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Assessment: Reference genomes

Q1: Reference genome discovery

1/1 point (graded)

How many Bioconductor packages provide reference genomic sequence for zebrafish (*Danio rerio*)? Exclude the packages with suffix ".masked", which we will discuss later.



Submit

You have used 1 of 5 attempts

✓ Correct (1/1 point)

Q2: Masking structures for genome gaps and repetitions

1/1 point (graded)

We have noted that the reference genome builds for complex organisms are works in progress. Genomic sequence "mask" structures have been defined to isolate ambiguous, unmappable, and low-complexity segments of genomes so that sequence analysis research can be targeted to reflect current knowledge of sequence regions that are more likely to be functionally informative.

Obtain **BSgenome.Hsapiens.UCSC.hg19.masked** (it is only a 20MB transfer.)

Run the commands:

```
library(BSgenome.Hsapiens.UCSC.hg19.masked)
c17m = BSgenome.Hsapiens.UCSC.hg19.masked$chr17
```

What is the class of `c17m` ?

MaskedDNASTring



Submit

You have used 2 of 2 attempts

✓ Correct (1/1 point)

Q3: Quantifying assembly gaps

1/1 point (graded)

When we print out the value of a *MaskedDNASTring*, we get a report on types of mask present. Part of the report for chromosome 17 in hg19 is:

```
81195210-letter "MaskedDNAString" instance (# for masking)
seq: AAGCTTCTCACCTGTTCTGCATAGATAATTGCAT...GTGGGTGTGGGTGTGGTGTGGGTGTGGGTGTGGT
masks:
  maskedwidth maskedratio active names          desc
1      3400000  0.04187439  TRUE AGAPS          assembly gaps
...
```

In build hg19, what percentage of the length of chromosome 22 is occupied by "assembly gaps"?
Reply with an integer between 0 and 100.



You have used 1 of 5 attempts

✓ Correct (1/1 point)

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Q1: answer not correct/up to date

When i enter the code in R, I find N+1 *Danio rerio* packages, while the answer to Q1 states it should be N.

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