Wraggling, Summarizing, and Plotting

Preliminaries

You don't need to import numpy to run pandas, but numpy comes in handy so often, we generally import it as well.

In [2]:
```
import numpy as np
import pandas as pd
import math
```

Let's re-use our function to load and clean up data from last time (but with a new name).

In [3]:
```
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
```

Load our data:

In [4]:
```
bcd = bcd_load_clean()
```

Now, for convenience, let's make a smaller data set to play with. We'll do this by dropping some of the columns.

We can do this in one of two ways. We can either `.drop` the columns we don't want, or `.copy` the columns we do. Here's the first method:

In [5]:
```
bcd2 = bcd.drop(labels = ['patient_id', 'cell_size_uniformity', 'cell_shape_uniformity',
                          'cell_shape_uniformity', 'marginal_adhesion', 'single_ep_cell_size
                          'bare_nuclei', 'normal_nucleoli', 'mitoses'],
                axis = 1,            # we're selecting column - default is rows
                inplace = False)     # we could modify bcd itself with True
```

In [5]:
```
bcd2
```

Out[5]:

	clump_thickness	bland_chromatin	class	doctor_name
0	5.0	3.0	benign	Doe
1	5.0	3.0	benign	Smith
2	3.0	3.0	benign	Lee
3	6.0	3.0	benign	Smith
4	4.0	3.0	benign	Wong
...	...	...	...	...
694	3.0	1.0	benign	Lee
695	2.0	1.0	benign	Smith
696	5.0	8.0	malignant	Lee
697	4.0	10.0	malignant	Lee
698	4.0	10.0	malignant	Wong

699 rows × 4 columns

In the cell below, make the same new data frame using column indexing and the `.copy()` method.

In [6]:
```
# make new bcd2 using .copy()
bcd2 = bcd[['clump_thickness', 'bland_chromatin', 'class', 'doctor_name']].copy()
```

In [7]:
```
# look at new bcd2
bcd2
```

Out[7]:

	clump_thickness	bland_chromatin	class	doctor_name
0	5.0	3.0	benign	Doe
1	5.0	3.0	benign	Smith
2	3.0	3.0	benign	Lee
3	6.0	3.0	benign	Smith
4	4.0	3.0	benign	Wong
...	...	...	...	...
694	3.0	1.0	benign	Lee
695	2.0	1.0	benign	Smith
696	5.0	8.0	malignant	Lee
697	4.0	10.0	malignant	Lee
698	4.0	10.0	malignant	Wong

699 rows × 4 columns

What might we want from this data set?

The main thing that comes to mind is whether any of the measures are related to the kind of tumor. To do this, we can

- group the data by the "class" column
- perform some operation, like computing the mean, separately for the groups.

We might also want to see if the doctors are behaving consistently with respect to one another.

The split-apply-combine workflow

Much of data wrangling can be thought of "split-apply-combine". This is where we

- *split* the data into groups
- do ("*apply*") some function or manipulation on a per-group basis
- *combine* the results back into a data frame, series, etc.

Happily, the "combine" step is often handled for you by the methods that do the "apply" step.

Splitting - the `groupby()` method

Grouping the data is easy using the `groupby()` method. We just provide the name of a grouping variable. Since the main question at hand is how the measurements might relate to the type of tumor, Let's group by tumor "class".

In [8]:
```
grpd = bcd2.groupby('class')
```

If we try to look at it:

In [9]:
```
grpd
```

Out[9]:
```
<pandas.core.groupby.generic.DataFrameGroupBy object at 0x7f8c91189580>
```

we see that the output of '.groupby() isn't a regular data frame, but rather a `DataFrameGroupBy` object. To interegate it, well need to use its methods or look at its attributes.

In the cell below, use the <TAB> key trick to browse the methods and properties that `grpd` has.

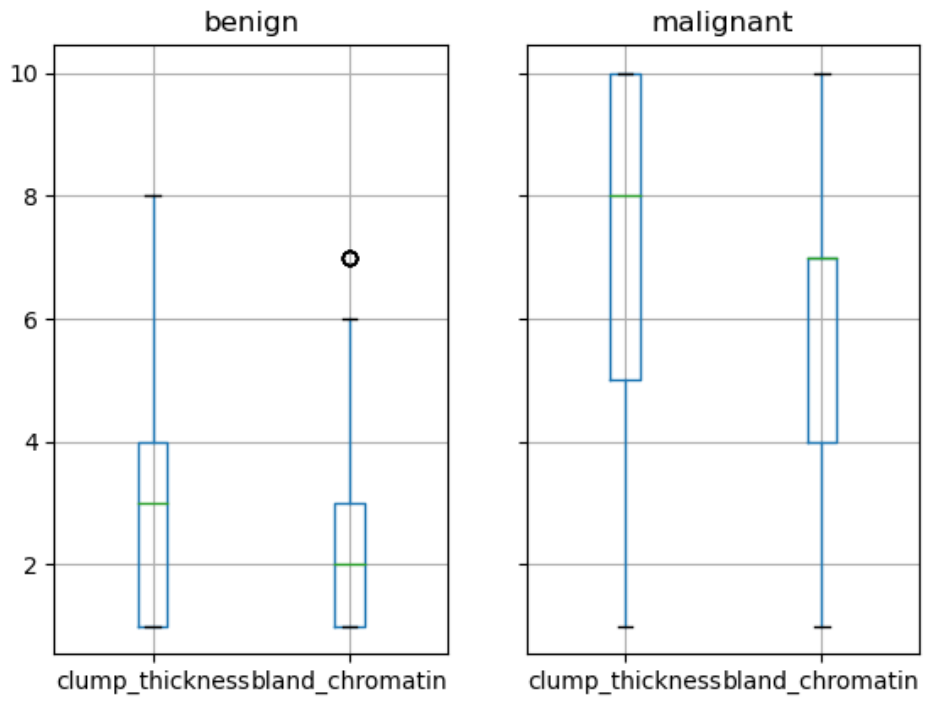
In [10]:
```
grpd.
```

```
  File "/var/folders/18/y5p3lwcd31j2dw1d0_k3lqsh0000gp/T/ipykernel_1204/1579351624.py", l
ine 1
    grpd.
         ^
SyntaxError: invalid syntax
```

One of the early methods on the list is `.boxplot` - see what that does in the cell below!

In [11]:
```
grpd.boxplot()
```

Out[11]:
```
benign            AxesSubplot(0.1,0.15;0.363636x0.75)
malignant    AxesSubplot(0.536364,0.15;0.363636x0.75)
dtype: object
```



While not the prettiest plot in the world, it does give us a hint that both of these variables might be related to tumor size.

(Make sure you remember or remind yourself what a box shows you.)

Now let's see if we can `.describe` the grouped data using the cell below.

In [12]:
```
  # some useful summary numbers
grpd.describe()
```

Out[12]:

	clump_thickness								bland_chromatin							
	count	mean	std	min	25%	50%	75%	max	count	mean	std	min	25%	50%	75%	max
class																
benign	458.0	2.956332	1.674318	1.0	1.0	3.0	4.0	8.0	455.0	2.105495	1.081417	1.0	1.0	2.0	3.0	7.0
malignant	240.0	7.204167	2.429763	1.0	5.0	8.0	10.0	10.0	240.0	5.991667	2.270406	1.0	4.0	7.0	7.0	10.0

What is the approximate mean difference between the groups for each of the two measures?

- Mean difference for clump thickness = 4.24
- Mean difference for bland chromatin = 3.88

Do a very rough guesstimate of Student's *t* for the clump thickness (e.g., just use the larger `std` and smaller `countn`). You can use the cell below as a calculator if you like.

In [13]:
```
clump_thickness_t_estimate = (4.24)/(2.43/math.sqrt(240))
bland_chromatin_t_estimate = (3.88)/(2.27/math.sqrt(240))
print(f'This is the approximate t for clump thickness: {clump_thickness_t_estimate}')
print(f'This is the approximate t for bland chromatin: {bland_chromatin_t_estimate}')
```

```
This is the approximate t for clump thickness: 27.031192408097855
This is the approximate t for bland chromatin: 26.479604199620756
```

What does that tell you?

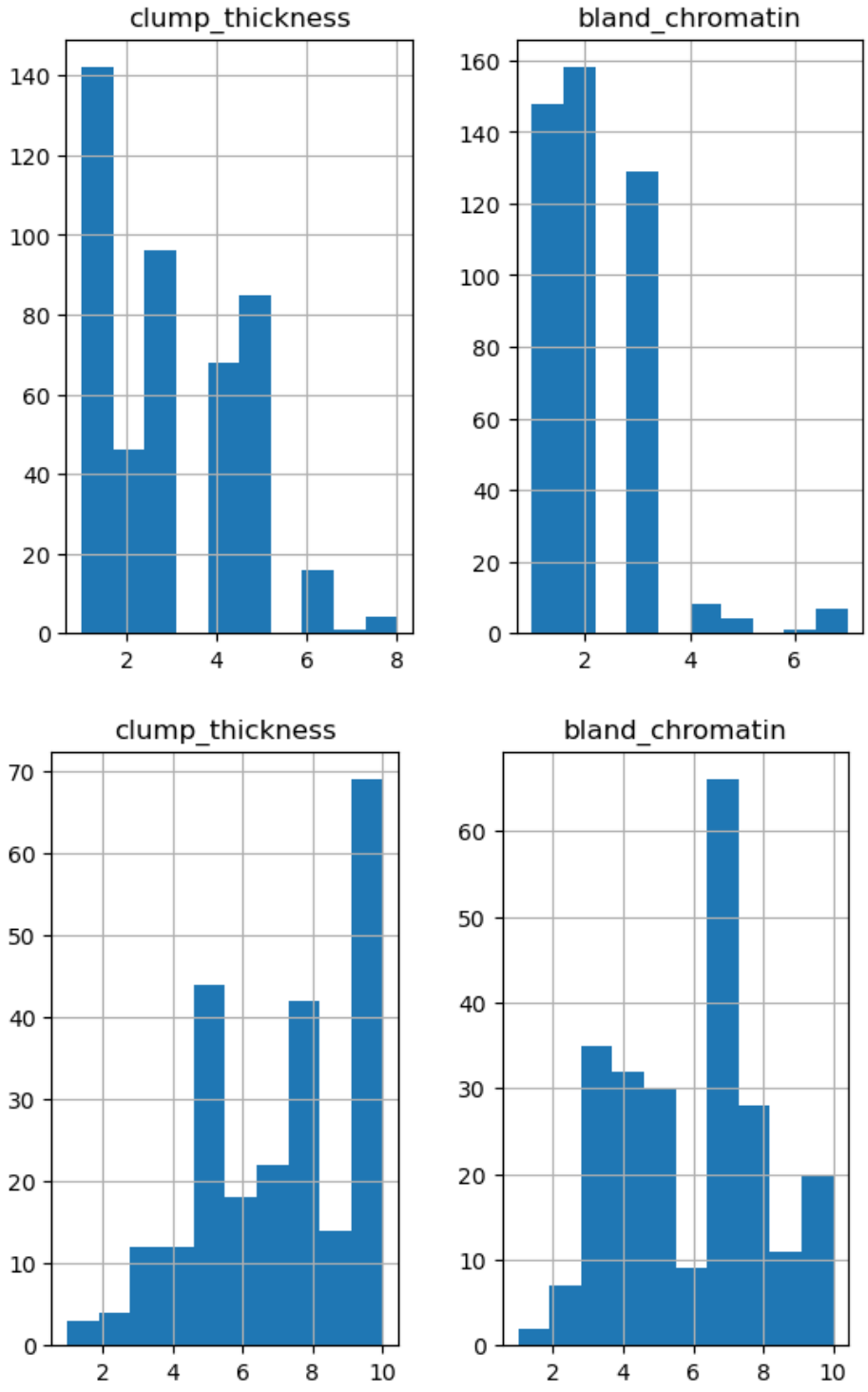
The t scores are very large, so there is likely a difference between the clump thickness and the bland chromatin of benign and malignant tumors

---

Now let's make a histogram of grouped data using the appropriate method.

In [14]:
```
grpd.hist()
```

Out[14]:
```
class
benign       [[AxesSubplot(0.125,0.11;0.336957x0.77), AxesS...
malignant    [[AxesSubplot(0.125,0.11;0.336957x0.77), AxesS...
dtype: object
```



Again, not the prettiest plot in the world. By comparison with the boxplot above, we can see that the top row of these histograms correspond to the benign tumors. We can also see that, consistent with the box plots, there is quite a bit overlap in the data values across groups. Is this consistent with your calculation of *t*?

I wouldn't have expected the distributions to overlap as much as they do given the t value. The t value suggests that there is large a difference between the characteristics of clump thickness and bland chromatin for benign and malignant tumors

---

We can also get the data for a specific group out of the grouped object. This will return a regular data frame the same width as the original, but only containing the requested group's data.

In [15]:
```
grpd.get_group('benign')
```

Out[15]:

	clump_thickness	bland_chromatin	class	doctor_name
0	5.0	3.0	benign	Doe
1	5.0	3.0	benign	Smith
2	3.0	3.0	benign	Lee
3	6.0	3.0	benign	Smith
4	4.0	3.0	benign	Wong
...	...	...	...	...
690	1.0	1.0	benign	Doe
692	3.0	1.0	benign	Wong
693	3.0	2.0	benign	Lee
694	3.0	1.0	benign	Lee
695	2.0	1.0	benign	Smith

458 rows × 4 columns

In the cell below, confirm that the returned object is indeed a pandas `DataFrame` .

In [16]:
```
type(grpd.get_group('benign'))
```

Out[16]:
```
pandas.core.frame.DataFrame
```

Applying - doing things to the data within groups

Once we have grouped data, we can easily caluculate things per group. Using the <TAB> trick, we can see that these objects produced by `groupby()` have methods for all the common statistical summaries.

Simple calculations

We can compute the mean for each measure *by group*

In [17]:
```
my_means = grpd.mean(numeric_only = True)
my_means
```

Out[17]:

class	clump_thickness	bland_chromatin
benign	2.956332	2.105495
malignant	7.204167	5.991667

In the cells below, compute and show the

standard deviations:

In [18]:
```
my_sds =  grpd.std()# compute
my_sds # show
```

Out[18]:

class	clump_thickness	bland_chromatin
benign	1.674318	1.081417
malignant	2.429763	2.270406

and the counts

In [19]:
```
my_counts = grpd.count() # compute
my_counts = my_counts[['clump_thickness', 'bland_chromatin']] # got rid of doctor counts
my_counts # show
```

Out[19]:

class	clump_thickness	bland_chromatin
benign	458	455
malignant	240	240

We can easily do simple maths on data frames of a compatible size. Here's a comparison of how many z-scores above zero each of the means are:

In [20]:
```
my_zeds = my_means/my_sds
my_zeds
```

Out[20]:

class	clump_thickness	bland_chromatin
benign	1.765693	1.946977
malignant	2.964967	2.639029

We can look at the difference between the z-scores for each measure using the `diff()` method, which takes the first difference down the rows.

In [21]:
```
my_zeds.diff()
```

Out[21]:

class	clump_thickness	bland_chromatin
benign	NaN	NaN
malignant	1.199274	0.692052

This difference in z-scores – how far apart two means are in terms of the standard deviation of the data – is roughly what statisticians call "effect size".

Why do the NaNs appear in the first row?

There is no row before the first row to calculate the first rows difference from the previous rows difference

In the cell below, extract just the row with the numbers from `my_zeds` into a new series. (hint: using `.loc` is probably easiest)

In [22]:
```
my_zeds.diff()
```

Out[22]:

class	clump_thickness	bland_chromatin
benign	NaN	NaN
malignant	1.199274	0.692052

In [23]:
```
my_zeds_diff = my_zeds.diff()
my_zeds_diff = my_zeds_diff.loc['malignant']    # extract
my_zeds_diff # show
```

Out[23]:
```
clump_thickness    1.199274
bland_chromatin    0.692052
Name: malignant, dtype: float64
```

We could also compute the difference by using `.loc[]` row indexing and simple maths.

In [24]:
```
my_zeds.loc['malignant'] - my_zeds.loc['benign']
```

Out[24]:
```
clump_thickness    1.199274
bland_chromatin    0.692052
dtype: float64
```

Mulitiple caclulations with `agg()`

We can do multiple calculation at once by placing function names inside the `agg()`) or `aggregate()`) methods (they are synonyms). Here's where importing numpy comes in handy.

In [25]:
```
grpd.agg([np.mean, np.std])
```

```
/var/folders/18/y5p3lwcd31j2dw1d0_k3lqsh0000gp/T/ipykernel_1204/1757925766.py:1: FutureWa
rning: ['doctor_name'] did not aggregate successfully. If any error is raised this will r
aise in a future version of pandas. Drop these columns/ops to avoid this warning.
  grpd.agg([np.mean, np.std])
```

Out[25]:

	clump_thickness		bland_chromatin	
	mean	std	mean	std
class				
benign	2.956332	1.674318	2.105495	1.081417
malignant	7.204167	2.429763	5.991667	2.270406

That worked, but pandas still complained to us because `grpd` has the doctors' names in it, and we obviously can't compute the means and standard deviations of those!

In the cell below, repeat the above calculation without triggering the warning.

In [26]:
```
bcd2.drop('doctor_name', axis=1).groupby('class').agg([np.mean, np.std])
```

Out[26]:

	clump_thickness		bland_chromatin	
	mean	std	mean	std
class				
benign	2.956332	1.674318	2.105495	1.081417
malignant	7.204167	2.429763	5.991667	2.270406

We can use the pandas versions of functions by placing them in quotes. This is handy because, for example, pandas has a `count` and numpy doesn't.

In [27]:
```
grpd[['clump_thickness', 'bland_chromatin']].agg([np.mean, 'std', 'count'])
```

Out[27]:

	clump_thickness			bland_chromatin		
	mean	std	count	mean	std	count
class						
benign	2.956332	1.674318	458	2.105495	1.081417	455
malignant	7.204167	2.429763	240	5.991667	2.270406	240

MultiIndexing - getting at our summary data

Let's store our summary table little summary table above in its own data frame. This is going to complete our *split-apply-combine* by creating and naming a `DataFrame` object.

In [28]:
```
my_summary = grpd[['clump_thickness', 'bland_chromatin']].agg([np.mean, 'std', 'count'])
my_summary
```

Out[28]:

	clump_thickness			bland_chromatin		
	mean	std	count	mean	std	count
class						
benign	2.956332	1.674318	458	2.105495	1.081417	455
malignant	7.204167	2.429763	240	5.991667	2.270406	240

Notice that this data frame has hierachical column labels. In other words, there is a "clump_thickness" meta-column that contains three colums of its own, and that these subcolumns have the same names as those in the other meta-column. Thus saying "look at the mean column" would be ambiguous because the meta-column wasn't specified.

In pandas, this is known at "multiIndexing".

Getting a meta-column is easy - it's just like getting a regular column from a data frame.

In [29]:
```
my_summary['clump_thickness']
```

Out[29]:

	mean	std	count
class			
benign	2.956332	1.674318	458
malignant	7.204167	2.429763	240

To get a subcolumn, we can index the meta-column, and then index the subcolumn from that.

In [30]:
```
my_summary['clump_thickness']['mean']
```

Out[30]:
```
class
benign       2.956332
malignant    7.204167
Name: mean, dtype: float64
```

If this looks confusing, consider the same thing broken up into two steps:

In [31]:
```
meta_c = my_summary['clump_thickness']
meta_c
```

Out[31]:

	mean	std	count
class			
benign	2.956332	1.674318	458
malignant	7.204167	2.429763	240

In [32]:
```
meta_c['mean']
```

Out[32]:
```
class
benign       2.956332
malignant    7.204167
Name: mean, dtype: float64
```

In the cell below, extract the mean and std of "bland_chromatin" in one go.

In [33]:
```
my_summary['bland_chromatin'][['mean', 'std']]
```

Out[33]:

class	mean	std
benign	2.105495	1.081417
malignant	5.991667	2.270406

If we want values from a row, we need to get a bit more fancy and use `.loc`.

We can get a whole row using `df.loc[row_index(s)]`

In [34]:
```
my_summary.loc['benign']
```

Out[34]:
```
clump_thickness  mean       2.956332
                 std        1.674318
                 count    458.000000
bland_chromatin  mean       2.105495
                 std        1.081417
                 count    455.000000
Name: benign, dtype: float64
```

(note: that this gave us a hierarchical index!)

We can get a row and and a particular column with `df.loc[row_index(s), (metacolumn_index, subcolumn_index)]`

In [35]:
```
my_summary.loc['benign', ('clump_thickness', 'mean')]
```

Out[35]:
```
2.9563318777292578
```

We can also get bigger slices of the data with the colon `:` operator:

In [36]:
```
my_summary.loc['benign', ('clump_thickness', 'mean'):('bland_chromatin', 'std')]
```

Out[36]:
```
clump_thickness  mean       2.956332
                 std        1.674318
                 count    458.000000
bland_chromatin  mean       2.105495
                 std        1.081417
Name: benign, dtype: float64
```

In the cell below, extract the mean and std of the bland chromatin meta-column.

In [37]:
```
my_summary['bland_chromatin'][['mean', 'std']]
```

Out[37]:

class	mean	std
benign	2.105495	1.081417
malignant	5.991667	2.270406

Simple caculations with pivot tables

Pivot tables are summary data with the levels of one variable running down the row names (the index), the levels of another running across the column names, and values populating the interior. This should be made concrete by making one with the `pivot_table()` method:

In [38]:
```
bcd2.pivot_table(index = 'doctor_name', columns = 'class', values = 'bland_chromatin')
```

Out[38]:

doctor_name	class	benign	malignant
Doe		2.000000	5.456140
Lee		2.067227	6.150000
Smith		1.980392	6.459459
Wong		2.388889	5.714286

By default, `pivot_table()` computes the group (row x column) means, but we can compute any of the standard summary statistics we wish. We just specify it using the `aggfunc` argument:

In [39]:
```
bcd2.pivot_table(index = 'doctor_name',
                 columns = 'class',
                 values = 'bland_chromatin',
                 aggfunc = 'std')
```

Out[39]:

doctor_name	class	benign	malignant
Doe		1.003992	2.260453
Lee		1.014564	2.121920
Smith		0.943769	2.330202
Wong		1.303004	2.263846

These are called "pivot tables" because their implementation makes it easy to pivot our view of the data summary.

In the cell below, "pivot" our view of the means so we have "class" down the rows, doctor name across the columns, and the means of clump thickness inside the table.

In [40]:
```
bcd2.pivot_table(index = 'class', columns = 'doctor_name', values = 'bland_chromatin')
```

Out[40]:

doctor_name	Doe	Lee	Smith	Wong
class				
benign	2.00000	2.067227	1.980392	2.388889
malignant	5.45614	6.150000	6.459459	5.714286

Because clumb thickness and bland chromatin only have the values 1 to 10, we could use either one as a grouping variable in a pivot table:

In [41]:
```
bcd2.pivot_table(index = 'clump_thickness', columns = 'class', values = 'bland_chromatin')
```

Out[41]:

class	benign	malignant
clump_thickness		
1.0	1.978723	5.666667
2.0	2.090909	5.000000
3.0	2.145833	5.500000
4.0	2.117647	7.916667
5.0	2.011765	5.818182
6.0	3.062500	6.666667
7.0	2.000000	5.818182
8.0	3.750000	5.761905
9.0	NaN	5.142857
10.0	NaN	6.147059

Notice the NaNs – no benign tumors have a thickness of 9 or 10.

Grouped plotting

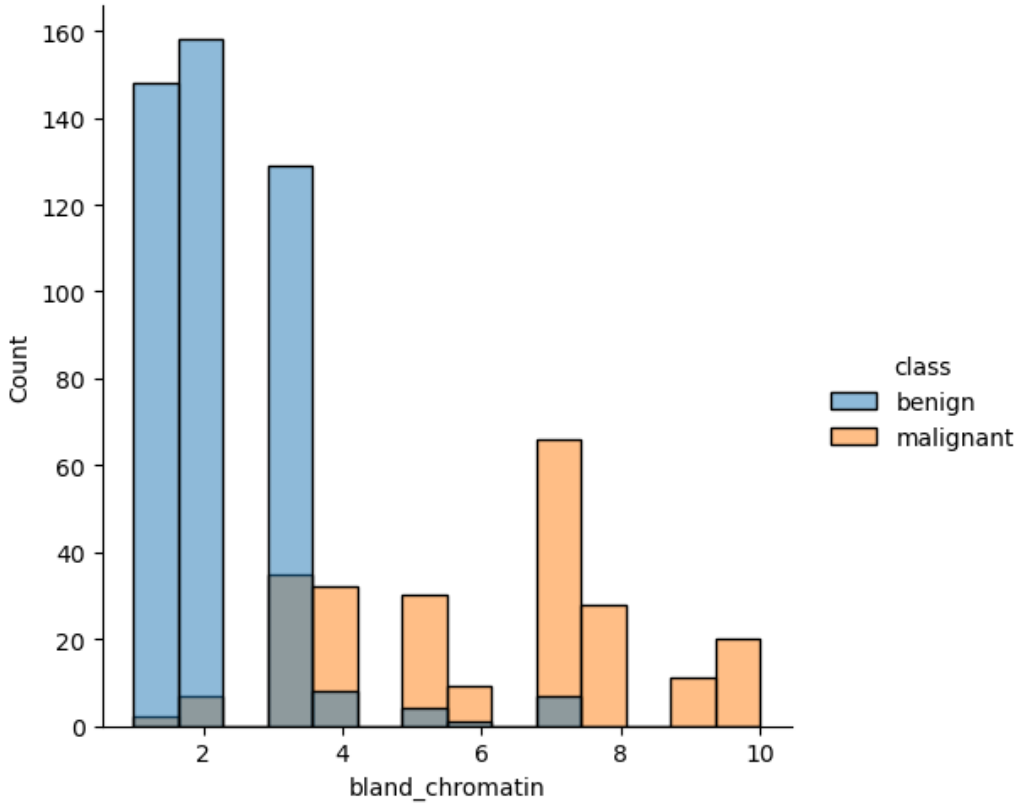
As we have already seen, the seaborn package can take care of grouping for us – we just need to assign a grouping variable to color ('hue'), style, etc. And we already know how to do all this!

In [7]:
```
import seaborn as sns
```

Make a distribution plot (like a histogram) of bland chromatin values grouped by tumor type.

In [43]:
```
sns.displot(data=bcd2, x='bland_chromatin', hue='class')
```

Out[43]:
```
<seaborn.axisgrid.FacetGrid at 0x7f8c30058a00>
```



Make a joint plot grouped by tumor type:

In [81]:
```
bcd2
```

Out[81]:

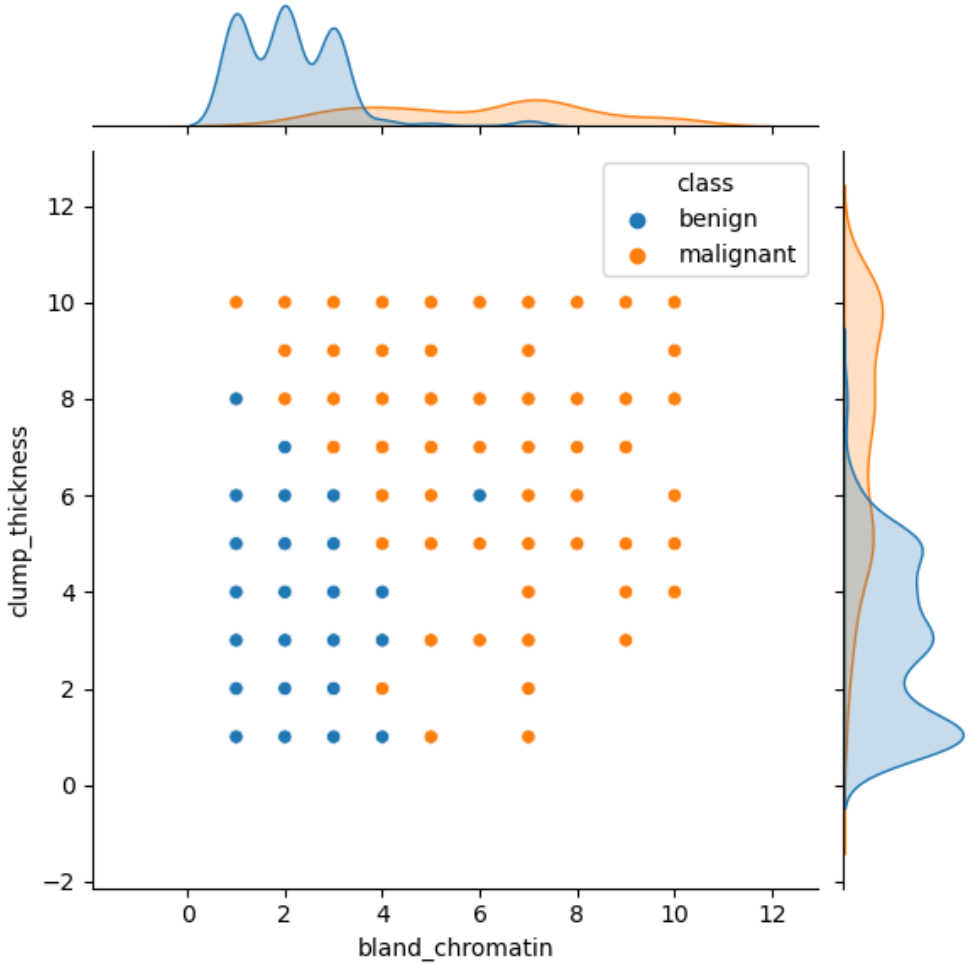
	clump_thickness	bland_chromatin	class	doctor_name
0	5.0	3.0	benign	Doe
1	5.0	3.0	benign	Smith
2	3.0	3.0	benign	Lee
3	6.0	3.0	benign	Smith
4	4.0	3.0	benign	Wong
...	...	...	...	...
694	3.0	1.0	benign	Lee
695	2.0	1.0	benign	Smith
696	5.0	8.0	malignant	Lee
697	4.0	10.0	malignant	Lee
698	4.0	10.0	malignant	Wong

699 rows × 4 columns

In [23]:
```
%matplotlib inline
```

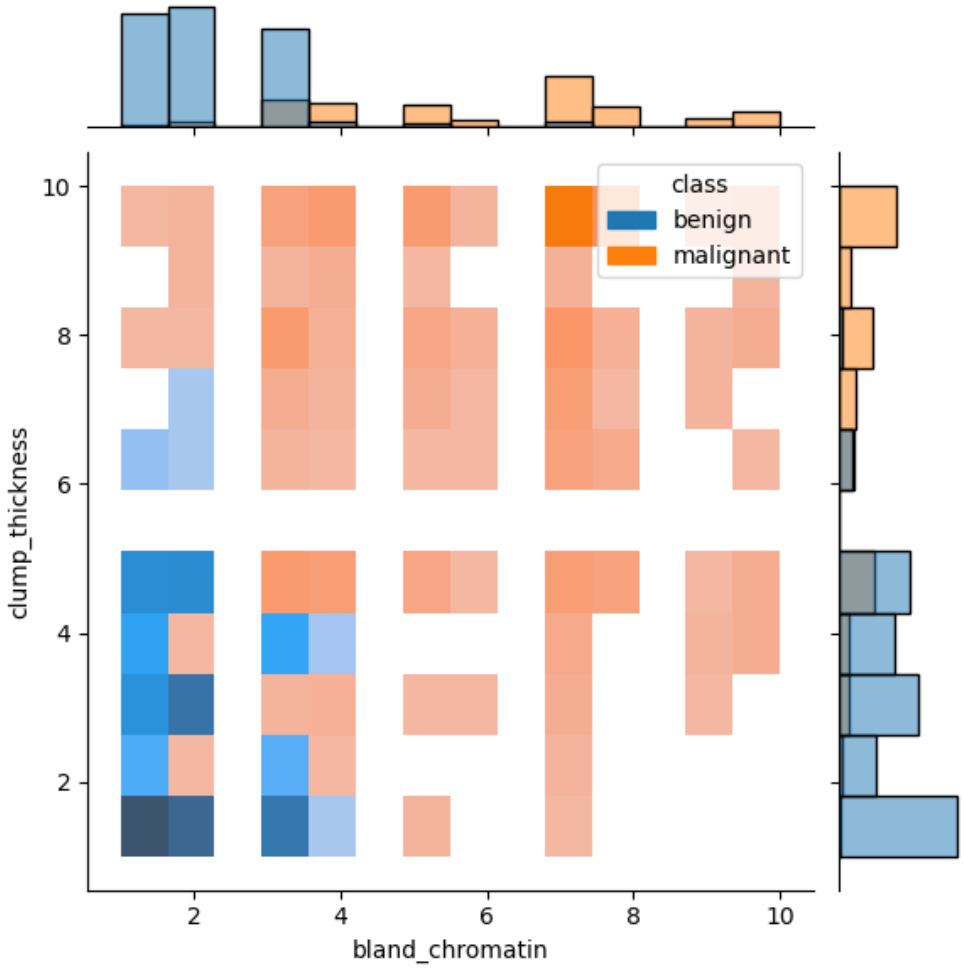
In [24]:
```
sns.jointplot(data=bcd2, x='bland_chromatin', y='clump_thickness', hue='class')
```

Out[24]:
```
<seaborn.axisgrid.JointGrid at 0x7f7dca69ea60>
```



In [25]:
```
sns.jointplot(data=bcd2, x='bland_chromatin', y='clump_thickness', hue='class', kind='hist'
```

Out[25]:
```
<seaborn.axisgrid.JointGrid at 0x7f7dca82c820>
```

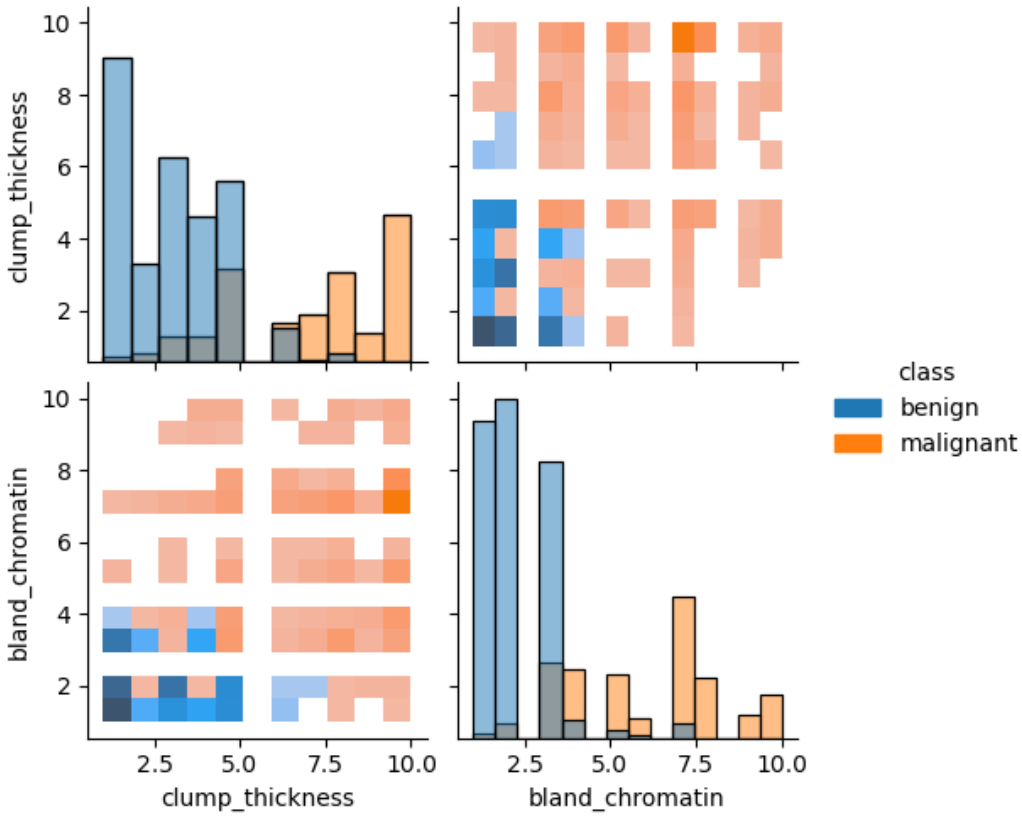


Make a pairplot of our two measurement variables grouped by tumor type.

Make a pairplot of our two measurement variables grouped by tumor type and with `kind = 'hist'` in order to make histograms in the off-diagonal plots.

In [8]:
```
sns.pairplot(data=bcd2, hue='class', kind='hist')
```

Out[8]:
```
<seaborn.axisgrid.PairGrid at 0x7f7db93d5730>
```

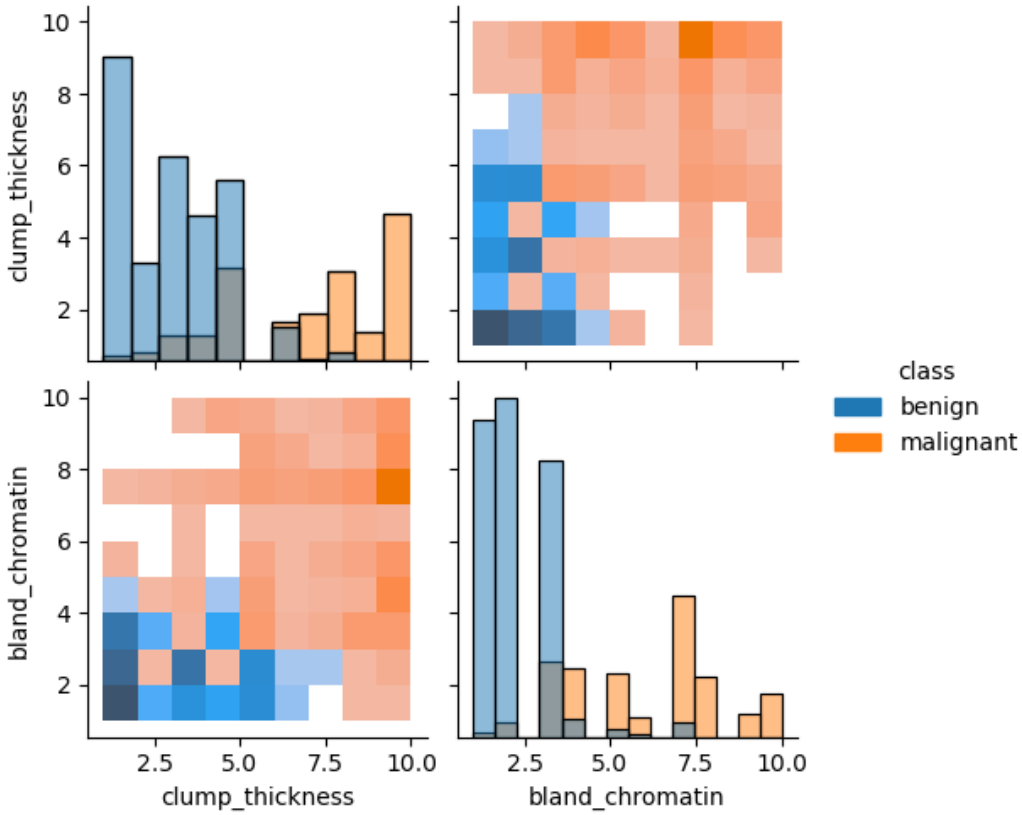


The plot above is okay except for the white space in the diagonal plots that aren't actually missing data. To fix this, we need to set our binwidth to 1, so that it matches the data (which are integers from 1 to 10).

Use the cell below to remake the plot with a binwidth of 1 for the diagonal plot. Hint: use the `plot_kws` argument to adjust this.

In [11]:
```
import matplotlib.pyplot as plt
```

In [14]:
```
sns.pairplot(bcd2, hue = 'class', kind = 'hist', plot_kws=dict(binwidth=1))
plt.show()
```



Your conclusions

In the cell below, briefly state your conclusions from our analysis above. Are either or both of the measurements related to tumor type?

Both of the measures are related to tumor type individually, but using them together can be even better to determine the tumor type. Individually, when either measure is greater, the tumor is more likely to be cancerous. Together, when bland chromatin and clump thickness are greater, a tumor is more likely to be cancerous

Summary

In this tutorial, we learned to analyze data by group:

- the split-apply-combine concept
- grouping using `groupby()`
- doing simple grouped calculations
- doing multiple calculations with `agg()`
- multiIndexing
- simple summaries with pivot tables