

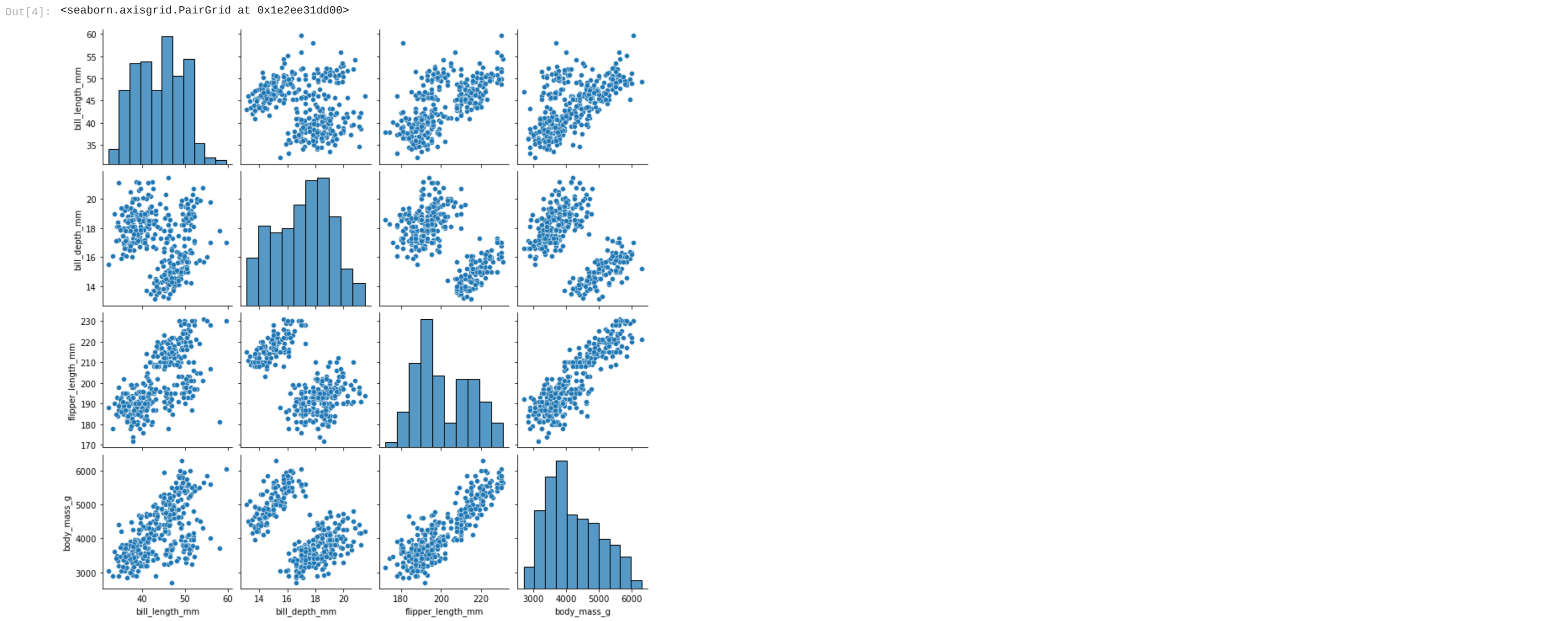
```
In [1]: import pandas as pd
import seaborn as sns
penguins = sns.load_dataset("penguins")
```

```
In [2]: penguins.head()
```

Out[2]:

| | species | island | bill_length_mm | bill_depth_mm | flipper_length_mm | body_mass_g | sex |
|---|---------|-----------|----------------|---------------|-------------------|-------------|--------|
| 0 | Adelie | Torgersen | 39.1 | 18.7 | 181.0 | 3750.0 | Male |
| 1 | Adelie | Torgersen | 39.5 | 17.4 | 186.0 | 3800.0 | Female |
| 2 | Adelie | Torgersen | 40.3 | 18.0 | 195.0 | 3250.0 | Female |
| 3 | Adelie | Torgersen | NaN | NaN | NaN | NaN | NaN |
| 4 | Adelie | Torgersen | 36.7 | 19.3 | 193.0 | 3450.0 | Female |

```
In [4]: sns.pairplot(penguins)
```



In each graph clusters can be found. the biggest cluster are the top right and bottom left.

```
In [7]: from sklearn.cluster import KMeans
```

```
In [8]: penguinsNan = penguins.dropna()
```

```
In [9]: features = ['bill_length_mm','bill_depth_mm','flipper_length_mm', 'body_mass_g']
km = KMeans(n_clusters=2, random_state=42).fit(penguinsNan[features])
```

```
In [13]: penguinsNan.head()
```

Out[13]:

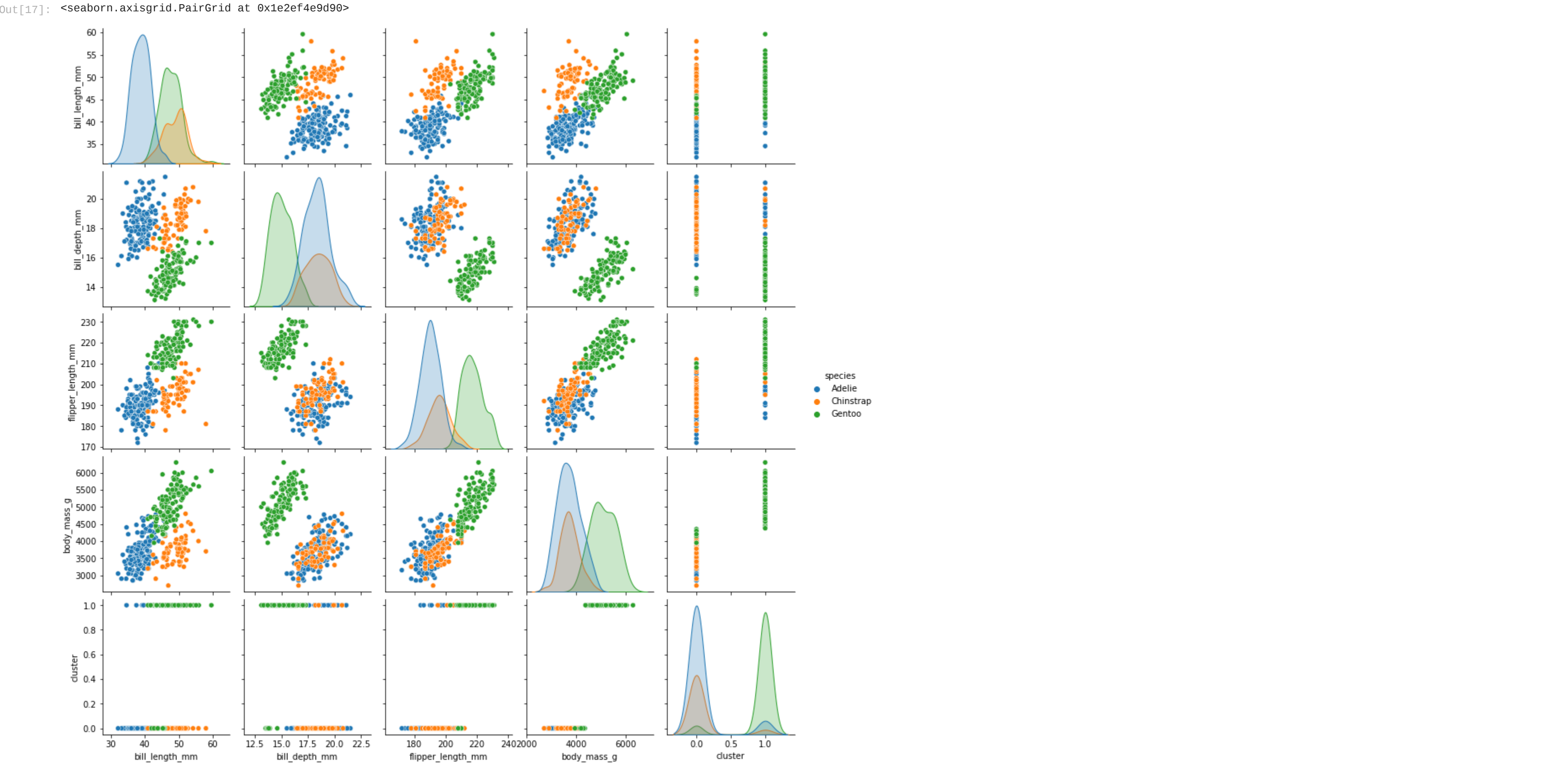
| | species | island | bill_length_mm | bill_depth_mm | flipper_length_mm | body_mass_g | sex | cluster |
|---|---------|-----------|----------------|---------------|-------------------|-------------|--------|---------|
| 0 | Adelie | Torgersen | 39.1 | 18.7 | 181.0 | 3750.0 | Male | 0 |
| 1 | Adelie | Torgersen | 39.5 | 17.4 | 186.0 | 3800.0 | Female | 0 |
| 2 | Adelie | Torgersen | 40.3 | 18.0 | 195.0 | 3250.0 | Female | 0 |
| 4 | Adelie | Torgersen | 36.7 | 19.3 | 193.0 | 3450.0 | Female | 0 |
| 5 | Adelie | Torgersen | 39.3 | 20.6 | 190.0 | 3650.0 | Male | 0 |

```
In [14]: from sklearn import metrics
from sklearn.metrics import pairwise_distances
```

```
In [16]: metrics.silhouette_score(penguinsNan[features], km.labels_, metric='euclidean')
```

```
Out[16]: 0.6307117469850305
```

```
In [17]: sns.pairplot(penguinsNan, hue="species")
```



```
In [18]: contingency_table = penguinsNan.groupby(['species', 'cluster']).size().unstack('cluster', fill_value=0)
contingency_table
```

Out[18]:

| | cluster | 0 | 1 |
|-----------|---------|-----|-----|
| species | | | |
| Adelie | | 132 | 14 |
| Chinstrap | | 63 | 5 |
| Gentoo | | 8 | 111 |

There were no exact matches