	<pre>import pandas as pd import numpy as np import random import matplotlib.pyplot as plt %natplotlib inline import seaborn as sns sns.set_style('darkgrid') #We are setting the seed to assure you get the same answers on quizzes as we set up random.seed(42)</pre> 1. Now, read in the ab_data.csv data. Store it in df. Use your dataframe to answer the questions
	in Quiz 1 of the classroom. a. Read in the dataset and take a look at the top few rows here: df = pd.read_csv('ab_data.csv') df.head() user_id timestamp group landing_page converted 0 851104 2017-01-21 22:11:48.556739 control old_page 0 1 804228 2017-01-12 08:01:45.159739 control old_page 0 2 661590 2017-01-11 16:55:06.154213 treatment new_page 0 3 853541 2017-01-08 18:28:03.143765 treatment new_page 0
n [3]: ut[3]:	4 864975 2017-01-21 01:52:26.210827 control old_page 1 b. Use the below cell to find the number of rows in the dataset. df.shape[0] 294478 c. The number of unique users in the dataset. df['user_id'].nunique()
n [5]: ut[5]:	<pre>d. The proportion of users converted. converted = df.query('converted == 1') converted.shape[0] /df.shape[0] 9.11965919355605512 e. The number of times the _new_page and _treatment don't line up. df.query('group == "treatment" and landing_page != "new_page"').shape[0] +\ df.query('group != "treatment" and landing_page == "new_page"').shape[0]</pre>
ut[6]: n [7]:	f. Do any of the rows have missing values? df.info() <class 'pandas.core.frame.dataframe'=""> RangeIndex: 294478 entries, 0 to 294477 Data columns (total 5 columns): # Column Non-Null Count Dtype</class>
	dtypes: int64(2), object(3) memory usage: 11.2+ MB No, there is'nt missing values. 2. For the rows where treatment is not aligned with new_page or control is not aligned with old_page, we cannot be sure if this row truly received the new or old page. Use Quiz 2 in the classroom to provide how we should handle these rows. a. Now use the answer to the quiz to create a new dataset that meets the specifications from the quiz. Store your new dataframe in df2. df2=df df2.drop(df.query("(group == 'treatment' and landing_page == 'old_page') or (group == 'droup == 'treatment' and landing_page == 'old_page') or (group == 'treatment' and 'tre
n [9]: ut[9]: [10]:	<pre>'control' and landing_page == 'new_page')").index, inplace=frue) # Double Check all of the correct rows were removed - this should be 0 df2[((df2['group'] == 'treatment') == (df2['landing_page'] == 'new_page')) == False].shape[0] 9 3. Use df2 and the cells below to answer questions for Quiz3 in the classroom. a. How many unique user_ids are in df2? df2['user_id'].nunique()</pre>
[11]: t[11]:	b. There is one user_id repeated in df2. What is it? df2[df2.duplicated(['user_id'], keep=rolse)]['user_id'].unique() array([773192]) c. What is the row information for the repeat user_id? df2[df2.duplicated(['user_id'], keep=rolse)] user_id timestamp group landing_page converted
[13]:	1899 773192 2017-01-09 05:37:58.781806 treatment new_page 0 2893 773192 2017-01-14 02:55:59.590927 treatment new_page 0 d. Remove one of the rows with a duplicate user_id, but keep your dataframe as df2. df2.drop(df2.loc[[1899]].index, inplace=True) 4. Use df2 in the below cells to answer the quiz questions related to Quiz 4 in the classroom. a. What is the probability of an individual converting regardless of the page they receive? prob_convert = df2.query('converted == 1').shape[0] / df2.shape[0] prob_convert
[15]: t[15]:	
[16]: t[16]:	<pre>treatment_population = df2.query('group == "treatment"') treatment_converted = control_converted = df2.query('converted == 1 and group == "treatment"') (treatment_converted.shape[0] / treatment_population.shape[0]) 9.11880806551510564 d. What is the probability that an individual received the new page? #For further analysis, we are querying now individual who received old page received_new_page = df2.query('landing_page == "new_page"')</pre>
	received_new_page = df2.query('landing_page == "new_page"') received_old_page = df2.query('landing_page == "old_page"') received_new_page.shape[0] / df2.shape[0] 0.5000619442226688 e. Consider your results from a. through d. above, and explain below whether you think there is sufficient evidence to say that the new treatment page leads to more conversions. Once control group converting rate is higher than treatment group, we fail to reject the null hypothesis.
	Part II - A/B Test Notice that because of the time stamp associated with each event, you could technically run a hypothesis test continuously as each observation was observed. However, then the hard question is do you stop as soon as one page is considered significantly better than another or does it need to happen consistently for a certain amount of time? How long do you run to render a decision that neither page is better than another? These questions are the difficult parts associated with A/B tests in general. 1. For now, consider you need to make the decision just based on all the data provided. If you want to
	assume that the old page is better unless the new page proves to be definitely better at a Type I error rate of 5%, what should your null and alternative hypotheses be? You can state your hypothesis in terms of words or in terms of p_{old} and p_{new} , which are the converted rates for the old and new pages. $H_0: p_{old} >= p_{new}$ $H_1: p_{old} < p_{new}$ 2. Assume under the null hypothesis, p_{new} and p_{old} both have "true" success rates equal to the converted success rate regardless of page - that is p_{new} and p_{old} are equal. Furthermore, assume they are equal to the converted rate in ab_data.csv regardless of the page.
	Use a sample size for each page equal to the ones in $ab_data.csv$. Perform the sampling distribution for the difference in $converted$ between the two pages over 10,000 iterations of calculating an estimate from the null. Use the cells below to provide the necessary parts of this simulation. If this doesn't make complete sense right now, don't worry - you are going to work through the problems below to complete this problem. You can use $Quiz 5$ in the classroom to make sure you are on the right track.
[18]: t[18]: [19]:	p_new = df2['converted'].mean() p_new
[20]: t[20]:	c. What is n_{new} ?
[22]: t[22]:	e. Simulate n_{new} transactions with a convert rate of p_{new} under the null. Store these n_{new} 1's and 0's in $new_page_converted$.
[24]: t[24]:	g. Find p_{new} - p_{old} for your simulated values from part (e) and (f).
	<pre>for _ in range(int(1e5)): new_page_converted = np.random.binomial(n_new,p_new) old_page_converted = np.random.binomial(n_old, p_old) p_diff = new_page_converted/n_new - old_page_converted/n_old p_diffs.append(p_diff) i. Plot a histogram of the p_diffs. Does this plot look like what you expected? Use the matching problem in the classroom to assure you fully understand what was computed here. plt.title('Simulated p-values') plt.ylabel('Frequency') plt.xlabel('p-values')</pre>
	plt.hist(p_diffs); Simulated p-values 25000 25000 10000
[27]: t[27]:	j. What proportion of the p_diffs are greater than the actual difference observed in ab_data.csv ? p_diff_orig = (treatment_population['converted'].mean() - control_population['converted']).mean() p_diff_orig
[28]:	-0.0015782389853555795
	p_diffs = np.array(p_diffs) p_diff_proportion = (p_diff_orig < p_diffs).mean() print('proportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) proportion of p_diffs greater than p_diffs from ab_data.csv : 0.90443 k. In words, explain what you just computed in part j. What is this value called in scientific studies? What does this value mean in terms of whether or not there is a difference between the new and old pages? A p-value is the probability of observing your statistic if the null hypothesis is true. The null hypothesis was that the difference in means would be equal or less than 0, and the alternative was the difference would be greater than 0. However, the difference is less than zero, and the p-value is
	p_diffs = np.array(p_diffs) p_diff_proportion = (p_diff_orig < p_diffs).mean() print('proportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) Troportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) Troportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) Troportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) Troportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion) Troportion of p_diffs greater than p_diffs from ab_data.csv : ',p_diff_proportion The null hypothesis was that you just computed in part j. What is this value called in scientific studies? What does this value mean in terms of whether or not there is a difference between the new and old pages? A p-value is the probability of observing your statistic if the null hypothesis is true. The null hypothesis was that the difference in means would be equal or less than 0, and the alternative was the difference would be greater than 0. However, the difference is less than 2ero, and the p-value is very large. We do not have evidence to rejust the null. I. We could also use a built-in to achieve similar results. Though using the built-in might be easier to code, the above portions are a walkthrough of the ideas that are critical to correctly thinking about statistical significance. Fill in the below to calculate the number of conversions for each page, as well as the number of individuals who received each page. Let n_old and n_new refer the the number of rows associated with the old page and new pages, respectively. The port statsmodels.api sm convert_old = df2.query('landing page == "lold_page" & converted == True').shape[s] convert_new = df2.query('landing page == "new_page" & converted == True').shape[s]
[29]:	p_diffs = np.array(p_diffs) p_difff_proportion = (p_difff_orig < p_diffs).mean() print('proportion of p_diffs greater than p_diffs from ab_data.csv.' , p_diff_proportion) reportion of p_diffs greater than p_diffs from ab_data.csv.' k. In words, explain what you just computed in part j. What is this value called in scientific studies? What does this value mean in terms of whether or not there is a difference between the new and old pages? A p-value is the probability of observing your statistic if the null hypothesis is true. The null hypothesis was that the difference in means would be equal or less than 0, and the alternative was the difference would be greater than 0. However, the difference is less than zero, and the p-value is very large. We do not have evidence to rejust the null. I. We could also use a built-in to achieve similar results. Though using the built-in might be easier to code, the above portions are a walkthrough of the ideas that are critical to correctly thinking about statistical significance. Fill in the below to calculate the number of conversions for each page, as well as the number of individuals who received each page. Let n_old and n_new refer the the number of rows associated with the old page and new pages, respectively.
[29]:	p_diffs = np.array(p_diffs) p_difff_proportion = (p_diff_orig < p_diffs).mean() print('proportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion) reportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion) reportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion' reportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion' reportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion' reportion of p_diffs greater than p_diffs from ab_data.csv.' ',p_diff_proportion defs greater than p_diffs from ab_data.csv.' ',p_diff_proportion from ab_data.csv.' ',p_diff_prop
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[30]:	p_diffs = np.array(p_diffs) p_diff_proportion = (p_diff_crig < p_diffs).mean() print("proportion = (p_diff_crig < p_diffs).mean() print("proportion of p_diffs greater than p_diffs from abcusta.cov") p_diff_proportion p_di
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