Making and Utilizing TxDB Objects

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1 Introduction

The GenomicFeatures package retrieves and manages transcript-related features from the UCSC Genome Bioinformatics\footnote{http://genome.ucsc.edu/} and BioMart\footnote{http://www.biomart.org/} data resources. The package is useful for ChIP-chip, ChIP-seq, and RNA-seq analyses.

```r
library("GenomicFeatures")
## Loading required package: BiocGenerics
## Loading required package: parallel
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:parallel':
##
##  clusterApply, clusterApplyLB, clusterCall, clusterEvalQ, clusterExport,
##  clusterMap, parApply, parCapply, parLapply, parLapplyLB, parRapply,
##  parSapply, parSapplyLB

## The following objects are masked from 'package:stats':
##
##  IQR, mad, xtabs

## The following objects are masked from 'package:base':
##
##  Filter, Find, Map, Position, Reduce, anyDuplicated, append, as.data.frame,
##  cbind, colnames, do.call, duplicated, eval, evalq, get, grep, grepl,
##  intersect, is.unsorted, lapply, lengths, mapply, match, mget, order, paste,
##  pmax, pmax.int, pmin, pmin.int, rank, rbind, rownames, sapply, setdiff,
##  sort, table, tapply, union, unique, unsplit, which, which.max, which.min

## Loading required package: S4Vectors
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
```
2 TxDB Objects

The GenomicFeatures package uses TxDB objects to store transcript metadata. This class maps the 5' and 3' untranslated regions (UTRs), protein coding sequences (CDSs) and exons for a set of mRNA transcripts to their associated genome. TxDB objects have numerous accessors functions to allow such features to be retrieved individually or grouped together in a way that reflects the underlying biology.

All TxDB objects are backed by a SQLite database that manages genomic locations and the relationships between pre-processed mRNA transcripts, exons, protein coding sequences, and their related gene identifiers.

3 Retrieving Data from TxDB objects

3.1 Loading Transcript Data

There are two ways that users can load pre-existing data to generate a TxDB object. One method is to use the loadDb method to load the object directly from an appropriate .sqlite database file.

Here we are loading a previously created TxDB object based on UCSC known gene data. This database only contains a small subset of the possible annotations for human and is only included to demonstrate and test the functionality of the GenomicFeatures package as a demonstration.

```r
txdb <- loadDb(samplefile, package="GenomicFeatures")
txdb

# TxDB object:
# # Db type: TxDB
# # Supporting package: GenomicFeatures
```
In this case, the *TxDb* object has been returned by the *loadDb* method.

More commonly however, we expect that users will just load a *TxDb* annotation package like this:

```r
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb <- TxDb.Hsapiens.UCSC.hg19.knownGene # shorthand (for convenience)
```

Loading the package like this will also create a *TxDb* object, and by default that object will have the same name as the package itself.
3.2 Pre-filtering data based on Chromosomes

It is possible to filter the data that is returned from a TxDb object based on its chromosome. This can be a useful way to limit the things that are returned if you are only interested in studying a handful of chromosomes.

To determine which chromosomes are currently active, use the seqlevels method. For example:

```r
head(seqlevels(txdb))
```

```markdown
## [1] "chr1" "chr2" "chr3" "chr4" "chr5" "chr6"
```

Will tell you all the chromosomes that are active for the TxDb.Hsapiens.UCSC.hg19.knownGene TxDb object (by default it will be all of them).

If you then wanted to only set Chromosome 1 to be active you could do it like this:

```r
seqlevels(txdb) <- "chr1"
```

So if you ran this, then from this point on in your R session only chromosome 1 would be consulted when you call the various retrieval methods... If you need to reset back to the original seqlevels (i.e. to the seqlevels stored in the db), then set the seqlevels to seqlevels0(txdb).

```r
seqlevels(txdb) <- seqlevels0(txdb)
```

Exercise 1

*Use seqlevels to set only chromosome 15 to be active. BTW, the rest of this vignette will assume you have succeeded at this.*

Solution:

```r
seqlevels(txdb) <- "chr15"
```

3.3 Retrieving data using the select method

The TxDb objects inherit from AnnotationDb objects (just as the ChipDb and OrgDb objects do). One of the implications of this relationship is that these object ought to be used in similar ways to each other. Therefore we have written supporting columns, keytypes, keys and select methods for TxDb objects.

These methods can be a useful way of extracting data from a TxDb object. And they are used in the same way that they would be used to extract information about a ChipDb or an OrgDb object. Here is a simple example of how to find the UCSC transcript names that match with a set of gene IDs.

```r
keys <- c("100033416", "100033417", "100033420")
columns(txdb)
```

```markdown
## [1] "CDSCHROM" "CDSID" "CDSNAME" "CDSSTART" "CDSSTRAND" "EXONCHROM" "EXONEND" "EXONID" "EXONNAME" "EXONRANK" "EXONSTART" "EXONSTRAND" "GENEID" "TXCHROM" "TXEND" "TXID" "TXNAME"
```

```r
keytypes(txdb)
```

```markdown
## [1] "CDSID" "CDSNAME" "EXONID" "EXONNAME" "GENEID" "TXID" "TXNAME"
```
select(txdb, keys = keys, columns="TXNAME", keytype="GENEID")

## 'select()' returned 1:1 mapping between keys and columns

## GENEID   TXNAME
## 1 100033416 uc001yxl.4
## 2 100033417 uc001yxo.3
## 3 100033420 uc001yxr.3

**Exercise 2**

*For the genes in the example above, find the chromosome and strand information that will go with each of the transcript names.*

**Solution:**

columns(txdb)

## [1] "CDSCHROM" "CDSEND" "CDSID" "CDSNAME" "CDSSTART" "CDSSTRAND"
## [7] "EXONCHROM" "EXONEND" "EXONID" "EXONNAME" "EXONRANK" "EXONSTART"
## [13] "EXONSTRAND" "GENEID" "TXCHROM" "TXEND" "TXID" "TXNAME"
## [19] "TXSTART" "TXSTRAND" "TXTYPE"

cols <- c("TXNAME", "TXSTRAND", "TXCHROM")

select(txdb, keys=keys, columns=cols, keytype="GENEID")

## 'select()' returned 1:1 mapping between keys and columns

## GENEID   TXNAME TXCHROM TXSTRAND
## 1 100033416 uc001yxl.4 chr15  +
## 2 100033417 uc001yxo.3 chr15  +
## 3 100033420 uc001yxr.3 chr15  +

### 3.4 Methods for returning GRanges objects

Retrieving data with select is useful, but sometimes it is more convenient to extract the result as GRanges objects. This is often the case when you are doing counting or specialized overlap operations downstream. For these use cases there is another family of methods available.

Perhaps the most common operations for a TxDb object is to retrieve the genomic coordinates or ranges for exons, transcripts or coding sequences. The functions transcripts, exons, and cds return the coordinate information as a GRanges object.

As an example, all transcripts present in a TxDb object can be obtained as follows:

GR <- transcripts(txdb)

GR[1:3]

## GRanges object with 3 ranges and 2 metadata columns:
## seqnames ranges strand | tx_id tx_name
## <Rle> <IRanges> <Rle> | <integer> <character>
## [1] chr15 [20362688, 20364420]  + | 53552 uc001yte.1
## 
## seqinfo: 1 sequence from hg19 genome

The `transcripts` function returns a `GRanges` class object. You can learn a lot more about the manipulation of these objects by reading the *GenomicRanges* introductory vignette. The `show` method for a `GRanges` object will display the ranges, seqnames (a chromosome or a contig), and strand on the left side and then present related metadata on the right side. At the bottom, the `seqLengths` display all the possible seqnames along with the length of each sequence.

In addition, the `transcripts` function can also be used to retrieve a subset of the transcripts available such as those on the + strand of chromosome 1.

```
GR <- transcripts(txdb, filter=list(tx_chrom = "chr15", tx_strand = "+"))
length(GR)
## [1] 1732

unique(strand(GR))
## [1] +
## Levels: + - *
```

The `exons` and `cds` functions can also be used in a similar fashion to retrieve genomic coordinates for exons and coding sequences.

**Exercise 3**

*Use* `exons` to retrieve all the exons from chromosome 15. *How does the length of this compare to the value returned by `transcripts`?*

**Solution:**

```
EX <- exons(txdb)
EX[1:4]
```

```
## GRanges object with 4 ranges and 1 metadata column:
##   seqnames ranges strand | exon_id
##       <Rle> <IRanges> <Rle> | <integer>
## [1] chr15 [20362688, 20362858] + | 192986
## -------
## seqinfo: 1 sequence from hg19 genome

length(EX)
## [1] 10771

length(GR)
## [1] 1732
```
### 3.5 Working with Grouped Features

Often one is interested in how particular genomic features relate to each other, and not just their location. For example, it might be of interest to group transcripts by gene or to group exons by transcript. Such groupings are supported by the `transcriptsBy`, `exonsBy`, and `cdsBy` functions.

The following call can be used to group transcripts by genes:

```r
GRList <- transcriptsBy(txdb, by = "gene")
length(GRList)
## [1] 799
names(GRList)[10:13]
## [1] "100033424" "100033425" "100033427" "100033428"

GRList[11:12]
## GRangesList object of length 2:
## $100033425
## GRanges object with 1 range and 2 metadata columns:
## seqnames ranges strand | tx_id tx_name
## <Rle> <IRanges> <Rle> | <integer> <character>
## [1] chr15 [25324204, 25325381] + | 53638 uc001yxw.4
##
## $100033427
## GRanges object with 1 range and 2 metadata columns:
## seqnames ranges strand | tx_id tx_name
## <Rle> <IRanges> <Rle> | <integer> <character>
## [1] chr15 [25326433, 25326526] + | 53640 uc001yxz.3
##
## -------
## seqinfo: 1 sequence from hg19 genome
```

The `transcriptsBy` function returns a `GRangesList` class object. As with `GRanges` objects, you can learn more about these objects by reading the `GenomicRanges` introductory vignette. The `show` method for a `GRangesList` object will display as a list of `GRanges` objects. And, at the bottom the seqlengths will be displayed once for the entire list.

For each of these three functions, there is a limited set of options that can be passed into the by argument to allow grouping. For the `transcriptsBy` function, you can group by gene, exon or cds, whereas for the `exonsBy` and `cdsBy` functions can only be grouped by transcript (tx) or gene.

So as a further example, to extract all the exons for each transcript you can call:

```r
GRList <- exonsBy(txdb, by = "tx")
length(GRList)
## [1] 3337
names(GRList)[10:13]
## [1] "53561" "53562" "53563" "53564"

GRList[[12]]
```
## GRanges object with 1 range and 3 metadata columns:
## 
## seqnames ranges strand | exon_id exon_name exon_rank
## <Rle> <IRanges> <Rle> | <integer> <character> <integer>
## [1] chr15 [22043463, 22043502] + | 193028 <NA> 1
## -------
## seqinfo: 1 sequence from hg19 genome

As you can see, the GRangesList objects returned from each function contain locations and identifiers grouped into a list like object according to the type of feature specified in the by argument. The object returned can then be used by functions like findOverlaps to contextualize alignments from high-throughput sequencing.

The identifiers used to label the GRanges objects depend upon the data source used to create the TxDB object. So the list identifiers will not always be Entrez Gene IDs, as they were in the first example. Furthermore, some data sources do not provide a unique identifier for all features. In this situation, the group label will be a synthetic ID created by GenomicFeatures to keep the relations between features consistent in the database this was the case in the 2nd example. Even though the results will sometimes have to come back to you as synthetic IDs, you can still always retrieve the original IDs.

### Exercise 4

*Starting with the tx_ids that are the names of the GRList object we just made, use select to retrieve that matching transcript names. Remember that the list used a by argument = "tx", so the list is grouped by transcript IDs.*

#### Solution:

```r
GRList <- exonsBy(txdb, by = "tx")
tx_ids <- names(GRList)
head(select(txdb, keys=tx_ids, columns="TXNAME", keytype="TXID"))
```

```r
## 'select()' returned 1:1 mapping between keys and columns
##
## TXID TXNAME
## 1 53552 uc001yte.1
## 2 53553 uc001ytf.1
## 3 53554 uc001ytj.3
## 4 53555 uc021sex.1
## 5 53556 uc010tzb.1
## 6 53557 uc021sey.1
```

Finally, the order of the results in a GRangesList object can vary with the way in which things were grouped. In most cases the grouped elements of the GRangesList object will be listed in the order that they occurred along the chromosome. However, when exons or CDS are grouped by transcript, they will instead be grouped according to their position along the transcript itself. This is important because alternative splicing can mean that the order along the transcript can be different from that along the chromosome.

### 3.6 Predefined grouping functions

The intronsByTranscript, fiveUTRsByTranscript and threeUTRsByTranscript are convenience functions that provide behavior equivalent to the grouping functions, but in prespecified form. These functions
return a \texttt{GRangesList} object grouped by transcript for introns, 5’ UTR’s, and 3’ UTR’s, respectively. Below are examples of how you can call these methods.

\begin{verbatim}
length(intronsByTranscript(txdb))
## [1] 3337
length(fiveUTRsByTranscript(txdb))
## [1] 1825
length(threeUTRsByTranscript(txdb))
## [1] 1803
\end{verbatim}

### 3.7 Getting the actual sequence data

The \textit{GenomicFeatures} package also provides functions for converting from ranges to actual sequence (when paired with an appropriate \textit{BSgenome} package).

\begin{verbatim}
library(BSgenome.Hsapiens.UCSC.hg19)
## Loading required package: BSgenome
## Loading required package: Biostrings
## Loading required package: XVector
## Loading required package: rtracklayer
tx_seqs1 <- extractTranscriptSeqs(Hsapiens, TxDb.Hsapiens.UCSC.hg19.knownGene, use.names=TRUE)
\end{verbatim}

And, once these sequences have been extracted, you can translate them into proteins with \texttt{translate}:

\begin{verbatim}
suppressWarnings(translate(tx_seqs1))
## A AAStringSet instance of length 3337
## width seq names
## [1] 125 EDQDDEARVYEGFRPGMYVEIQV...QRLLKYPQHMHCGAFAW*FSDSCH uc001yte.1
## [2] 288 RIAS*GRAEFSSAQTSEIRRRRSVLL...IFLFFESYFVSYFNYGNNCFVTVD uc001ytf.1
## [3] 588 RSGQRLPEQPEAEAGDGGQKIGRRAEH...KVICERDLENETHYLCIKICFSS uc001ytj.3
## [4] 10 HHLNCRPQQTG uc021sex.1
## [5] 9 STVTLPQHSG uc010tzb.1
## ... ... ...
## [3333] 10 QVPMRVQVQG uc021syy.1
## [3334] 306 MVTEFIFGLSDFSLQELQTFLMLFFVF...TLRNKDMKTAIRRLKWDHSSVKF* uc002cdf.1
## [3335] 550 LAVSLFDLFFLFLMCCCLLAAQTSRVL...RRQSLTPRLHPAQLILEY*KHTVGF uc002cde.2
## [3336] 496 LAVSLFDLFFLFLMCCCLLAAQTSRVL...EAVTDPEFASCTARDPLLKAHCWFL uc010utv.1
## [3337] 531 LAVSLFDLFFLFLMCCCLLAAQTSRVL...RRQSLTPRLHPAQLILEY*KHTVGF uc010utw.1
\end{verbatim}

**Exercise 5**

\textit{But of course this is not a meaningful translation, because the call to \texttt{extractTranscriptSeqs} will have extracted all the transcribed regions of the genome regardless of whether or not they are translated. Look}
at the manual page for \texttt{extractTranscriptSeqs} and see how you can use \texttt{cdsBy} to only translate only the coding regions.

Solution:

\begin{verbatim}
cds_seqs <- extractTranscriptSeqs(Hsapiens,
                                   cdsBy(txdb, by="tx", use.names=TRUE))
translate(cds_seqs)
\end{verbatim}

\begin{verbatim}
## A AAStringSet instance of length 1875
## width seq names
## [1] 102 MYVRVEIENPCEFVNIDPHYPIILG...EDHNGRQLLKYTPQHMHCAGAFAW* uc001yte.1
## [2] 435 MEWKLEQSMREQALLKATQLTQLQESLK...QEHPGLGSCOVFFCWAWPPRRRR* uc010tzc.1
## [3] 317 MKIANNTVTEFILLGTQSQDIQLLLV...QERVSMKRLSRSRHVCQVDIIRN* uc001yuc.1
## [4] 314 METANYTKEFVLTLGSDQTPQVLV...YTLRNKEVKAAMRKLYTVILYCEK* uc010tzu.2
## [5] 317 MKIANNTVTEFILLGTQSQDIQLLLV...QERVSMKRLSRSRHVCQVDIIRN* uc010tzv.2
## ... ... ...
## [1871] 186 MAGGVLPLRGLRMLCRVLLFSQFCIL...RDHVCHCLGRSEFKDIDCQNVFLQVY* uc010ush.1
## [1872] 258 MNSKLEWASGWHQYSENMTFEI...GMMWYPNFWLCLTELTTIVV* uc002b3.1
## [1873] 803 MAEEALAAEAASVERSALQQEDIRWLWS...ILVTSAIDKLKNLRKTRLN...EAEAF* uc002bxm.3
## [1874] 306 MVTEFIFLGLSDQHELTFMLFVFFV...TLRKKDMKTAIRRLKWDHAHSVFK* uc002cdf.1
## [1875] 134 MSESIFSHNLQLLSSPVRCPMGMG...QSCYKGETQESVESRVLPGPRHRH* uc010utv.1
\end{verbatim}

4 Creating New TxDb Objects or Packages

The \textit{GenomicFeatures} package provides functions to create \textit{TxDb} objects based on data downloaded from UCSC Genome Bioinformatics or BioMart. The following subsections demonstrate the use of these functions. There is also support for creating \textit{TxDb} objects from custom data sources using \texttt{makeTxDb}; see the help page for this function for details.

4.1 Using \texttt{makeTxDbFromUCSC}

The function \texttt{makeTxDbFromUCSC} downloads UCSC Genome Bioinformatics transcript tables (e.g. "knownGene", "refGene", "ensGene") for a genome build (e.g. "mm9", "hg19"). Use the \texttt{supportedUCSTables} utility function to get the list of tables known to work with \texttt{makeTxDbFromUCSC}.

\begin{verbatim}
supportedUCSTables(genome="mm9")
\end{verbatim}

\begin{verbatim}
##   tablename track subtrack
##  1 knownGene  UCSC  Genes  <NA>
##  2 knownGeneOld8 Old  UCSC  Genes  <NA>
##  3 knownGeneOld7 Old  UCSC  Genes  <NA>
##  4 knownGeneOld6 Old  UCSC  Genes  <NA>
##  5 knownGeneOld5 Old  UCSC  Genes  <NA>
##  6 knownGeneOld4 Old  UCSC  Genes  <NA>
##  7 ccdsGene  CCDS  <NA>
\end{verbatim}
The function `makeTxDbFromUCSC` also takes an important argument called `circ_seqs` to label which chromosomes are circular. The argument is a character vector of strings that correspond to the circular chromosomes (as labeled by the source). To discover what the source calls their chromosomes, use the `getChromInfoFromUCSC` function to list them. By default, there is a supplied character vector that will attempt to label all the mitochondrial chromosomes as circular by matching to them. This is the `DEFAULT_CIRCSEQS` vector. It contains strings that usually correspond to mitochondrial chromosomes. Once the database has been generated with the circular chromosomes tagged in this way, all subsequent analysis of these chromosomes will be able to consider their circularity for analysis. So it is important for the user to make sure that they pass in the correct strings to the `circ_seqs` argument to ensure that the correct sequences are tagged as circular by the database.

```r
head(getChromInfoFromUCSC("hg19"))
```

## 4.2 Using `makeTxDbFromBiomart`

Retrieve data from BioMart by specifying the mart and the data set to the `makeTxDbFromBiomart` function (not all BioMart data sets are currently supported):
As with the `makeTxDbFromUCSC` function, the `makeTxDbFromBiomart` function also has a `circ.seqs` argument that will default to using the contents of the `DEFAULT_CIRC_SEQS` vector. And just like those UCSC sources, there is also a helper function called `getChromInfoFromBiomart` that can show what the different chromosomes are called for a given source.

Using the `makeTxDbFromBiomart` `makeTxDbFromUCSC` functions can take a while and may also require some bandwidth as these methods have to download and then assemble a database from their respective sources. It is not expected that most users will want to do this step every time. Instead, we suggest that you save your annotation objects and label them with an appropriate time stamp so as to facilitate reproducible research.

### 4.3 Using `makeTxDbFromGFF`

You can also extract transcript information from either GFF3 or GTF files by using the `makeTxDbFromGFF` function. Usage is similar to `makeTxDbFromBiomart` and `makeTxDbFromUCSC`.

### 4.4 Saving and Loading a TxDb Object

Once a `TxDb` object has been created, it can be saved to avoid the time and bandwidth costs of recreating it and to make it possible to reproduce results with identical genomic feature data at a later date. Since `TxDb` objects are backed by a SQLite database, the save format is a SQLite database file (which could be accessed from programs other than R if desired). Note that it is not possible to serialize a `TxDb` object using R's `save` function.

```r
saveDb(mm9KG_txdb, file="fileName.sqlite")
```

And as was mentioned earlier, a saved `TxDb` object can be initialized from a .sqlite file by simply using `loadDb`.

```r
mm9KG_txdb <- loadDb("fileName.sqlite")
```

### 4.5 Using `makeTxDbPackageFromUCSC` and `makeTxDbPackageFromBiomart`

It is often much more convenient to just make an annotation package out of your annotations. If you are finding that this is the case, then you should consider the convenience functions: `makeTxDbPackageFromUCSC` and `makeTxDbPackageFromBiomart`. These functions are similar to `makeTxDbFromUCSC` and `makeTxDbFromBiomart` except that they will take the extra step of actually wrapping the database up into an annotation package for you. This package can then be installed and used as of the standard TxDb packages found on in the Bioconductor repository.

### 5 Session Information

```r
## R version 3.3.1 (2016-06-21)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Ubuntu 16.04.1 LTS
```
## locale:

```
[1] LC_CTYPE=en_US.UTF-8 LC_NUMERIC=C LC_TIME=en_US.UTF-8
[4] LC_COLLATE=C LC_MONETARY=en_US.UTF-8 LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8 LC_NAME=C LC_ADDRESS=C
[10] LC_TELEPHONE=C LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

## attached base packages:

```
[1] stats4 parallel stats graphics grDevices utils datasets methods
[9] base
```

## other attached packages:

```
[1] BSgenome.Hsapiens.UCSC.hg19_1.4.0 BSgenome_1.42.0
[3] rtracklayer_1.34.0 Biostrings_2.42.0
[5] XVector_0.14.0 TxDb.Hsapiens.UCSC.hg19.knownGene_3.2.2
[7] GenomicFeatures_1.26.0 AnnotationDbi_1.36.0
[9] Biobase_2.34.0 GenomicRanges_1.26.0
[11] GenomeInfoDb_1.10.0 IRanges_2.8.0
[13] S4Vectors_0.12.0 BiocGenerics_0.20.0
```

## loaded via a namespace (and not attached):

```
[1] knitr_1.14 magrittr_1.5 GenomicAlignments_1.10.0
[4] zlibbioc_1.20.0 BiocParallel_1.8.0 lattice_0.20-34
[7] highr_0.6 stringr_1.1.0 tools_3.3.1
[10] grid_3.3.1 SummarizedExperiment_1.4.0 DBI_0.5-1
[13] Matrix_1.2-7.1 formatR_1.4 bitops_1.0-6
[16] RCurl_1.95-4.8 biomaRt_2.30.0 evaluate_0.10
[19] RSQLite_1.0.0 stringi_1.1.2 Rsamtools_1.26.0
[22] XML_3.98-1.4 BiocStyle_2.2.0
```