

# An Introduction to *GenomeInfoDb*

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Modified: 26 June, 2020. Compiled: October 26, 2021

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## 1 Introduction

---

The *GenomeInfoDb* 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.

## 2 Functionality for all existing organisms

### 2.1 genomeStyles

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

```
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
```

Oragnism's supported by GenomeInfoDb can be found by :

```
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.

```
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
```

## An Introduction to *GenomeInfoDb*

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 :

```
"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`

```
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).

```
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`

```
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`. 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 :

```
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:

```
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.

```
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.

```
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.

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

## chrII chrIII chrM
```

```
## "II" "III" "MT"
```

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

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

## GRanges object with 35 ranges and 0 metadata columns:
##      seqnames      ranges strand
##      <Rle> <IRanges> <Rle>
## [1]   ch1         1-5      *
## [2]   ch2         2-6      *
## [3]   ch3         3-7      *
## [4]   ch4         4-8      *
## [5]   ch5         5-9      *
## ...           ...           ...
## [31]  ch31        31-35     *
## [32]  ch32        32-36     *
## [33]  ch33        33-37     *
## [34]  ch34        34-38     *
## [35]  ch35        35-39     *
## -----
## seqinfo: 35 sequences from an unspecified genome; no seqlengths
```

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.

```
newnames <- paste0("chr",1:35)
names(newnames) <- paste0("ch",1:35)
head(newnames)

##   ch1   ch2   ch3   ch4   ch5   ch6
## "chr1" "chr2" "chr3" "chr4" "chr5" "chr6"

gr <- renameSeqlevels(gr,newnames)
gr

## 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      *
## ...           ...           ...
## [31]  chr31        31-35     *
```

```
## [32] chr32 32-36 *
## [33] chr33 33-37 *
## [34] chr34 34-38 *
## [35] chr35 35-39 *
## -----
## seqinfo: 35 sequences from an unspecified genome; no seqlengths
```

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.

```
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 *
## ... ... ... ...
## [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
```

## 2.12 keepStandardChromosomes

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

```
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      *
## ...      ...      ...      ...
## [31] chr31     31-35    *
## [32] chr32     32-36    *
## [33] chr33     33-37    *
## [34] chr34     34-38    *
## [35] chr35     35-39    *
## -----
## seqinfo: 35 sequences from an unspecified genome; no seqlengths
```

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

```
plantgr <- GRanges(c(1:5,"MT","Pltd"), IRanges(1:7,width=5))
keepStandardChromosomes(plantgr,species="Arabidopsis thaliana",
pruning.mode="coarse")

## 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
```

### 3 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.
x <- Seqinfo(seqnames=c("chr1", "chr2", "chr3", "chrM"),
             seqlengths=c(100, 200, NA, 15),
             isCircular=c(NA, FALSE, FALSE, TRUE),
             genome="toy")

length(x)
## [1] 4

seqnames(x)
## [1] "chr1" "chr2" "chr3" "chrM"

names(x)
## [1] "chr1" "chr2" "chr3" "chrM"

seqlevels(x)
## [1] "chr1" "chr2" "chr3" "chrM"

seqlengths(x)
## chr1 chr2 chr3 chrM
## 100 200 NA 15

isCircular(x)
## chr1 chr2 chr3 chrM
## NA FALSE FALSE TRUE

genome(x)
## chr1 chr2 chr3 chrM
## "toy" "toy" "toy" "toy"

x[c("chrY", "chr3", "chr1")] # 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 (NA, toy):
## 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     FALSE  toy
## chr4      NA      NA     <NA>
## chrM      15      TRUE   toy
## chr1      100     NA     toy
## chr2      200     FALSE  toy

## This contradicts what 'x' says about circularity of chr3 and chrM:
isCircular(y)[c("chr3", "chrM")] <- c(TRUE, FALSE)
y

## Seqinfo object with 3 sequences (1 circular) from an unspecified genome:
## 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

```
txdb <- 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:UCSC to NCBI), we can use the functionality provided by GenomeInfoDb 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".

```
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",
```

```
x <- keepSeqlevels(x, auto) group="auto")
```

## 5 Session Information

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

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

- R Under development (unstable) (2021-10-19 r81077), x86\_64-pc-linux-gnu
- Locale: LC\_CTYPE=en\_US.UTF-8, LC\_NUMERIC=C, LC\_TIME=en\_GB, 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 20.04.3 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.15-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.15-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, stats, stats4, utils
- Other packages: AnnotationDbi 1.57.0, Biobase 2.55.0, BiocGenerics 0.41.0, GenomeInfoDb 1.31.0, GenomicFeatures 1.47.0, GenomicRanges 1.47.0, IRanges 2.29.0, S4Vectors 0.33.0, TxDb.Dmelanogaster.UCSC.dm3.ensGene 3.2.2
- Loaded via a namespace (and not attached): BiocFileCache 2.3.0, BiocIO 1.5.0, BiocManager 1.30.16, BiocParallel 1.29.0, BiocStyle 2.23.0, Biostrings 2.63.0, DBI 1.1.1, DelayedArray 0.21.0, GenomeInfoDbData 1.2.7, GenomicAlignments 1.31.0, KEGGREST 1.35.0, Matrix 1.3-4, MatrixGenerics 1.7.0, R6 2.5.1, RCurl 1.98-1.5, RSQLite 2.2.8, Rcpp 1.0.7, Rsamtools 2.11.0, SummarizedExperiment 1.25.0, XML 3.99-0.8, XVector 0.35.0, assertthat 0.2.1, biomaRt 2.51.0, bit 4.0.4, bit64 4.0.5, bitops 1.0-7, blob 1.2.2, cachem 1.0.6, compiler 4.2.0, crayon 1.4.1, curl 4.3.2, dbplyr 2.1.1, digest 0.6.28, dplyr 1.0.7, ellipsis 0.3.2, evaluate 0.14, fansi 0.5.0, fastmap 1.1.0, filelock 1.0.2, generics 0.1.1, glue 1.4.2, grid 4.2.0, highr 0.9, hms 1.1.1, htmltools 0.5.2, httr 1.4.2, knitr 1.36, lattice 0.20-45, lifecycle 1.0.1, magrittr 2.0.1, matrixStats 0.61.0, memoise 2.0.0, parallel 4.2.0, pillar 1.6.4, pkgconfig 2.0.3, png 0.1-7, prettyunits 1.1.1, progress 1.2.2, purrr 0.3.4, rappdirs 0.3.3, restfulr 0.0.13, rjson 0.2.20, rlang 0.4.12, rmarkdown 2.11, rtracklayer 1.55.0, stringi 1.7.5, stringr 1.4.0, tibble 3.1.5, tidyselect 1.1.1, tools 4.2.0, utf8 1.2.2, vctrs 0.3.8, xfun 0.27, xml2 1.3.2, yaml 2.2.1, zlibbioc 1.41.0