Demo 1: Free text search of ENCODE data

1. Go to https://www.encodeproject.org
2. Enter “skin” into the search box on the upper right hand corner
3. All matches on the website will be shown
4. Select “Experiments”
5. View all ENCODE assays that contain a match to “skin”
Demo 2: Browsing and filtering of ENCODE data

1. Go to https://www.encodeproject.org
2. Under the “Data” menu bar, select “Assays”

3. All publicly available assays are shown. The categories on the left are metadata describing the assays. They can be used to filter your results.
5. View all ENCODE assays that are filtered by selecting “skin of body”. Note that the results are not straight text matches. For example, “fibroblast of arm”, and “keratinocytes” are included in the results list.
1. Go to https://www.encodeproject.org
2. Enter “skin” into the search box on the upper right hand corner
3. All matches on the website will be shown
4. Select “Experiments”
Demo 3: Combine search & filter of ENCODE data

1. Go to https://www.encodeproject.org
2. Enter “skin” into the search box on the upper right hand corner
3. All matches on the website will be shown
4. Select “Experiments”
5. View all ENCODE assays that contain a match to “skin”

![ENCODE Assay Table]

6. If looking for RNA-seq data from adult samples, select “RNA-seq” under Assay and “adult” under Life Stage.

![ENCODE Assay Table]
Demo 4: Visualize data

Details of how to configure tracks will be presented during the UCSC Genome Browser workshop. This demo just shows what to expect as you are connected to the browser.

1. Get the list of assays illustrated in Demo 3.
2. Select “Visualize” button on the upper right corner. This will automatically create a trackhub to visualize the results.

3. An intermediate page listing the reference genome is shown. Trackhubs can be made with different reference genomes.

4. The trackhub will be connected. Enter a gene name or enter submit. Details of how to configure tracks will be presented during the UCSC Genome Browser workshop.
5. The track hub is listed as “Hub (search)"

6. Hover over tracks to view file-related metadata.

7. Click on left hand grouping to configure tracks and view more metadata, including file download links and links back to the ENCODE Portal.
8. ENCODE metadata for the track hub
Demo 5: Batch download data

1. Get the list of assays illustrated in Demo 3.
2. Select “Download” button on the upper right corner.

3. Instructions on the command to batch download files is displayed. Click on ‘Download’ again. This will download a file called ‘files.txt’
4. Open files.txt. This includes a list of links to all the files for those experiments. The first link contains the metadata. You can select the subset of files by using the ‘available data’ facet.

5. Transfer this file to your server and use
   xargs -n 1 curl -O -L < files.txt
Exercises using the ENCODE Portal

Exercise 1: ChIP-seq assays
- How many ChIP-seq assays are available against H3K27me3 in mouse
- How many unique antibodies are used?
- Of the antibodies used, which one(s) have been fully characterized to current ENCODE standards?

Exercise 2: Controls
- What is the accession for control experiment for ENCSR778SIU?
- How many assays use this control?

Exercise 3: Recently released data
- What was the total number of assays released in June 2015?
- How many of each kind?

Exercise 4: Files
- What are the accession(s) and md5sum(s) to the fastq files for biological replicate 1 in assay ENCSR000AFI?
- What are the accessions of the alignment (bam) files made from the fastq’s?
- Which software tool and version was used to generate them?

Exercise 5: Protein factors
- Which assays have been performed against IGF2BP1?
Pre-requisites: download or install these tools to help you get started
- A JSON pretty-printer plugin for your web browser, such as JSONView (for Chrome or Firefox) or JSON Formatter (for Safari)
- A few python modules
  - pip install requests
  - pip install json
  - pip install jsonschema

Help document: https://www.encodeproject.org/help/rest-api/
Sample script: https://github.com/ENCODE-DCC/submission_sample_scripts/blob/master/get.py

Try the exercises listed on the previous page. They can be performed programmatically as well.