[n [2]:	<pre>import pandas as pd import numpy as np import seaborn as sns import scipy.stats as ss import statsmodels.stats.api as sms import matplotlib.pyplot as plt pd.set_option('display.max_columns', None) from matplotlib.pyplot import figure</pre>
n [3]:	<pre># read data T1 = pd.read_csv('t1_user_active_min.csv') T2 = pd.read_csv('t2_user_variant.csv') T3 = pd.read_csv('t3_user_active_min_pre.csv') T4 = pd.read_csv('t4_user_attributes.csv') # look at data T1.head(10)</pre>
ut[3]:	uid dt active_mins 0 0 2019-02-22 5.0 1 0 2019-03-11 5.0 2 0 2019-03-18 3.0 3 0 2019-03-22 4.0 4 0 2019-04-03 9.0 5 0 2019-04-17 1.0 7 0 2019-05-07 3.0 8 0 2019-05-14 1.0 9 0 2019-05-19 1.0
	T2.head(10) vid variant_number dt signup_date 0 0 0 2019-02-06 2018-09-24 1 1 0 2019-02-06 2016-11-07 2 2 0 2019-02-06 2018-09-17 3 3 0 2019-02-06 2018-03-04 4 4 0 2019-02-06 2017-03-09 5 5 0 2019-02-06 2018-06-25 6 6 0 2019-02-06 2017-01-22 7 7 0 2019-02-06 2016-08-12 8 8 0 2019-02-06 2019-01-18
[5]: t[5]:	9 9 0 2019-02-06 2018-05-02 T3.head(10) uid dt active_mins 0 0 2018-09-24 3.0 1 0 2018-11-08 4.0 2 0 2018-11-24 3.0 3 0 2018-11-28 6.0 4 0 2018-12-02 6.0 5 0 2018-12-04 1.0
[6]: t[6]:	6 0 2018-12-07 8.0 7 0 2018-12-09 5.0 8 0 2018-12-14 8.0 9 0 2018-12-15 2.0 T4. head (10) wid gender user_type 0 0 male non_reader 1 1 male reader 2 2 male non_reader
	3 3 male non_reader 4 4 male non_reader 5 5 female non_reader 6 6 female non_reader 7 7 male non_reader 8 8 male new_user 9 9 female non_reader Hypothesis: Changes implemented for group B has increased user engagement I will also break down whether 1) Active usership time increased or decreased
[7]: [t[7]:	2) Frequency of visits increased or decreased 3) Do the above two points for old/new users, male/female users, and if they are readers/non-readers. # see number of control group users and test group users. T2['variant_number'].value_counts() # 80% in control(40k), 20% in treatment/test group (10k) 0 40000 1 10000 Name: variant_number, dtype: int64 # load users into control and treatment/test group arrays.
[9]: [[10]:	<pre>user_control = [] user_treatment = [] for index,row in T2.iterrows(): if row['variant_number'] == 0: user_control.append(row['uid']) else: user_treatment.append(row['uid']) # merge attributes table and variant table. var_gen_ageinquora = pd.merge(T2,T4,how = "inner", on = "uid") var_gen_ageinquora.head()</pre>
	uid variant_number dt signup_date gender user_type 0 0 0 2019-02-06 2018-09-24 male non_reader 1 1 0 2019-02-06 2016-11-07 male reader 2 2 0 2019-02-06 2018-09-17 male non_reader 3 3 0 2019-02-06 2018-03-04 male non_reader 4 4 0 2019-02-06 2017-03-09 male non_reader # split var_gen_ageinquora_into control and treatment groups. var_gen_ageinquora_control = var_gen_ageinquora[var_gen_ageinquora[var_into_number]] == 0] var_gen_ageinquora_treatment = var_gen_ageinquora[var_gen_ageinquora[var_into_number]] == 1] 1 cat_cols = ['gender', 'user_type']
[12]: [13]:	<pre>cont_cols = ['days_since_joined_till_AB_tested'] # sort control and treatment groups into arrays based on if they are in treatment or control and date they joined before ab test. uid_control</pre>
	886958 40000 2019-03-02 18.0 886959 40000 2019-03-12 4.0 886960 40001 2019-02-14 16.0 886961 40001 2019-02-17 5.0 after_AB_control.head() uid dt active_mins 0 0 2019-02-22 5.0 1 0 2019-03-11 5.0
[15]: [15]:	2 0 2019-03-18 3.0 3 0 2019-03-22 4.0 4 0 2019-04-03 9.0 before_AB_treatment.head() uid dt active_mins 989489 40001 2018-08-12 1.0 989490 40001 2018-08-21 1.0
	989491 40001 2018-09-21 5.0 989492 40001 2018-09-23 3.0 989493 40001 2018-10-03 1.0 before_AB_control.head() uid dt active_mins 0 0 2018-09-24 3.0 1 0 2018-11-08 4.0 2 0 2018-11-24 3.0
[17]:	<pre>3 0 2018-11-28 6.0 4 0 2018-12-02 6.0 # merge the control/test and date tables with the attributes table before_AB_control_base_table</pre>
[18]:	# renaming some columns before_AB_control_base_table.rename(columns = {"dt_x":"date", "dt_y":"AB_Date"}, inplace = True) before_AB_treatment_base_table.rename(columns = {"dt_x":"date", "dt_y":"AB_Date"}, inplace = True) after_AB_control_base_table.rename(columns = {"dt_x":"date", "dt_y":"AB_Date"}, inplace = True) after_AB_treatment_base_table.rename(columns = {"dt_x":"date", "dt_y":"AB_Date"}, inplace = True) after_AB_control_base_table.rename(columns = {"dt_x":"date", "dt_y":"AB_Date"}, inplace = True) before_AB_control_base_table.head() uid
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[21]:	<pre># plot of male readers for before (orange) and after (blue) data f, axes = plt.subplots(1, 2) plt.style.use('ggplot') pd.set_option('display.max_rows', None) sns.distplot(before_AB_treatment_base_table_noout[(before_AB_treatment_base_table_noout["gender"] == 'female')&(before_AB_treatment_base_table_</pre>
	C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and we be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and we be removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and we have a function for kernel density plots). warnings.warn(msg, FutureWarning) 0.08 0.07 0.08 0.09 0.00 0.0
[22]:	# plot of male readers for before (orange) and after (blue) data f, axes = plt.subplots(1, 2) plt.style.use('ggplot')
	<pre>pd.set_option('display.max_rows', None) sns.distplot(before_AB_treatment_base_table_noout[(before_AB_treatment_base_table_noout["gender"] == 'male')&(before_AB_treatment_base_table_noout</pre>
	C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: 'distplot' is a deprecated function and we removed in a future version. Please adapt your code to use either 'displot' (a figure-level function with similar flexibility) or 'kdeplot' (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: 'distplot' is a deprecated function and we removed in a future version. Please adapt your code to use either 'displot' (a figure-level function with similar flexibility) or 'kdeplot' (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: 'distplot' is a deprecated function and we have removed in a future version. Please adapt your code to use either 'displot' (a figure-level function with similar flexibility) or 'kdeplot' (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: 'distplot' is a deprecated function and we removed in a future version. Please adapt your code to use either 'displot' (a figure-level function with similar flexibility) or 'kdeplot' (a xes-level function for kernel density plots). warnings.warn(msg, FutureWarning) 0.08 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.06 - 0.07 - 0.07 - 0.08 - 0.09 - 0.09 - 0.09 - 0.09 - 0.00 -
[23]:	user_count_before_AB = pd.DataFrame(before_AB_treatment_base_table_noout['uid'].value_counts()) user_count_before_AB.reset_index(inplace = True) user_count_before_AB.rename(columns = {'uid':'before_count', 'index':'uid'}, inplace = True) user_count_after_AB = pd.DataFrame(after_AB_treatment_base_table_noout['uid'].value_counts()) user_count_after_AB.reset_index(inplace = True) user_count_after_AB.reset_index(inplace = True) user_count_after_AB.rename(columns = {'uid':'after_count', 'index':'uid'}, inplace = True)
	fig = plt.figure(figsize=(10,6)) plt.style.use('ggplot') pd.set_option('display.max_rows', None) sns.distplot(user_count_before_AB['before_count'], hist=False, color='red', axlabel = "Frequency of Visit") sns.distplot(user_count_after_AB['after_count'], hist=False, color='blue', axlabel = "Frequency of Visit") plt.legend() plt.show() C:\Users\avand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and we removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a xavand\anaconda3\envs\Data_sci\lib\site-packages\seaborn\distributions.py:2557: FutureWarning: `distplot` is a deprecated function and we removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a removed in a future version. Please adapt your code to use either `displot` (a figure-level function with similar flexibility) or `kdeplot` (a figure-level function for kernel density plots).
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[25]:	after_AB_control_base_table_noout = after_AB_control_base_table[after_AB_control_base_table.active_mins < np.percentile(after_AB_control_base_table_noout = after_AB_treatment_base_table[after_AB_treatment_base_table.active_mins < np.percentile(after_AB_treatment_base_table) after_AB_treatment_base_table.active_mins < np.percentile(after_AB_treatment_bas
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	1 0 2019-03-11 5.0 0 2019-02-06 2018-09-24 male non_reader 2 0 2019-03-18 3.0 0 2019-02-06 2018-09-24 male non_reader 3 0 2019-03-22 4.0 0 2019-02-06 2018-09-24 male non_reader 4 0 2019-04-03 9.0 0 2019-02-06 2018-09-24 male non_reader # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment data after the ab date # plot of male/female readers for control and treatment base_table_noout["gender"] == 'female')&(after_AB_control_base_table_noout["user_nab_control_base_table_noout["gender"] == 'male')&(after_AB_treatment_base_table_noout["user_nab_control_base_table_noout["defter_AB_control_base_table_noout["user_nab_control_base_table_noout[(after_AB_control_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout[(after_AB_treatment_base_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_table_noout["user_nab_t
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