Exercise 1
a. Generate a random DNAString of length 2000. (You will need: sample(), DNA_BASES, paste(), DNAString().)
b. Create views on it.
c. Invert the views.
d. Count the frequencies of the DNA letters: (a) in the DNAString object, (b) inside the views, (c) outside the views. Do a sanity check.

Exercise 2
a. Load Affymetrix hgu95av2 probe sequences into a DNAStringSet object.
b. Remove the first 10 probes.
c. Which probes contain more than 16 A’s?
d. Reverse complement the probes.
e. Trim the first (5’) and last (3’) two bases.
f. Generate the sequences of the mismatch probes (MM probes) by replacing the middle nucleotide of each PM probe by its reverse complement.
g. Which probes contain more than 9 consecutive A’s? (You can use vcountPattern() for this.) Display their sequences.

Exercise 3
a. Load BSgenome data package for hg19.
b. Count the number of times each Affymetrix hgu95av2 probe hits Human chr22. (You will need: PDict(), countPDict().)
c. Which probes have more than 2000 hits? Display their sequences.
Exercise 4

The goal of this exercise is to count the nb of times each Human transcript is hit by a hgu95av2 probe. We use the TxDb.Hsapiens.UCSC.hg19.knownGene package for the locations of the transcripts and their exons.

a. Extract the Human transcriptome with `extractTranscriptsFromGenome()` (defined in the GenomicFeatures package).

b. Use `vcountPDict()` (with ‘collapse=2’) to count the nb of hits per transcript.