tu15_DataWranglingIII

March 7, 2023

1 Wrangling III

In this tutorial, we'll round out our focus on data wrangling by looking

- handling duplicate values
- data transformations

1.1 Preliminaries

As usual, we'll load some libraries we'll be likely to use.

[1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
```

Now we'll get set up to work by

- loading the cancer data and cleaning it up (as before)
- trim out some columns so we can look at the data frame more easily
- shorten up some of the column names to save ourselves some typing

Let's reuse our function to do the loading and cleaning.

[2]:

```
def bcd_load_clean():
    bcd = pd.read_csv('./data/breast_cancer_data.csv')
    bcd['patient_id'] = bcd['patient_id'].astype('string')
    bcd['doctor_name'] = bcd['doctor_name'].str.split().str[1]
    bcd['bare_nuclei'] = bcd['bare_nuclei'].replace('?', '')
    bcd['bare_nuclei'] = pd.to_numeric(bcd['bare_nuclei'])

    return bcd
```

[3]:

```
bcd = bcd_load_clean()
```

Make a little version with just two numeric columns to play with.

[4]:

```
bcd2 = bcd[['patient_id', 'clump_thickness', 'bland_chromatin', 'class']].copy()
```

Let's give the columns shorter names to save some typing.

```
[5]: bcd2 = bcd2.rename(columns={'clump_thickness': 'thick',
                                 'bland_chromatin': 'chrom',
                                 'patient_id': 'id'})
```

1.2 Duplicate entries

As we have already seen, datasets can contain strange things that we have to overcome prior to analysis. One of the most common issues in a dataset are duplicate entries. These are common with large datasets that have been transcribed by humans at some point. Humands get bored, lose their place, etc.

Let's look at the shape of our cancer data frame (remember data frames have a `shape` attribute).

```
[7]: bcd2.shape
```

```
[7]: (699, 4)
```

Now let's look at the number of unique entries using the `nunique()` data frame method; this will return the number of distinct values in each column.

```
[10]: bcd2.nunique()
```

```
[10]: id       645
      thick     10
      chrom     10
      class      2
      dtype: int64
```

So we can see that, while there are 699 observations in our data, there are only 645 unique patient ids. This tells us that several patients have multiple entries. These could be from patients making multiple visits to the doctor, or they could be a mistakes, or some combination thereof.

We can find out which rows – which entire observations – are identical with the `duplicated()` method.

```
[9]: bcd2.duplicated()
```

```
[9]: 0      False
     1      False
     2      False
     3      False
     4      False
            …
     694    False
     695    False
```

```
696    False
697    False
698     True
Length: 699, dtype: bool
```

That's not terribly helpful by itself, but…

In the cell below, count the number of duplicated rows (remember a True is a 1).

```
[21]: sum(bcd2.duplicated())
```

```
[21]: 12
```

We can also use the output of `.duplicated()` to do logical indexing to see the observations that have duplicates. Do that in the cell below.

```
[22]: bcd2[bcd2.duplicated()]
```

```
[22]:
          id  thick  chrom      class
208  1218860    1.0    3.0     benign
253  1100524    6.0    7.0  malignant
254  1116116    9.0    3.0  malignant
258  1198641    3.0    3.0     benign
272   320675    3.0    7.0  malignant
322   733639    3.0    3.0     benign
338   704097    1.0    2.0     benign
443   734111    1.0    1.0     benign
561  1321942    5.0    3.0     benign
684   466906    1.0    1.0     benign
690   654546    1.0    1.0     benign
698   897471    4.0   10.0  malignant
```

This is promising but, if we look at what is listed, we don't actually see any duplicates. So what is `duplicates()` doing?

Use the cell below to get help on `duplicated()` using `help()` or `?`.

```
[143]: #help(bcd2.duplicated())
```

… we can see that it has a "keep" argument. By default, `duplicated()` it gives us the *first* instance of any duplicated rows. We can make it show all the rows with `keep=False`.

Go ahead and do that in the cell below.

```
[36]: bcd2[bcd2.duplicated(keep = False)]
```

```
[36]:          id  thick  chrom      class
      42   1100524    6.0    7.0  malignant
      62   1116116    9.0    3.0  malignant
      168  1198641    3.0    3.0     benign
      207  1218860    1.0    3.0     benign
      208  1218860    1.0    3.0     benign
      253  1100524    6.0    7.0  malignant
      254  1116116    9.0    3.0  malignant
      258  1198641    3.0    3.0     benign
      267   320675    3.0    7.0  malignant
      272   320675    3.0    7.0  malignant
      314   704097    1.0    2.0     benign
      321   733639    3.0    3.0     benign
      322   733639    3.0    3.0     benign
      338   704097    1.0    2.0     benign
      442   734111    1.0    1.0     benign
      443   734111    1.0    1.0     benign
      560  1321942    5.0    3.0     benign
      561  1321942    5.0    3.0     benign
      683   466906    1.0    1.0     benign
      684   466906    1.0    1.0     benign
      689   654546    1.0    1.0     benign
      690   654546    1.0    1.0     benign
      697   897471    4.0   10.0  malignant
      698   897471    4.0   10.0  malignant
```

Hm. That's somewhat helpful. If we look near the bottom, we see that the last 5 or so duplicates occur in successive rows, perhaps indicating a data entry mistake. Perhaps looking at the data sorted by patient ID would be more helpful.

In the cell below, use the the `.sort_values()` method to look at our duplicates sorted by ID.

```
[40]: bcd2.sort_values(by = 'id)
```

```
[40]:          id  thick  chrom      class
      42   1100524    6.0    7.0  malignant
      253  1100524    6.0    7.0  malignant
      62   1116116    9.0    3.0  malignant
      254  1116116    9.0    3.0  malignant
      168  1198641    3.0    3.0     benign
      258  1198641    3.0    3.0     benign
```

```
207  1218860    1.0    3.0     benign
208  1218860    1.0    3.0     benign
561  1321942    5.0    3.0     benign
560  1321942    5.0    3.0     benign
272   320675    3.0    7.0  malignant
267   320675    3.0    7.0  malignant
684   466906    1.0    1.0     benign
683   466906    1.0    1.0     benign
690   654546    1.0    1.0     benign
689   654546    1.0    1.0     benign
314   704097    1.0    2.0     benign
338   704097    1.0    2.0     benign
321   733639    3.0    3.0     benign
322   733639    3.0    3.0     benign
442   734111    1.0    1.0     benign
443   734111    1.0    1.0     benign
697   897471    4.0   10.0  malignant
698   897471    4.0   10.0  malignant
```

So most of the duplicates occur in adjacent rows, but others do not. Perhaps we should check and see if the same patients occur multiple times with different measurements, indicating multiple visits to the doctor.

Use the cell below and the `subset` argument to `duplicated()` to look at multiple entries for any patients that have them.

[48]:
```
bcd2[bcd2.duplicated(subset = 'id', keep = False)]
```

[48]:
```
          id  thick  chrom      class
4    1017023    4.0    3.0     benign
8    1033078    2.0    1.0     benign
9    1033078    4.0    2.0     benign
29   1070935    1.0    1.0     benign
30   1070935    3.0    2.0     benign
..       …    …    …        …
689   654546    1.0    1.0     benign
690   654546    1.0    1.0     benign
691   695091    5.0    4.0  malignant
697   897471    4.0   10.0  malignant
698   897471    4.0   10.0  malignant

[100 rows x 4 columns]
```

Now, in the cell below, do the same thing but sort the output by patient ID.

[50]:

```
bcd2[bcd2.duplicated(keep = False)].sort_values(by = 'id')
```

[50]:

```
          id  thick  chrom      class
42   1100524    6.0    7.0  malignant
253  1100524    6.0    7.0  malignant
62   1116116    9.0    3.0  malignant
254  1116116    9.0    3.0  malignant
168  1198641    3.0    3.0     benign
258  1198641    3.0    3.0     benign
207  1218860    1.0    3.0     benign
208  1218860    1.0    3.0     benign
561  1321942    5.0    3.0     benign
560  1321942    5.0    3.0     benign
272   320675    3.0    7.0  malignant
267   320675    3.0    7.0  malignant
684   466906    1.0    1.0     benign
683   466906    1.0    1.0     benign
690   654546    1.0    1.0     benign
689   654546    1.0    1.0     benign
314   704097    1.0    2.0     benign
338   704097    1.0    2.0     benign
321   733639    3.0    3.0     benign
322   733639    3.0    3.0     benign
442   734111    1.0    1.0     benign
443   734111    1.0    1.0     benign
697   897471    4.0   10.0  malignant
698   897471    4.0   10.0  malignant
```

So it looks like patients do come in multiple times and the values can change between visits.

We can look at repeat patient's number of visits directly if we want. We'll take advantage of the fact that the `.size` of a `groupby()` object returns the number of rows for each group.

[51]:

```
repeat_patients = bcd2.groupby('id').size().sort_values(ascending =False)
```

[53]:

```
repeat_patients
```

[53]:

```
id
1182404    6
1276091    5
1198641    3
1299596    2
1158247    2
          ..
1200892    1
1200952    1
```

```
1201834    1
1201870    1
95719      1
Length: 645, dtype: int64
```

So one patient came in 6 times.

Use the cell below look at the data for the patient with 6 visits.

```
[52]: bcd2[bcd2['id'] == '1182404']
```

```
[52]:          id  thick  chrom   class
     136  1182404    4.0    2.0  benign
     256  1182404    3.0    1.0  benign
     257  1182404    3.0    2.0  benign
     265  1182404    5.0    3.0  benign
     448  1182404    1.0    1.0  benign
     497  1182404    4.0    1.0  benign
```

So it appears that some patients have multiple legitimate entries in the data frame.

If you were put in charge of analyzing these data, what would you do with duplicate observations in this data frame, and why?

1.3 Transforming data

Sometimes we wish to apply a transform to data by pushing each data value through some function. Common transformations are unit conversions (miles to kilometers, for example), log or power transformations, and normalizing data (for example, converting data to z-scores).

1.3.1 Transforming data with a built-in function

Consider the following data…

```
[54]: df = pd.DataFrame({'x': range(6),
                         'y': [0.1, 0.9, 4.2, 8.7, 15.9, 26]})
```

```
[55]: df
```

```
[55]:    x     y
     0  0   0.1
     1  1   0.9
```

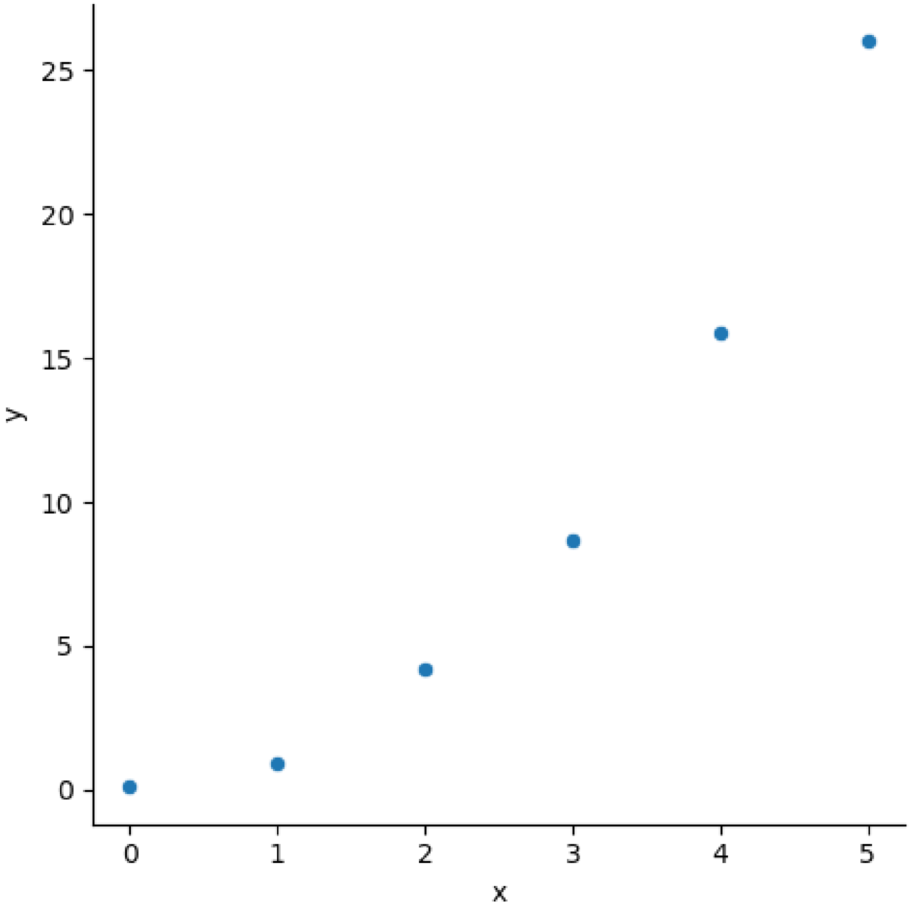
```
2  2   4.2
3  3   8.7
4  4  15.9
5  5  26.0
```

Plot the data (y vs. x) (seaborn's `relplot()` is handy).

[56]:
```
%matplotlib inline
```

[68]:
```
# plot y vs. x
sns.relplot(data = df, x = 'x', y = 'y')
```

[68]:
```
<seaborn.axisgrid.FacetGrid at 0x7f9118402460>
```



These data look non-linear, like they are following a power law. If that's true, we should get a straight line if we plot the log of the values against one another. In order to get these values, we will use the `transform()` method to convert the values into their logs.

[69]:

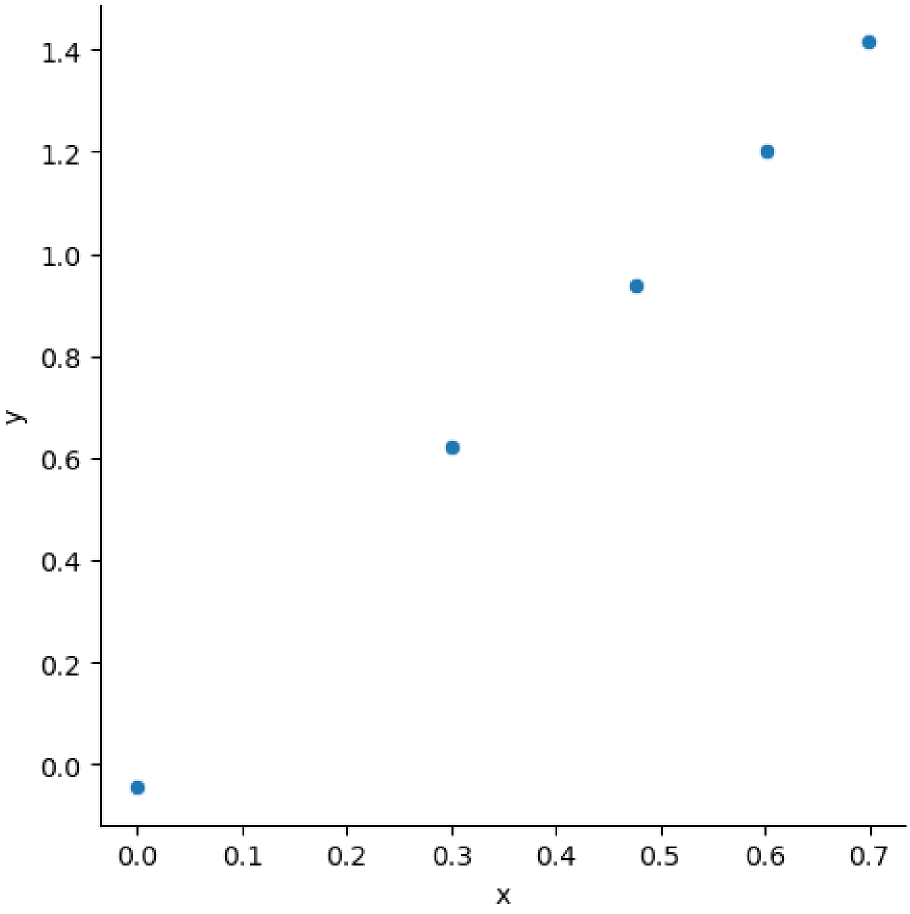
```
df_trans = df.copy()
df_trans['y'] = df['y'].transform(np.log10)
df_trans['x'] = df['x'].transform(np.log10)
```

[70]:

```
# plot new y vs. new x
sns.relplot(data = df_trans, x = 'x', y = 'y')
```

[70]:

```
<seaborn.axisgrid.FacetGrid at 0x7f9118555c70>
```



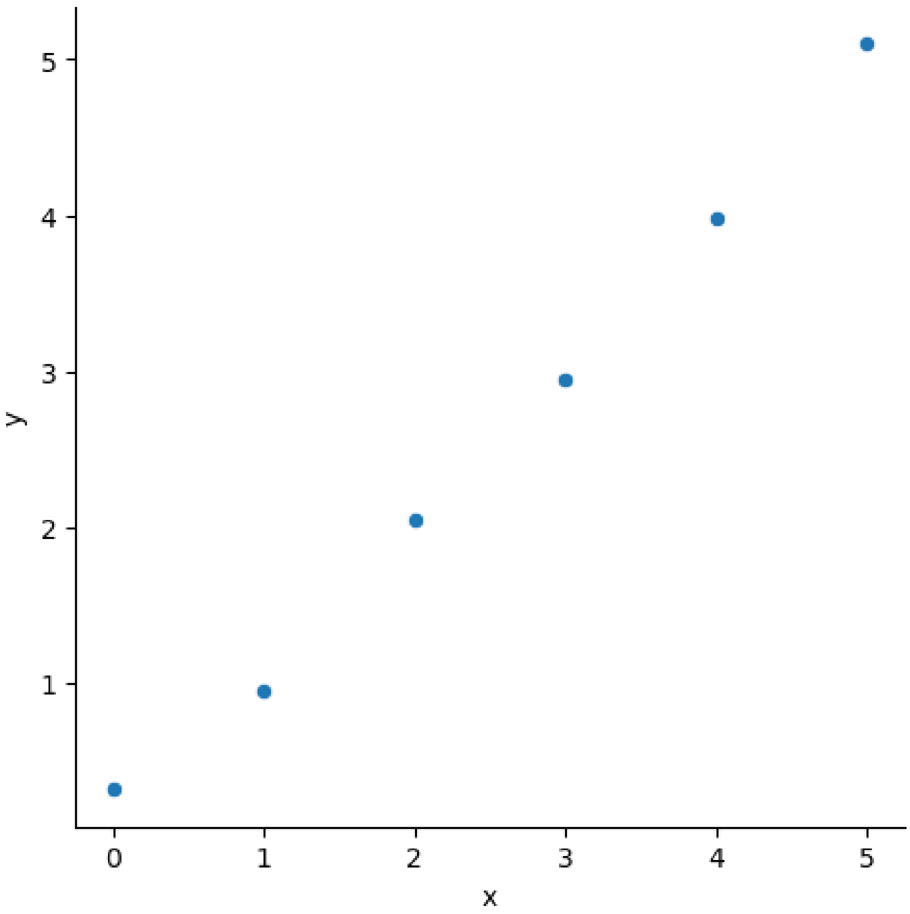
Sure enough. The slope of the line should tell us the exponent of the power law, and it looks to be about 2. If that's the case, then transforming the original y-values with a square-root function should also produce a straight line.

In the cells below, use `transform()` to get the square root of the original y values, and plot them against the x values.

```
[64]: # get sqrts
      df_trans2 = df.copy()
      df_trans2['y'] = df['y'].transform(np.sqrt)
```

```
[66]: #plot
      sns.relplot(data = df_trans2, x = 'x', y = 'y')
```

```
[66]: <seaborn.axisgrid.FacetGrid at 0x7f90fc4c43a0>
```



We could also transform our cancer data. In the cell below, create a new data frame in which the numeric values are the natural log of the original values.

```
[96]: # compute log vals
      bcd_log10 = bcd2.copy()
```

```
[111]: bcd_log10[['thick','chrom']] = bcd_log10[['thick','chrom']].transform(np.log10)
```

[112]:

```
bcd_log10
```

[112]:

```
          id     thick     chrom      class
0    1000025  0.698970  0.477121     benign
1    1002945  0.698970  0.477121     benign
2    1015425  0.477121  0.477121     benign
3    1016277  0.778151  0.477121     benign
4    1017023  0.602060  0.477121     benign
..       …         …         …          …
694   776715  0.477121  0.000000     benign
695   841769  0.301030  0.000000     benign
696   888820  0.698970  0.903090  malignant
697   897471  0.602060  1.000000  malignant
698   897471  0.602060  1.000000  malignant

[699 rows x 4 columns]
```

1.3.2 Applying a custom function to data

A great thing about `transform()` (and some other data frame methods) is you can use your own fuctions, not just built in ones.

For `transform()`, the only requirement is that your function

- be able to take a data frame as input
- produce output the same size as the input, or
- produce a single value

Here's a function to "center" data by subtracting the mean from each value.

[98]:

```
def center_data(grp):
    grp_mean = grp.mean(numeric_only = True)

    grp = (grp - grp_mean)

    return grp
```

In the cell below, use our new function to create a new version of our cancer data frame with the mean removed from each group of data. The `.transform()` method works column-by-column, so you don't need to worry about grouping the data.

[108]:

```
bcd_centered = bcd2.copy()
bcd_centered[['thick','chrom']] = bcd_centered[['thick','chrom']].
  ↪transform(center_data)
```

[109]:

```
bcd_centered
```

```
[109]:          id     thick     chrom      class
       0    1000025  0.583095 -0.447482     benign
       1    1002945  0.583095 -0.447482     benign
       2    1015425 -1.416905 -0.447482     benign
       3    1016277  1.583095 -0.447482     benign
       4    1017023 -0.416905 -0.447482     benign
       ..       …        …        …        …
       694   776715 -1.416905 -2.447482     benign
       695   841769 -2.416905 -2.447482     benign
       696   888820  0.583095  4.552518  malignant
       697   897471 -0.416905  6.552518  malignant
       698   897471 -0.416905  6.552518  malignant

       [699 rows x 4 columns]
```

Confirm this worked by computing the mean for each column of your transformed data.

```
[113]: bcd_centered[['thick','chrom']].mean()
```

```
[113]: thick    3.333850e-16
       chrom   -1.004472e-15
       dtype: float64
```

In the cells below, write a function to convert the cancer data to z-scores, and use your new function to convert the numeric columns of our cancer data frame.

```
[114]: # my z-score function!
       def zscore_data(grp):
           grp_mean = grp.mean(numeric_only = True)
           grp_std = grp.std(numeric_only = True)

           grp = (grp - grp_mean)/grp_std

           return grp
```

```
[116]: # run transform() with my function
       bcd_zscore = bcd2.copy()
       bcd_zscore[['thick','chrom']] = bcd_zscore[['thick','chrom']].
         ↪transform(zscore_data)
```

```
[117]: # look at the transformed data
       bcd_zscore
```

```
[117]:          id     thick     chrom      class
       0    1000025  0.206942 -0.183305     benign
```

```
1    1002945  0.206942 -0.183305     benign
2    1015425 -0.502864 -0.183305     benign
3    1016277  0.561845 -0.183305     benign
4    1017023 -0.147961 -0.183305     benign
..       …         …         …          …
694   776715 -0.502864 -1.002577     benign
695   841769 -0.857766 -1.002577     benign
696   888820  0.206942  1.864876  malignant
697   897471 -0.147961  2.684148  malignant
698   897471 -0.147961  2.684148  malignant

[699 rows x 4 columns]
```

[120]:
```
# see what the means are
bcd_zscore.mean(numeric_only = True)
```

[120]:
```
thick   -1.492757e-16
chrom    1.214057e-16
dtype: float64
```

[121]:
```
# see what the ... are
bcd_zscore.std(numeric_only = True)
```

[121]:
```
thick    1.0
chrom    1.0
dtype: float64
```

---

lambda functions Lambda functions, also know as anonymous functions, are short, one-off functions that are often used in situation in which ***all*** you need the function for is get passed to a method such as `transform()`

While the structure of a normal function is:

[125]:
```
def func_name(input_arg) :
    calculations
    ret_val = more calculations

    return ret_val
```

```
  File "/var/folders/zc/6v283x0929j5f38j6cvlvbwr0000gn/T/ipykernel_17066/
↪272322305.py", line 2
    calculations
    ^
IndentationError: unexpected indent
```

The structure of a lambda function is:

[ ]:

```
lambda input_arg : calculation of ret_val
```

Here's how we would compute z-scores using a lambda function:

[126]:

```
trans_data = bcd2[['thick', 'chrom']].transform(
    lambda col_vals: (col_vals - col_vals.mean()) / col_vals.std()
)
```

Note that the entire lambda function is the one and only input to `transform()`.

In the cell below, confirm that the lambda function method worked.

[127]:

```
trans_data
```

[127]:

```
        thick     chrom
0    0.206942 -0.183305
1    0.206942 -0.183305
2   -0.502864 -0.183305
3    0.561845 -0.183305
4   -0.147961 -0.183305
..        …         …
694 -0.502864 -1.002577
695 -0.857766 -1.002577
696  0.206942  1.864876
697 -0.147961  2.684148
698 -0.147961  2.684148

[699 rows x 2 columns]
```

For very simple transformations, using a lambda function makes a lot of sense. For more complicated transformations, we'd probably want to just create a regular function, or the code could become unreadable.

How complicated is too complicated? That's up to you, but anything more complicated than applying an offset and a scale factor (like computing a z-score), probably deserves its own function.

In the cell below, transform the numeric cancer data so the values range from 0 to 1 using a lambda function. You can assume that the maximum value is 10 and the minimum value is 1.

[130]:

```
range_data = bcd2[['thick', 'chrom']].transform(
    lambda col_vals: (col_vals-1)/9
)
range_data
```

```
[130]:         thick     chrom
       0    0.444444  0.222222
       1    0.444444  0.222222
       2    0.222222  0.222222
       3    0.555556  0.222222
       4    0.333333  0.222222
       ..        …         …
       694  0.222222  0.000000
       695  0.111111  0.000000
       696  0.444444  0.777778
       697  0.333333  1.000000
       698  0.333333  1.000000

       [699 rows x 2 columns]
```

In the cell below, us a regular function to rescale the values from 0 to 1. In this case, however, do not assume you know the minimum and maximum values ahead of time.

```
[141]: def change_data(grp) :
           grp_min = grp.min()
           grp_max = grp.max()

           grp = (grp - grp_min)/grp_max

           return grp

       # comute min of the data subtract min of all data, comute max and divide by␣
        ↪that max
```

```
[142]: bcd_range = bcd2.copy()
       bcd_range[['thick','chrom']] = bcd_range[['thick','chrom']].
        ↪transform(change_data)
       bcd_range
```

```
[142]:          id  thick  chrom      class
       0    1000025    0.4    0.2     benign
       1    1002945    0.4    0.2     benign
       2    1015425    0.2    0.2     benign
       3    1016277    0.5    0.2     benign
       4    1017023    0.3    0.2     benign
       ..       …      …      …         …
       694   776715    0.2    0.0     benign
       695   841769    0.1    0.0     benign
       696   888820    0.4    0.7  malignant
       697   897471    0.3    0.9  malignant
       698   897471    0.3    0.9  malignant
```

```
[699 rows x 4 columns]
```