Full genome sequences for Drosophila melanogaster (UCSC version dm2)
Examples

BSgenome.Dmelanogaster.UCSC.dm2
genome <- BSgenome.Dmelanogaster.UCSC.dm2
seqlengths(genome)
genome$chr2L # same as genome[["chr2L"]]

## ---------------------------------------------------------------------
## Upstream sequences
## ---------------------------------------------------------------------
## Starting with BioC 3.0, the upstream1000, upstream2000, and
## upstream5000 sequences for dm2 are not included in the BSgenome data
## package anymore. However they can easily be extracted from the full
## genome sequences with something like:

library(GenomicFeatures)
txdb <- makeTranscriptDbFromUCSC("dm2", "refGene")
 gn <- sort(genes(txdb))
up1000 <- flank(gn, width=1000)
up1000seqs <- getSeq(genome, up1000)

## IMPORTANT: Make sure you use a TxDb package (or TranscriptDb object),
## that contains a gene model based on the exact same reference genome
## as the BSgenome object you pass to getSeq(). Note that you can make
## your own custom TranscriptDb object from various annotation resources.
## See the makeTranscriptDbFromUCSC(), makeTranscriptDbFromBiomart(),
## and makeTranscriptDbFromGFF() functions in the GenomicFeatures
## package.

## ---------------------------------------------------------------------
## Genome-wide motif searching
## ---------------------------------------------------------------------
## See the GenomeSearching vignette in the BSgenome software
## package for some examples of genome-wide motif searching using
## Biostrings and the BSgenome data packages:
if (interactive())
  vignette("GenomeSearching", package="BSgenome")
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