

```
In [1]: # import all the packages needed
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

```
In [3]: # Reading the data from the file.
exercise007 = pd.read_csv("/Users/paulwen/OneDrive - The University of Texa
```

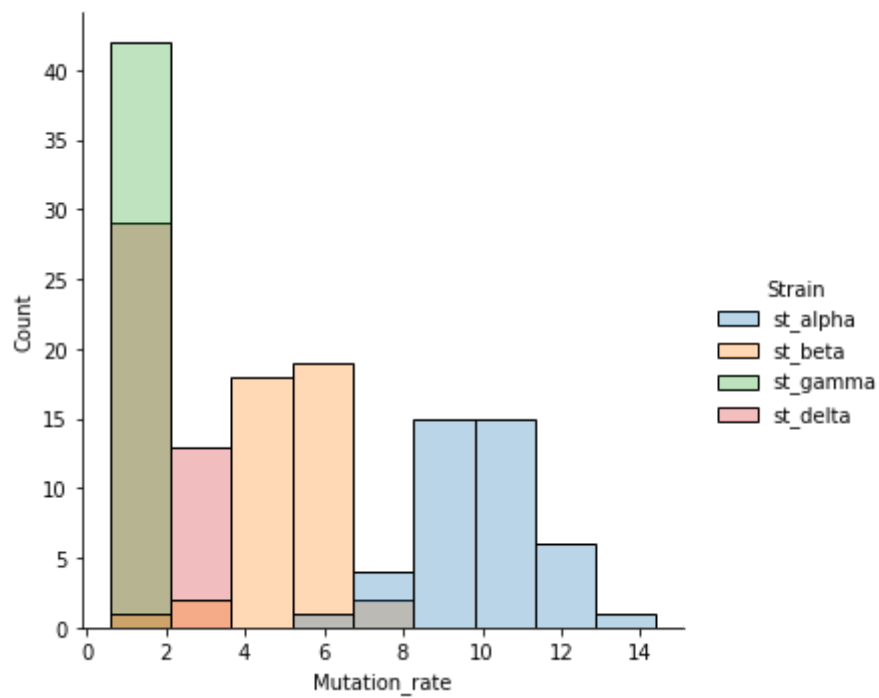
```
In [4]: display(exercise007)
```

	Strain	Mutation_rate
0	st_alpha	10.612005
1	st_alpha	12.586371
2	st_alpha	8.997583
3	st_alpha	11.681775
4	st_alpha	14.408237
...	...	...
163	st_delta	2.716249
164	st_delta	2.467378
165	st_delta	2.119801
166	st_delta	1.316537
167	st_delta	2.060472

168 rows × 2 columns

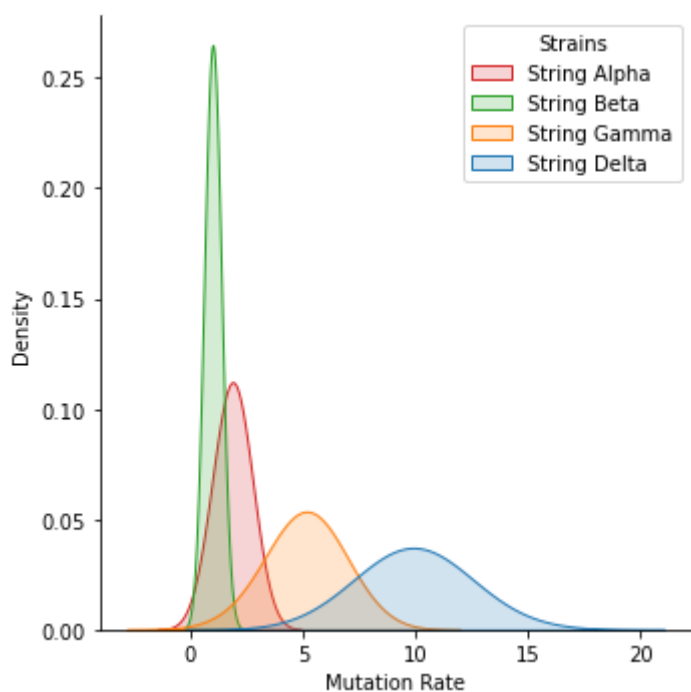
```
In [16]: # Histograms
sns.displot(exercise007, x="Mutation_rate", hue = "Strain", kind="hist", alp
```

```
Out[16]: <seaborn.axisgrid.FacetGrid at 0x7feadc270970>
```



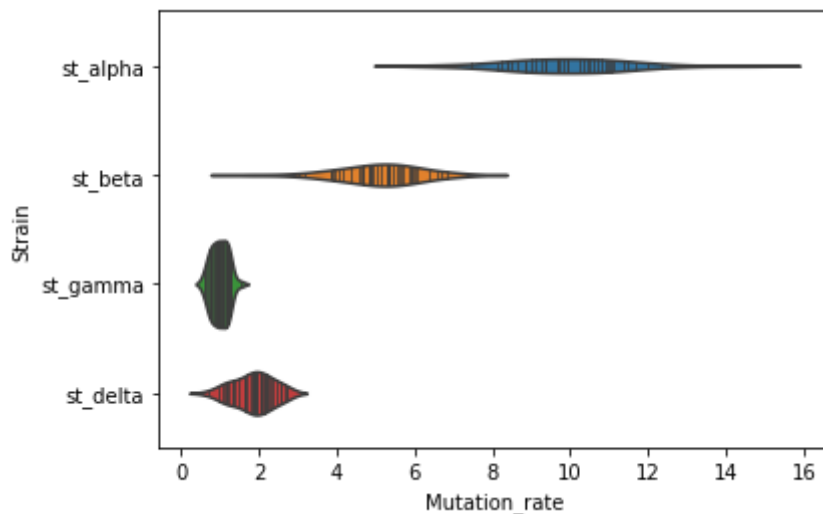
```
In [31]: # Most pretty graph I picked
# Kernel Density Estimate (KDE) plots
kde_plot = sns.displot(exercise007, x="Mutation_rate", hue="Strain", kind="
plt.legend(title='Strains', labels=['String Alpha', 'String Beta', 'String Ga
plt.xlabel('Mutation Rate')
kde_plot
```

Out[31]: <seaborn.axisgrid.FacetGrid at 0x7feadcca0190>



```
In [12]: # Violin plots
sns.violinplot(data=exercise007, x="Mutation_rate", y="Strain", inner="stic
```

Out[12]: <AxesSubplot:xlabel='Mutation\_rate', ylabel='Strain'>



```
In [13]: # box plots
sns.boxplot(data=exercise007, x="Mutation_rate", y="Strain")
```

```
Out[13]: <AxesSubplot:xlabel='Mutation_rate', ylabel='Strain'>
```

