Data Visualization

Lesson 8 - 8/13/19

(Please sign-in on the counter near the back door)

Penn
University of Pennsylvania

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Exercise 7 Review

How to measure run time?

- See “Extra Problem: `time` practice” in lab6
- At the top of your jupyter cell you can type **%%timeit** which runs the functions in the cell multiple times, and print the average and standard deviation of the runtimes it obtained

```
%%timeit

list_x = list(range(0,50000)) #50000 numbers
series_x = pd.Series(list_x)

series_squared = series_x.apply(lambda x: x**2)
```

```
26.8 ms ± 394 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)
```

```
%%timeit

list_x = list(range(0,50000)) #50000 numbers
series_x = pd.Series(list_x)

list_squared=[]
for val in series_x:
    list_squared.append(val**2)
```

```
22 ms ± 299 µs per loop (mean ± std. dev. of 7 runs, 10 loops each)
```

Using the pandas series apply function is marginally faster than looping right the series.

Review of Python Bootcamp

- In this class, you may have learned about:
  - Print statements
  - Data Types: Strings, Ints, Floats, Booleans, etc.
  - Conditionals (If/Else if/Else)
  - Loops (For/While)
  - Custom Functions
  - Lists, Dictionaries, Tuples
  - Reading and Writing Files lines by line
  - Writing scripts and importing libraries
  - Importing, exporting, slicing, joining, and grouping pandas series and dataframes

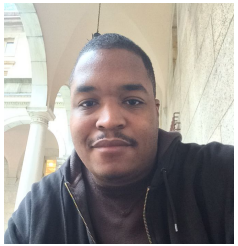
Review of Python Bootcamp

- What we hope you take away from this class is
  - Confidence and encouragement
  - A desire to write “clean” code that is well-commented and easy-to-understand variable names
  - An interest to learn more and make your code more efficient
  - **An ability to solve some more complex problems**

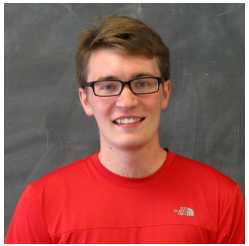
Today's TAs

Ben

Sammy

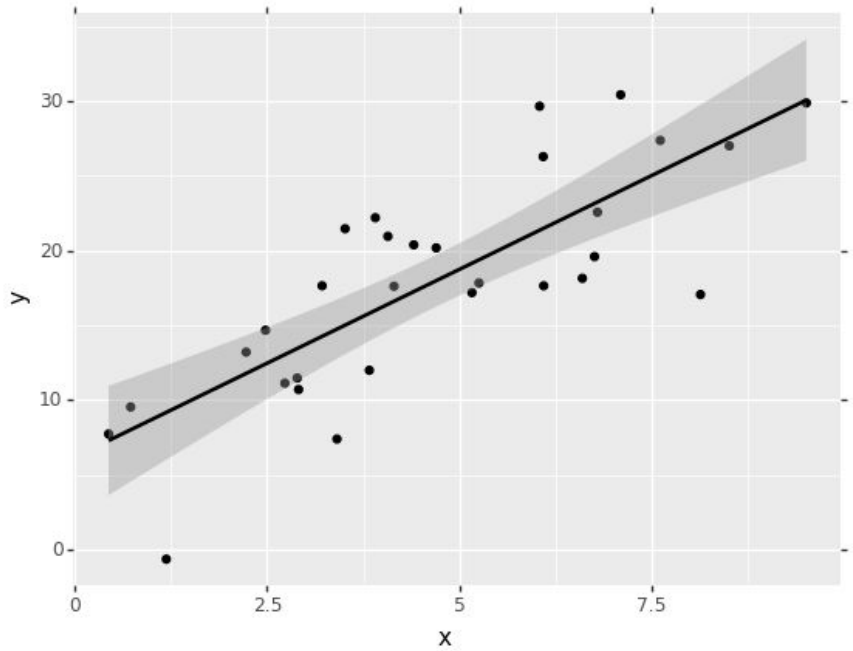


David



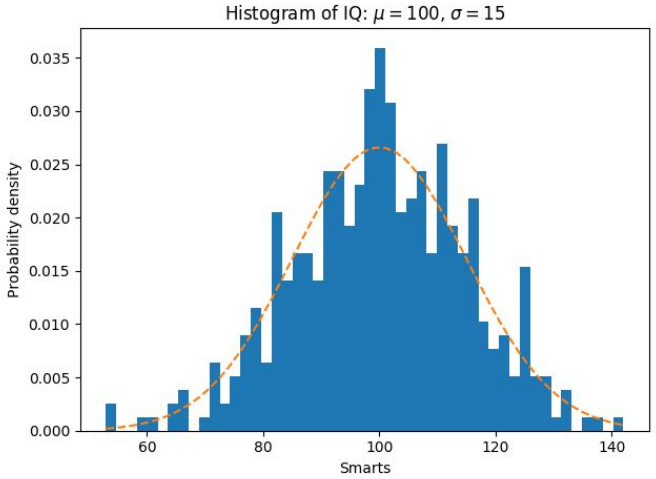
Louis

Why Data Visualization?

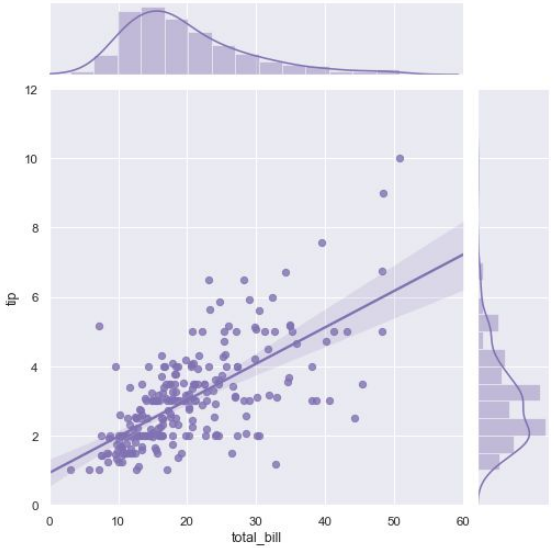


Visualization Options

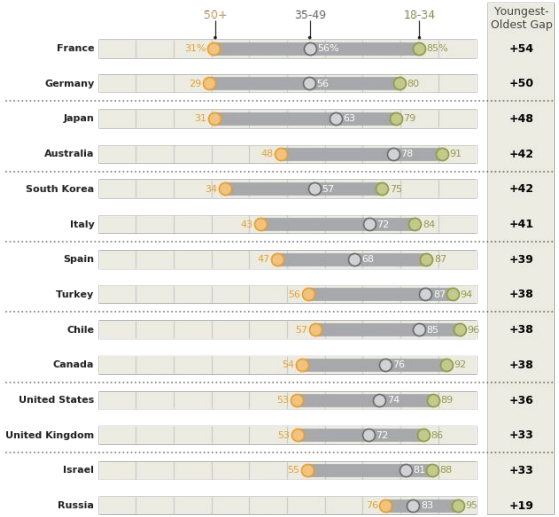
Matplotlib



Seaborn

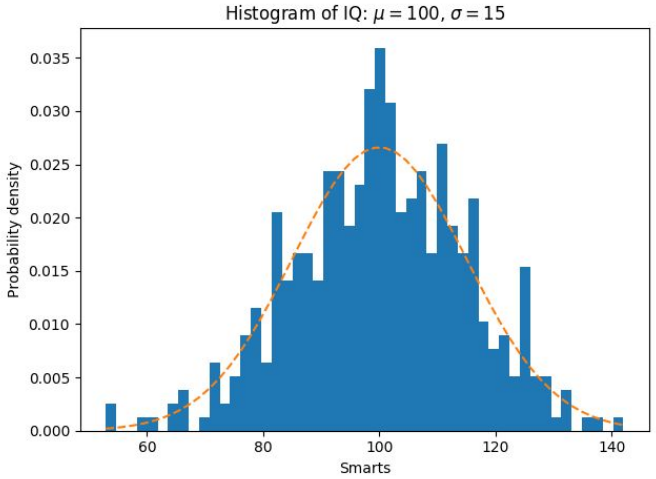


Plotnine

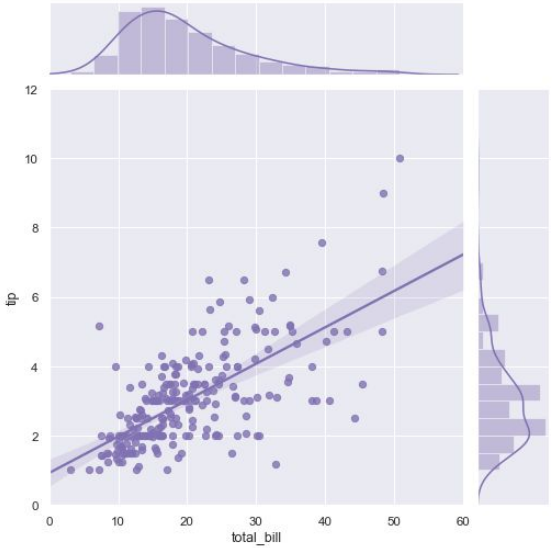


Visualization Options

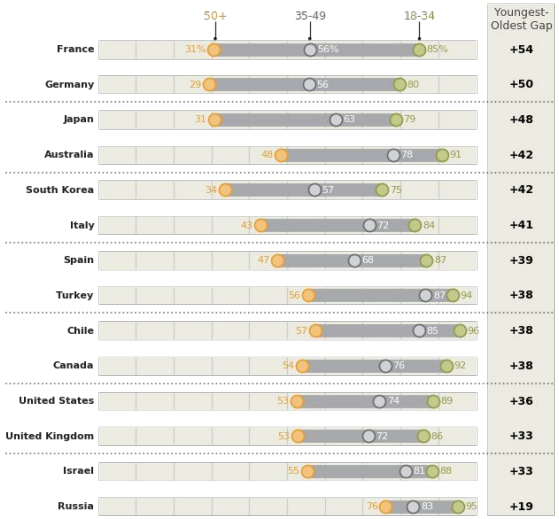
Matplotlib



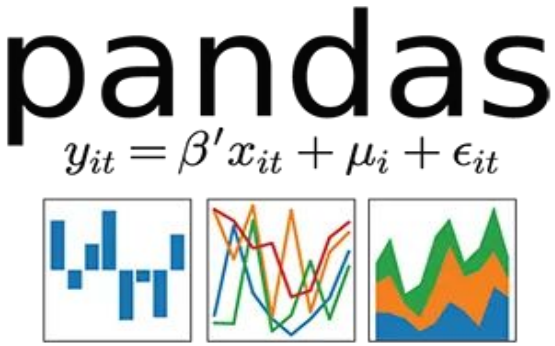
Seaborn



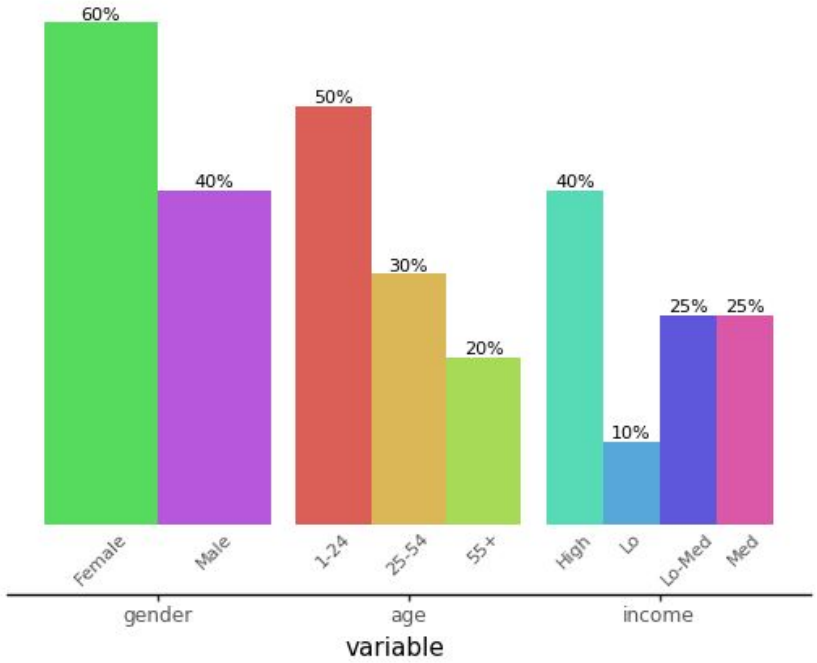
Plotnine



Connection between Pandas, R, and Plotnine



What do you need to make a plot?



1. Data

1. Data
2. Geometric Objects

1. Data
2. Geometric Objects
3. Color

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3. Color
4. Annotations

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Setup

In [34]:

```
import math
from plotnine import *

import pandas
import numpy as np

import warnings
warnings.filterwarnings('ignore')
```

Setup

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import math
from plotnine import *

import pandas
import numpy as np

import warnings
warnings.filterwarnings('ignore')
```

Read in data from Zenodo

In [35]:
```
dataframe = pandas.read_csv('volcano_data.tsv', sep='\t')
dataframe['neg_log_p_val'] = -np.log(dataframe['adj.P.Val'])
```

Setup

In [34]:
```
import math
from plotnine import *

import pandas
import numpy as np

import warnings
warnings.filterwarnings('ignore')
```

Read in data from Zenodo

In [35]:
```
dataframe = pandas.read_csv('volcano_data.tsv', sep='\t')
dataframe['neg_log_p_val'] = -np.log(dataframe['adj.P.Val'])
```

In [36]:
```
dataframe.head()
```

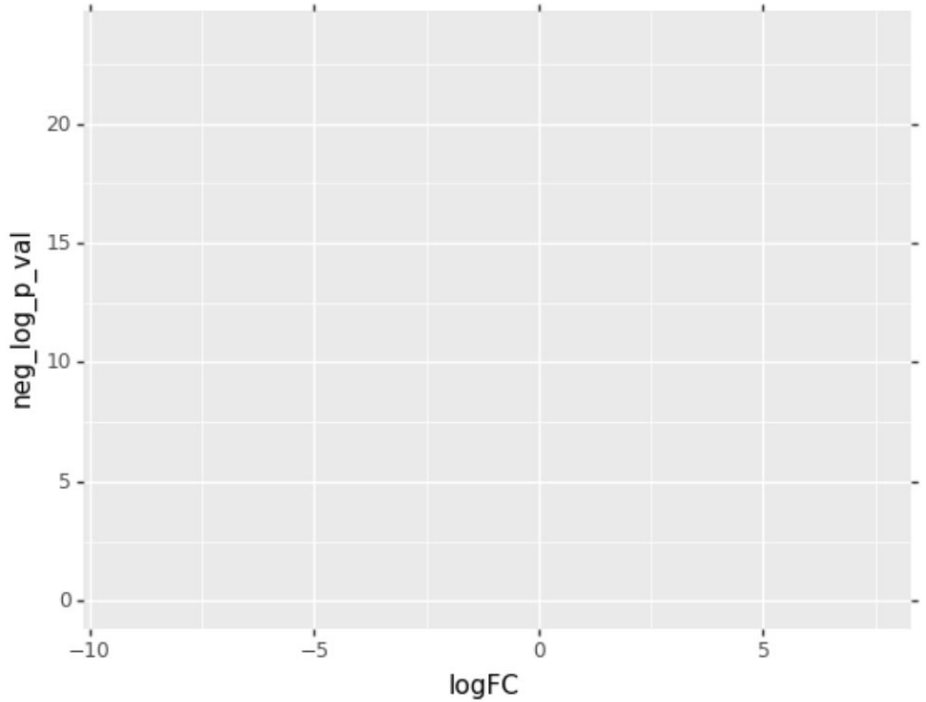
Out[36]:

	ENTREZID	SYMBOL	GENENAME	logFC	AveExpr	t	P.Value	adj.P.Val	neg_log_p_val
0	12992	Csn1s2b	casein alpha s2-like B	-8.603611	3.562950	-43.796498	3.830650e-15	6.053959e-11	23.527724
1	13358	Slc25a1	solute carrier family 25 (mitochondrial carrie...	-4.124175	5.779699	-29.907849	1.758595e-13	1.389642e-09	20.394220
2	11941	Atp2b2	ATPase, Ca++ transporting, plasma membrane 2	-7.386986	1.282143	-27.819499	4.836363e-13	2.432800e-09	19.834223
3	20531	Slc34a2	solute carrier family 34 (sodium phosphate), m...	-4.177812	4.278629	-27.072723	6.157428e-13	2.432800e-09	19.834223
4	100705	Acacb	acetyl-Coenzyme A carboxylase beta	-4.314320	4.440914	-25.223566	1.499977e-12	4.741129e-09	19.166991

Data from zenodo.org

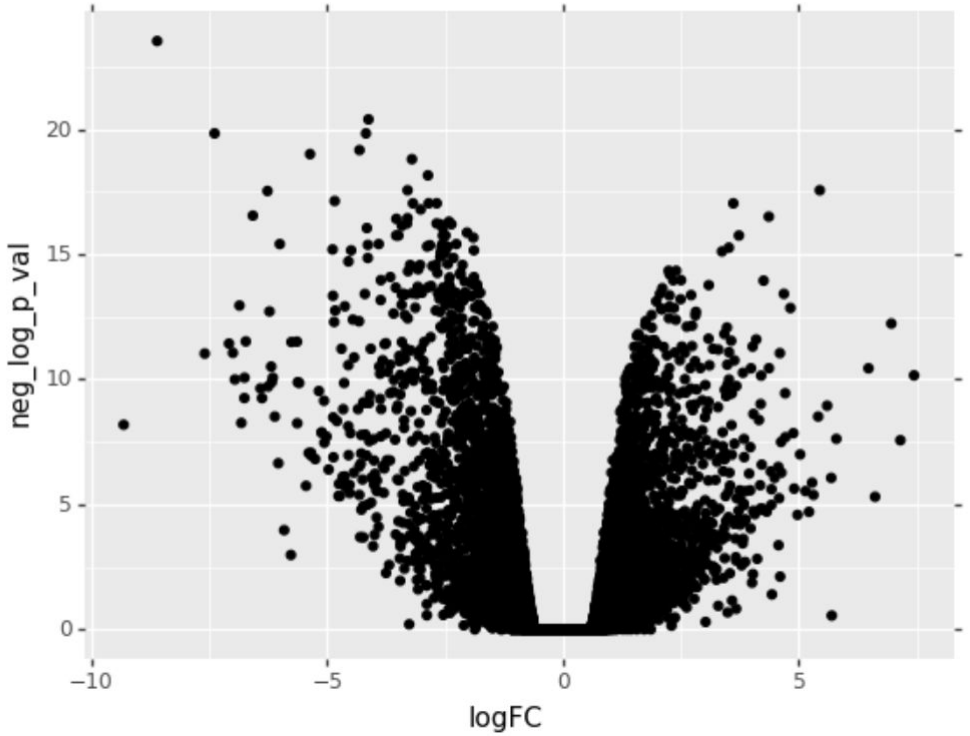
Data

```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val'))
```

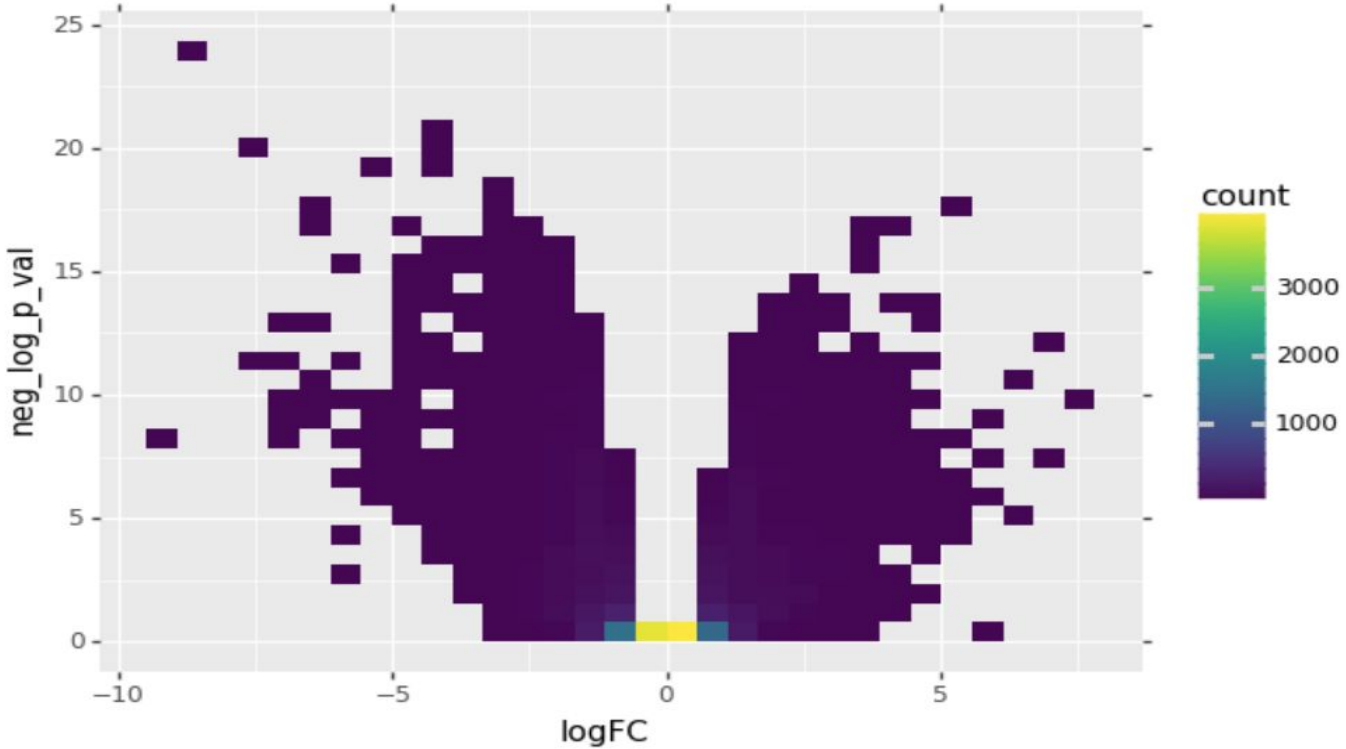


1. Data
2. Geometric Objects
3. Color
4. Annotations

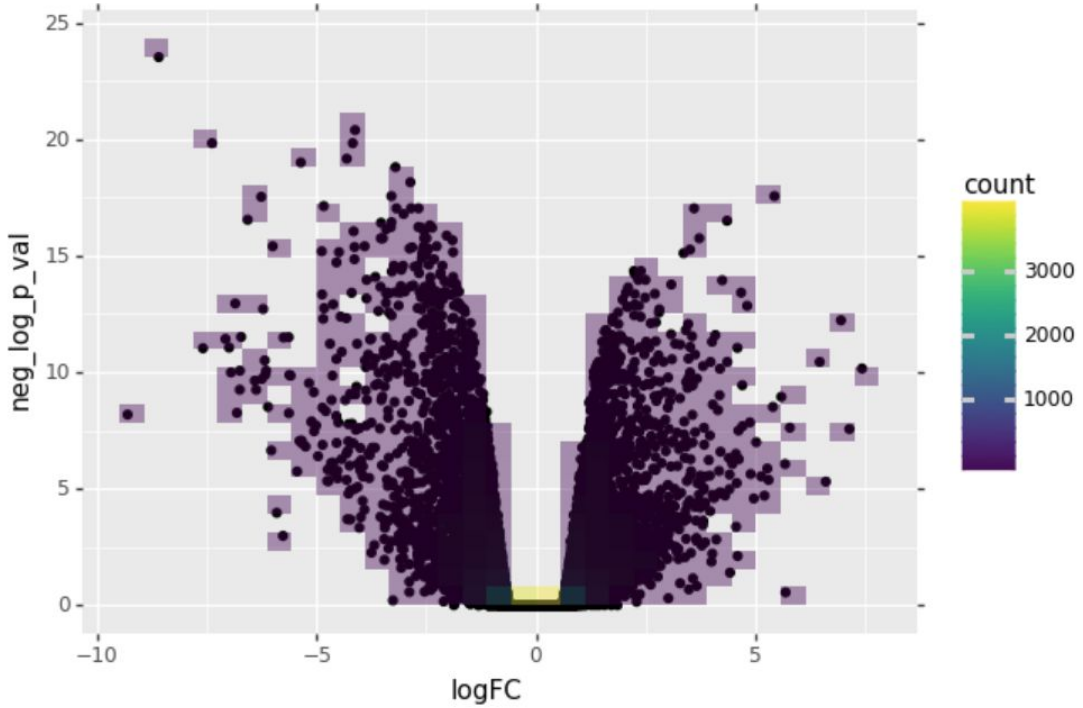
```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) + geom_point()
```



```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) + geom_bin2d()
```



```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val'))
+ geom_point()
+ geom_bin2d(alpha=.4)
```



1. Data
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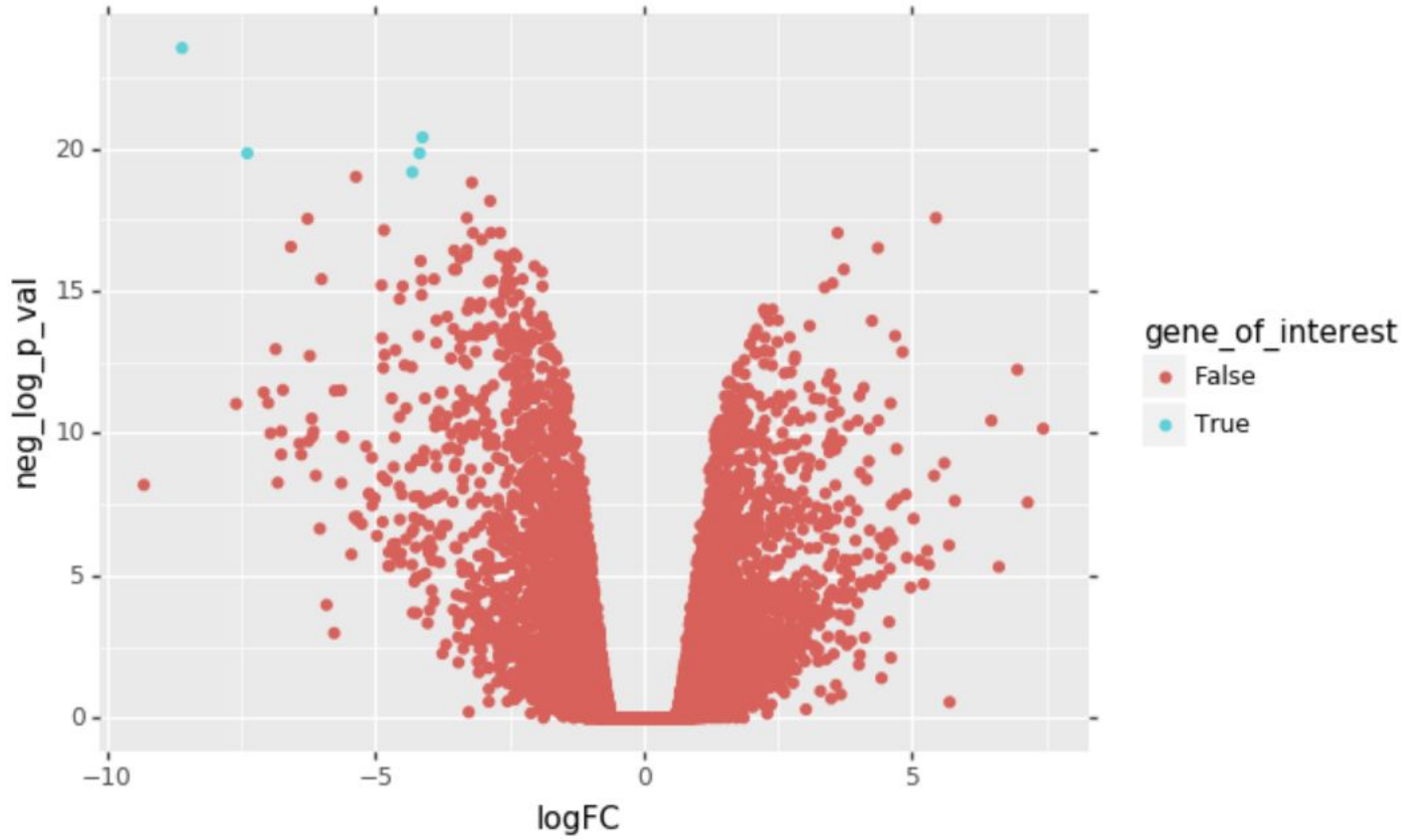
```
genes_of_interest = ['Csn1s2b', 'Slc25a1', 'Atp2b2', 'Slc34a2', 'Acacb']

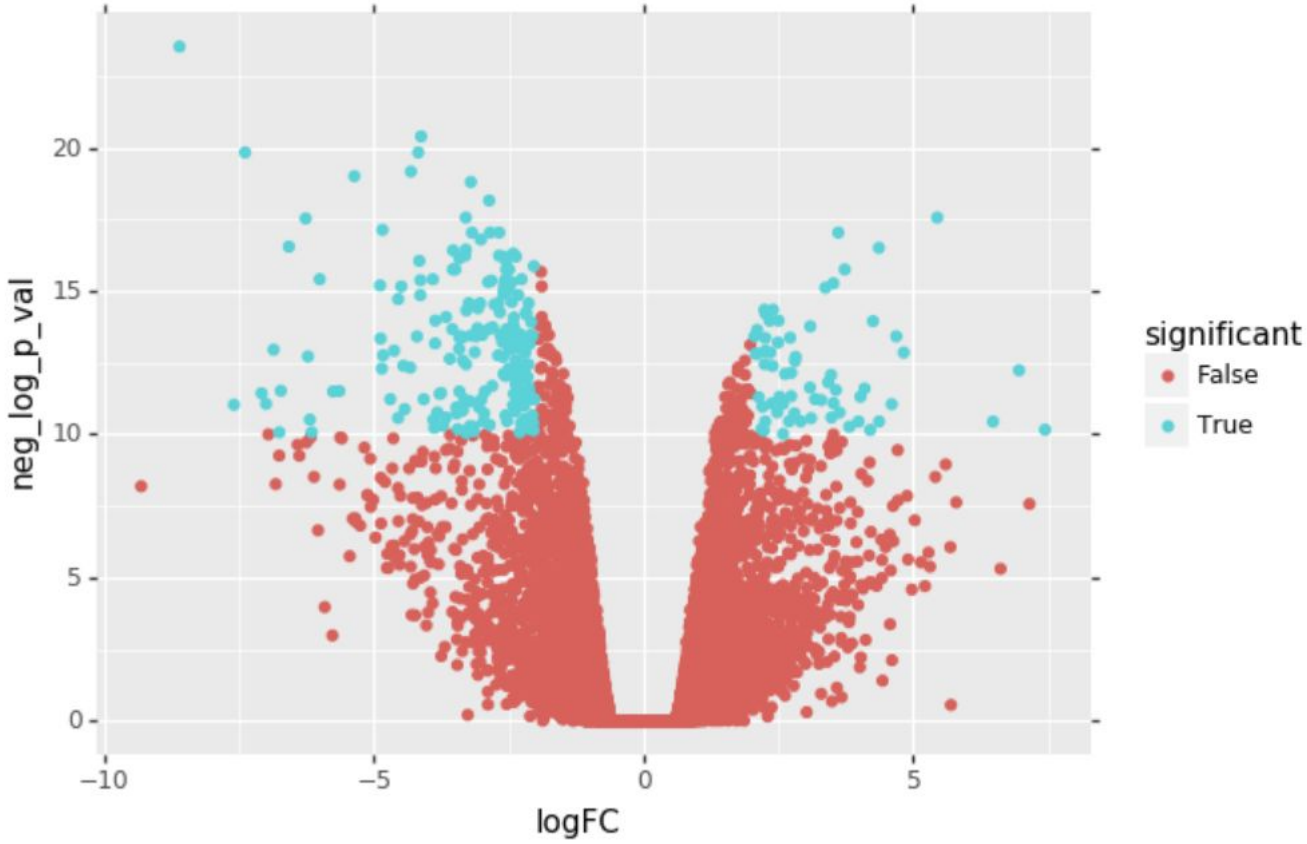
dataframe['gene_of_interest'] = dataframe['SYMBOL'].isin(genes_of_interest)

ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) + geom_point(aes(color='gene_of_interest'))
```

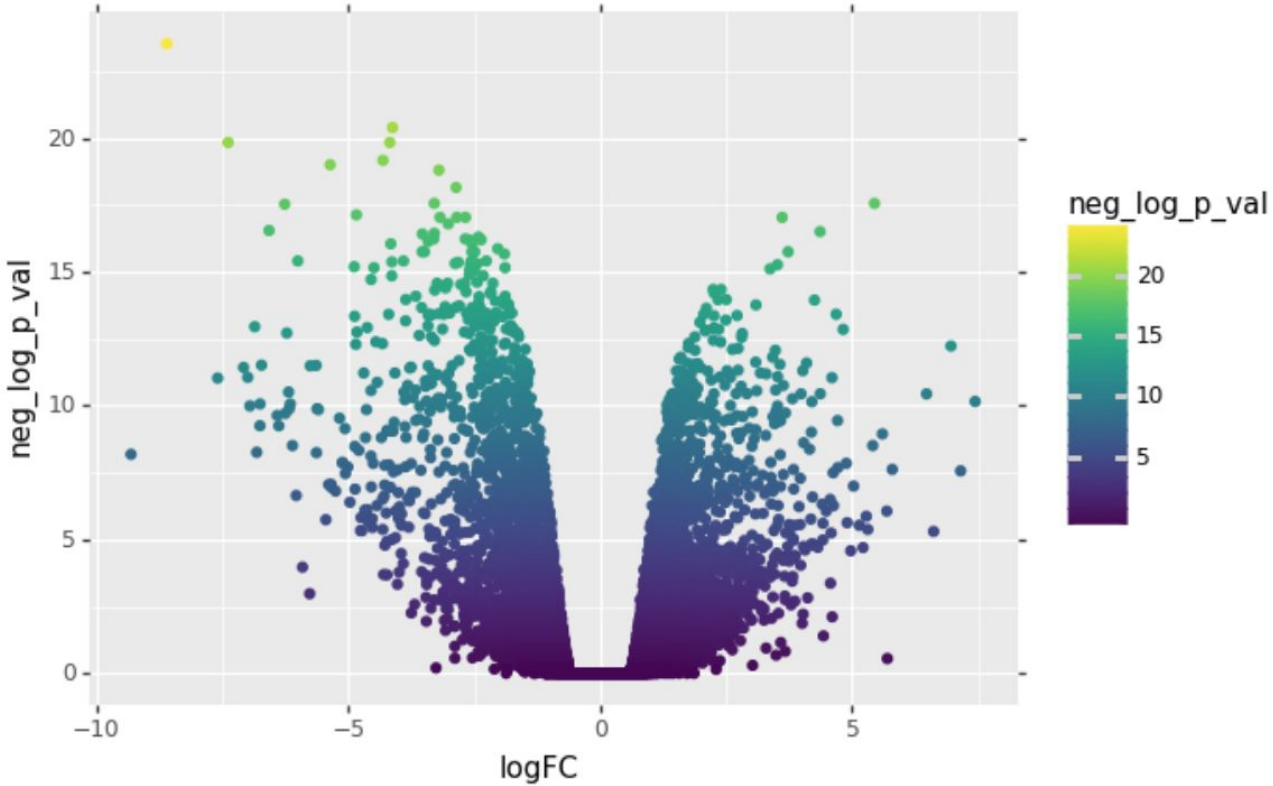


In [47]:
```
condition1 = dataframe['neg_log_p_val'] >= 10
condition2 = abs(dataframe['logFC']) > 2
dataframe['significant'] = condition1 & condition2

ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) + geom_point(aes(color='significant'))
```



```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val'))
+ geom_point(aes(color='neg_log_p_val'))
```



1. Data
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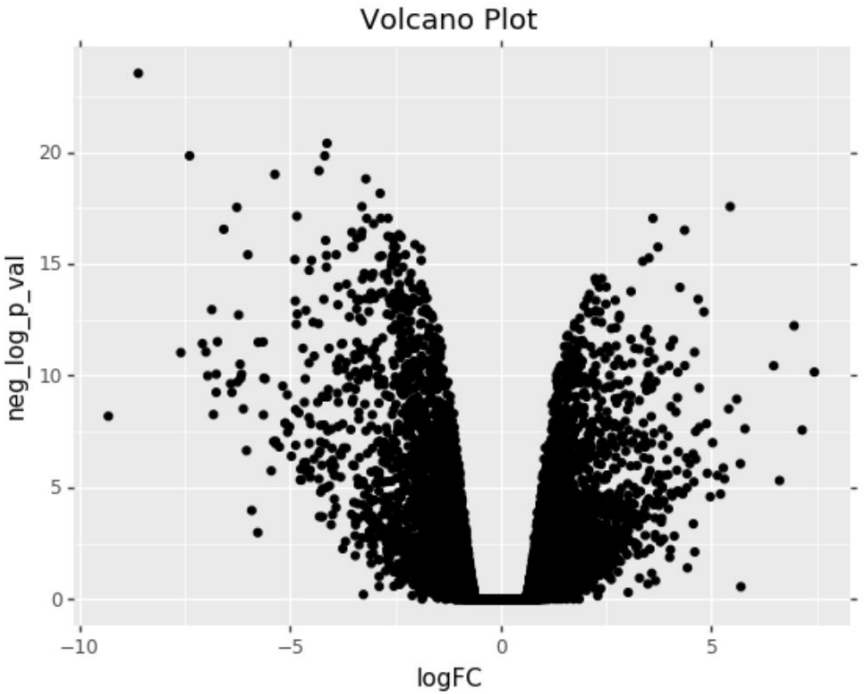
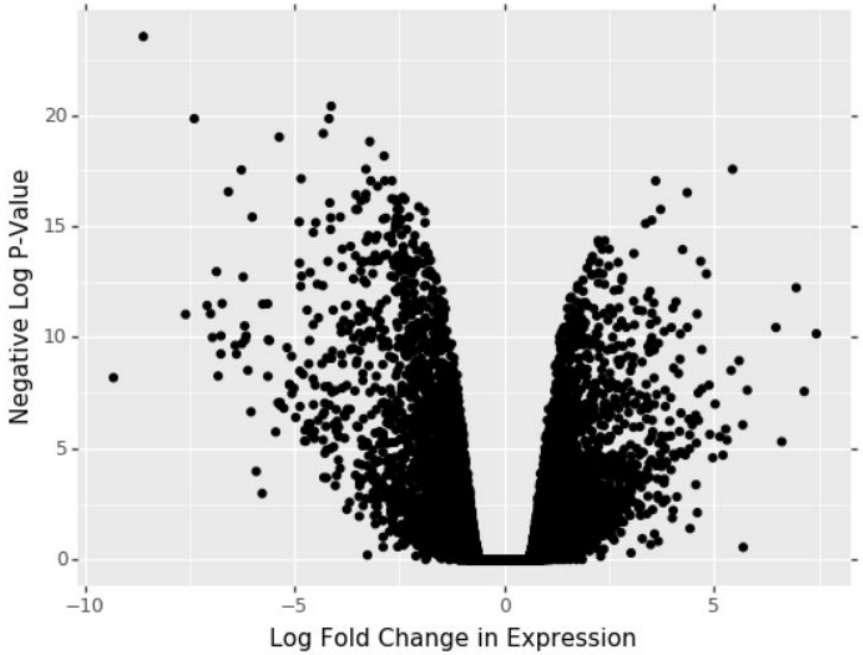
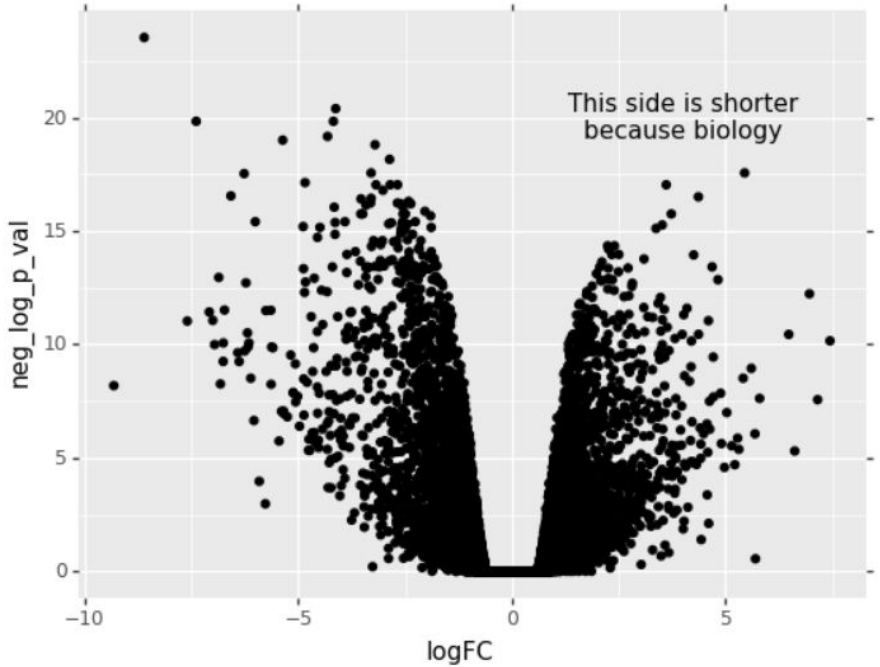
```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) \
+ geom_point()\
+ ggtitle('Volcano Plot')
```



```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val')) \
+ geom_point()\
+ xlab('Log Fold Change in Expression')\
+ ylab('Negative Log P-Value')
```



```
ggplot(dataframe, aes(x='logFC', y='neg_log_p_val', label='SYMBOL')) \
+ geom_point()\
+ annotate("text", x = 4, y = 20, label = "This side is shorter\nbecause biology")
```



Common Use Cases: Bar Plot (Setup)

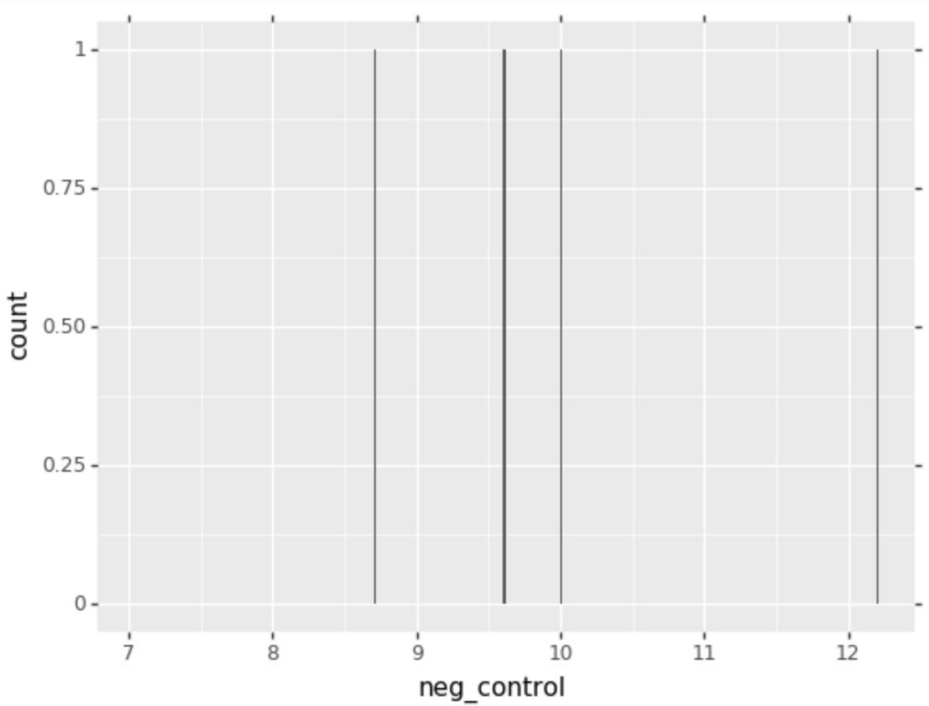
```
neg_control = np.random.normal(size=40) + 10
pos_control = np.random.normal(size=40) + 15
experiment = np.random.normal(size=40) + 14


data = {'neg_control': neg_control, 'pos_control': pos_control, 'experiment': experiment}
bar_df = pandas.DataFrame(data)
bar_df
```

	neg_control	pos_control	experiment
0	10.573405	15.795453	12.646862
1	10.266933	14.978045	12.372353
2	8.398704	14.365767	12.897853
3	9.794511	15.033012	14.688481

Bar Plot Attempt One

```
ggplot(bar_df, aes(x='neg_control')) + geom_bar()
```



Reshape Data

```
bar_df = pandas.melt(bar_df)
bar_df.head()
```

	neg_control	pos_control
0	10.573405	15.795453
1	10.266933	14.978045
2	8.398704	14.365767
3	9.794511	15.033012
4	8.888123	15.898007

Reshape Data

Convert data from columns with values to variable:value pairs

```
bar_df = pandas.melt(bar_df)
bar_df.head()
```

	neg_control	pos_control
0	10.573405	15.795453
1	10.266933	14.978045
2	8.398704	14.365767
3	9.794511	15.033012
4	8.888123	15.898007

Reshape Data

Convert data from columns with values to variable:value pairs

```
bar_df = pandas.melt(bar_df)
bar_df.head()
```

	neg_control	pos_control
0	10.573405	15.795453
1	10.266933	14.978045
2	8.398704	14.365767
3	9.794511	15.033012
4	8.888123	15.898007

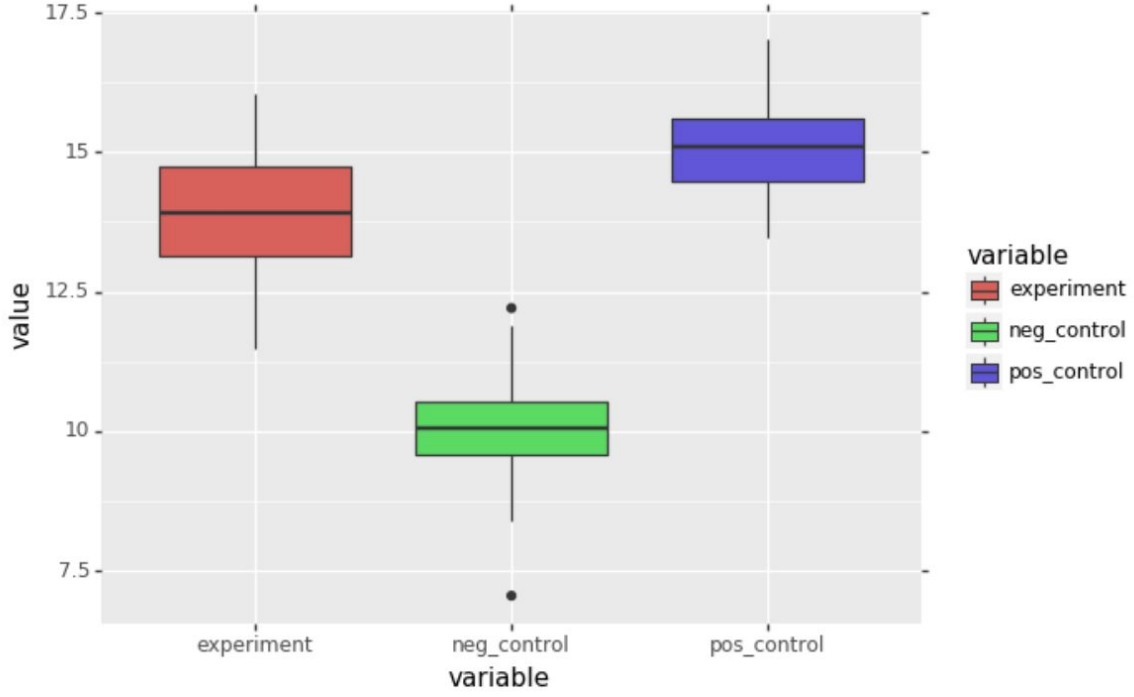
	variable	value
0	neg_control	10.573405
1	neg_control	10.266933
2	neg_control	8.398704
3	neg_control	9.794511
4	neg_control	8.888123

Box Plot Attempt 2

```
(ggplot(bar_df, aes(x='variable', y='value', fill='variable'))
+ geom_boxplot())
```

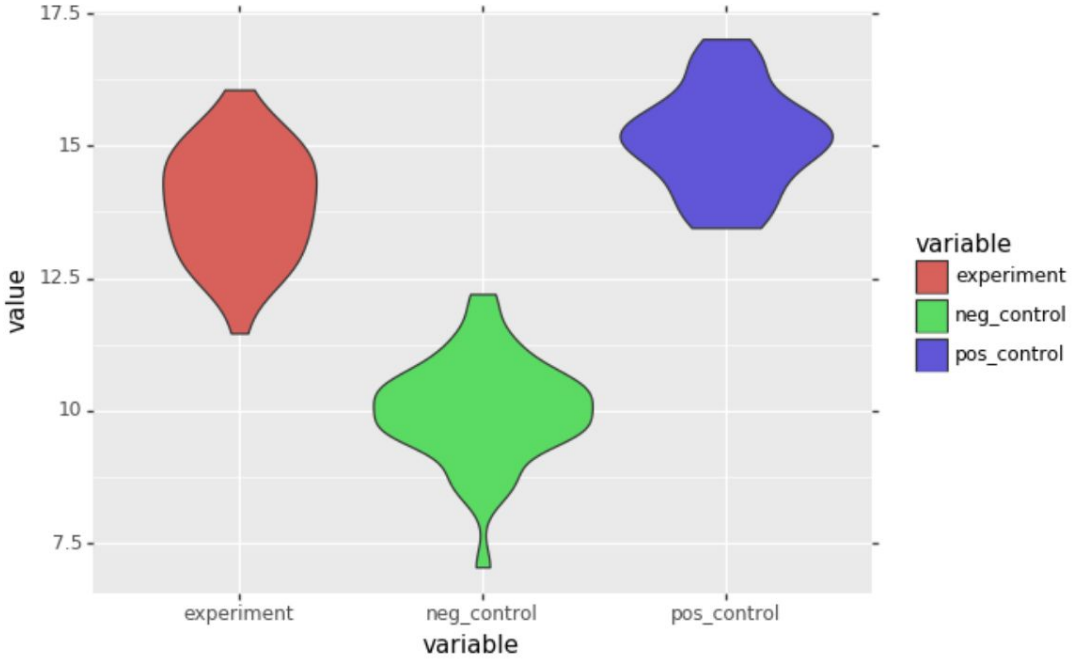
Box Plot Attempt 2

```
(ggplot(bar_df, aes(x='variable', y='value', fill='variable'))
+ geom_boxplot())
```



Bonus Box Plot

```
ggplot(bar_df, aes(x='variable', y='value', fill='variable'))\
+ geom_violin()
```

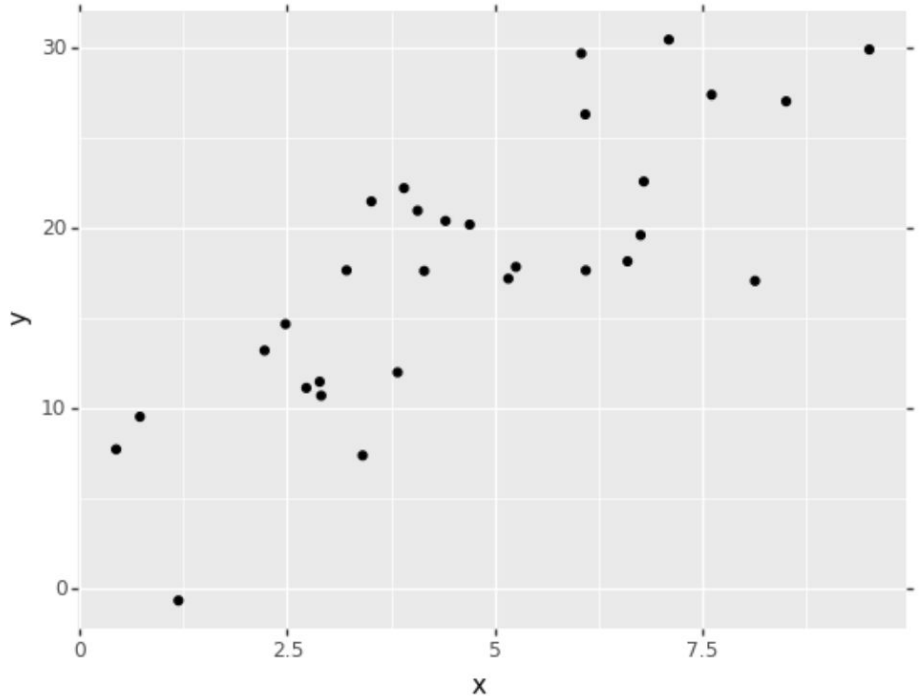


Common Use Cases: Scatter Plot

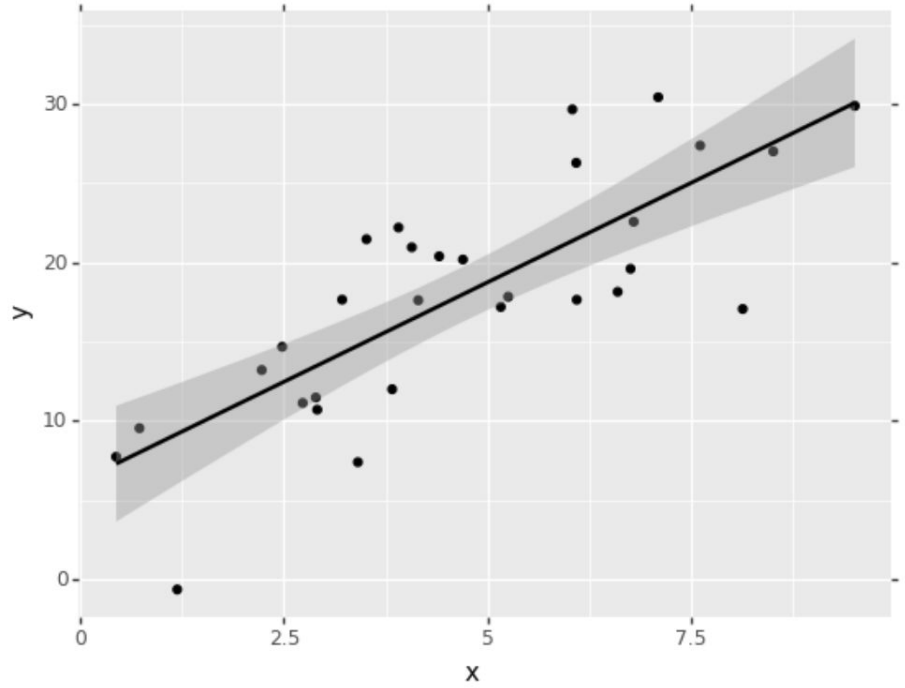
```
# Set the x range to be [0, 10)
scatter_x = np.random.random(30) * 10
# Give the line a slope of 3 and a y-intercept of 4
scatter_y = scatter_x * 3 + 4
# Add noise
scatter_y += np.random.normal(size=30) * 4

scatter_df = pandas.DataFrame({'x': scatter_x, 'y': scatter_y})
scatter_df.head()
```

```
ggplot(scatter_df, aes(x='x', y='y')) \
+ geom_point()
```



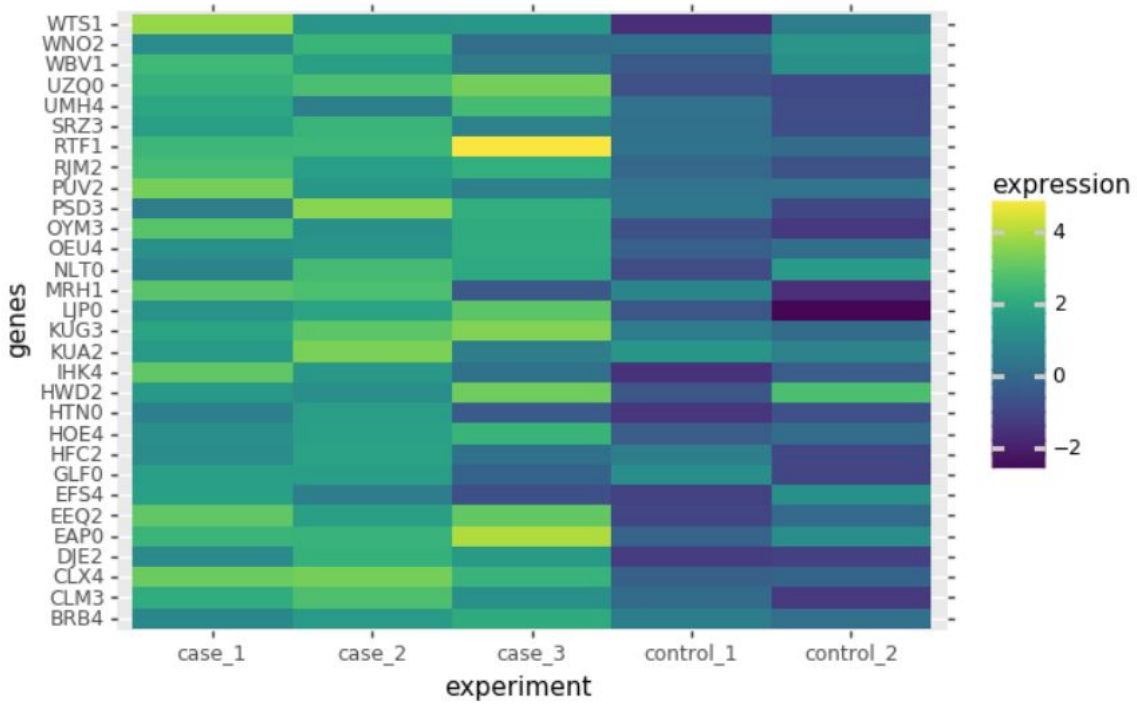
```
ggplot(scatter_df, aes(x='x', y='y'))\
+ geom_point()\
+ geom_smooth(method='lm')
```



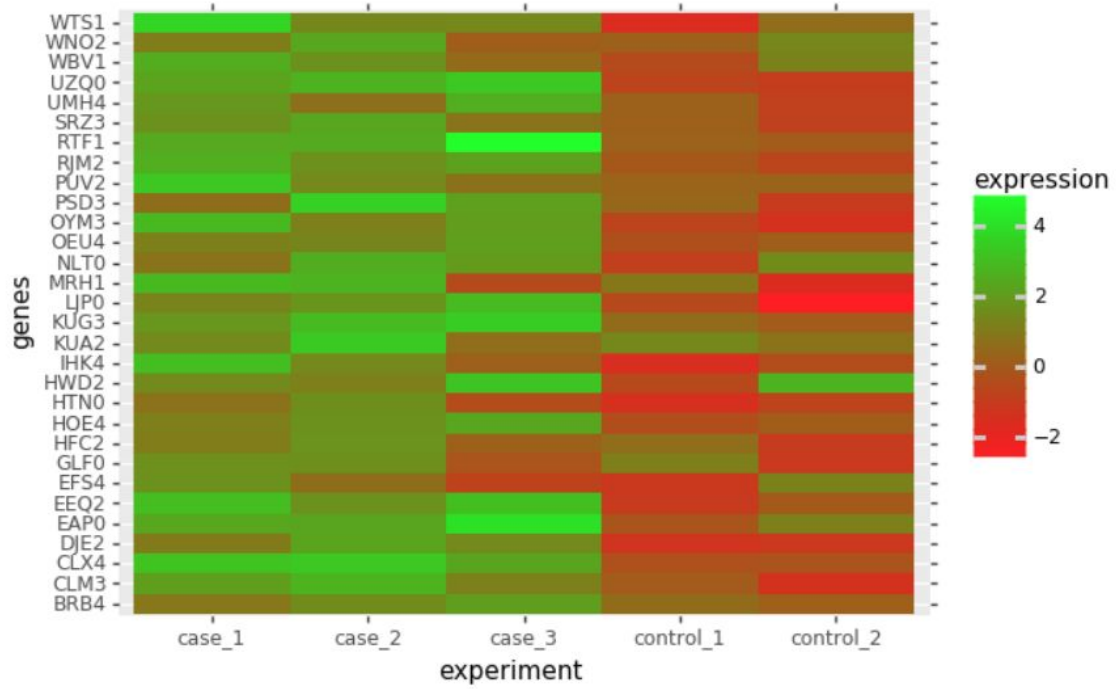
Common Use Cases: Heatmap

	genes	experiment	expression
0	WNO2	case_1	1.050926
1	NLT0	case_1	0.826808
2	RJM2	case_1	2.507592
3	EEQ2	case_1	2.911344
4	GLF0	case_1	1.611909

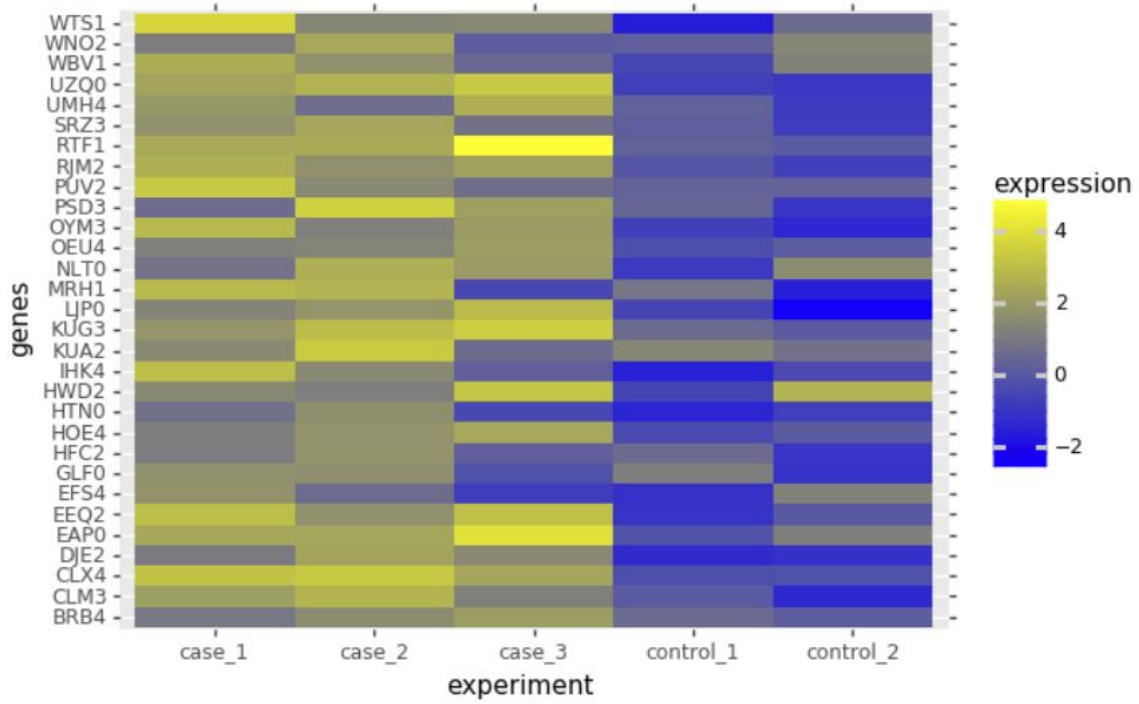
```
ggplot(heatmap_df, aes(x='experiment', y='genes'))\
+ geom_tile(aes(fill='expression'))\
```



```
ggplot(heatmap_df, aes(x='experiment', y='genes'))\
+ geom_tile(aes(fill='expression'))\
+ scale_fill_gradient(low='red', high='lime')
```



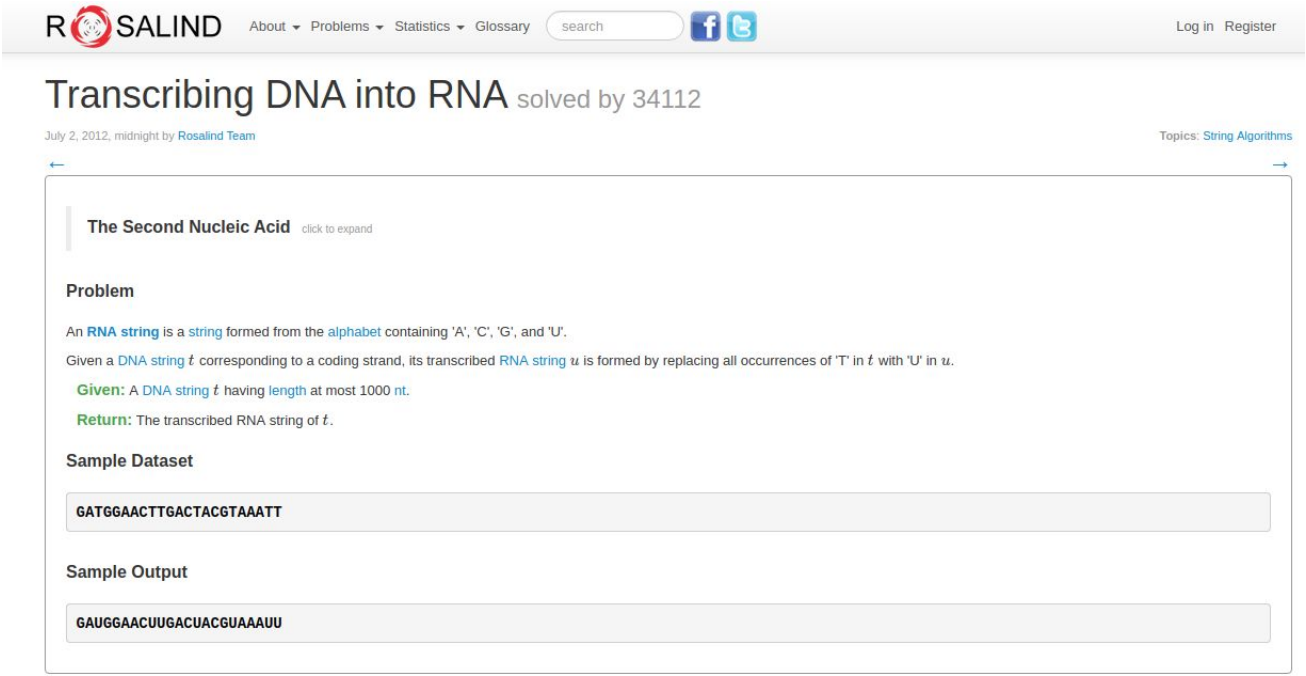
```
ggplot(heatmap_df, aes(x='experiment', y='genes'))\
+ geom_tile(aes(fill='expression'))\
+ scale_fill_gradient(low='blue', high='yellow')
```



Next Steps/Further Training

Rosalind

Codecademy



Next Steps/Further Training

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Don’t get discouraged!

Further Reading

http://vita.had.co.nz/papers/layered-grammar.pdf