

# PH525.5x Section 4: Genomic annotation with Bioconductor

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## Representing Reference Sequence

- Annotation concept hierarchy
- Base - reference genomic sequence for an organism
- Above this, organize the chromosomal sequence into regions of interest - i.e. genes, transcripts
- SNPs and CpG sites are also regions of interest
- SNPS are single nucleotide
- Other variants – indels, structural variants, fusions can constitute regions of interest but are more complicated to express + represent
- Within ROI, identify platform oriented annotation provided by assay manufacturer
- Once manufacturing happens, genomic annotation proceeds and annotations must be updated to account for ambiguities or updates for assay probe elements
- Above genomic sequence ROIs, annotations concerning groups with shared structural or functional properties
- Pathways with nodes being genes and paths being relationships between gene products, i.e. protein protein interaction, promotion, enhancement, repression (3rd level of hierarchy)
- Begin with reference genomes
- Biostrings package - **available.genomes** - packages that represent reference genomic sequences for many different organisms
- Homo sapiens reference - some have repeat masking and there are versions which include the masked regions
  - different numbers of sequences in the two builds due to contigs that haven't been placed on chromosomes yet
- Operations defined for BSgenome objects - substring, extract chromosomal information
- Bases in full sequence aren't completely resolved
- Application of iteration - count the number of bases in a number of chromosomes
- If you have enough RAM, it is possible to operate on chromosomes in parallel and performing operations using multicore programming

```
library(BSgenome)
```

```
## 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, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##   anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##   dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##   grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##   order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##   rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##   union, unique, unsplit, which.max, which.min
## Loading required package: S4Vectors
## Loading required package: stats4
##
## Attaching package: 'S4Vectors'
## The following object is masked from 'package:base':
##
##   expand.grid
## Loading required package: IRanges
## Loading required package: GenomeInfoDb
## Warning: package 'GenomeInfoDb' was built under R version 4.0.5
## Loading required package: GenomicRanges
## Loading required package: Biostrings
## Loading required package: XVector
##
## Attaching package: 'Biostrings'
## The following object is masked from 'package:base':
##
##   strsplit
## Loading required package: rtracklayer
library(Biostrings)
ag = available.genomes()
grep("Scerev", ag, value=TRUE)

## [1] "BSgenome.Scerevisiae.UCSC.sacCer1" "BSgenome.Scerevisiae.UCSC.sacCer2"
## [3] "BSgenome.Scerevisiae.UCSC.sacCer3"
grep("Hsap", ag, value=TRUE)

```

```
## [1] "BSgenome.Hsapiens.1000genomes.hs37d5"
## [2] "BSgenome.Hsapiens.NCBI.GRCh38"
## [3] "BSgenome.Hsapiens.UCSC.hg17"
## [4] "BSgenome.Hsapiens.UCSC.hg17.masked"
## [5] "BSgenome.Hsapiens.UCSC.hg18"
## [6] "BSgenome.Hsapiens.UCSC.hg18.masked"
## [7] "BSgenome.Hsapiens.UCSC.hg19"
## [8] "BSgenome.Hsapiens.UCSC.hg19.masked"
## [9] "BSgenome.Hsapiens.UCSC.hg38"
## [10] "BSgenome.Hsapiens.UCSC.hg38.masked"

# inspect the human genome
library(BSgenome.Hsapiens.UCSC.hg19)
Hsapiens

## Human genome:
## # organism: Homo sapiens (Human)
## # genome: hg19
## # provider: UCSC
## # release date: June 2013
## # 298 sequences:
## #   chr1             chr2             chr3
## #   chr4             chr5             chr6
## #   chr7             chr8             chr9
## #   chr10            chr11            chr12
## #   chr13            chr14            chr15
## #   ...             ...             ...
## #   chr19_gl949749_alt chr19_gl949750_alt chr19_gl949751_alt
## #   chr19_gl949752_alt chr19_gl949753_alt chr20_gl383577_alt
## #   chr21_gl383578_alt chr21_gl383579_alt chr21_gl383580_alt
## #   chr21_gl383581_alt chr22_gl383582_alt chr22_gl383583_alt
## #   chr22_kb663609_alt
## # (use 'seqnames()' to see all the sequence names, use the '$' or '[' operator
## # to access a given sequence)

length(Hsapiens)

## [1] 298

class(Hsapiens)

## [1] "BSgenome"
## attr(,"package")
## [1] "BSgenome"

methods(class="BSgenome")

## [1] [[           $           as.list         bsgenomeName
## [5] coerce       commonName    countPWM      export
## [9] extractAt    getSeq       injectSNPs    length
## [13] masknames    matchPWM     metadata      metadata<-
## [17] mseqnames    names        organism      provider
## [21] providerVersion releaseDate  releaseName   seqinfo
## [25] seqinfo<-    seqnames    seqnames<-    show
## [29] snpcount     SNPlocs_pkgname snplocs       sourceUrl
## [33] vcountPattern vcountPDict  Views         vmatchPattern
## [37] vmatchPDict
```



- Introduction to TxDb package architecture

```
# Import TxDb transcript database
library(TxDb.Hsapiens.UCSC.hg19.knownGene)

## Loading required package: GenomicFeatures
## Warning: package 'GenomicFeatures' was built under R version 4.0.4
## Loading required package: AnnotationDbi
## Loading required package: Biobase
## Welcome to Bioconductor
##
## Vignettes contain introductory material; view with
## 'browseVignettes()'. To cite Bioconductor, see
## 'citation("Biobase")', and for packages 'citation("pkgname")'.

txdb = TxDb.Hsapiens.UCSC.hg19.knownGene
class(txdb)

## [1] "TxDb"
## attr(,"package")
## [1] "GenomicFeatures"
methods(class="TxDb")

## [1] $                                $<-                                annotatedDataFrameFrom
## [4] as.list                          asBED                             asGFF
## [7] assayData                        assayData<-                       cds
## [10] cdsBy                           cdsByOverlaps                     coerce
## [13] columns                         combine                            contents
## [16] dbconn                          dbfile                            dbInfo
## [19] dbmeta                          dbschema                          disjointExons
## [22] distance                        exons                             exonsBy
## [25] exonsByOverlaps                 ExpressionSet                      extractUpstreamSeqs
## [28] featureNames                    featureNames<-                    fiveUTRsByTranscript
## [31] genes                           initialize                        intronsByTranscript
## [34] isActiveSeq                     isActiveSeq<-                     isNA
## [37] keys                             keytypes                          mapIds
## [40] mapIdsToRanges                  mappedkeys                        mapRangesToIds
## [43] mapToTranscripts                metadata                          microRNAs
## [46] nhit                            organism                          promoters
## [49] revmap                          sample                            sampleNames
## [52] sampleNames<-                  saveDb                            select
## [55] seqinfo                         seqinfo<-                        seqlevels<-
## [58] seqlevels0                      show                              species
## [61] storageMode                     storageMode<-                     taxonomyId
## [64] threeUTRsByTranscript           transcripts                        transcriptsBy
## [67] transcriptsByOverlaps           tRNAs                             updateObject
## see '?methods' for accessing help and source code

# extract and inspect genes from TxDb
genes(txdb)

## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
```

```
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
```

```
## GRanges object with 23056 ranges and 1 metadata column:
```

```
##      seqnames      ranges strand |      gene_id
##      <Rle>        <IRanges> <Rle> | <character>
##      1      chr19  58858172-58874214 - |          1
##     10      chr8  18248755-18258723  + |         10
##    100     chr20  43248163-43280376 - |        100
##   1000     chr18  25530930-25757445 - |       1000
##  10000     chr1  243651535-244006886 - |      10000
##     ...      ...      ...      ... .      ...
##   9991     chr9  114979995-115095944 - |      9991
##   9992     chr21  35736323-35743440  + |      9992
##   9993     chr22  19023795-19109967 - |      9993
##   9994     chr6   90539619-90584155  + |      9994
##   9997     chr22  50961997-50964905 - |      9997
## -----
```

```
## seqinfo: 93 sequences (1 circular) from hg19 genome
```

```
table(strand(genes(txdb)))
```

```
## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
```

```
##
##      +      -      *
## 11737 11319      0
```

```
summary(width(genes(txdb)))
```

```
## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##       20   5666   20116   60660   58175 24187703
```

```
# inspect largest gene in genome
```

```
id = which.max(width(genes(txdb)))
```

```
## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
```

```
genes(txdb)[id]
```

```
## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
```

```
## GRangesList object, or use suppressMessages() to suppress this message.
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand |      gene_id
##      <Rle>         <IRanges> <Rle> | <character>
## 286297      chr9 42844370-67032072 - |      286297
## -----
## seqinfo: 93 sequences (1 circular) from hg19 genome
library(org.Hs.eg.db)

##
select(org.Hs.eg.db, keys="286297", keytype="ENTREZID", columns=c("SYMBOL", "GENENAME"))

## 'select()' returned 1:1 mapping between keys and columns
##      ENTREZID      SYMBOL
## 1      286297 LOC286297
##
##                                     GENENAME
## 1 methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1 like pseudogene
# compare total size of exons to total size of genes
ex = exons(txdb)
rex = reduce(ex)
ex_width = sum(width(rex)) # bases in exons
gene_width = sum(width(genes(txdb))) # bases in genes

## 403 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
ex_width/gene_width

## [1] 0.06380062
```

## ensemblDb, EnsDb: annotation from EMBL

- European initiative for annotating genome called ensembl
- Ensemble-based representations managed in package called EmsembleDb
- Different packages representing different builds of ensembl annotation for different organisms
- More direct relationship to database and database tables - gene, transcript, transcript to exon mapping tables.
- More details provided to user through Ensembl transcripts method - get info on transcripts but also associated proteins, genes and biotype

```
# inspect data available from Ensembl
library(ensemblDb)
```

```
## Loading required package: AnnotationFilter
##
## Attaching package: 'ensemblDb'
## The following object is masked from 'package:stats':
##
##      filter
```

```
library(EnsDb.Hsapiens.v75)
names(listTables(EnsDb.Hsapiens.v75))
```

```
## [1] "gene"          "tx"            "tx2exon"       "exon"
## [5] "chromosome"    "protein"       "uniprot"       "protein_domain"
## [9] "entrezgene"    "metadata"
```

```
# extract Ensembl transcripts
```

```
edb = EnsDb.Hsapiens.v75 # abbreviate
```

```
txs <- transcripts(edb, filter = GeneNameFilter("ZBTB16"),
                  columns = c("protein_id", "uniprot_id", "tx_biotype"))
```

```
txs
```

```
## GRanges object with 20 ranges and 5 metadata columns:
```

```
##          seqnames          ranges strand |      protein_id
##          <Rle>            <IRanges> <Rle> |      <character>
## ENST00000335953      11 11930315-114121398   + | ENSP00000338157
## ENST00000335953      11 11930315-114121398   + | ENSP00000338157
## ENST00000335953      11 11930315-114121398   + | ENSP00000338157
## ENST00000335953      11 11930315-114121398   + | ENSP00000338157
## ENST00000335953      11 11930315-114121398   + | ENSP00000338157
## ...                ...                ...   ... | ...
## ENST00000392996      11 11931229-114121374   + | ENSP00000376721
## ENST00000539918      11 11935134-114118066   + | ENSP00000445047
## ENST00000545851      11 114051488-114118018   + |          <NA>
## ENST00000535379      11 114107929-114121279   + |          <NA>
## ENST00000535509      11 114117512-114121198   + |          <NA>
##          uniprot_id          tx_biotype          tx_id
##          <character>          <character>          <character>
## ENST00000335953  ZBT16_HUMAN      protein_coding ENST00000335953
## ENST00000335953  Q71UL7_HUMAN      protein_coding ENST00000335953
## ENST00000335953  Q71UL6_HUMAN      protein_coding ENST00000335953
## ENST00000335953  Q71UL5_HUMAN      protein_coding ENST00000335953
## ENST00000335953  F5H6C3_HUMAN      protein_coding ENST00000335953
## ...                ...                ...                ...
## ENST00000392996  F5H5Y7_HUMAN      protein_coding ENST00000392996
## ENST00000539918          <NA> nonsense_mediated_de.. ENST00000539918
## ENST00000545851          <NA> processed_transcript ENST00000545851
## ENST00000535379          <NA> processed_transcript ENST00000535379
## ENST00000535509          <NA> retained_intron ENST00000535509
##          gene_name
##          <character>
## ENST00000335953      ZBTB16
## ENST00000335953      ZBTB16
## ENST00000335953      ZBTB16
## ENST00000335953      ZBTB16
## ENST00000335953      ZBTB16
## ...                ...
## ENST00000392996      ZBTB16
## ENST00000539918      ZBTB16
## ENST00000545851      ZBTB16
## ENST00000535379      ZBTB16
## ENST00000535509      ZBTB16
## -----
## seqinfo: 1 sequence from GRCh37 genome
```



```
# compare Ensembl and UCSC transcripts
alltx = transcripts(edb) # Ensembl is larger
utx = transcripts(txdb) # UCSC is smaller
```

```
# table of biological types of transcripts
table(alltx$tx_biotype)
```

```
##
##          3prime_overlapping_ncrna          antisense
##                29                10058
##          IG_C_gene          IG_C_pseudogene
##                31                13
##          IG_D_gene          IG_J_gene
##                64                24
##          IG_J_pseudogene          IG_V_gene
##                6                185
##          IG_V_pseudogene          lincRNA
##                264                12101
##          LRG_gene          miRNA
##                477                3424
##          misc_RNA          Mt_rRNA
##                2190                2
##          Mt_tRNA          non_stop_decay
##                22                63
##          nonsense_mediated_decay          polymorphic_pseudogene
##                13812                70
##          processed_pseudogene          processed_transcript
##                11321                31417
##          protein_coding          pseudogene
##                90273                664
##          retained_intron          rRNA
##                28579                570
##          sense_intronic          sense_overlapping
##                827                342
##          snoRNA          snRNA
##                1621                2074
##          TR_C_gene          TR_D_gene
##                6                3
##          TR_J_gene          TR_J_pseudogene
##                82                4
##          TR_V_gene          TR_V_pseudogene
##                150                40
## transcribed_processed_pseudogene transcribed_unprocessed_pseudogene
##                476                986
## translated_processed_pseudogene          unitary_pseudogene
##                1                189
##          unprocessed_pseudogene
##                3187
```

## Assessment: Gene and transcript model

```
library(devtools)
```

```

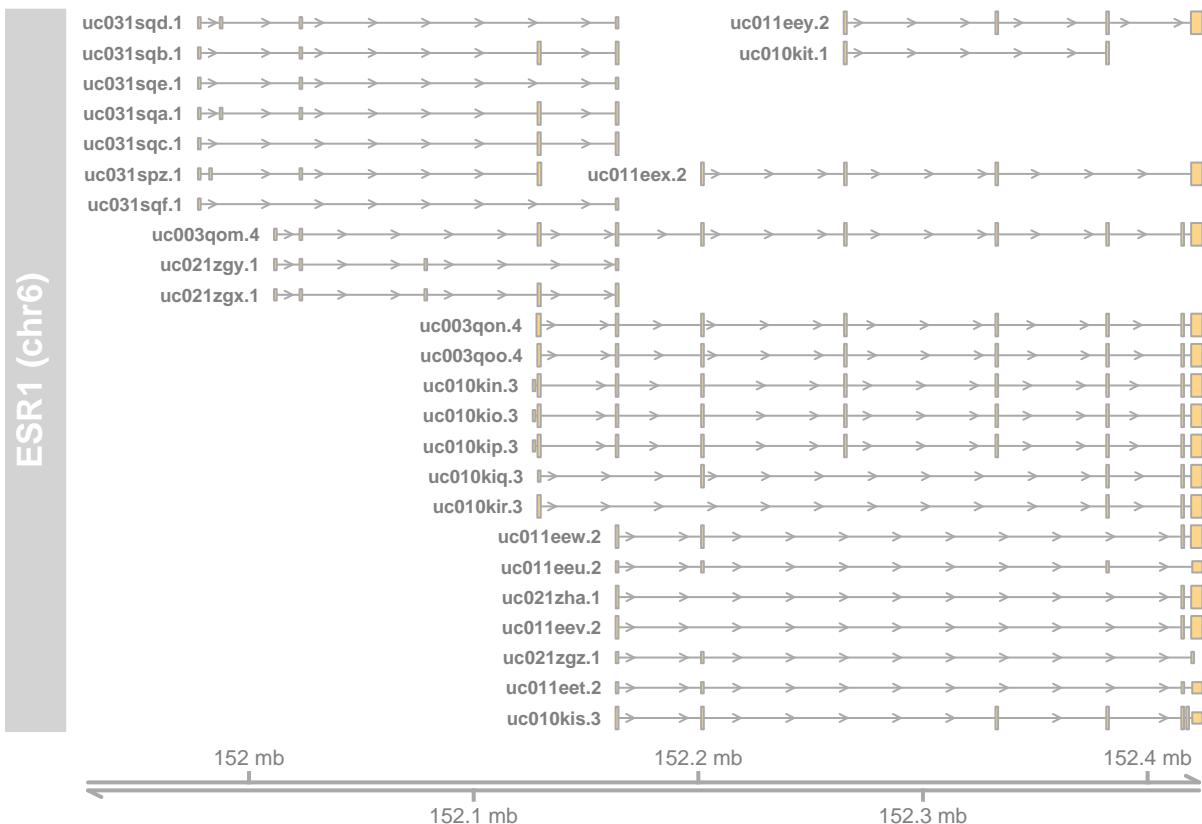
## Loading required package: usethis
install_github("genomicsclass/ph525x")

## Skipping install of 'ph525x' from a github remote, the SHA1 (e83c0d57) has not changed since last in
##   Use `force = TRUE` to force installation
library(ph525x)

## Loading required package: png
## Loading required package: grid
## Loading required package: Homo.sapiens
## Loading required package: OrganismDbi
## Loading required package: GO.db
##
stopifnot(packageVersion("ph525x") >= "0.0.16") # do over if fail
modPlot("ESR1", useGeneSym=FALSE, collapse=FALSE)

## Loading required package: Gviz
## Warning: package 'Gviz' was built under R version 4.0.4
##
## Attaching package: 'Gviz'
## The following object is masked from 'package:AnnotationFilter':
##
##   feature
## 'select()' returned 1:many mapping between keys and columns

```



```
library(TxDb.Hsapiens.UCSC.hg19.knownGene)
txdb = TxDb.Hsapiens.UCSC.hg19.knownGene
e_id <- select(edb, keys="ESR1", keytype="GENENAME", columns=c("ENTREZID"))[1, "ENTREZID"]
n_transcripts <- length(transcripts(txdb, filter=list(gene_id=e_id)))
paste("Number of transcripts comprising model of ESR1: ", n_transcripts)
```

```
## [1] "Number of transcripts comprising model of ESR1: 27"
```

## AnnotationHub: finding and caching important information

- Central hub for genomic annotation files maintained by Bioconductor community
- Includes annotation files from UCSC, ENSEMBL, and the Broad Institute
- **AnnotationHub** allows you to search and download resources from inside R session

```
library(AnnotationHub)
```

```
## Loading required package: BiocFileCache
```

```
## Loading required package: dbplyr
```

```
##
```

```
## Attaching package: 'AnnotationHub'
```

```
## The following object is masked from 'package:Biobase':
```

```
##
```

```
## cache
```

```
ah <- AnnotationHub()
```

```
## snapshotDate(): 2020-10-27
ah

## AnnotationHub with 57231 records
## # snapshotDate(): 2020-10-27
## # $dataprovder: Ensembl, BroadInstitute, UCSC, ftp://ftp.ncbi.nlm.nih.gov/g...
## # $species: Homo sapiens, Mus musculus, Drosophila melanogaster, Bos taurus,...
## # $rdataclass: GRanges, TwoBitFile, BigWigFile, EnsDb, Rle, OrgDb, ChainFile...
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH5012"]]'
##
##           title
## AH5012 | Chromosome Band
## AH5013 | STS Markers
## AH5014 | FISH Clones
## AH5015 | Recomb Rate
## AH5016 | ENCODE Pilot
## ...
## AH91566 | Zonotrichia_albicollis.Zonotrichia_albicollis-1.0.1.ncrna.2bit
## AH91567 | Zosterops_lateralis_melanops.ASM128173v1.cdna.all.2bit
## AH91568 | Zosterops_lateralis_melanops.ASM128173v1.dna_rm.toplevel.2bit
## AH91569 | Zosterops_lateralis_melanops.ASM128173v1.dna_sm.toplevel.2bit
## AH91570 | Zosterops_lateralis_melanops.ASM128173v1.ncrna.2bit

length(unique(ah$species))

## [1] 2643

ah_human <- subset(ah, species == "Homo sapiens")
ah_human

## AnnotationHub with 26461 records
## # snapshotDate(): 2020-10-27
## # $dataprovder: BroadInstitute, UCSC, Ensembl, GENCODE, UWashington, Stanfo...
## # $species: Homo sapiens
## # $rdataclass: GRanges, BigWigFile, Rle, ChainFile, TwoBitFile, list, data.f...
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH5012"]]'
##
##           title
## AH5012 | Chromosome Band
## AH5013 | STS Markers
## AH5014 | FISH Clones
## AH5015 | Recomb Rate
## AH5016 | ENCODE Pilot
## ...
## AH83216 | Ensembl 101 EnsDb for Homo sapiens
## AH83362 | Sequences of snoRNA targets of Homo sapiens hg38
## AH84122 | org.Hs.eg.db.sqlite
## AH89180 | Ensembl 102 EnsDb for Homo sapiens
## AH89426 | Ensembl 103 EnsDb for Homo sapiens
```

```
query(ah, "HepG2")
```

```
## AnnotationHub with 440 records
## # snapshotDate(): 2020-10-27
## # $dataprovder: UCSC, BroadInstitute, Pazar
## # $species: Homo sapiens, NA
## # $rdataclass: GRanges, BigWigFile
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH22246"]]'
##
##           title
## AH22246 | pazari_CEBPA_HEPG2_Schmidt_20120522.csv
## AH22249 | pazari_CTCF_HEPG2_Schmidt_20120522.csv
## AH22273 | pazari_HNF4A_HEPG2_Schmidt_20120522.csv
## AH22309 | pazari_STAG1_HEPG2_Schmidt_20120522.csv
## AH22348 | wgEncodeAffyRnaChipFiltTransfragsHepg2CytosolLongnonpolya.broadP...
## ...
## AH41564 | E118-H4K5ac.imputed.pval.signal.bigwig
## AH41691 | E118-H4K8ac.imputed.pval.signal.bigwig
## AH41818 | E118-H4K91ac.imputed.pval.signal.bigwig
## AH46971 | E118_15_coreMarks_mnemonics.bed.gz
## AH49484 | E118_RRBS_FractionalMethylation.bigwig
```

```
query(ah, c("HepG2", "H3K4me3"))
```

```
## AnnotationHub with 11 records
## # snapshotDate(): 2020-10-27
## # $dataprovder: BroadInstitute, UCSC
## # $species: Homo sapiens
## # $rdataclass: GRanges, BigWigFile
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH23311"]]'
##
##           title
## AH23311 | wgEncodeBroadHistoneHepg2H3k4me3StdPk.broadPeak.gz
## AH27201 | wgEncodeUwHistoneHepg2H3k4me3StdHotspotsRep1.broadPeak.gz
## AH27202 | wgEncodeUwHistoneHepg2H3k4me3StdHotspotsRep2.broadPeak.gz
## AH27203 | wgEncodeUwHistoneHepg2H3k4me3StdPkRep1.narrowPeak.gz
## AH27204 | wgEncodeUwHistoneHepg2H3k4me3StdPkRep2.narrowPeak.gz
## ...
## AH30771 | E118-H3K4me3.narrowPeak.gz
## AH31712 | E118-H3K4me3.gappedPeak.gz
## AH32893 | E118-H3K4me3.fc.signal.bigwig
## AH33925 | E118-H3K4me3.pval.signal.bigwig
## AH40296 | E118-H3K4me3.imputed.pval.signal.bigwig
```

```
hepg2 <- query(ah, "HepG2")
```

```
hepg2_h3k4me3 <- query(hepg2, c("H3k4me3"))
```

```
hepg2_h3k4me3
```

```
## AnnotationHub with 11 records
```

```
## # snapshotDate(): 2020-10-27
## # $dataprovder: BroadInstitute, UCSC
## # $species: Homo sapiens
## # $rdataclass: GRanges, BigWigFile
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH23311"]]'
##
##           title
## AH23311 | wgEncodeBroadHistoneHepg2H3k4me3StdPk.broadPeak.gz
## AH27201 | wgEncodeUwHistoneHepg2H3k4me3StdHotspotsRep1.broadPeak.gz
## AH27202 | wgEncodeUwHistoneHepg2H3k4me3StdHotspotsRep2.broadPeak.gz
## AH27203 | wgEncodeUwHistoneHepg2H3k4me3StdPkRep1.narrowPeak.gz
## AH27204 | wgEncodeUwHistoneHepg2H3k4me3StdPkRep2.narrowPeak.gz
## ...
## AH30771 | E118-H3K4me3.narrowPeak.gz
## AH31712 | E118-H3K4me3.gappedPeak.gz
## AH32893 | E118-H3K4me3.fc.signal.bigwig
## AH33925 | E118-H3K4me3.pval.signal.bigwig
## AH40296 | E118-H3K4me3.imputed.pval.signal.bigwig
```

```
hepg2_h3k4me3$tags
```

```
## [1] "wgEncode, ChipSeq, broadPeak, HepG2 cell, Bernstein grant"
## [2] "wgEncode, ChipSeq, broadPeak, HepG2 cell, Stam grant"
## [3] "wgEncode, ChipSeq, broadPeak, HepG2 cell, Stam grant"
## [4] "wgEncode, ChipSeq, narrowPeak, HepG2 cell, Stam grant"
## [5] "wgEncode, ChipSeq, narrowPeak, HepG2 cell, Stam grant"
## [6] "EpigenomeRoadMap, peaks, consolidated, broadPeak, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 Hepa"
## [7] "EpigenomeRoadMap, peaks, consolidated, narrowPeak, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 Hepa"
## [8] "EpigenomeRoadMap, peaks, consolidated, gappedPeak, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 Hepa"
## [9] "EpigenomeRoadMap, signal, consolidated, macs2signal, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 H"
## [10] "EpigenomeRoadMap, signal, consolidated, macs2signal, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 H"
## [11] "EpigenomeRoadMap, signal, consolidatedImputed, H3K4me3, E118, ENCODE2012, LIV.HEPG2.CNCR, HepG2 H"
```

```
# display(query(ah, "HepG2"))
```

```
e118_broadpeak <- query(hepg2_h3k4me3, c("E118", "broadPeak"))
id <- e118_broadpeak$ah_id
id
```

```
## [1] "AH29728"
```

```
hepg2_h3k4me3_broad <- ah[["AH29728"]]
```

```
## loading from cache
```

```
hepg2_h3k4me3_broad
```

```
## GRanges object with 60638 ranges and 5 metadata columns:
```

	seqnames	ranges	strand	name	score	signalValue
	<Rle>	<IRanges>	<Rle>	<character>	<numeric>	<numeric>
## [1]	chr14	24614467-24618166	*	Rank_1	850	20.3233
## [2]	chr20	3183140-3185609	*	Rank_2	830	25.7534
## [3]	chr14	24700096-24704098	*	Rank_3	811	17.2931
## [4]	chr14	24766070-24770499	*	Rank_4	763	18.9677

```
##      [5] chr20 44420138-44421910 * | Rank_5 755 24.0763
##      ...      ...      ...      ...      ...
## [60634] chr2 11928736-11929617 * | Rank_60634 0 1.73093
## [60635] chr10 97229724-97230412 * | Rank_60635 0 1.73015
## [60636] chr2 39896310-39896946 * | Rank_60636 0 1.73014
## [60637] chr6 3978391-3978677 * | Rank_60637 0 1.73015
## [60638] chr6 49433554-49434110 * | Rank_60638 0 1.73014
##      pValue qValue
##      <numeric> <numeric>
##      [1] 88.3475 85.0287
##      [2] 86.2138 83.0301
##      [3] 84.3213 81.1706
##      [4] 79.3876 76.3449
##      [5] 78.6304 75.5947
##      ...      ...      ...
## [60634] 1.00441 0
## [60635] 1.00357 0
## [60636] 1.00357 0
## [60637] 1.00357 0
## [60638] 1.00357 0
## -----
## seqinfo: 298 sequences (2 circular) from hg19 genome
```

```
alt_format <- ah[[id]]
```

```
## loading from cache
```

```
identical(hepg2_h3k4me3_broad, alt_format)
```

```
## [1] TRUE
```

## Assessment: AnnotationHub

```
library(AnnotationHub)
ah = AnnotationHub()
```

```
## snapshotDate(): 2020-10-27
```

```
mah = mcols(ah)
names(mah)
```

```
## [1] "title" "dataprovder" "species"
## [4] "taxonomyid" "genome" "description"
## [7] "coordinate_1_based" "maintainer" "rdatadateadded"
## [10] "preparerclass" "tags" "rdataclass"
## [13] "rdatapath" "sourceurl" "sourcetype"
```

```
sort(table(mah$species), decreasing=TRUE)[1:10]
```

```
##
## Homo sapiens Mus musculus Drosophila melanogaster
## 26461 1617 422
## Bos taurus Pan troglodytes Rattus norvegicus
## 318 306 305
## Danio rerio Gallus gallus Monodelphis domestica
## 297 265 242
```

```
##           Felis catus
##           235
n_ctcf_binding_hepg2 <- length(names(query(query(ah, "HepG2"), "CTCF")))
paste("Number of entries addressing CTCF binding in HepG2: ", n_ctcf_binding_hepg2)

## [1] "Number of entries addressing CTCF binding in HepG2: 13"
```

## liftOver: Translating between reference builds

- Genomic annotations typically defined for fixed genome build
- Human is often hg19
- When analysis is performed on different genome build, annotations must be translated to the coordinates of the new build before use
- Process of translating called **lifting**
- Implemented in **liftOver()** function of **rtracklayer** Bioconductor package
- Tutorial will move features from genome build hg38 -> hg19

```
# liftOver from rtracklayer
library(rtracklayer)
?liftOver

# chromosome 1 gene locations in hg38
library(TxDb.Hsapiens.UCSC.hg38.knownGene)
tx38 <- TxDb.Hsapiens.UCSC.hg38.knownGene
seqlevels(tx38, pruning.mode="coarse") = "chr1"
g1_38 <- genes(tx38)
```

```
## 12 genes were dropped because they have exons located on both strands
## of the same reference sequence or on more than one reference sequence,
## so cannot be represented by a single genomic range.
## Use 'single.strand.genes.only=FALSE' to get all the genes in a
## GRangesList object, or use suppressMessages() to suppress this message.
```

```
# Download hg38 to hg19 chain file
library(AnnotationHub)
ah <- AnnotationHub()
```

```
## snapshotDate(): 2020-10-27
ah.chain <- subset(ah, rdataclass == "ChainFile" & species == "Homo sapiens")
query(ah.chain, c("hg19", "hg38"))
```

```
## AnnotationHub with 4 records
## # snapshotDate(): 2020-10-27
## # $dataprovder: UCSC, NCBI
## # $species: Homo sapiens
## # $rdataclass: ChainFile
## # additional mcols(): taxonomyid, genome, description,
## #   coordinate_1_based, maintainer, rdatadateadded, preparerclass, tags,
## #   rdatapath, sourceurl, sourcetype
## # retrieve records with, e.g., 'object[["AH14108"]]'
##
##           title
## AH14108 | hg38ToHg19.over.chain.gz
## AH14150 | hg19ToHg38.over.chain.gz
```



```

## AH78915 | Chain file for Homo sapiens rRNA hg19 to hg38
## AH78916 | Chain file for Homo sapiens rRNA hg38 to hg19
ch <- ah [["AH14108"]]

## loading from cache
# perform the liftOver
g1_19L <- liftOver(g1_38, ch)
g1_19L

## GRangesList object of length 2696:
## $`10000`
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand |      gene_id
##      <Rle>         <IRanges> <Rle> | <character>
## [1]      chr1 243651535-244014381     - |      10000
## -----
##      seqinfo: 19 sequences from an unspecified genome; no seqlengths
##
## $`100034743`
## GRanges object with 3 ranges and 1 metadata column:
##      seqnames      ranges strand |      gene_id
##      <Rle>         <IRanges> <Rle> | <character>
## [1]      chr1 147466094-147484530     - |      100034743
## [2]      chr1 147484532-147484551     - |      100034743
## [3]      chr1 147484553-147487188     - |      100034743
## -----
##      seqinfo: 19 sequences from an unspecified genome; no seqlengths
##
## $`100126331`
## GRanges object with 1 range and 1 metadata column:
##      seqnames      ranges strand |      gene_id
##      <Rle>         <IRanges> <Rle> | <character>
## [1]      chr1 117637265-117637350      + |      100126331
## -----
##      seqinfo: 19 sequences from an unspecified genome; no seqlengths
##
## ...
## <2693 more elements>

```