

AnnotationHub Exercisess

Getting started

The `AnnotationHub` package provides a client interface to resources stored at the AnnotationHub web service.

```
library(AnnotationHub)
```

Start by creating an `AnnotationHub` object

```
ah = AnnotationHub()
```

Exercises

- Query the `ah` object to find a `TxDb` object for hg38. How many such records are there?

```
library(AnnotationHub)
ah = AnnotationHub()
query(ah, c('hg38', 'TxDb'))
```

- Access the record in the first exercise and assign it to the `txdb` variable.

```
txdb = ah[["AH52260"]]
```

- Use the `transcripts` method to get a set of `GRanges` associated with transcripts.

```
tx = transcripts(txdb)
tx
```

- Perform a query on `ah` to find the narrow peak `RoadMapEpigenome` objects. How many records are available?

```
ah_roadmap = query(ah, c("RoadMap", "narrowpeak"))
length(ah_roadmap)
```

- Further filter to keep only DNase data. How many records are available?

```
dnase = query(ah_roadmap, 'dnase')
dnase
```

- Load the last DNase record into a variable. What does the track store in it? What is the class of the record?

```
dnase_track = dnase[['AH45295']]
dnase_track
class(dnase_track)
```