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Assessment: Setup and GRanges

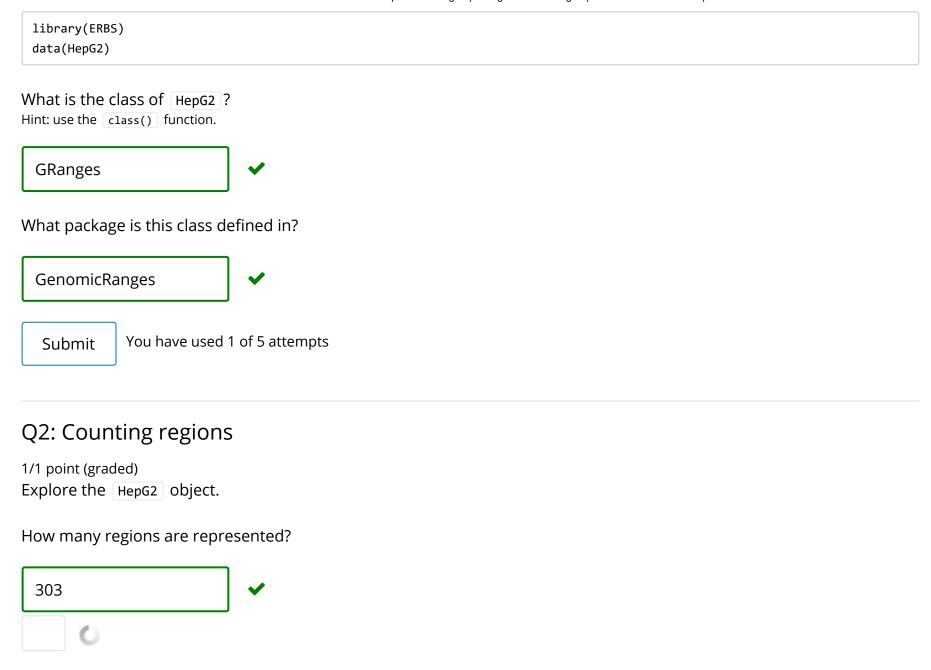
This week we are using two sets of genomic regions as examples. These are the reported ESRRA binding sites obtained for a ENCODE ChIP-seq experiment on two cell lines: HepG2 and GM12878. We have put these regions into an R package for your convenience. If you have not done so already, please download and install the **ERBS** package:

BiocManager::install("genomicsclass/ERBS")

Q1: Classes for genomic ranges

2/2 points (graded)

Load the **ERBS** library and then the HepG2 object.



You have used 1 of 5 attempts Submit

Discussion

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