Startup Assessment

Stephen Blatti

November 11, 2017

The following problems check that you have a grip on a) how to look up and assess the experimental method underlying an experimental data package, b) how to answer a basic question about the human reference genomic sequence.

Package annotation check

Which of the following biocViews terms is not employed to annotate the Hiiragi2013 experimental data package?

```
qPCRdata
MicroarrayData
RNASeqData
ReproducibleResearch
```

RNASeq Data See http://bioconductor.org/packages/release/data/experiment/html/Hiiragi2013.html

Reference chromosome lengths

In human genome reference build hg19, what is the length of chromosome 16?

```r
library(BSgenome.Hsapiens.UCSC.hg19)
```

```
## Warning: package 'GenomeInfoDb' was built under R version 3.4.2
```

```
## Warning: package 'GenomicRanges' was built under R version 3.4.2
```

```
## Warning: package 'rtracklayer' was built under R version 3.4.2
```

```r
length(Hsapiens$chr16)
```

```
## [1] 90354753
```

```r
# or nchar(Hsapiens$chr16)
```