpsByOverlaps</code> , or <code>snpsById</code> to <i>infer</i> the reference allele (a.k.a. <i>ref</i> allele) and alternate allele(s) (a.k.a. <i>alt</i> allele(s)) for each SNP in the returned GPos object. The inferred <i>ref</i> allele and <i>alt</i> allele(s) are returned in additional metadata columns <code>ref_allele</code> (character) and <code>alt_alleles</code> (CharacterList). For <code>inferRefAndAltAlleles</code> : 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 <code>getBSgenome</code> function (e.g. "GRCh38") and the corresponding BSgenome data package needs to be already installed (see <code>?getBSgenome</code> 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 <code>alleles_as_ambig</code> like obtained when using any of the SNP extractor <code>snpsBySeqname</code> , <code>snpsByOverlaps</code> , or <code>snpsById</code> on a SNPlocs 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.

`snpBySeqname`, `snpByOverlaps`, and `snpById` 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 `snpById` 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`.

`inferRefAndAltAlleles` 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

```

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

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

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

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

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

## 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)

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

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

## 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")
}

## -----
## Obtaining 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.
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
## 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]

```

XtraSNPlocs-class *XtraSNPlocs* objects

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

```

## S4 method for signature 'XtraSNPlocs'
snpcount(x)

## S4 method for signature 'XtraSNPlocs'
snpsBySeqname(x, seqnames,
              columns=c("seqnames", "start", "end", "strand", "RefSNP_id"),
              drop.rs.prefix=FALSE, as.DataFrame=FALSE)

## S4 method for signature 'XtraSNPlocs'

```

```

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

## S4 method for signature 'XtraSNPlocs'
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

<code>x</code>	An XtraSNPlocs object.
<code>seqnames</code>	The names of the sequences for which to get SNPs. NAs and duplicates are not allowed. The supplied seqnames must be a subset of <code>seqlevels(x)</code> .
<code>columns</code>	The names of the columns to return. Valid column names are: <code>seqnames</code> , <code>start</code> , <code>end</code> , <code>width</code> , <code>strand</code> , <code>RefSNP_id</code> , <code>alleles</code> , <code>snpClass</code> , <code>loctype</code> . See Details section below for a description of these columns.
<code>drop.rs.prefix</code>	Should the <code>rs</code> prefix be dropped from the returned RefSNP ids? (RefSNP ids are stored in the <code>RefSNP_id</code> metadata column of the returned object.)
<code>as.DataFrame</code>	Should the result be returned in a DataFrame instead of a GRanges object?
<code>ranges</code>	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 "ch14:5201-5300".
<code>...</code>	Additional arguments, for use in specific methods. Arguments passed to the <code>snpsByOverlaps</code> method for XtraSNPlocs objects through <code>...</code> are used internally in the call to subsetByOverlaps() . See <code>?IRanges::subsetByOverlaps</code> in the IRanges package and <code>?GenomicRanges::subsetByOverlaps</code> in the GenomicRanges package for more information about the <code>subsetByOverlaps()</code> generic and its method for GenomicRanges objects.
<code>ids</code>	The RefSNP ids to look up (a.k.a. <i>rs ids</i>). Can be integer or character vector, with or without the "rs" prefix. NAs are not allowed.
<code>ifnotfound</code>	What to do if SNP ids are not found.
<code>do.NULL, prefix</code>	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 metadata 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().
```

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