1 Introduction

The *GenomInfoDb* provides an interface to access seqlevelsStyles (such as UCSC, NCBI, Ensembl) and their supported mappings for organisms. For instance, for Homo sapiens, seqlevelsStyle "UCSC" maps to "chr1", "chr2", ..., "chrX","chrY". The section below introduces these functions with examples.
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## Functionality for all existing organisms

### 2.1 genomeStyles

The `genomeStyles` lists out for each organism, the `seqlevelsStyles` and their mappings.

```r
seqmap <- genomeStyles()
head(seqmap, n=2)
```

```
## $Arabidopsis_thaliana
## circular auto sex NCBI TAIR9 Ensembl
## 1 FALSE TRUE FALSE  1 Chr1 1
## 2 FALSE TRUE FALSE  2 Chr2 2
## 3 FALSE TRUE FALSE  3 Chr3 3
## 4 FALSE TRUE FALSE  4 Chr4 4
## 5 FALSE TRUE FALSE  5 Chr5 5
## 6 TRUE FALSE FALSE  MT ChrM Mt
## 7 TRUE FALSE TRUE  Pltd ChrC Pt
##
## $Caenorhabditis_elegans
## circular auto sex NCBI UCSC Ensembl
## 1 FALSE TRUE FALSE  I chrI I
## 2 FALSE TRUE FALSE  II chrII II
## 3 FALSE TRUE FALSE  III chrIII III
## 4 FALSE TRUE FALSE  IV chrIV IV
## 5 FALSE TRUE FALSE  V chrV V
## 6 FALSE FALSE TRUE  X chrX X
## 7 TRUE TRUE FALSE  MT chrM MtDNA
```

Organism’s supported by GenomInfoDb can be found by:

```r
names(genomeStyles())
```

```
## [1] "Arabidopsis_thaliana"  "Caenorhabditis_elegans"
## [3] "Canis_familiaris"      "Cyanidioschyzon_merolae"
## [5] "Drosophila_melanogaster" "Homo_sapiens"
## [7] "Mus_musculus"          "Oryza_sativa"
## [9] "Populus_trichocarpa"   "Rattus norvegicus"
##[11] "Saccharomyces_cerevisiae" "Zea_mays"
```

If one knows the organism one is interested in, then we can directly access the information for the given organism along. Each function accepts an argument called species which as "genus species", the default is "Homo sapiens". In the following example we list out only the first five entries returned by the code snippet.

```r
head(genomeStyles("Homo_sapiens"), 5)
```

```
## circular auto sex NCBI UCSC dbSNP Ensembl
## 1 FALSE TRUE FALSE  1 chr1 ch1 1
## 2 FALSE TRUE FALSE  2 chr2 ch2 2
## 3 FALSE TRUE FALSE  3 chr3 ch3 3
## 4 FALSE TRUE FALSE  4 chr4 ch4 4
## 5 FALSE TRUE FALSE  5 chr5 ch5 5
```
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We can also check if a given style is supported by GenomeInfoDb for a given species. For example, if we want to know if "UCSC" mapping is supported for "Homo sapiens" we can ask:

```r
"UCSC" %in% names(genomeStyles("Homo_sapiens"))
## [1] TRUE
```

### 2.2 extractSeqlevels

We can also extract the desired seqlevelsStyle from a given organism using the `extractSeqlevels` function:

```r
extractSeqlevels(species="Arabidopsis_thaliana", style="NCBI")
## [1] "1" "2" "3" "4" "5" "MT" "Pltd"
```

### 2.3 extractSeqlevelsByGroup

We can also extract the desired seqlevelsStyle from a given organism based on a group (Group - 'auto' denotes autosomes, 'circular' denotes circular chromosomes and 'sex' denotes sex chromosomes; the default is all chromosomes are returned):

```r
extractSeqlevelsByGroup(species="Arabidopsis_thaliana", style="NCBI", group="auto")
## [1] "1" "2" "3" "4" "5"
```

### 2.4 seqlevelsStyle

We can find the seqname Style for a given character vector by using the `seqlevelsStyle` function:

```r
seqlevelsStyle(paste0("chr",c(1:30)))
## [1] "UCSC"
seqlevelsStyle(c("2L","2R","X","Xhet"))
## [1] "NCBI"
```

### 2.5 seqlevelsInGroup

We can also subset a given character vector containing seqnames using the `seqlevelsInGroup` function. We currently support 3 groups: 'auto' for autosomes, 'sex' for allosomes/sex chromosomes and circular for 'circular' chromosomes. The user can also provide the style and species they are working with. In the following examples, we extract the sex, auto and circular chromosomes for Homo sapiens:
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```r
newchr <- paste0("chr", c(1:22, "X", "Y", "M", "1_gl000192_random", "4_ctg9_hap1"))
seqlevelsInGroup(newchr, group="sex")
## [1] "chrX" "chrY"

seqlevelsInGroup(newchr, group="auto")
## [1] "chr1" "chr2" "chr3" "chr4" "chr5" "chr6" "chr7" "chr8" "chr9"
## [10] "chr10" "chr11" "chr12" "chr13" "chr14" "chr15" "chr16" "chr17" "chr18"
## [19] "chr19" "chr20" "chr21" "chr22"

seqlevelsInGroup(newchr, group="circular")
## [1] "chrM"

seqlevelsInGroup(newchr, group="sex","Homo_sapiens","UCSC")
## [1] "chrX" "chrY"
```

if we have a vector containing seqnames and we want to verify the species and style for them, we can use:

```r
seqnames <- c("chr1", "chr9", "chr2", "chr3", "chr10")
all(seqnames %in% extractSeqlevels("Homo_sapiens", "UCSC"))
## [1] TRUE
```

### 2.6 orderSeqlevels

The `orderSeqlevels` can return the order of a given character vector which contains seqnames. In the following example, we show how you can find the order for a given seqnames character vector.

```r
seqnames <- c("chr1", "chr9", "chr2", "chr3", "chr10")
orderSeqlevels(seqnames)
## [1] 1 3 4 2 5

seqnames[orderSeqlevels(seqnames)]
## [1] "chr1" "chr2" "chr3" "chr9" "chr10"
```

### 2.7 rankSeqlevels

The `rankSeqlevels` can return the rank of a given character vector which contains seqnames. In the following example, we show how you can find the rank for a given seqnames character vector.

```r
seqnames <- c("chr1", "chr9", "chr2", "chr3", "chr10")
rankSeqlevels(seqnames)
## [1] 1 4 2 3 5
```
2.8 mapSeqlevels

Returns a matrix with 1 column per supplied sequence name and 1 row per sequence renaming map compatible with the specified style. If `best.only` is `TRUE` (the default), only the "best" renaming maps (i.e. the rows with less NAs) are returned.

```r
c(mapSeqlevels(c("chrII", "chrIII", "chrM"), "NCBI"))
```

We also have several seqlevel utility functions. Let us construct a basic GRanges and show how these functions can be used.

```r
gr <- GRanges(paste0("ch",1:35), IRanges(1:35, width=5))
gr
```

As you can see, we have "ch" instead of "chr" for chromosome names. We can use `renameSeqlevels` to change the "ch" to "chr".

2.9 renameSeqlevels

As the first argument - it takes the object whose seqlevels we need to change, and as the second argument it takes a named vector which has the changes.

```r
newnames <- paste0("chr",1:35)
names(newnames) <- paste0("ch",1:35)
head(newnames)
gr <- renameSeqlevels(gr,newnames)
gr
```
Humans have just 22 primary chromosomes - but here we have some extra seqlevels which
we want to remove - there are several ways we can achieve this:

### 2.10 dropSeqlevels

Here the second argument is the seqlevels that you want to drop. Because these seqlevels are
in use (i.e. have ranges on them), the ranges on these sequences need to be removed before
the seqlevels can be dropped. We call this pruning. The pruning.mode argument controls
how to prune gr. Unlike for list-like objects (e.g. GRangesList) for which pruning can be
done in various ways, pruning a GRanges object is straightforward and achieved by specifying
pruning.mode="coarse".

```
dropSeqlevels(gr, paste0("chr",23:35), pruning.mode="coarse")
```

## GRanges object with 22 ranges and 0 metadata columns:
## seqnames ranges strand
## <Rle> <IRanges> <Rle>
## [1] chr1 1-5 *
## [2] chr2 2-6 *
## [3] chr3 3-7 *
## [4] chr4 4-8 *
## [5] chr5 5-9 *
## ... ... ... ... 
## [18] chr18 18-22 *
## [19] chr19 19-23 *
## [20] chr20 20-24 *
## [21] chr21 21-25 *
## [22] chr22 22-26 *
## -------
## seqinfo: 22 sequences from an unspecified genome; no seqlengths
### 2.11 keepSeqlevels

Here the second argument is the seqlevels that you want to keep.

```r
keepSeqlevels(gr, paste0("chr",1:22), pruning.mode="coarse")
```

```
## GRanges object with 22 ranges and 0 metadata columns:
## seqnames ranges strand
## <Rle> <IRanges> <Rle>
## [1] chr1  1-5  *
## [2] chr2  2-6  *
## [3] chr3  3-7  *
## [4] chr4  4-8  *
## [5] chr5  5-9  *
## ...  ...  ...  ...
## [19] chr19 19-23 *
## [20] chr20 20-24 *
## [21] chr21 21-25 *
## [22] chr22 22-26 *
## -------
##      ## seqinfo: 22 sequences from an unspecified genome; no seqlengths
```

### 2.12 keepStandardChromosomes

This function internally uses the pre-defined tables inside GenomInfoDb to find the correct seqlevels according to the sequence style of the object.

```r
keepStandardChromosomes(gr, pruning.mode="coarse")
```

```
## GRanges object with 35 ranges and 0 metadata columns:
## seqnames ranges strand
## <Rle> <IRanges> <Rle>
## [1] chr1  1-5  *
## [2] chr2  2-6  *
## [3] chr3  3-7  *
## [4] chr4  4-8  *
## [5] chr5  5-9  *
## ...  ...  ...  ...
## [19] chr19 19-23 *
## [20] chr20 20-24 *
## [21] chr21 21-25 *
## [22] chr22 22-26 *
## .......
##      ## seqinfo: 35 sequences from an unspecified genome; no seqlengths
```

One can also specify the optional species argument to be more precise.

```r
plantgr <- GRanges(c(1:5,"MT","Pltd"), IRanges(1:7,width=5))
keepStandardChromosomes(plantgr, species="Arabidopsis thaliana")
```
## GRanges object with 7 ranges and 0 metadata columns:
## seqnames ranges strand
## <Rle> <IRanges> <Rle>
## [1] 1 1-5 *
## [2] 2 2-6 *
## [3] 3 3-7 *
## [4] 4 4-8 *
## [5] 5 5-9 *
## [6] MT 6-10 *
## [7] Pltd 7-11 *
## -------
## seqinfo: 7 sequences from an unspecified genome; no seqlengths

### Seqinfo objects

--

Note that all the arguments (except 'genome') must have the same length. 'genome' can be of length 1, whatever the lengths of the other arguments are.

```r
x <- Seqinfo(seqnames=c("chr1", "chr2", "chr3", "chrM"),
  seqlengths=c(100, 200, NA, 15),
  isCircular=c(NA, FALSE, FALSE, TRUE),
  genome="toy")
```

- **length(x)**
  ```r```
  ## [1] 4
  ```

- **seqnames(x)**
  ```r```
  ## [1] "chr1" "chr2" "chr3" "chrM"
  ```

- **names(x)**
  ```r```
  ## [1] "chr1" "chr2" "chr3" "chrM"
  ```

- **seqlevels(x)**
  ```r```
  ## [1] "chr1" "chr2" "chr3" "chrM"
  ```

- **seqlengths(x)**
  ```r```
  ## chr1 chr2 chr3 chrM
  ## 100 200 NA 15
  ```

- **isCircular(x)**
  ```r```
  ## chr1 chr2 chr3 chrM
  ## NA FALSE FALSE TRUE
  ```

- **genome(x)**
  ```r```
  ## chr1 chr2 chr3 chrM
  ## "toy" "toy" "toy" "toy"
  ```

- **x[c("chrY", "chr3", "chr1")]**
  ```r```
  # subset by names
## Seqinfo object with 3 sequences from 2 genomes (NA, toy):
## seqnames seqlengths isCircular genome
## chrY NA NA <NA>
## chr3 NA FALSE toy
## chr1 100 NA toy

## Rename, drop, add and/or reorder the sequence levels:
xx <- x
seqlevels(xx) <- sub("chr", "ch", seqlevels(xx)) # rename
xx

## Seqinfo object with 4 sequences (1 circular) from toy genome:
## seqnames seqlengths isCircular genome
## ch1 100 NA toy
## ch2 200 FALSE toy
## ch3 NA FALSE toy
## chM 15 TRUE toy

seqlevels(xx) <- rev(seqlevels(xx)) # reorder
xx

## Seqinfo object with 4 sequences (1 circular) from toy genome:
## seqnames seqlengths isCircular genome
## chM 15 TRUE toy
## ch3 NA FALSE toy
## ch2 200 FALSE toy
## ch1 100 NA toy

seqlevels(xx) <- c("ch1", "ch2", "chY") # drop/add/reorder
xx

## Seqinfo object with 3 sequences from 2 genomes (toy, NA):
## seqnames seqlengths isCircular genome
## ch1 100 NA toy
## ch2 200 FALSE toy
## chY NA NA <NA>

seqlevels(xx) <- c(chY="Y", ch1="1", "22") # rename/reorder/drop/add
xx

## Seqinfo object with 3 sequences from 2 genomes (toy, NA):
## seqnames seqlengths isCircular genome
## Y NA NA <NA>
## 1 100 NA toy
## 22 NA NA <NA>

y <- Seqinfo(seqnames=c("chr3", "chr4", "chrM"),
            seqlengths=c(300, NA, 15))

y

## Seqinfo object with 3 sequences from an unspecified genome:
## seqnames seqlengths isCircular genome
## chr3 300 NA <NA>
## chr4 NA NA <NA>
## chrM 15 NA <NA>
merge(x, y) # rows for chr3 and chrM are merged

## Warning in .Seqinfo.mergexy(x, y): Each of the 2 combined objects has sequence
levels not in the other:
## - in 'x': chr1, chr2
## - in 'y': chr4
## Make sure to always combine/compare objects based on the same reference
## genome (use suppressWarnings() to suppress this warning).

## Seqinfo object with 5 sequences (1 circular) from 2 genomes (toy, NA):
##  seqnames seqlengths isCircular genome
##  chr1 100 NA toy
##  chr2 200 FALSE toy
##  chr3 300 FALSE toy
##  chrM 15  TRUE toy
##  chr4 NA NA <NA>

suppressWarnings(merge(x, y))

## Seqinfo object with 5 sequences (1 circular) from 2 genomes (toy, NA):
##  seqnames seqlengths isCircular genome
##  chr1 100 NA toy
##  chr2 200 FALSE toy
##  chr3 300 FALSE toy
##  chrM 15  TRUE toy
##  chr4 NA NA <NA>

## Note that, strictly speaking, merging 2 Seqinfo objects is not
## a commutative operation, i.e., in general 'z1 <- merge(x, y)'
## is not identical to 'z2 <- merge(y, x)'. However 'z1' and 'z2'
## are guaranteed to contain the same information (i.e. the same
## rows, but typically not in the same order):

suppressWarnings(merge(y, x))

## Seqinfo object with 5 sequences (1 circular) from 2 genomes (toy, NA):
##  seqnames seqlengths isCircular genome
##  chr3 300  TRUE <NA>
##  chr4 NA NA <NA>
##  chrM 15  FALSE <NA>

if (interactive()) {
  merge(x, y) # raises an error
}
4 Examples

4.1 converting seqlevel styles (eg:UCSC to NCBI)

A quick example using Drosophila Melanogaster. The txdb object contains seqlevels in UCSC style, we want to convert them to NCBI

```r
taxdb <- TxDb.Dmelanogaster.UCSC.dm3.ensGene
seqlevels(txdb)
## [1] "chr2L"  "chr2R"  "chr3L"  "chr3R"  "chr4"  "chrX"
## [7] "chrU"   "chrM"   "chr2LHet" "chr2RHet" "chr3LHet" "chr3RHet"
## [13] "chrXHet" "chrYHet" "chrUextra"

genomeStyles("Drosophila melanogaster")
## circular sex auto  NCBI   UCSC    Ensembl
##  1 FALSE  FALSE  TRUE  2L    chr2L  2L
##  2 FALSE  FALSE  TRUE  2R    chr2R  2R
##  3 FALSE  FALSE  TRUE  3L    chr3L  3L
##  4 FALSE  FALSE  TRUE  3R    chr3R  3R
##  5 FALSE  FALSE  TRUE  4     chr4   4
##  6 FALSE  TRUE   FALSE X     chrX   X
##  7 FALSE  TRUE   FALSE Y     chrY   Y
##  8 TRUE   FALSE  FALSE MT    chrM  dmel_mitochondrion_genome
##  9 FALSE  FALSE  FALSE 2LHet chr2LHet 2LHet
## 10 FALSE  FALSE  FALSE 2RHet chr2RHet 2RHet
## 11 FALSE  FALSE  FALSE 3LHet chr3LHet 3LHet
## 12 FALSE  FALSE  FALSE 3RHet chr3RHet 3RHet
## 13 FALSE  FALSE  FALSE XHet chrXHet XHet
## 14 FALSE  FALSE  FALSE YHet chrYHet YHet
## 15 FALSE  FALSE  FALSE Un    chrU   U
## 16 FALSE  FALSE  FALSE <NA>  chrUextra Uextra

mapSeqlevels(seqlevels(txdb), "NCBI")
## chr2L  chr2R  chr3L  chr3R  chr4  chrX  chrU
##  "2L"  "2R"  "3L"  "3R"  "4"  "X"  "Un"
## chrM  chr2LHet chr2RHet chr3LHet chr3RHet chrXHet chrYHet
##  "MT"  "2LHet" "2RHet" "3LHet" "3RHet" "XHet" "YHet"
## chrUextra
## NA
```

4.2 converting styles and removing unwanted seqlevels

Suppose we read in a Bam file or a BED file and the resulting GRanges have a lot of seqlevels which are not required by your analysis or you want to rename the seqlevels from the current style to your own style (eg:USCS to NCBI), we can use the functionality provided by GenomelInfoDb to do that.

Let us say that we have extracted the seqlevels of the Seqinfo object(say GRanges from a BED file) in a variable called "sequence".
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```r
sequence <- seqlevels(x)

## sequence is in UCSC format and we want NCBI style
newStyle <- mapSeqlevels(sequence,"NCBI")
newStyle <- newStyle[complete.cases(newStyle)] # removing NA cases.

## rename the seqlevels
x <- renameSeqlevels(x,newStyle)

## keep only the seqlevels you want (say autosomes)
auto <- extractSeqlevelsByGroup(species="Homo sapiens", style="NCBI",
group="auto")
x <- keepSeqlevels(x,auto)
```

5  Session Information

Here is the output of `sessionInfo()` on the system on which this document was compiled:

```r
toLatex(sessionInfo())
```

- R version 4.0.2 (2020-06-22), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 18.04.4 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.12-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.12-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils
- Other packages: AnnotationDbi 1.51.0, Biobase 2.49.0, BiocGenerics 0.35.4, GenomeInfoDb 1.25.5, GenomicFeatures 1.41.0, GenomicRanges 1.41.5, IRanges 2.23.10, S4Vectors 0.27.12, TxBd.Dmelanogaster.UCSC.dm3.ensGene 3.2.2
- Loaded via a namespace (and not attached): BiocFileCache 1.13.0, BiocManager 1.30.10, BiocParallel 1.23.0, BiocStyle 2.17.0, Biostrings 2.57.2, DBI 1.1.0, DelayedArray 0.15.6, GenomeInfoDbData 1.2.3, GenomicAlignments 1.25.3, Matrix 1.2-18, R6 2.4.1, RCurl 1.98-1.2, RSQLite 2.2.0, Rcpp 1.0.4.6, Rsamtools 2.5.3, SummarizedExperiment 1.19.5, XML 3.99-0.3, XVector 0.29.3, askpass 1.1, assertthat 0.2.1, biomaRt 2.45.1, bit 1.1-15.2, bit64 0.9-7, bitops 1.0-6, blob 1.2.1, compiler 4.0.2, crayon 1.3.4, curl 4.3, dplyr 1.4.4, digest 0.6.25, dplyr 1.0.0, ellipsis 0.3.1, evaluate 0.14, generics 0.0.2, glue 1.4.1, grid 4.0.2, highr 0.8, hms 0.5.3, htmltools 0.5.0, htr 1.4.1, knitr 1.29, lattice 0.20-41, lifecycle 0.2.0, magrittr 1.5, matrixStats 0.56.0, memoise 1.1.0, openssl 1.4.2, pillar 1.4.4, pkgconfig 2.0.3, prettyunits 1.1.1, progress 1.2.2,
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purrr 0.3.4, rappdirs 0.3.1, rlang 0.4.6, rmarkdown 2.3, rtracklayer 1.49.3,
stringi 1.4.6, stringr 1.4.0, tibble 3.0.1, tidyselect 1.1.0, tools 4.0.2, vctrs 0.3.1,
xfun 0.15, yaml 2.2.1, zlibbioc 1.35.0