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## Assessment: Introduction to GenomicRanges

We will continue using the ERBS example introduced in the video.

### Q1: Statistics on peak scores

1/1 point (graded)

In the video we used the `values()` method to extract meta-data on the regions. An alternative, and actually preferred approach going forward, is `mcols()`.

What is the median of the `signalValue` column for the HepG2 data?





You have used 1 of 5 attempts

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✓ Correct (1/1 point)

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## Q2: Locating the largest peak

1/1 point (graded)

In what chromosome is the region with the highest `signalValue` (copy and paste your answer)?

You have used 2 of 5 attempts

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✓ Correct (1/1 point)

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## Q3: Tabulating by chromosome

1/1 point (graded)

How many regions are from chromosome 16?





You have used 1 of 5 attempts

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✓ Correct (1/1 point)

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## Q4: Statistics on peak widths

1/1 point (graded)

Make a histogram of the widths of the regions from all chromosomes (not just chr16). Note it has a heavy right tail.

What is the median width?



You have used 1 of 5 attempts

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✓ Correct (1/1 point)

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## Discussion

**Topic:** Section 2 / Introduction to GenomicRanges

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