1. Basic IPython usage

- 1. Try the 2 iPython modes
- 2. Create new cells above and below your current one
- 3. Try the following:
 - (a) In the 1st cell, set the variable name to your name. Execute the cell.
 - (b) In the 2nd cell, execute print name. Execute the cell.
 - (c) In the 3rd cell, redefine name to something else. Execute the cell.
 - (d) What will happen if you now rerun 2nd cell? Why? Would this be different if the notebook was a regular Python script?

2. DataFrames

Create a dummy dataframe:

- 1. Use head, tail and describe
- 2. Use the loc method to...
 - (a) select rows 1-3.
 - (b) select all rows of the sample column.
 - (c) select rows 1-3 of chrom and cov.
- 3. Use the iloc method to select the first 5 rows and columns

3. Basic DataFrames

- 1. Load the quasar dataset into a pandas DataFrame using read_csv
- 2. Try out what happens if you load the DataFrame without using the correct sep argument
- 3. Try again the row/column selection you used on the dummy DataFrame
- 4. Save a subset of df into df2 and compare the outputs of describe.

4. Counting and Boolean Indexing

- 1. How many different genes are there in the dataset?
- 2. Use boolean indexing to select all rows with FAO > 50.
- 3. How many rows are there with FAO > 500? And for FAO > 1500?
- 4. How many rows have an effect of either 'STOP_GAINED' or 'FRAME_SHIFT'? Hint: this is possible in one command by using the <code>.isin(list)</code> method.

5. Column creation

- 1. Replace the "Effect_Impact" column with a lowercase version of itself. Hint: the str method exposes a column as a string so you can use all the standard Python string functions.
- 2. Create a new column called DP as the sum of FAO and FDP.
- 3. Create a new column called len as the combined length of ref and alt.
- 4. Write a function that parses the Effect from a row and returns "strong" if it's in 'STOP_GAINED' or 'FRAME_SHIFT', otherwise "weak". Test the function using a dictionary (to simulate a row).
- 5. Create a new column "Binary Impact" by applying the function using df.apply(function, axis=1)