Wrangling III

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

- handling duplicate values
- data transformations

Preliminaries

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

In [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.

In [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
```

In [3]:
```
bcd = bcd_load_clean()
```

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

In [4]:
```
bcd2 = bcd[['patient_id', 'clump_thickness', 'bland_chromatin', 'class']].copy()
```

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

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

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).

In [6]:
```
bcd2.shape
```

Out[6]:
```
(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.

In [7]:
```
bcd2.nunique()
```

Out[7]:
```
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.

In [8]:
```
bcd2.duplicated()
```

Out[8]:
```
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).

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

Out[9]:
```
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.

In [10]:
```
bcd2.loc[bcd2.duplicated()]
```

Out[10]:

	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 `?`.

In [11]:
```
help(bcd2.duplicated())
```

```
|       Examples
|       --------
|       >>> s1 = pd.Series([1, 2, 3])
|       >>> s2 = pd.Series([4, 5, 6])
|       >>> s3 = pd.Series([4, 5, 6], index=[3, 4, 5])
|       >>> s1.append(s2)
|       0    1
|       1    2
|       2    3
|       0    4
|       1    5
|       2    6
|       dtype: int64
|
|       >>> s1.append(s3)
|       0    1
|       1    2
|       2    3
|       3    4
|       4    5
```

... 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.

In [12]:
```
bcd2[bcd2.duplicated(keep=False)]
```

Out[12]:

	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.

In [13]:
```
bcd2[bcd2.duplicated(keep=False)].sort_values(by='id')
```

Out[13]:

	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.

In [14]:
```
bcd2[bcd2.duplicated(subset='id', keep=False)]
```

Out[14]:

	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 × 4 columns

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

In [15]:
```
bcd2[bcd2.duplicated(subset='id', keep=False)].sort_values(by='id')
```

Out[15]:

	id	thick	chrom	class
4	1017023	4.0	3.0	benign
252	1017023	6.0	3.0	benign
8	1033078	2.0	1.0	benign
9	1033078	4.0	2.0	benign
618	1061990	4.0	2.0	benign
...	...	...	...	...
527	798429	4.0	3.0	benign
344	822829	7.0	9.0	malignant
612	822829	8.0	10.0	malignant
697	897471	4.0	10.0	malignant
698	897471	4.0	10.0	malignant

100 rows × 4 columns

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.

In [16]:
```
repeat_patients = bcd2.groupby('id').size().sort_values(ascending =False)
```

In [17]:
```
repeat_patients
```

Out[17]:
```
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.

In [18]:
```
bcd2[bcd2['id'] == '1182404']
```

Out[18]:

	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?

I would only get rid of duplicate entries in which the whole row is duplicated since patients can visit multiple times

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).

Transforming data with a built-in function

Consider the following data...

In [19]:
```
df = pd.DataFrame({'x': range(6),
                   'y': [0.1, 0.9, 4.2, 8.7, 15.9, 26]})
```

In [20]:
```
df
```

Out[20]:

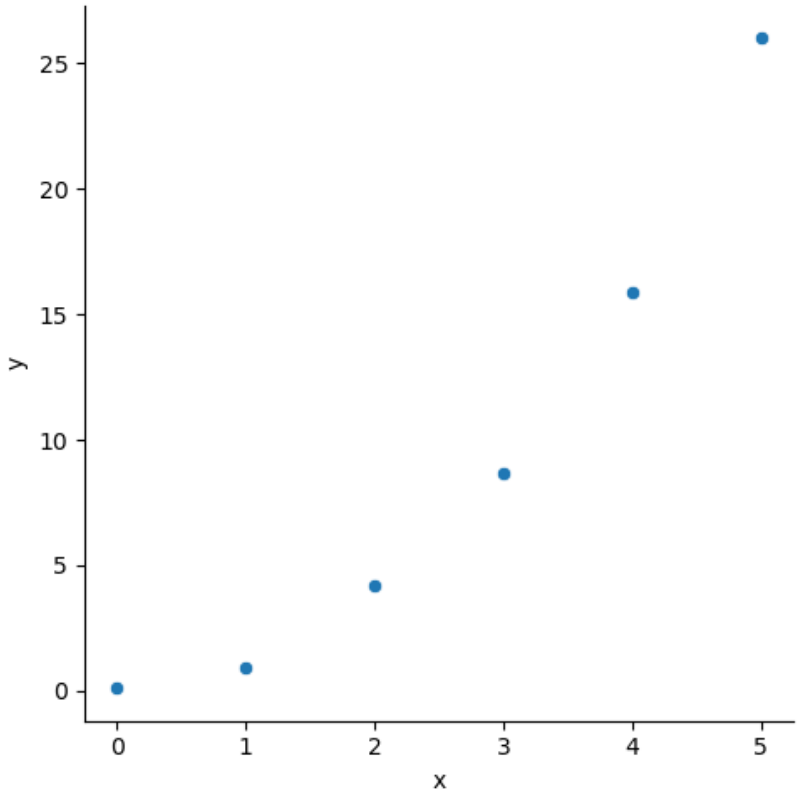
	x	y
0	0	0.1
1	1	0.9
2	2	4.2
3	3	8.7
4	4	15.9
5	5	26.0

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

In [21]:
```
%matplotlib inline
```

In [22]:
```
# plot y vs. x
sns.relplot(data=df, x='x', y='y')
```

Out[22]:
```
<seaborn.axisgrid.FacetGrid at 0x7fd140ef7b80>
```

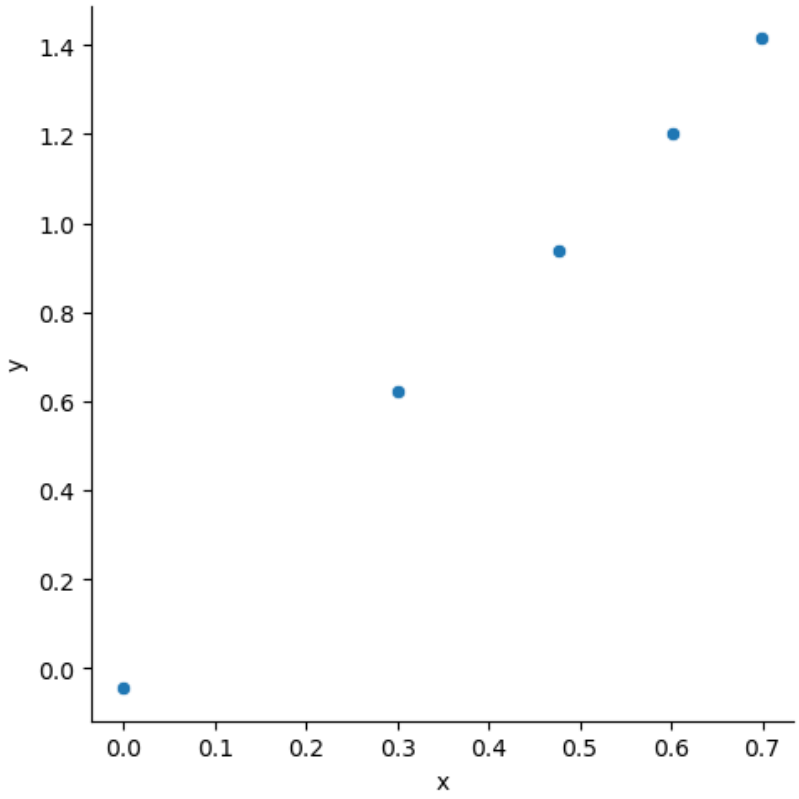


These data look non-linear, like they are following a power law. If that's true, we should get a straight line if we plot the log of the values against one another. In order to get these values, we will use the `transform()` method to convert the values into their logs.

In [23]:
```
df_trans = df.copy()
df_trans['y'] = df_trans['y'].transform(np.log10)
df_trans['x'] = df_trans['x'].transform(np.log10)
```

In [24]:
```
# plot new y vs. new x
sns.relplot(data=df_trans, x='x', y='y')
```

Out[24]:
```
<seaborn.axisgrid.FacetGrid at 0x7fd163ec1310>
```



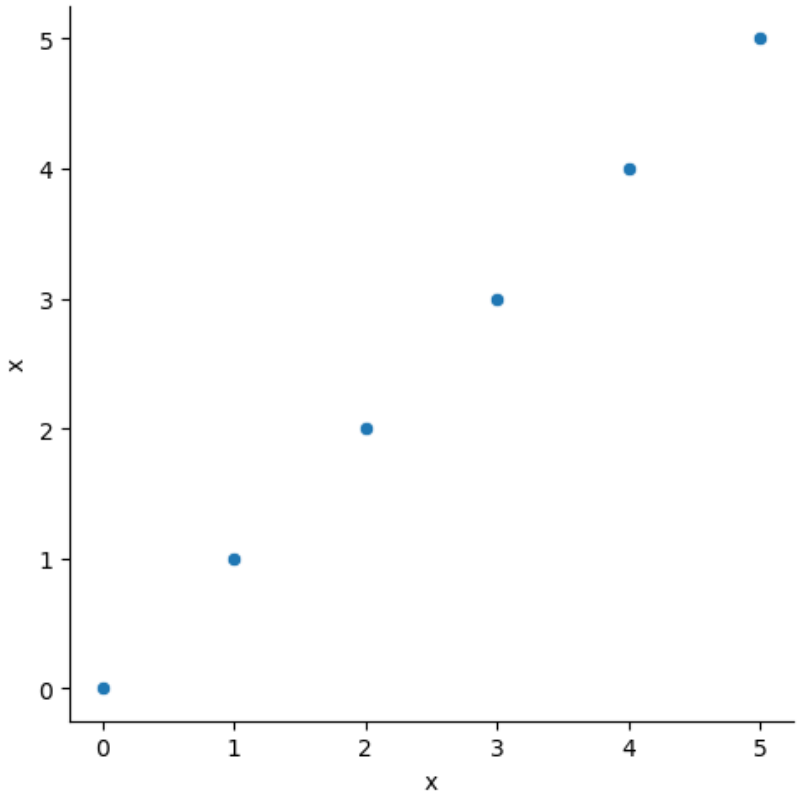
Sure enough. The slope of the line should tell us the exponent of the power law, and it looks to be about 2. If that's the case, then transforming the original y-values with a square-root function should also produce a straight line.

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

In [25]:
```
# get sqrts
df_trans2 = df.copy()
df_trans2['y'] = df_trans2['y'].transform(np.sqrt)
```

In [26]:
```
# plot
sns.relplot(data=df_trans2, x='x', y='x')
```

Out[26]:
```
<seaborn.axisgrid.FacetGrid at 0x7fd1411fa970>
```



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.

In [27]:
```
# compute log vals
bcd2_natural_log = bcd2.copy()
bcd2_natural_log[['thick', 'chrom']] = bcd2_natural_log[['thick', 'chrom']].transform(np.log
```

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.

In [28]:
```
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.

In [29]:
```
bcd2_centered = bcd2.copy()
bcd2_centered[['thick', 'chrom']] = bcd2_centered[['thick', 'chrom']].transform(center_data)
bcd2_centered
```

Out[29]:

	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 × 4 columns

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

In [30]:
```
print('It worked since the means are practically 0')
bcd2_centered[['thick', 'chrom']].mean()
```

```
It worked since the means are practically 0
```

Out[30]:
```
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.

In [31]:
```
# my z-score function!
def z_score(col):
    col_mean = col.mean(numeric_only=True)
    sd = col.std(numeric_only=True)
    col = (col - col_mean)/sd

    return col
```

In [32]:
```
# run transform() with my function
bcd2_z = bcd2.copy()
bcd2_z[['thick', 'chrom']] = bcd2_z[['thick', 'chrom']].transform(z_score)
```

In [33]:
```
# look at the transformed data
bcd2_z
```

Out[33]:

	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 × 4 columns

In [34]:
```
# see what the means are
bcd2_z[['thick', 'chrom']].mean()
```

Out[34]:
```
thick   -1.492757e-16
chrom    1.214057e-16
dtype: float64
```

In [35]:
```
# see what the sd are
bcd2_z.std(numeric_only=True)
```

Out[35]:
```
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:

In [36]:
```
def func_name(input_arg) :
    caluculations
    ret_val = more calculations

    return ret_val
```

```
  File "/var/folders/18/y5p3lwcd31j2dw1d0_k3lqsh0000gp/T/ipykernel_6100/989757355.py", lin
e 3
    ret_val = more calculations
                   ^
SyntaxError: invalid syntax
```

The structure of a lambda function is:

In [ ]:
```
lambda input_arg : calculation of ret_val
```

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

In [37]:
```
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.

In [38]:
```
trans_data.mean(numeric_only=True)
```

Out[38]:
```
thick   -1.492757e-16
chrom    1.214057e-16
dtype: float64
```

In [39]:
```
trans_data.std(numeric_only=True)
```

Out[39]:
```
thick    1.0
chrom    1.0
dtype: float64
```

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.

In [42]:
```
bcd2
```

Out[42]:

	id	thick	chrom	class
0	1000025	5.0	3.0	benign
1	1002945	5.0	3.0	benign
2	1015425	3.0	3.0	benign
3	1016277	6.0	3.0	benign
4	1017023	4.0	3.0	benign
...	...	...	...	...
694	776715	3.0	1.0	benign
695	841769	2.0	1.0	benign
696	888820	5.0	8.0	malignant
697	897471	4.0	10.0	malignant
698	897471	4.0	10.0	malignant

699 rows × 4 columns

In [48]:
```
range_data = bcd2[['thick', 'chrom']].transform(
    lambda col_vals: (col_vals - 1) / 9
)
```

In [49]:
```
range_data
```

Out[49]:

	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 × 2 columns

In [46]:
```
range_data = bcd2[['thick', 'chrom']].transform(
    lambda col_vals : (col_vals - col_vals.min())/col_vals.max()
)
```

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.

In [50]:
```
def rescale(col_vals):
    col_vals = (col_vals - col_vals.min())/col_vals.max()

    return col_vals
```

In [51]:
```
range_data2 = bcd2.copy()
range_data2[['thick', 'chrom']] = range_data2[['thick', 'chrom']].transform(rescale)
range_data2
```

Out[51]:

	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 × 4 columns