Dave530Week3

December 14, 2024

```
[111]: # 3.2 Exercise: Preparing for Exploratory Data Analysis Using Python
```

```
[112]: # Exercise 1: Page 11: 1-1
       # Execute existing cells and solve exercise as directed.
```

```
[202]: import warnings
       # Suppress all warnings
       warnings.filterwarnings("ignore")
       import nsfg
```

```
[204]: preg = nsfg.ReadFemPreg()
       preg.head()
```

```
[204]:    caseid  pregordr  howpreg_n  howpreg_p  moscurrp  nowprgdk  pregend1  \
       0       1         1        NaN        NaN       NaN       NaN       6.0
       1       1         2        NaN        NaN       NaN       NaN       6.0
       2       2         1        NaN        NaN       NaN       NaN       5.0
       3       2         2        NaN        NaN       NaN       NaN       6.0
       4       2         3        NaN        NaN       NaN       NaN       6.0

          pregend2  nbrnaliv  multbrth  …  laborfor_i  religion_i  metro_i  \
       0       NaN       1.0       NaN  …           0           0        0
       1       NaN       1.0       NaN  …           0           0        0
       2       NaN       3.0       5.0  …           0           0        0
       3       NaN       1.0       NaN  …           0           0        0
       4       NaN       1.0       NaN  …           0           0        0

              basewgt  adj_mod_basewgt      finalwgt  secu_p  sest  cmintvw  \
       0  3410.389399      3869.349602   6448.271112       2     9      NaN
       1  3410.389399      3869.349602   6448.271112       2     9      NaN
       2  7226.301740      8567.549110  12999.542264       2    12      NaN
       3  7226.301740      8567.549110  12999.542264       2    12      NaN
       4  7226.301740      8567.549110  12999.542264       2    12      NaN

          totalwgt_lb
       0       8.8125
       1       7.8750
       2       9.1250
```

```
3       7.0000
4       6.1875

[5 rows x 244 columns]
```

Print the column names.

```
[205]: preg.columns
```

```
[205]: Index(['caseid', 'pregordr', 'howpreg_n', 'howpreg_p', 'moscurrp', 'nowprgdk',
              'pregend1', 'pregend2', 'nbrnaliv', 'multbrth',
              …
              'laborfor_i', 'religion_i', 'metro_i', 'basewgt', 'adj_mod_basewgt',
              'finalwgt', 'secu_p', 'sest', 'cmintvw', 'totalwgt_lb'],
             dtype='object', length=244)
```

Select a single column name.

```
[206]: preg.columns[1]
```

```
[206]: 'pregordr'
```

Select a column and check what type it is.

```
[120]: pregordr = preg['pregordr']
       type(pregordr)
```

```
[120]: pandas.core.series.Series
```

Print a column.

```
[122]: pregordr
```

```
[122]: 0        1
       1        2
       2        1
       3        2
       4        3
               ..
       13588    1
       13589    2
       13590    3
       13591    4
       13592    5
       Name: pregordr, Length: 13593, dtype: int64
```

Select a single element from a column.

```
[124]: pregordr[0]
```

```
[124]: 1
```

Select a slice from a column.

```
[126]: pregordr[2:5]
```

```
[126]: 2    1
       3    2
       4    3
       Name: pregordr, dtype: int64
```

Select a column using dot notation.

```
[128]: pregordr = preg.pregordr
```

Count the number of times each value occurs.

```
[130]: preg.outcome.value_counts().sort_index()
```

```
[130]: outcome
       1    9148
       2    1862
       3     120
       4    1921
       5     190
       6     352
       Name: count, dtype: int64
```

Check the values of another variable.

```
[132]: preg.birthwgt_lb.value_counts().sort_index()
```

```
[132]: birthwgt_lb
       0.0        8
       1.0       40
       2.0       53
       3.0       98
       4.0      229
       5.0      697
       6.0     2223
       7.0     3049
       8.0     1889
       9.0      623
       10.0     132
       11.0      26
       12.0      10
       13.0       3
       14.0       3
       15.0       1
       Name: count, dtype: int64
```

Make a dictionary that maps from each respondent's `caseid` to a list of indices into the pregnancy `DataFrame`. Use it to select the pregnancy outcomes for a single respondent.

[134]:
```
caseid = 10229
preg_map = nsfg.MakePregMap(preg)

#jyoti

indices = preg_map[caseid]
preg.outcome[indices].values
```

[134]:
```
array([4, 4, 4, 4, 4, 4, 1], dtype=int64)
```

0.1 Exercises

Select the `birthord` column, print the value counts, and compare to results published in the codebook

[137]:
```
birthord = preg['birthord']
birthord
```

[137]:
```
0        1.0
1        2.0
2        1.0
3        2.0
4        3.0
        …
13588    1.0
13589    NaN
13590    NaN
13591    2.0
13592    3.0
Name: birthord, Length: 13593, dtype: float64
```

We can also use `isnull` to count the number of nans.

[139]:
```
preg.birthord.isnull().sum()
```

[139]:
```
4445
```

Select the `prglngth` column, print the value counts, and compare to results published in the codebook

[141]:
```
prglngth = preg['prglngth']
print(prglngth)
preg.prglngth.value_counts().sort_index()
```

```
0        39
1        39
2        39
```

```
3        39
4        39
         ..
13588    39
13589     6
13590     5
13591    39
13592    39
Name: prglngth, Length: 13593, dtype: int64
```

```
[141]: prglngth
       0        15
       1         9
       2        78
       3       151
       4       412
       5       181
       6       543
       7       175
       8       409
       9       594
       10      137
       11      202
       12      170
       13      446
       14       29
       15       39
       16       44
       17      253
       18       17
       19       34
       20       18
       21       37
       22      147
       23       12
       24       31
       25       15
       26      117
       27        8
       28       38
       29       23
       30      198
       31       29
       32      122
       33       50
       34       60
       35      357
```

```
36     329
37     457
38     609
39    4744
40    1120
41     591
42     328
43     148
44      46
45      10
46       1
47       1
48       7
50       2
Name: count, dtype: int64
```

To compute the mean of a column, you can invoke the `mean` method on a Series. For example, here is the mean birthweight in pounds:

```
[143]: preg.totalwgt_lb.mean()
```

```
[143]: 7.265628457623368
```

Create a new column named totalwgt_kg that contains birth weight in kilograms. Compute its mean. Remember that when you create a new column, you have to use dictionary syntax, not dot notation.

```
[145]: # homework
       # convert totalwgt_lb to totalwgt_kg and create a ne column
       preg['totalwgt_kg'] = preg.totalwgt_lb * 0.453592
       preg.totalwgt_kg.mean()
```

```
[145]: 3.2956309433502984
```

`nsfg.py` also provides `ReadFemResp`, which reads the female respondents file and returns a `DataFrame`:

```
[147]: resp = nsfg.ReadFemResp()
```

`DataFrame` provides a method `head` that displays the first five rows:

```
[149]: resp.head()
```

```
[149]:    caseid  rscrinf  rdormres  rostscrn  rscreenhisp  rscreenrace  age_a  \
       0    2298        1         5         5            1          5.0     27
       1    5012        1         5         1            5          5.0     42
       2   11586        1         5         1            5          5.0     43
       3    6794        5         5         4            1          5.0     15
       4     616        1         5         4            1          5.0     20
```

```
   age_r  cmbirth  agescrn  …  pubassis_i      basewgt  adj_mod_basewgt  \
0     27      902       27  …           0  3247.916977      5123.759559
1     42      718       42  …           0  2335.279149      2846.799490
2     43      708       43  …           0  2335.279149      2846.799490
3     15     1042       15  …           0  3783.152221      5071.464231
4     20      991       20  …           0  5341.329968      6437.335772

      finalwgt  secu_r  sest  cmintvw  cmlstyr  screentime   intvlngth
0  5556.717241       2    18     1234     1222    18:26:36  110.492667
1  4744.191350       2    18     1233     1221    16:30:59   64.294000
2  4744.191350       2    18     1234     1222    18:19:09   75.149167
3  5923.977368       2    18     1234     1222    15:54:43   28.642833
4  7229.128072       2    18     1233     1221    14:19:44   69.502667

[5 rows x 3087 columns]
```

Select the `age_r` column from `resp` and print the value counts. How old are the youngest and oldest respondents?

[151]:

```
# homework
# Select the age_r column from resp and print the value counts
resp.age_r.value_counts().sort_index()
```

[151]:

```
age_r
15     217
16     223
17     234
18     235
19     241
20     258
21     267
22     287
23     282
24     269
25     267
26     260
27     255
28     252
29     262
30     292
31     278
32     273
33     257
34     255
35     262
36     266
37     271
```

```
38    256
39    215
40    256
41    250
42    215
43    253
44    235
Name: count, dtype: int64
```

[152]:
```
# From the above result, The youngest one is 15 year old and oldest one is 44
```

We can use the **caseid** to match up rows from **resp** and **preg**. For example, we can select the row from **resp** for **caseid** 2298 like this:

[154]:
```
resp[resp.caseid==2298]
```

[154]:
```
   caseid  rscrinf  rdormres  rostscrn  rscreenhisp  rscreenrace  age_a  \
0    2298        1         5         5            1          5.0     27

   age_r  cmbirth  agescrn  …  pubassis_i      basewgt  adj_mod_basewgt  \
0     27      902       27  …           0  3247.916977      5123.759559

      finalwgt  secu_r  sest  cmintvw  cmlstyr  screentime   intvlngth
0  5556.717241       2    18     1234     1222    18:26:36  110.492667

[1 rows x 3087 columns]
```

And we can get the corresponding rows from **preg** like this:

[156]:
```
preg[preg.caseid==2298]
```

[156]:
```
      caseid  pregordr  howpreg_n  howpreg_p  moscurrp  nowprgdk  pregend1  \
2610    2298         1        NaN        NaN       NaN       NaN       6.0
2611    2298         2        NaN        NaN       NaN       NaN       6.0
2612    2298         3        NaN        NaN       NaN       NaN       6.0
2613    2298         4        NaN        NaN       NaN       NaN       6.0

      pregend2  nbrnaliv  multbrth  …  religion_i  metro_i      basewgt  \
2610       NaN       1.0       NaN  …           0        0  3247.916977
2611       NaN       1.0       NaN  …           0        0  3247.916977
2612       NaN       1.0       NaN  …           0        0  3247.916977
2613       NaN       1.0       NaN  …           0        0  3247.916977

      adj_mod_basewgt     finalwgt  secu_p  sest  cmintvw  totalwgt_lb  \
2610      5123.759559  5556.717241       2    18      NaN       6.8750
2611      5123.759559  5556.717241       2    18      NaN       5.5000
2612      5123.759559  5556.717241       2    18      NaN       4.1875
2613      5123.759559  5556.717241       2    18      NaN       6.8750
```

```
      totalwgt_kg
2610     3.118445
2611     2.494756
2612     1.899417
2613     3.118445

[4 rows x 245 columns]
```

How old is the respondent with `caseid` 1?

[158]:
```python
#homework
# filter the age based on caseid == 1

resp[resp.caseid==1].age_r
```

[158]:
```
1069    44
Name: age_r, dtype: int64
```

What are the pregnancy lengths for the respondent with `caseid` 2298?

[160]:
```python
#homework
# filter data based on caseid
preg[preg.caseid==2298].prglngth
```

[160]:
```
2610    40
2611    36
2612    30
2613    40
Name: prglngth, dtype: int64
```

What was the birthweight of the first baby born to the respondent with `caseid` 5013?

[162]:
```python
# homework

# use `pregordr` to select the first baby

preg[(preg.caseid==5013) & (preg.pregordr==1)].birthwgt_lb
```

[162]:
```
5516    7.0
Name: birthwgt_lb, dtype: float64
```

[163]:
```python
# # Exercise 2: Page 11: 1-2
# Find the value of pregnum
```

[164]:
```python
pregnum = preg.groupby('caseid').size()

# Display the first few rows
print(pregnum)
```

```
# Convert the result to a DataFrame
pregnancy_count_df = pregnum.reset_index(name='pregnum')

# Count how many respondents have the same pregnancy count
same_pregnancy_count = pregnancy_count_df['pregnum'].value_counts().
 ↪reset_index()
same_pregnancy_count.columns = ['pregnum', 'respondent_count']

# Sort by pregnancy_count
same_pregnancy_count = same_pregnancy_count.sort_values(by='pregnum')
# Display the result
print(same_pregnancy_count)
```

```
caseid
1        2
2        3
6        3
7        2
12       1
        ..
12566    2
12568    3
12569    2
12570    3
12571    5
Length: 5033, dtype: int64
    pregnum  respondent_count
1         1              1267
0         2              1432
2         3              1110
3         4               611
4         5               305
5         6               150
6         7                80
7         8                40
8         9                21
9        10                 9
10       11                 3
11       12                 2
12       14                 2
13       19                 1
```

[165]:

```
# To compare groups using summary statistics in Python, you can calculate␣
 ↪descriptive statistics like
#mean, median, standard deviation, count, etc., for each group. Using the␣
 ↪pandas library, this can be done efficiently.
```

[166]:

```
import numpy as np
# import math as math
import thinkstats2
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
%matplotlib inline
import thinkplot
```

[167]:

```
# # Exercise 3: Page 25: 2-1
# Do first baby arrive late?
```

[168]:

```
import nsfg
```

[169]:

```
preg = nsfg.ReadFemPreg()
live = preg[preg.outcome == 1]
```

[170]:

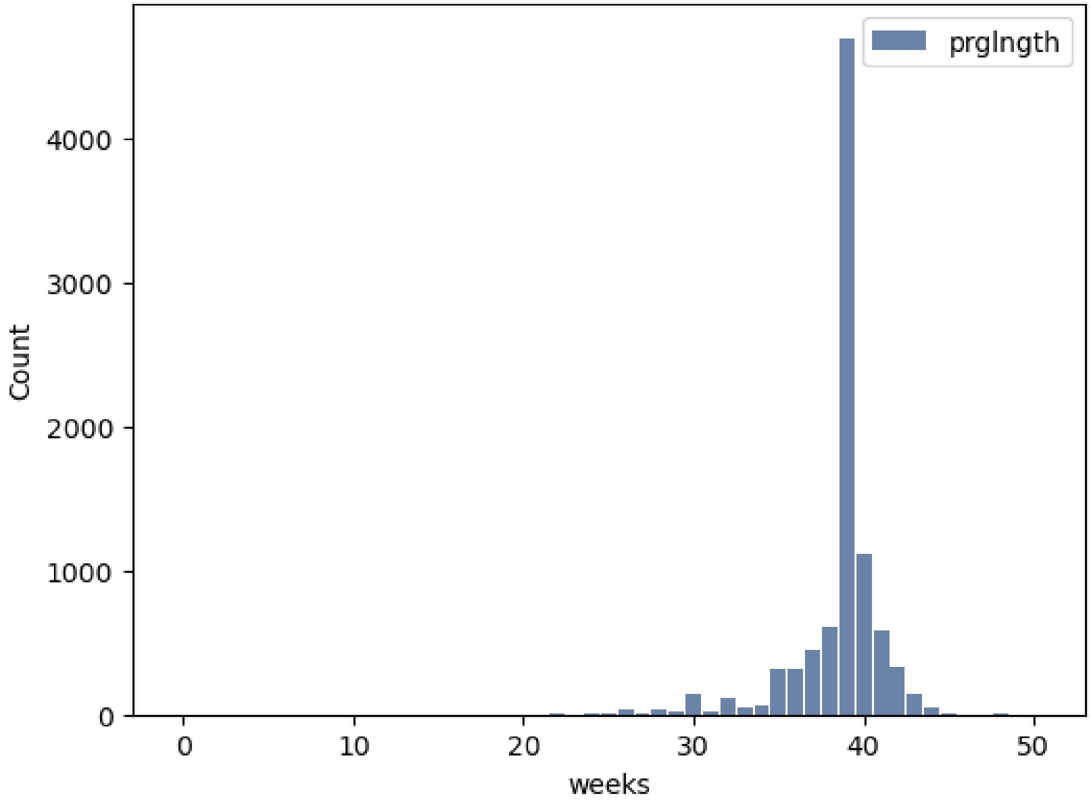
```
ages = np.floor(live.agepreg)
```

[171]:

```
# As an exercise, plot the histogram of pregnancy lengths (column prglngth).
```

[172]:

```
# Solution

hist = thinkstats2.Hist(live.prglngth, label='prglngth')
thinkplot.Hist(hist)
thinkplot.Config(xlabel='weeks', ylabel='Count')
```



[173]:

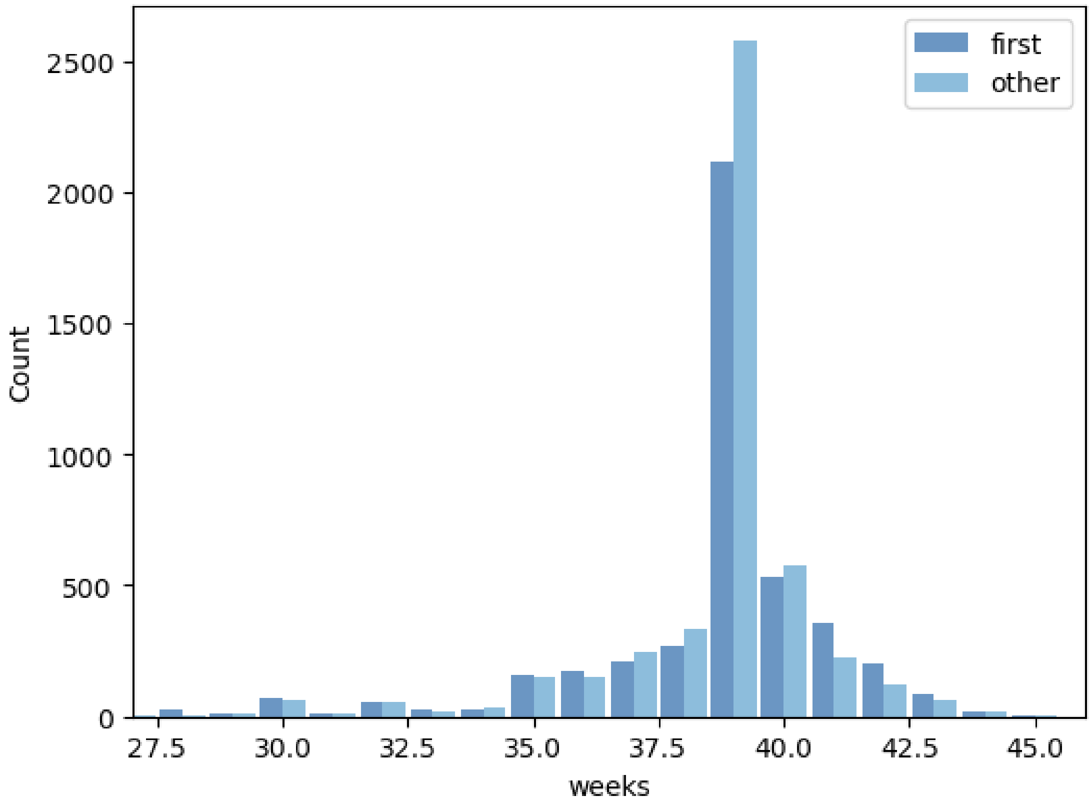
```
# From live births, we can select first babies and others using birthord,

# List item
# List item
# then compute histograms of pregnancy length for the two groups.
```

[174]:

```
firsts = live[live.birthord == 1]
others = live[live.birthord != 1]

first_hist = thinkstats2.Hist(firsts.prglngth, label='first')
other_hist = thinkstats2.Hist(others.prglngth, label='other')
```

[175]:

```
width = 0.45
thinkplot.PrePlot(2)
thinkplot.Hist(first_hist, align='right', width=width)
thinkplot.Hist(other_hist, align='left', width=width)
thinkplot.Config(xlabel='weeks', ylabel='Count', xlim=[27, 46])
```



[176]:
```
#Series provides methods to compute summary statistics:
mean = live.prglngth.mean()
var = live.prglngth.var()
std = live.prglngth.std()
```

[177]:
```
mean, std
```

[177]:
```
(38.56055968517709, 2.702343810070593)
```

[178]:
```
# Here's are the mean pregnancy lengths for first babies and others:

# List item
# List item
```

[179]:
```
firsts.prglngth.mean(), others.prglngth.mean()
```

[179]:
```
(38.60095173351461, 38.52291446673706)
```

[180]:
```
#Here's the difference (in weeks):
firsts.prglngth.mean() - others.prglngth.mean()
```

[180]:

```
0.07803726677754952
```

[181]:

```
# Distributions
# Summary statistics - mean, variance, median, etc. Dangerous because they␣
 ↪obscure the data.
# Alternative is to look at distributions of the data - describes how often␣
 ↪each value appears.

# Distributions are usually represented as histograms (raw frequencies binned␣
 ↪into equally spaced buckets).
# Normalized histogram is called Probability Mass Function (PMF).
```

[182]:

```
prglen_first_babies = firsts.prglngth
prglen_other_babies = others.prglngth

# setting up range of histogram and number of bins
first_baby_min_prglen = np.min(prglen_first_babies)
first_baby_max_prglen = np.max(prglen_first_babies)
other_baby_min_prglen = np.min(prglen_other_babies)
other_baby_max_prglen = np.max(prglen_other_babies)
print("first baby preg length min: %d, max: %d" %
      (first_baby_min_prglen, first_baby_max_prglen))
print("other baby preg length min: %d, max: %d" %
      (other_baby_min_prglen, other_baby_max_prglen))

bin_lb = min([first_baby_min_prglen, other_baby_min_prglen])
bin_ub = max([first_baby_max_prglen, other_baby_max_prglen])
nbr_bins = bin_ub - bin_lb
bin_range = (bin_lb, bin_ub)
print("range:", bin_range, "#-bins:", nbr_bins)

# building the histograms
first_baby_fdist = np.histogram(np.array(prglen_first_babies), bins=nbr_bins,␣
 ↪range=bin_range)
other_baby_fdist = np.histogram(np.array(prglen_other_babies), bins=nbr_bins,␣
 ↪range=bin_range)
```

```
first baby preg length min: 0, max: 48
other baby preg length min: 4, max: 50
range: (0, 50) #-bins: 50
```

[183]:

```
def mode(fdist):
    """ takes a histogram and returns the most frequent value """
    mode_idx = np.argmax(fdist[0])
    return fdist[1][mode_idx]

def all_modes(fdist):
    """ takes a histogram and returns (value, freq) pairs in desc freq """
    mode_idxs = np.argsort(fdist[0])[::-1]
    vf_pairs = []
    for i in range(mode_idxs.shape[0]):
        vf_pairs.append((int(fdist[1][mode_idxs[i]]), fdist[0][mode_idxs[i]]))
    return vf_pairs
```

[184]:

```
print("First baby arrival top week (mode): %d" % (mode(first_baby_fdist)))
print("Other baby arrival top week (mode): %d" % (mode(other_baby_fdist)))

print("First baby top 5 frequent weeks:", all_modes(first_baby_fdist)[0:5])
print("Other baby top 5 frequent weeks:", all_modes(other_baby_fdist)[0:5])
```

```
First baby arrival top week (mode): 39
Other baby arrival top week (mode): 39
First baby top 5 frequent weeks: [(39, 2114), (40, 536), (41, 360), (38, 272),
(37, 208)]
Other baby top 5 frequent weeks: [(39, 2579), (40, 580), (38, 335), (37, 247),
(41, 227)]
```

[185]:

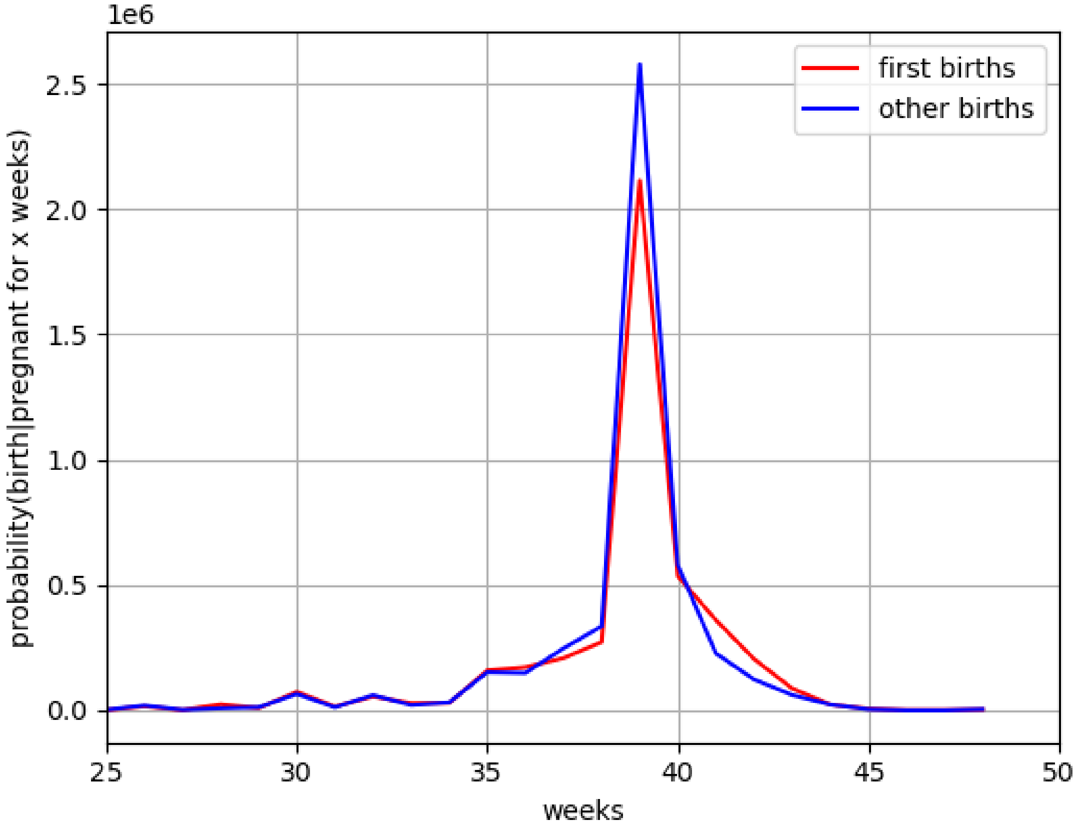
```
# Plotting Histograms
# From histogram below, it looks like until about week 41, other babies tend to␣
 ↪arrive sooner in aggregate,
#but after that more first babies arrive. So there seems to be evidence that␣
 ↪first babies do tend to arrive late.

# Other information from the plot:

# Mode - most common week for arrival seems to be 39 weeks.
# Shape - distribution is assymetric around the mode, drops of quicker to right␣
 ↪than left.
#Possible reason is because surgical intervention happens for late pregnancies.
# Outliers - babies born at 30 weeks are probably just unusual, but may also␣
 ↪reflect reporting errors.
```

[186]:

```
def remaining_lifetime(pmf, age):
    """ Takes PMF and age and returns PMF of remaining lifetime """
    ages = pmf[1][:-1]
    idxs = np.where(ages >= age)[0]
    r_probs = pmf[0][idxs]
    r_ages = ages[idxs]
    # generate a fake population with r_probs and r_ages
    fake_pop_size = 1000
    fake_pop = []
    for i in range(r_ages.shape[0]):
        num_aged = int(r_probs[i] * fake_pop_size)
        for j in range(num_aged):
            fake_pop.append(r_ages[i])
    # create a histogram and return
    r_nbins = r_ages.shape[0]
    r_range = (np.min(r_ages), np.max(r_ages))
    return np.histogram(np.array(fake_pop), bins=r_nbins, range=r_range)
```

[187]:

```
# compute PMFs for each distribution
pmf_first_babies = np.histogram(prglen_first_babies,
                                bins=nbr_bins, range=bin_range)
pmf_other_babies = np.histogram(prglen_other_babies,
                                bins=nbr_bins, range=bin_range)



def cond_prob(pmf, x):
    """ Returns probability that birth will occur at week x given person
        is pregnant at week x """
    return remaining_lifetime(pmf, x)[0][0]

first_birth_probs = []
other_birth_probs = []
for x in range(0, 49):
    first_birth_probs.append(cond_prob(pmf_first_babies, x))
    other_birth_probs.append(cond_prob(pmf_other_babies, x))

plt.plot(range(len(first_birth_probs)), first_birth_probs, color='r',␣
 ↪label="first births")
plt.plot(range(len(first_birth_probs)), other_birth_probs, color='b',␣
 ↪label="other births")

plt.ylabel("probability(birth|pregnant for x weeks)")
plt.xlabel("weeks")
plt.xlim([25, 50])
plt.legend(loc="best")
plt.grid()
plt.show()
```



[188]:
```
# The chart indicates that a first baby is less likely to be born until about␣
↪week 42, after which they are more likely to be born than other babies.
```

[189]:
```
# Reporting Results
# The evidence clearly indicates that first babies tend to arrive later than␣
↪others.
```

[190]:
```
# Exercise 4: Page 25: 2-4
#Using the variable totalwgt_lb, investigate whether first babies are lighter␣
↪or heavier than others.

#Compute Cohen's effect size to quantify the difference between the groups. How␣
↪does it compare to the difference in pregnancy length?
```

[191]:
```
# Compute the Cohen effect size for the difference in pregnancy length for␣
↪first babies and others.
# The Cohen's Effect Size measures the magnitude of the difference between two␣
↪groups.
```

[192]:

```
#This functon computes the Cohen effect size, which is the difference in means␣
 ↪expressed in number of standard deviations:
```

[193]:

```
def CohenEffectSize(group1, group2):
    """Computes Cohen's effect size for two groups.

    group1: Series or DataFrame
    group2: Series or DataFrame

    returns: float if the arguments are Series;
             Series if the arguments are DataFrames
    """
    diff = group1.mean() - group2.mean()

    var1 = group1.var()
    var2 = group2.var()
    n1, n2 = len(group1), len(group2)

    pooled_var = (n1 * var1 + n2 * var2) / (n1 + n2)
    d = diff / np.sqrt(pooled_var)
    return d
```

[194]:

```
# mean1, mean2: Compute the means of the two groups.
# std1, std2: Compute the standard deviations of the two groups (with ddof=1␣
 ↪for sample standard deviation).
# pooled_std: Calculate the pooled standard deviation using the formula.
# d: Compute Cohen's
# d by dividing the difference in means by the pooled standard deviation.

# Interpretation of Cohen’s
# d=0.2: Small effect size
# d=0.5: Medium effect size
# d=0.8: Large effect size
```

[195]:

```
# Solution
# Find the mean of total weight of the first and other babies in lb

firsts.totalwgt_lb.mean(), others.totalwgt_lb.mean()
```

[195]:

```
(7.201094430437772, 7.325855614973262)
```

[196]:

```
# Find the Cohen'd effect size

CohenEffectSize(firsts.totalwgt_lb, others.totalwgt_lb)
```

[196]:

```
-0.088672927072602
```

[197]:
```
# Conclusion: A Cohen's d of
# -0.088672927072602 suggests a very small difference between the firsts and␣
 ↪other babies group, with the other babiess group being slightly higher.
# A negative indicates that the mean of the other babies total wt group is␣
 ↪higher than the mean of the first total wt group.
```

[198]:
```
# How does it compare to the difference in pregnancy length?
```

[199]:
```
# Solution
firsts.prglngth.mean(), others.prglngth.mean()
```

[199]:
```
(38.60095173351461, 38.52291446673706)
```

[200]:
```
CohenEffectSize(firsts.prglngth, others.prglngth)
```

[200]:
```
0.028879044654449883
```

[201]:
```
# Conclusion: A Cohen's d of

# d=0.028879044654449883 falls well within the small effect size range and is␣
 ↪very close to zero, it indicates almost no meaningful difference between the␣
 ↪two groups.
# A positive d means the mean of prglngth of first group  is slightly higher␣
 ↪than the mean of prglngth of others group.
```