AB Testing Practice

February 2, 2021

1 A/B Testing

Notes summarized from https://medium.com/@RenatoFillinich/ab-testing-with-python-e5964dd66143

1. Designing our experiment
2. Collecting and preparing the data
3. Visualizing the results
4. Testing the hypothesis
5. Drawing conclusions

Scenario - online ecommerce business - current conversion rate of product page: 13% on average throughout the year - team would be happy with 2% increase (new design considered successful if it raises conversion rate to 15%)

1.0.1 1. Designing our experiment

Formulating hypothesis Two-tailed test to see if new design will perform better or worse or the same:
H_0: p = p_0
H_a: p != p_0
p is conversion rate of new design, p_0 is conversion rate of old design

$\alpha = 0.05$
- if probability of observing a result as extreme or more (p-value) is lower than α, then reject null.

(our independent variable)
Control: old design
Test: new design

(dependent variable - what we are tryna measure)
conversion rate:
- 0: user did not buy the product during this user session
- 1: user bought the product during this user session

Choosing sample size The number of people/user sessions we decide in each group will have an affect on the precision of our estimated conversion rates: the larger the sample size, the more precise our estimate (i.e. the smaller the C.I.), the higher the chance to detect a difference in two

groups, if present.
But also more expensive.

Power analysis:

- Power of the test (1 - β): probability of finding a statistical difference between the groups in our test when a difference is actually present (0.80 by convention)
  - have 80% chance to detect it as statistically significant in our test with the sample size we will calculate
- Alpha value: critical value (0.05)

- Effect size: how big of a difference we expect there to be between the conversion rates

[4]:
```
import numpy as np
import pandas as pd
import scipy.stats as stats
import statsmodels.stats.api as sms
import matplotlib as mpl
import matplotlib.pyplot as plt
import seaborn as sns
from math import ceil

# %matplotlib inline # will make your plot outputs appear and be stored within␣
↪the notebook
```

[5]:
```
effect_size = sms.proportion_effectsize(0.13, 0.15)
effect_size
```

[5]: -0.0576728617308947

What is ratio=1 in sample size calculation:
The documentation from statsmodels defines it as "ratio of the number of observations in sample 2 relative to sample 1". Essentially, you input the sample size for group 1 in the function and indicate sample size for group 2 as a ratio of group 1. In this case they are the same, hence ratio=1

[6]:
```
# for two sample
required_n = sms.NormalIndPower().solve_power(
    effect_size,
    power=0.8,
    alpha=0.05,
    ratio=1
    ) # Calculating sample size needed

required_n = ceil(required_n) # Rounding up to next whole number                ␣
↪

print(required_n) # required_n is the number needed for each group
```

4720

1.0.2 2. Collecting and preparing the data

[7]:
```
# see all objects in folder
! ls
```

```
AB Testing and Predictive Modeling.ipynb
README.md
ab_data.csv
```

[9]:
```
df = pd.read_csv('ab_data.csv')
df.head()
```

[9]:

	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
4	864975	2017-01-21 01:52:26.210827	control	old_page	1

[10]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 294478 entries, 0 to 294477
Data columns (total 5 columns):
 #   Column        Non-Null Count   Dtype
---  ------        --------------   -----
 0   user_id       294478 non-null  int64
 1   timestamp     294478 non-null  object
 2   group         294478 non-null  object
 3   landing_page  294478 non-null  object
 4   converted     294478 non-null  int64
dtypes: int64(2), object(3)
memory usage: 11.2+ MB
```

[14]:
```
# check that TC group is getting the correct new vs old page
pd.crosstab(df['group'], df['landing_page'])
```

[14]:

landing_page	new_page	old_page
group		
control	1928	145274
treatment	145311	1965

[18]:
```
session_counts = df['user_id'].value_counts(ascending=False) # counting num of␣
↪appearances for each unique user
```

```
multi_users = session_counts[session_counts > 1].count() # count the number of␣
↪users that appeared more than once

print(f'There are {multi_users} users that appear multiple times in the␣
↪dataset')
```

```
There are 3894 users that appear multiple times in the dataset
```

[21]:
```
users_to_drop = session_counts[session_counts > 1].index # index of users that␣
↪we are dropping

df = df[~df['user_id'].isin(users_to_drop)]
print(f'The updated dataset now has {df.shape[0]} entries')
```

```
The updated dataset now has 286690 entries
```

Sampling Setting random_state = 123 or some number to get reproducible results. DataFrame.sample() will perform simple random sampling.

[24]:
```
# perform simple random sampling

control_sample = df[df['group'] == 'control'].sample(n=required_n,␣
↪random_state=123)
treatment_sample = df[df['group'] == 'treatment'].sample(n=required_n,␣
↪random_state=123)
```

[26]:
```
ab_sample = pd.concat([control_sample, treatment_sample], axis=0)
ab_sample.reset_index(drop=True, inplace=True)

ab_sample.head()
```

[26]:

	user_id	timestamp	group	landing_page	converted
0	689587	2017-01-13 11:17:53.637947	control	old_page	0
1	708802	2017-01-17 06:26:13.317907	control	old_page	0
2	734166	2017-01-09 03:16:50.487997	control	old_page	0
3	679205	2017-01-21 08:14:08.970343	control	old_page	0
4	664151	2017-01-10 09:55:59.891293	control	old_page	0

[29]:
```
ab_sample['group'].value_counts()
```

[29]:
```
treatment    4720
control      4720
Name: group, dtype: int64
```

3. Visualizing the results ddof: Delta Degrees of Freedom
The standard deviation is the square root of the average of the squared deviations from the mean,

i.e., std = sqrt(mean(x)), where x = abs(a - a.mean())**2.

The average squared deviation is typically calculated as x.sum() / N, where N = len(x). If, however, ddof is specified, the divisor N - ddof is used instead.

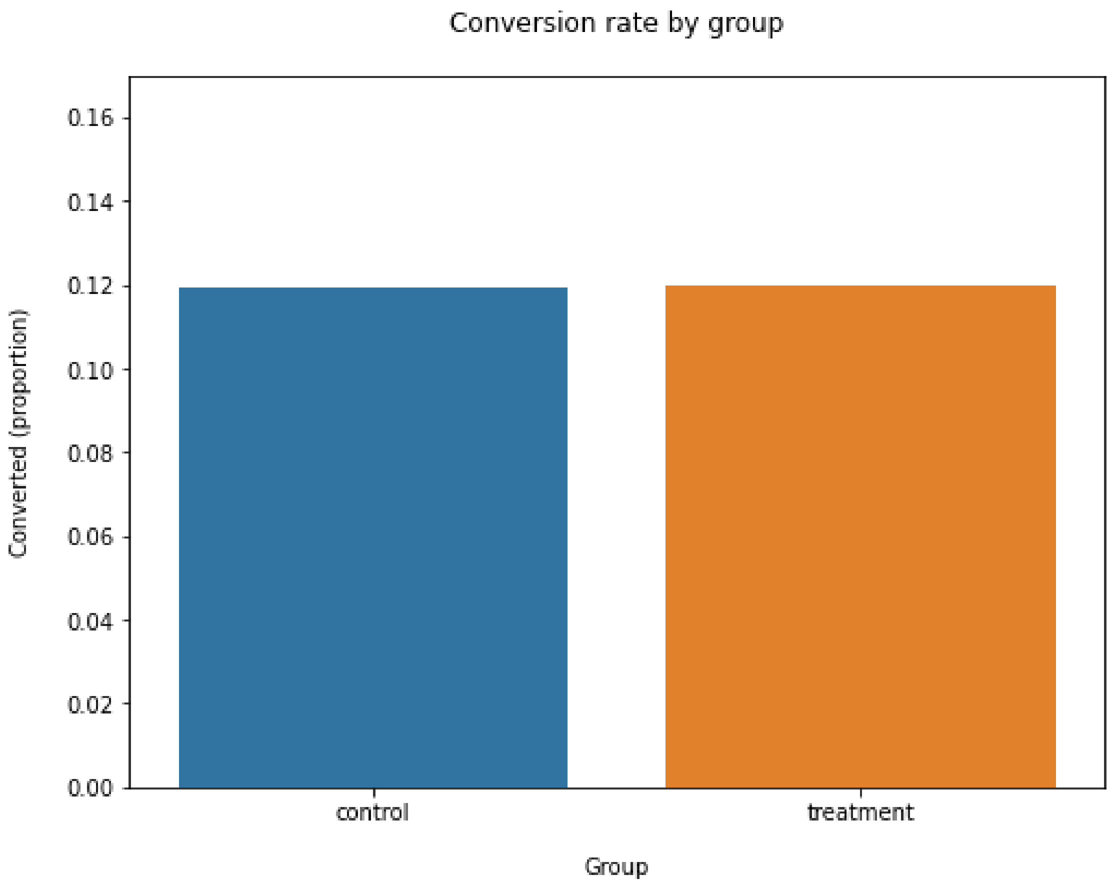
In standard statistical practice, ddof=1 provides an unbiased estimator of the variance of the infinite population.
ddof=0 provides a maximum likelihood estimate of the variance for normally distributed variables.

- Include ddof=1 if you're calculating np.std() for a sample taken from your full dataset.
- Ensure ddof=0 if you're calculating np.std() for the full population

[36]:
```
conversion_rates = ab_sample.groupby('group')['converted']

std_p = lambda x: np.std(x, ddof=0) # standard deviation of the proportion
se_p = lambda x: stats.sem(x, ddof=0) # standard error of the proportion (std /␣
↪sqrt(n))

conversion_rates = conversion_rates.agg([np.mean, std_p, se_p])
conversion_rates.columns = ['conversion_rate', 'std_deviation', 'std_error']


conversion_rates.style.format('{:.3f}')
```

[36]: <pandas.io.formats.style.Styler at 0x7f8c2d2eba50>

[38]:
```
plt.figure(figsize=(8,6))

sns.barplot(x=ab_sample['group'], y=ab_sample['converted'], ci=False)

plt.ylim(0, 0.17)
plt.title('Conversion rate by group', pad=20)
plt.xlabel('Group', labelpad=15)
plt.ylabel('Converted (proportion)', labelpad=15);
```



4. Testing the hypothesis We have a large sample - can use normal approximation (i.e. z-test) to calculate p-value.

[49]:
```
from statsmodels.stats.proportion import proportions_ztest, proportion_confint
```

[51]:
```
control_results = ab_sample[ab_sample['group'] == 'control']['converted'] #␣
↪converted column for all controls
treatment_results = ab_sample[ab_sample['group'] == 'treatment']['converted'] #␣
↪converted column for all treatment

n_con = control_results.count()
n_treat = treatment_results.count()

successes = [control_results.sum(), treatment_results.sum()] # count of␣
↪converted users in control and treatment group
nobs = [n_con, n_treat]

z_stat, pval = proportions_ztest(successes, nobs=nobs)
```

```
(lower_con, lower_treat), (upper_con, upper_treat) =␣
↪proportion_confint(successes, nobs=nobs, alpha=0.05)
```

[52]:
```
print(f'z statistic: {z_stat:.2f}')
print(f'p-value: {pval:.3f}')
print(f'ci 95% for control group: [{lower_con:.3f}, {upper_con:.3f}]')
print(f'ci 95% for treatment group: [{lower_treat:.3f}, {upper_treat:.3f}]')
```

```
z statistic: -0.10
p-value: 0.924
ci 95% for control group: [0.110, 0.128]
ci 95% for treatment group: [0.110, 0.129]
```

5. Drawing conclusions p-value is greater than $\alpha = 0.05$, we fail to reject null. New design did not perform significantly different than our old one.

Looking at CI for treatment group: [0.110, 0.129], it 1.) included baseline value of 13%, and 2.) it does not include our target value of 15%.
This means that it is more likely that the true conversion rate of the new design is similar to baseline.