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Programming Assignment 03: Classifying Unknown Animals as Mammal or Not Mammal

Date: 07-16-22

```
# imported for data management (dataframe)
import pandas as pd

# This package needs part of anaconda and needs to be installed
# conda install -c conda-forge-wordcloud

# Imported  to allow for the display of word clouds
import matplotlib.pyplot as plt

# Imported to create train/test partitioning of the data
from sklearn.model_selection import train_test_split

# Imported to get frequency counts
import collections

# Imported to use confusion matrix
from sklearn.metrics import confusion_matrix
from sklearn.metrics import accuracy_score
from sklearn.metrics import classification_report
```

Concept Description:

Train a system existing data to classify *animals* as either mammal or not mammal.

Data collection:

The data has been provided by Perry B. Koob, not professor or doctor as a part of our assignment on canvas.

Example Description:

Animmal name - This is a nominal attribute that contains the name of the animal.

Hair - This a nomianal and boolean attribute that describes if the animal has hair.

Feathers - This a nomianal and boolean attribute that describes if the animal has feathers.

Eggs - This a nomianal and boolean attribute that describes if the animal lays eggs.

Milk - This a nomianal and boolean attribute that describes if the animal gives milk

Airborne - This a nomianal and boolean attribute that describes if the animal is a airborne

Aquatic - This a nomianal and boolean attribute that describes if the animal lives in water

Predator - This a nomianal and boolean attribute that describes if the animal feeds on other animals

Toothed - This a nomianal and boolean attribute that describes if the animal has hteeth.

Backbone - This a nomianal and boolean attribute that describes if the animals have backbone

Breathes - This a nomianal and boolean attribute that describes if the animals breathes

Venemous - This a nomianal and boolean attribute that describes if the animal is venomous

Fine - This a nomianal and boolean attribute that describes if the animal has fins

Legs - This a nomianal and boolean attribute that describes if the animal has legs as: 0 legs 2 legs 4 legs 5 legs 6 legs 8 legs 12 legs

Tail - This a nomianal and boolean attribute that describes if the animal has tail

Domestic - This a nomianal and boolean attribute that describes if the animal is domestic

Catsize - This a nomianal and boolean attribute that describes if the animal is catsize.

Gestation - This is an interval attribute that describes the animal's gestation period and has missing values

Type - This a nomianal and boolean attribute used to identify the type of the animal

Ismammal - This is a binary class label generated from the type class label. It is a transformation of a nominal class label, so it is also nominal. The labels are now mammal and not mammal

Degestation - The values are discretized and generated from the interval attribute gestation.

Data Import and wrangling:

The results of each search is read from the respective excel into spearate dataframes. careful attrention is paid to make sure the data is read in as character strings.

```
df = pd.read_excel("/content/sample_data/animal-taxonomy.xlsx", dtype=str)
```

```
df.columns
```

```
Index(['animal name', 'hair', 'feathers', 'eggs', 'milk', 'airborne',
       'aquatic', 'predator', 'toothed', 'backbone', 'breathes', 'venomous',
```

```
           'fins', 'legs', 'tail', 'domestic', 'catsize', 'gestation', 'type'],
          dtype='object')
```

```
df.loc[(df['type'] == 'mammal'), 'ismammal'] = 'mammal'
df.loc[(df['type'] != 'mammal'), 'ismammal'] = 'non-mammal'

df.columns
```

```
Index(['animal name', 'hair', 'feathers', 'eggs', 'milk', 'airborne',
       'aquatic', 'predator', 'toothed', 'backbone', 'breathes', 'venomous',
       'fins', 'legs', 'tail', 'domestic', 'catsize', 'gestation', 'type',
       'ismammal'],
      dtype='object')
```

```
#dropping null values since gestation attribute has NaN
df = df[df['gestation'].notna()]

df.dropna()
```

	animal name	hair	feathers	eggs	milk	airborne	aquatic	predator	toothed	backbo
0	aardvark	True	False	False	True	False	False	True	True	Tr
1	anole	False	False	True	False	False	False	False	True	Tr
2	antelope	True	False	False	True	False	False	False	True	Tr
3	axolotl	False	False	True	False	False	True	False	True	Tr
4	bass	False	False	True	False	False	True	True	True	Tr
...	...	...	...	...	...	...	...	...	...	
126	wallaby	True	False	False	True	False	False	False	True	Tr
127	wasp	True	False	True	False	True	False	False	False	Fa
128	whale shark	False	False	False	False	False	False	False	True	Tr

```
df.isna().any()
```

```
animal name    False
hair           False
feathers       False
eggs           False
milk           False
airborne       False
```

```
aquatic        False
predator       False
toothed        False
backbone       False
breathes       False
venomous       False
fins           False
legs           False
tail           False
domestic       False
catsize        False
gestation      False
type           False
ismammal       False
dtype: bool
```

Partition the data into a training set and a test set using a 85/15 split.

```
X = df.drop(columns=['type','ismammal'])
Y = df[['ismammal']]
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, train_size = 0.85, random_state = 1
```

Exploratory Data Analysis:

Looking into what type of measure the attributes are.

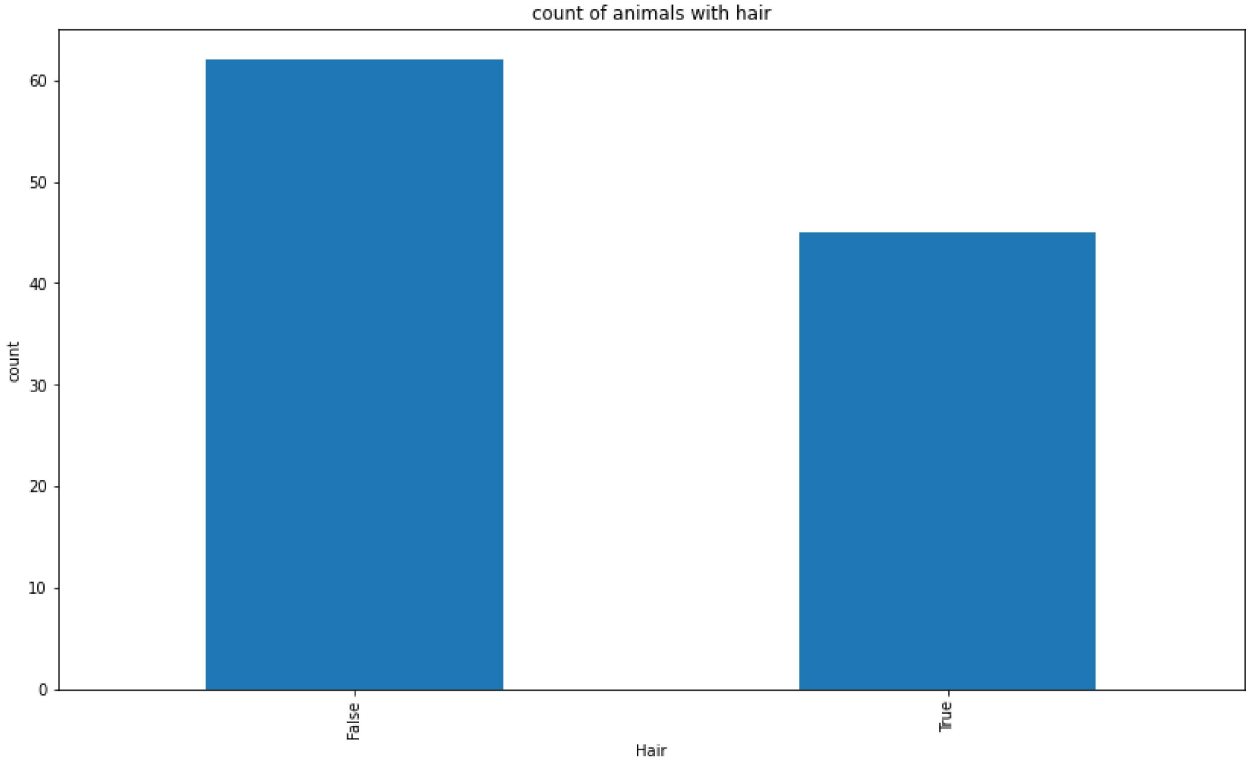
```
df.describe()
```

	animal name	hair	feathers	eggs	milk	airborne	aquatic	predator	toothed	bacl
count	126	126	126	126	126	126	126	126	126	
unique	126	2	2	2	2	2	2	2	2	
top	aardvark	False	False	True	False	False	False	True	True	

Here, I've plotted graphs for each attribute

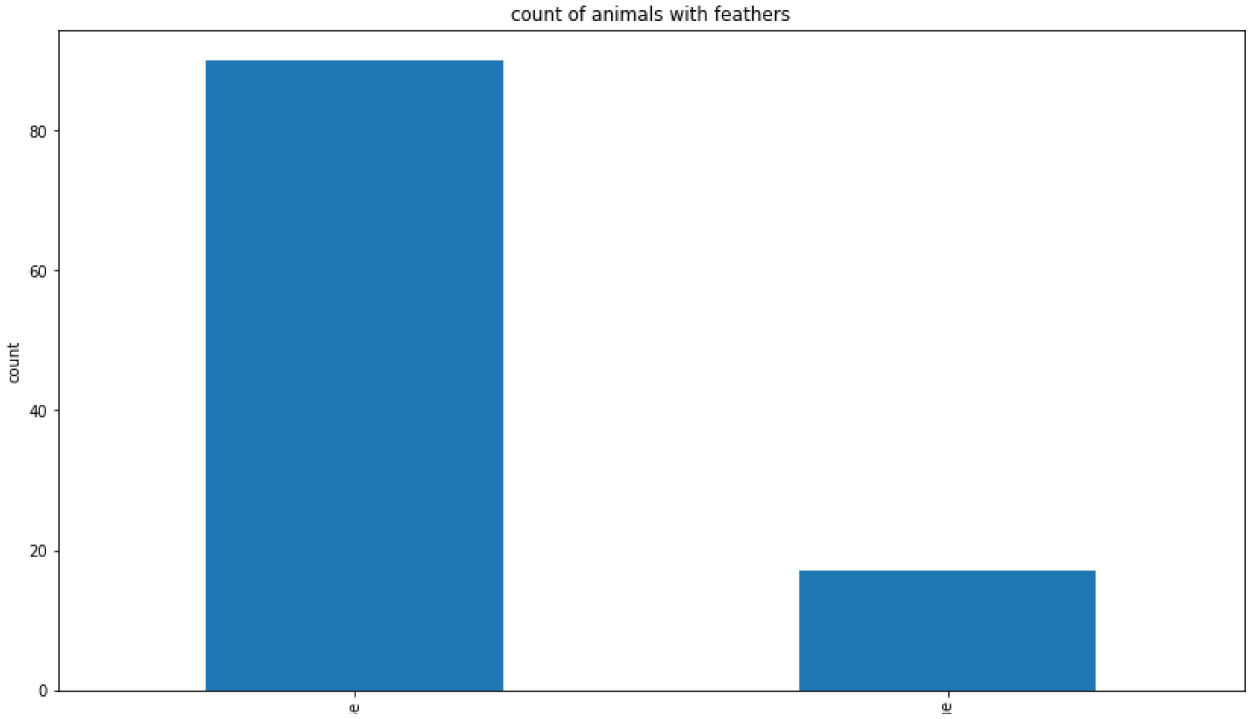
```
# Hair
plot = X_train['hair'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("Hair")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



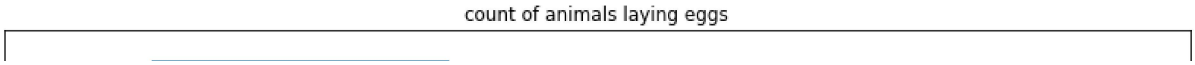

```
# Feathers
plot = X_train['feathers'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count c
plot.set_xlabel("feathers")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



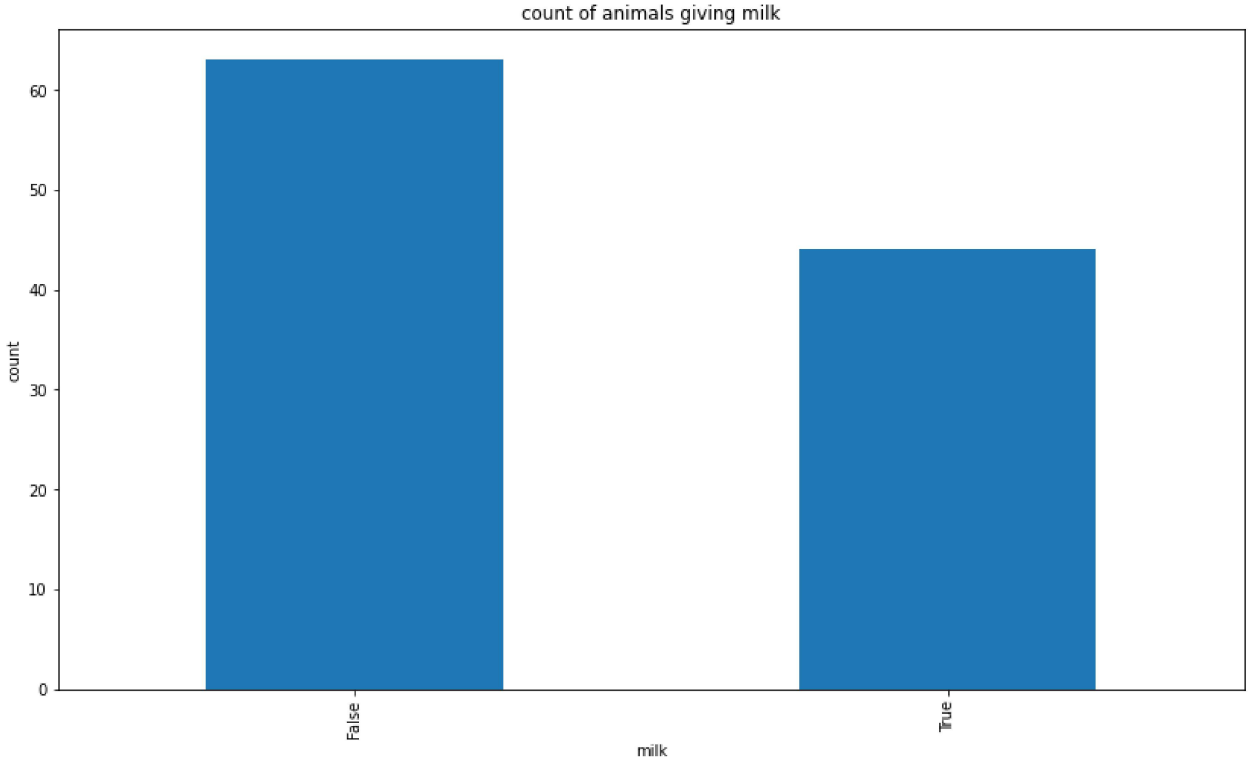

```
# EggS
plot = X_train['eggs'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("eggs")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



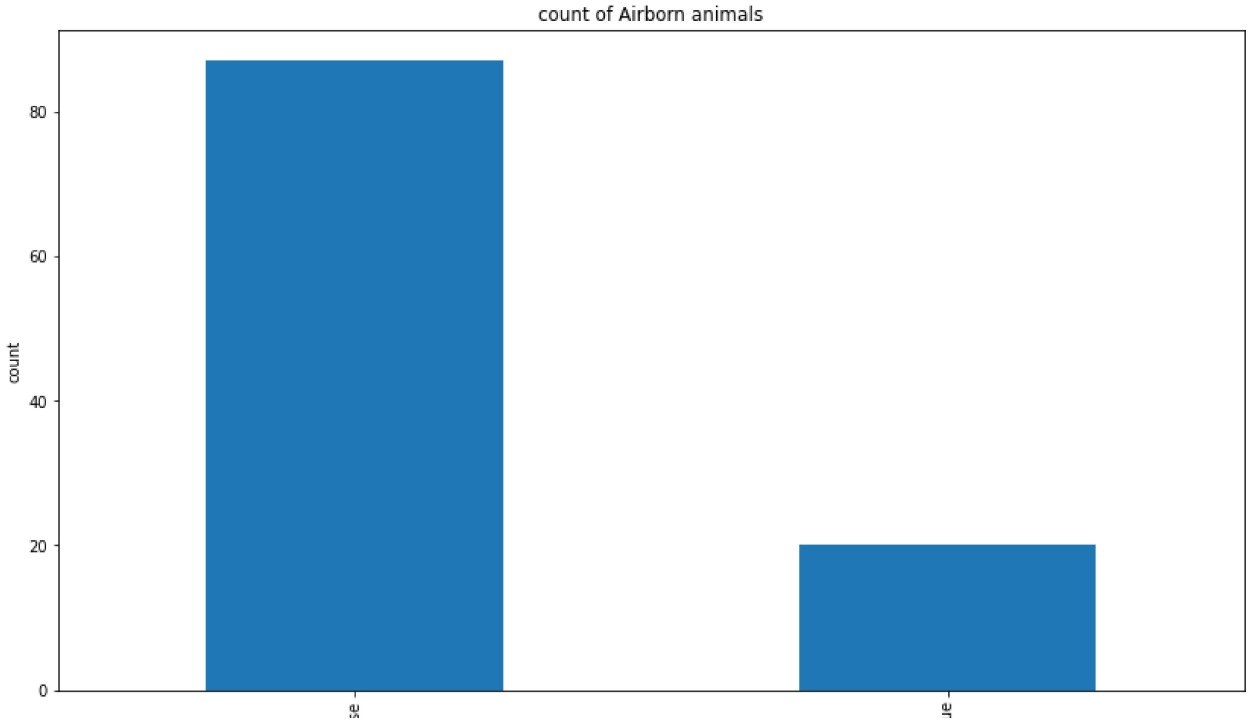

```
# Milk
plot = X_train['milk'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("milk")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



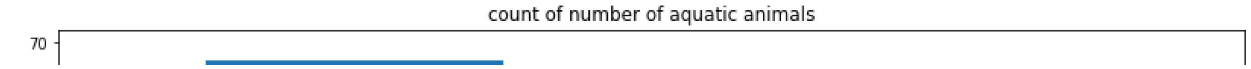

```
# Airbone
plot = X_train['airborne'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count c
plot.set_xlabel("airborne")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



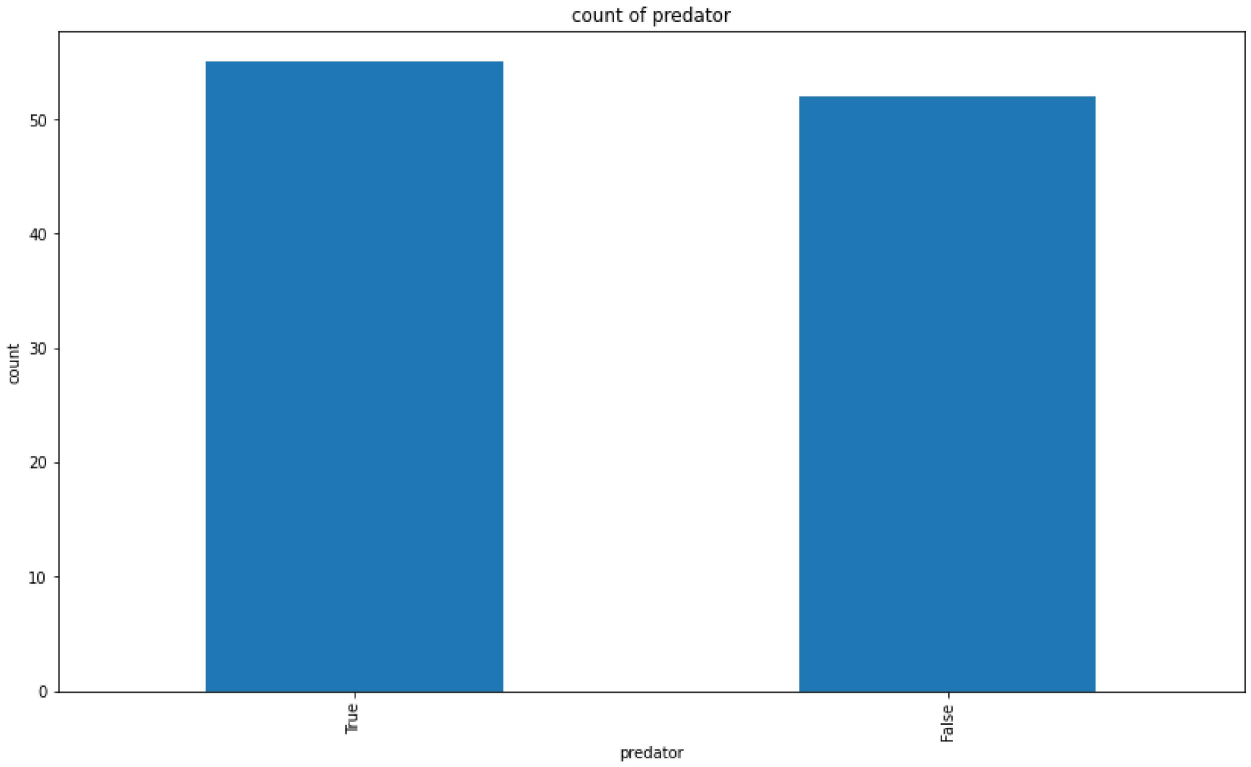

```
# Aquatic
plot = X_train['aquatic'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of
plot.set_xlabel("aquatic")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



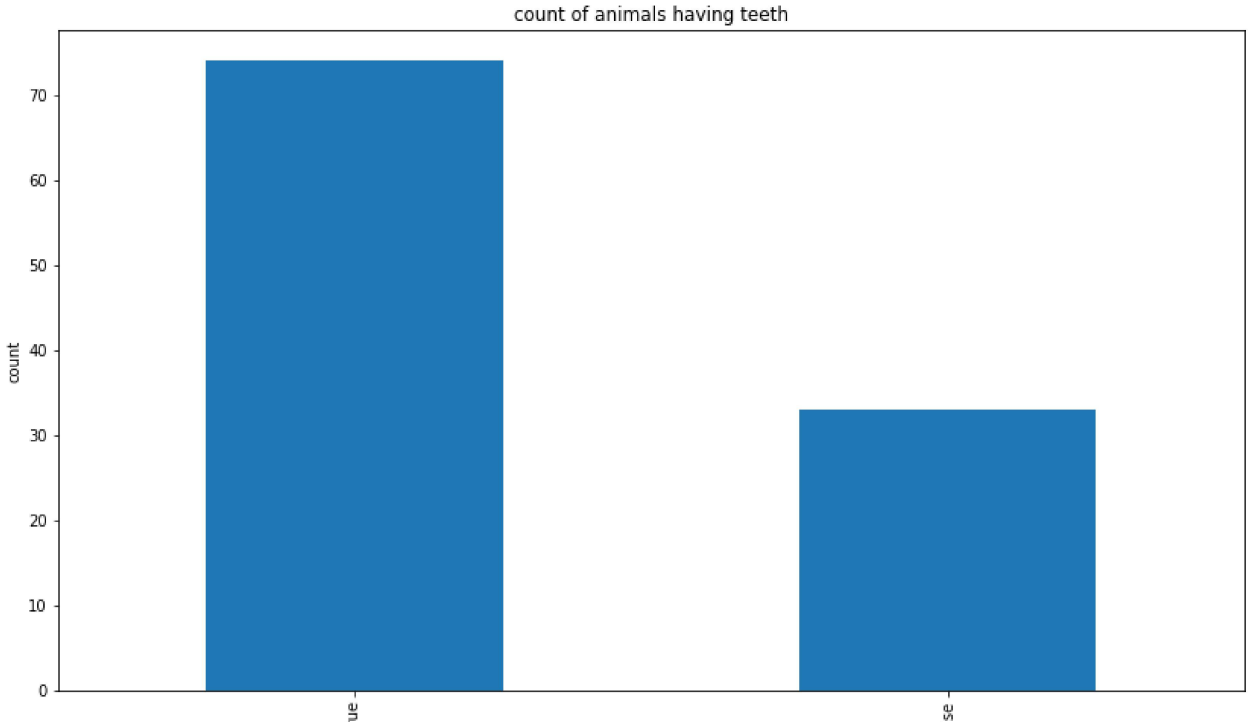

```
# Predator
plot = X_train['predator'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count c
plot.set_xlabel("predator")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



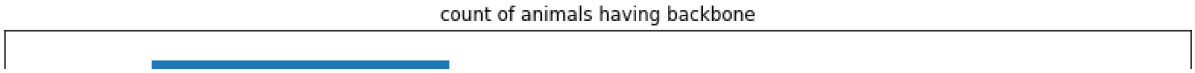

```
# Toothed
plot = X_train['toothed'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of
plot.set_xlabel("toothed")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



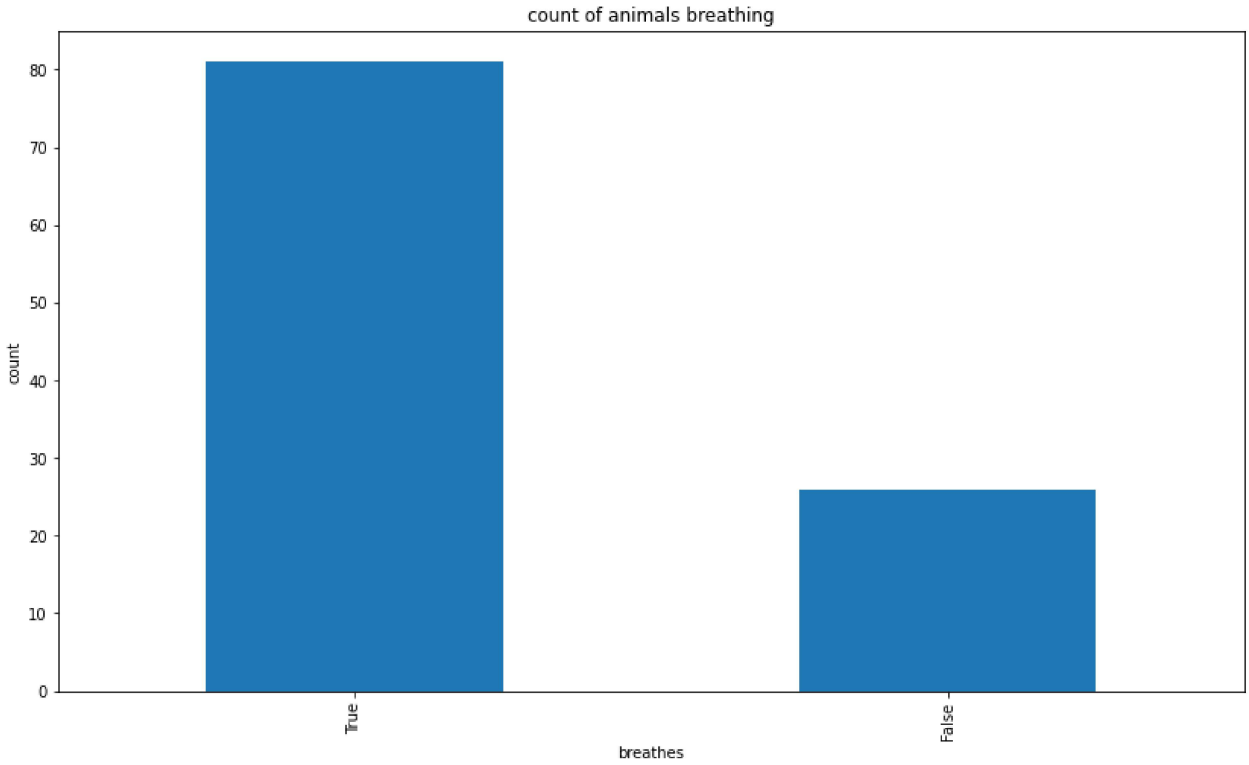

```
# Backbone
plot = X_train['backbone'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count o
plot.set_xlabel("backbone")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



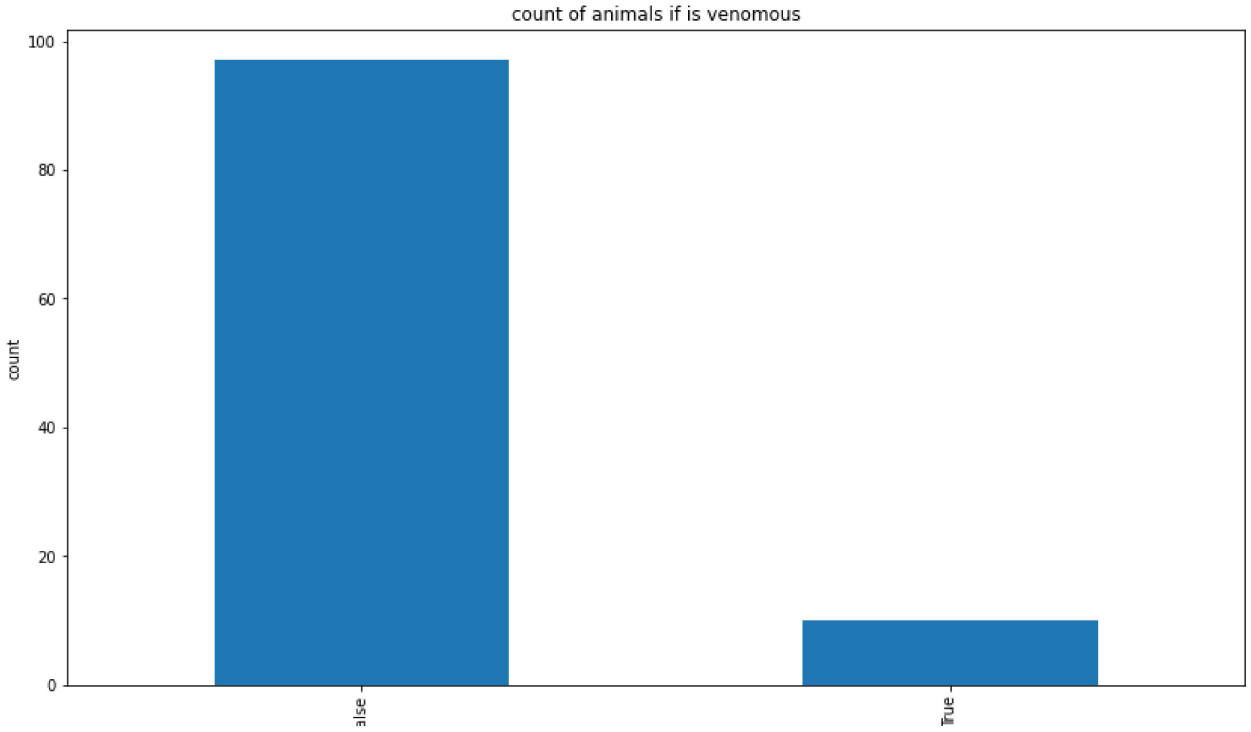

```
# Breathes
plot = X_train['breathes'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count o
plot.set_xlabel("breathes")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



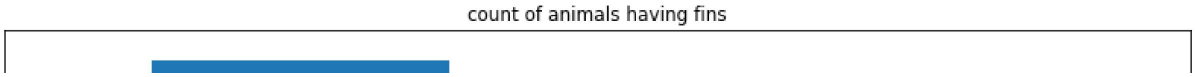

```
# Venomous
plot = X_train['venomous'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count o
plot.set_xlabel("venomous")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



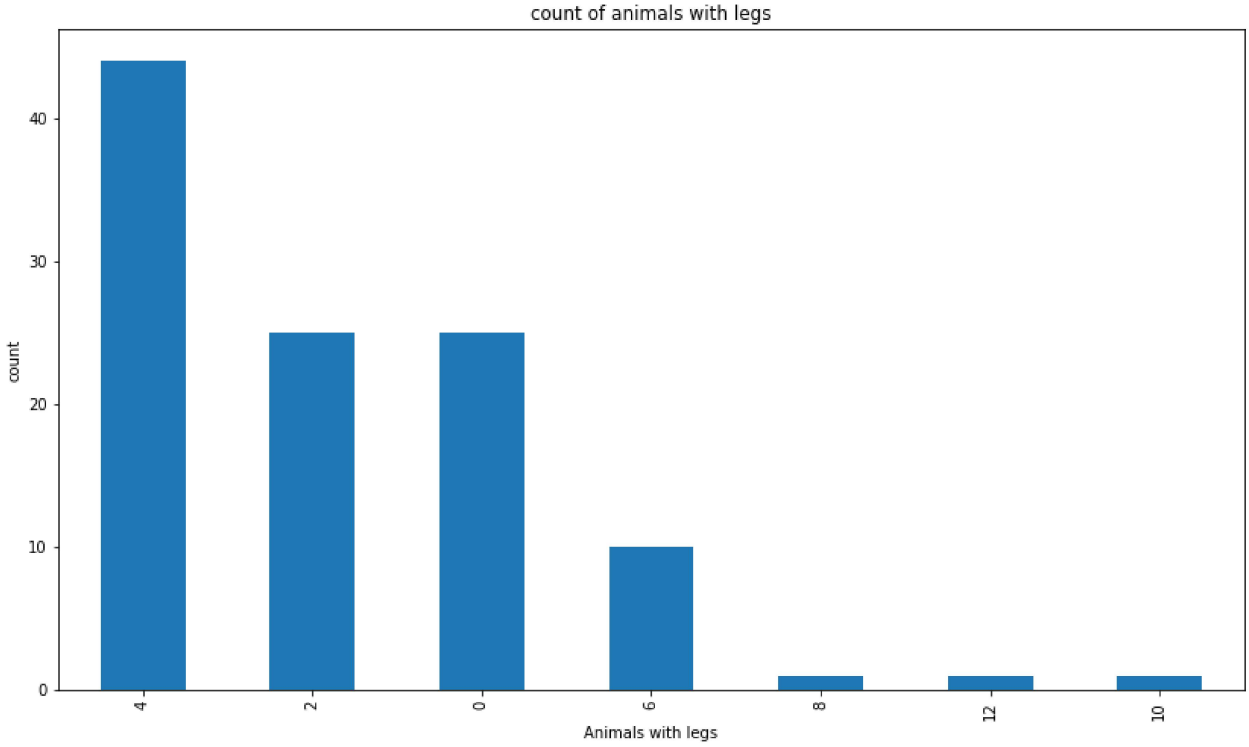

```
# Fins
plot = X_train['fins'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("fins")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



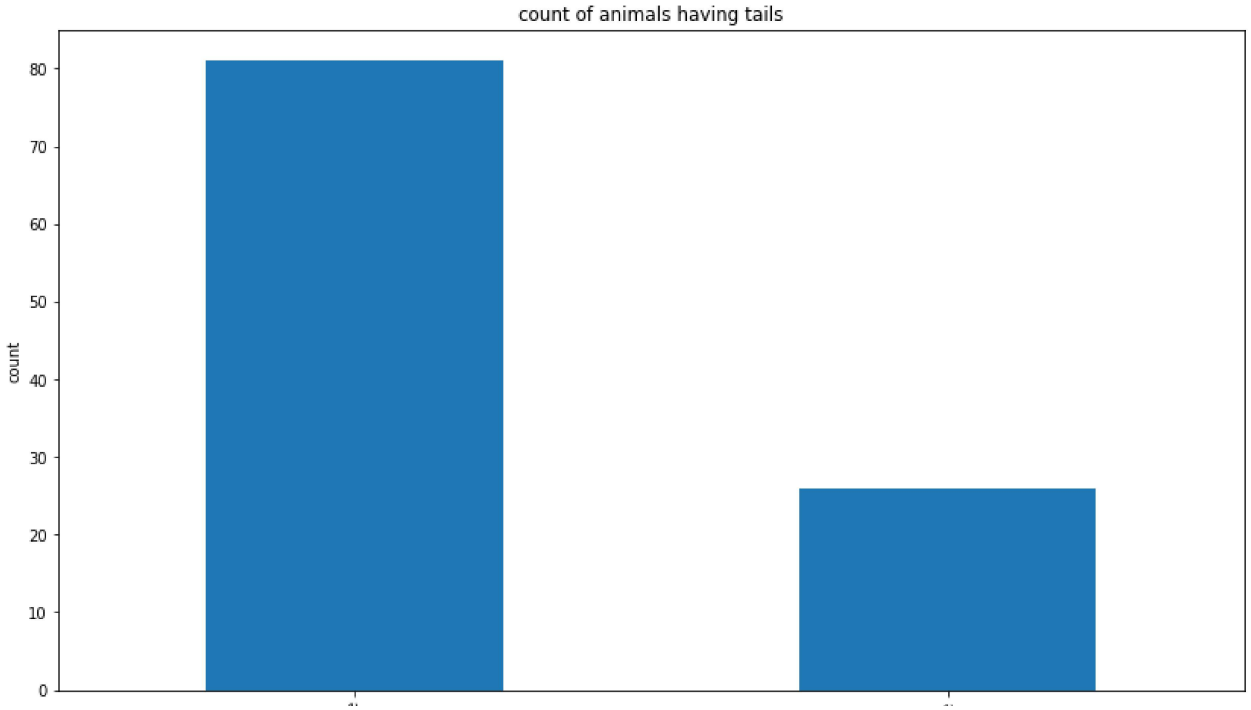

```
# Legs
plot = X_train['legs'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("Animals with legs")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



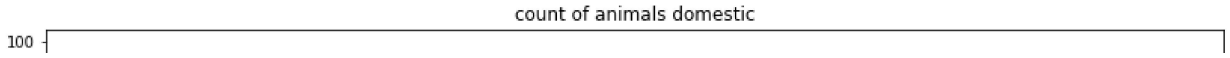

```
# Tail
plot = X_train['tail'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of ar
plot.set_xlabel("Tail")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```



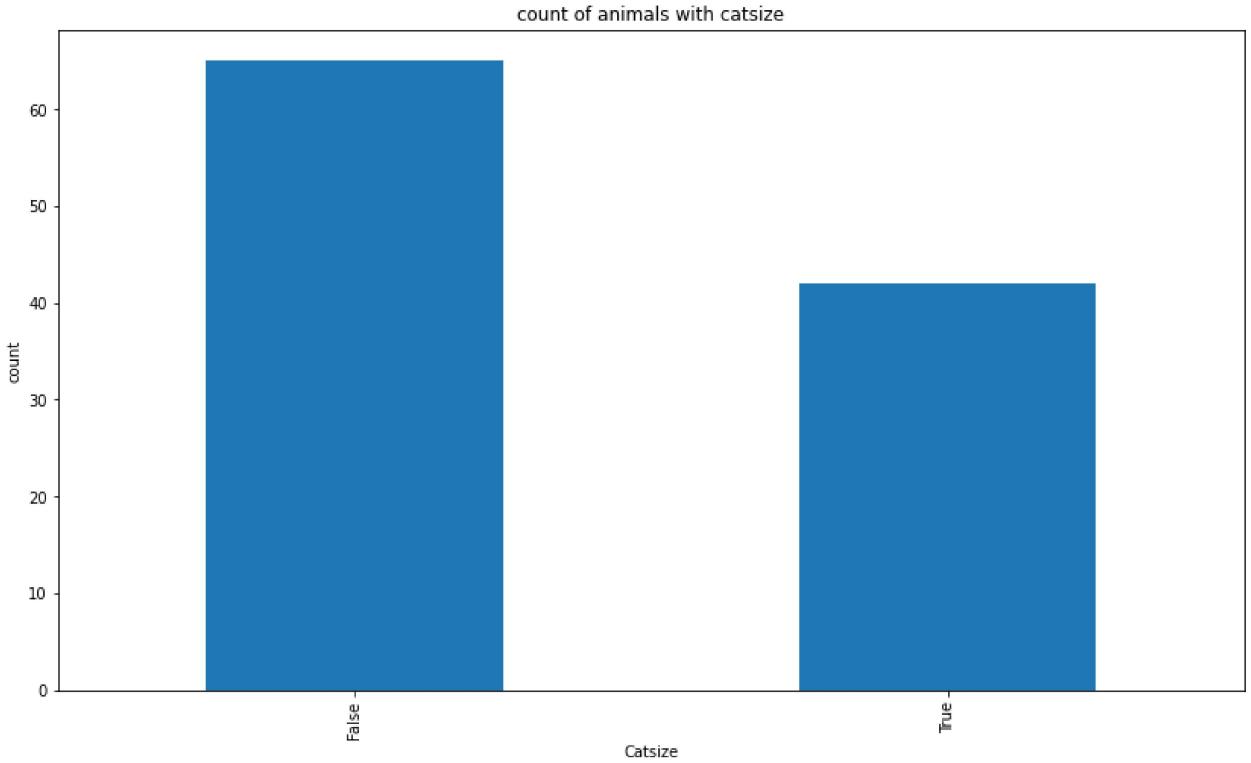

```
# Domestic
plot = X_train['domestic'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count o
plot.set_xlabel("domestic")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```




```
# Catsize
plot = X_train['catsize'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count of
plot.set_xlabel("Catsize")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```

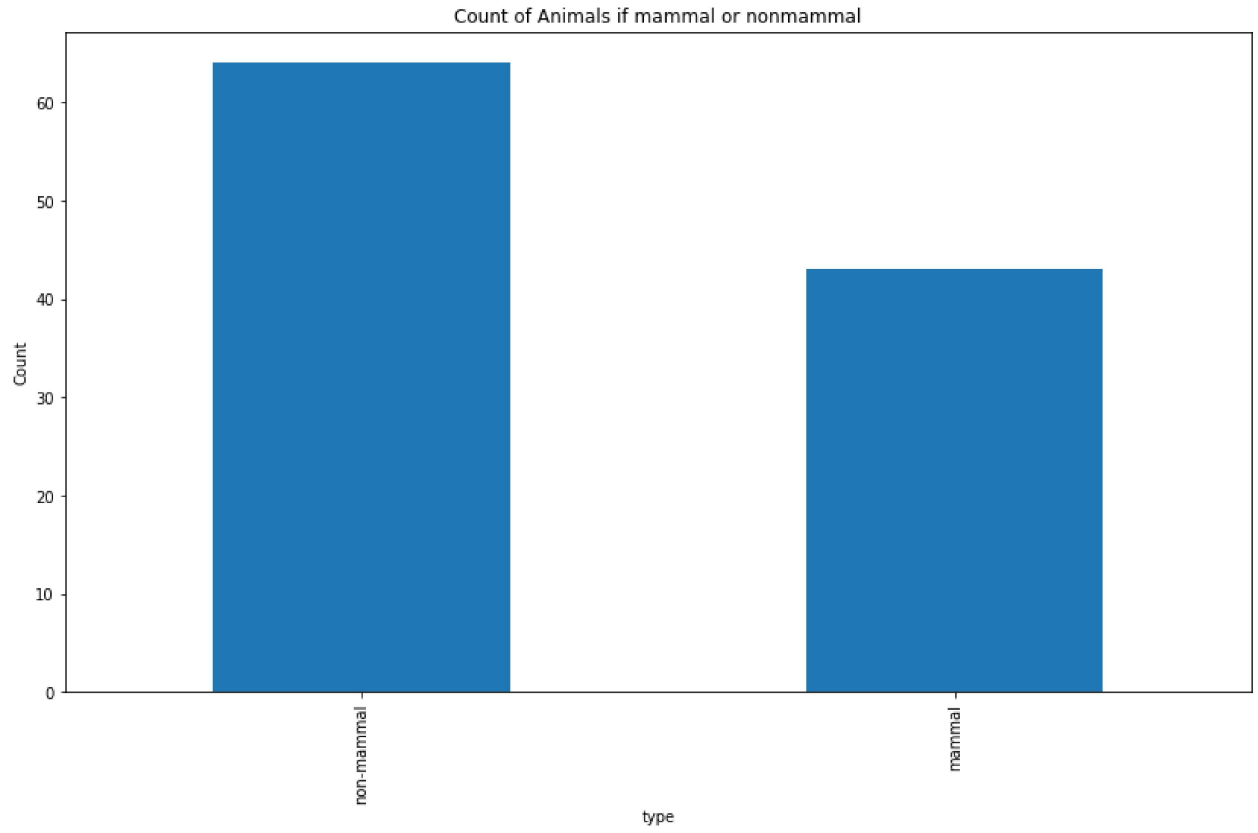



```
Y_train
```

	ismammal
2	mammal
55	non-mammal
111	non-mammal
116	non-mammal
49	non-mammal

```
#ismammal
plot = Y_train['ismammal'].value_counts().plot(kind='bar',
                                    figsize=(14,8),
                                    title="Count of Animals if mammal or nonmammal")
plot.set_xlabel("type")
plot.set_ylabel("Count")
```

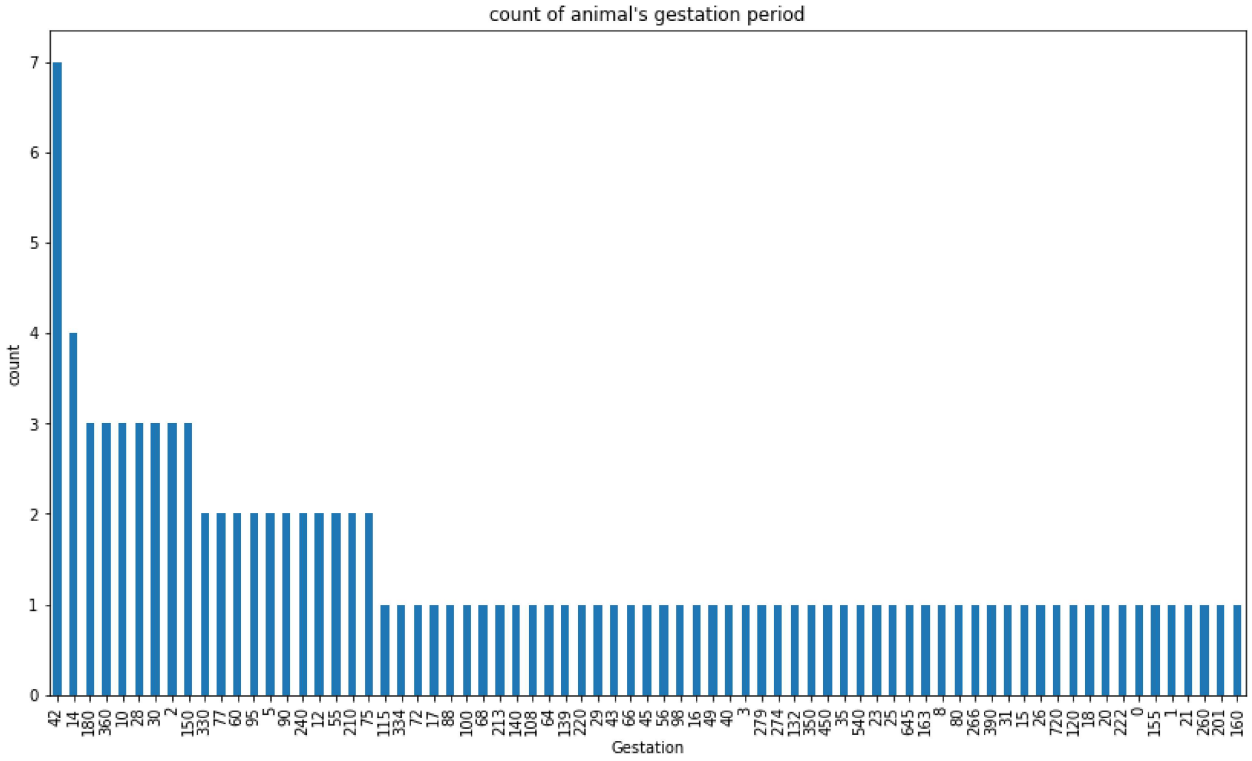
```
Text(0, 0.5, 'Count')
```




```
# gestation
```

```
plot = X_train['gestation'].value_counts().plot(kind = 'bar', figsize=(14,8), title = "count
plot.set_xlabel("Gestation")
plot.set_ylabel("count")
```

```
Text(0, 0.5, 'count')
```




```
X_train['gestation'].describe()
```

```
count     107
unique     73
top        42
freq        7
Name: gestation, dtype: object
```

```
X_train['gestation']= X_train['gestation'].astype('int')
X_train.loc[(X_train['gestation'] <= 2), 'degestation'] = 0
X_train.loc[(X_train['gestation'] > 2), 'degestation'] = 1
X_train = X_train.drop(columns = ['gestation'])
```

```
X_test['gestation']= X_test['gestation'].astype('int')
X_test.loc[(X_test['gestation'] <= 2), 'degestation'] = 0
X_test.loc[(X_test['gestation'] > 2), 'degestation'] = 1
X_test = X_test.drop(columns = ['gestation'])
```

Mining or Analytics:

using two way tables to get frequency per class.

```
# Hair
hair_col = pd.crosstab(index = X_train["hair"], columns = Y_train["ismammal"], margins = True
hair_col
```

ismammal hair	mammal	non-mammal	All
False	2	60	62
True	41	4	45
All	43	64	107

Based on the frequency of mammal count and mammal count, we can generate the following rule set for the hair attrbute:

True - mammal

False - non mammal

now we determine the error rate of the hair column rules.

```
error = 0
error += hair_col.loc['True', 'non-mammal']
error += hair_col.loc['False', 'mammal']
error_rate = error/hair_col.loc['All', 'All']
error_rate
```

```
0.056074766355140186
```

```
#feathers
feathers_col = pd.crosstab(index = X_train ["feathers"], columns = Y_train["ismammal"], margi
feathers_col
```

```
ismammal  mammal  non-mammal  All
```

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the feathers attribute

True - non-mammal False- non-mammal

Now we detemine the error rate of the feathers rules

```
error = 0
error += feathers_col.loc['True', 'non-mammal']
error += feathers_col.loc['False', 'mammal']
error_rate = error/feathers_col.loc['All', 'All']
error_rate
```

```
0.5607476635514018
```

```
# Eggs
eggs_col = pd.crosstab(index = X_train ["eggs"], columns = Y_train["ismammal"], margins= True
eggs_col
```

ismammal	mammal	non-mammal	All
eggs			
False	42	4	46
True	1	60	61
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the eggs attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the eggs rules

```
error = 0
error += eggs_col.loc['True', 'non-mammal']
error += eggs_col.loc['False', 'mammal']
error_rate = error/eggs_col.loc['All', 'All']
error_rate
```

```
0.9532710280373832
```

```
# Milk
milk_col = pd.crosstab(index = X_train ["milk"], columns = Y_train["ismammal"], margins= True
milk_col
```

ismammal	mammal	non-mammal	All
milk			
False	0	63	63
True	43	1	44
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the milk attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the milk rules

```
error = 0
error += milk_col.loc['True', 'non-mammal']
error += milk_col.loc['False', 'mammal']
error_rate = error/milk_col.loc['All', 'All']
error_rate
```

```
0.009345794392523364
```

```
# Airborn
airborn_col = pd.crosstab(index = X_train ["milk"], columns = Y_train["ismammal"], margins= T
airborn_col
```

ismammal	mammal	non-mammal	All
milk			
False	0	63	63
True	43	1	44
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the airborn attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the airborn rules

```
error = 0
error += airborn_col.loc['True', 'non-mammal']
error += airborn_col.loc['False', 'mammal']
error_rate = error/airborn_col.loc['All', 'All']
error_rate
```

```
0.009345794392523364
```

```
# aquatic
aquatic_col = pd.crosstab(index = X_train ["aquatic"], columns = Y_train["ismammal"], margins
aquatic_col
```

ismammal	mammal	non-mammal	All
aquatic			
False	36	32	68
True	7	32	39
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the aquatic attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the aquatic rules

```
error = 0
error += aquatic_col.loc['True', 'non-mammal']
error += aquatic_col.loc['False', 'mammal']
error_rate = error/aquatic_col.loc['All', 'All']
error_rate
```

```
0.6355140186915887
```

```
# predator
predator_col = pd.crosstab(index = X_train ["predator"], columns = Y_train["ismammal"], margi
predator_col
```

ismammal	mammal	non-mammal	All
predator			
False	21	31	52
True	22	33	55
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the predator attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the predator rules

```
error = 0
error += predator_col.loc['True', 'non-mammal']
error += predator_col.loc['False', 'mammal']
error_rate = error/predator_col.loc['All', 'All']
error_rate
```

```
0.5046728971962616
```

```
# toothed
toothed_col = pd.crosstab(index = X_train ["toothed"], columns = Y_train["ismammal"], margins
toothed_col
```

ismammal	mammal	non-mammal	All
toothed			
False	1	32	33
True	42	32	74
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the toothed attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the toothed rules

```
error = 0
error += toothed_col.loc['True', 'non-mammal']
error += toothed_col.loc['False', 'mammal']
error_rate = error/toothed_col.loc['All', 'All']
error_rate
```

```
0.308411214953271
```

```
# backbone
backbone_col = pd.crosstab(index = X_train ["backbone"], columns = Y_train["ismammal"], margi
backbone_col
```

ismammal	mammal	non-mammal	All
backbone			
False	0	18	18
True	43	46	89
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the backbone attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the backbone rules

```
error = 0
error += backbone_col.loc['True', 'non-mammal']
error += backbone_col.loc['False', 'mammal']
error_rate = error/backbone_col.loc['All', 'All']
error_rate
```

```
0.42990654205607476
```

```
# breathes
breathes_col = pd.crosstab(index = X_train ["breathes"], columns = Y_train["ismammal"], margi
breathes_col
```

ismammal	mammal	non-mammal	All
breathes			
False	0	26	26
True	43	38	81

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the breathes attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the breathes rules

```
error = 0
error += breathes_col.loc['True', 'non-mammal']
error += breathes_col.loc['False', 'mammal']
error_rate = error/breathes_col.loc['All', 'All']
error_rate
```

```
0.35514018691588783
```

```
# venomous
venomous_col = pd.crosstab(index = X_train ["venomous"], columns = Y_train["ismammal"], margi
venomous_col
```

ismammal	mammal	non-mammal	All
venomous			
False	42	55	97
True	1	9	10
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the venomous attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the venomous rules

```
error = 0
error += venomous_col.loc['True', 'non-mammal']
```

```
error += venomous_col.loc['False', 'mammal']
error_rate = error/venomous_col.loc['All', 'All']
error_rate
```

```
0.4766355140186916
```

```
# fins
fins_col = pd.crosstab(index = X_train ["fins"], columns = Y_train["ismammal"], margins= True
fins_col
```

ismammal fins	mammal	non-mammal	All
False	39	50	89
True	4	14	18
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the fins attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the fins rules

```
error = 0
error += fins_col.loc['True', 'non-mammal']
error += fins_col.loc['False', 'mammal']
error_rate = error/fins_col.loc['All', 'All']
error_rate
```

```
0.4953271028037383
```

```
# legs
legs_col = pd.crosstab(index = X_train ["legs"], columns = Y_train["ismammal"], margins= True
legs_col
```

ismammal	mammal	non-mammal	All
legs			
0	3	22	25
10	0	1	1
12	0	1	1
2	7	18	25
4	33	11	44

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the legs attribute

0 - non-mammal

2 - non-mammal

4 - mammal

6 - non-mammal

8 - non-mammal

12 - non-mammal

Now we detemine the error rate of the legs rules

```
error = 0
error += legs_col.loc['0', 'mammal']
error += legs_col.loc['2', 'mammal']
error += legs_col.loc['4', 'non-mammal']
error += legs_col.loc['6', 'mammal']
error += legs_col.loc['8', 'mammal']
error += legs_col.loc['12', 'mammal']
error_rate = error/legs_col.loc['All', 'All']
error_rate
```

```
0.19626168224299065
```

```
# tail
tail_col = pd.crosstab(index = X_train ["tail"], columns = Y_train["ismammal"], margins= True
tail_col
```

ismammal	mammal	non-mammal	All
tail			

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the tail attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the tail rules

```
error = 0
error += tail_col.loc['True', 'non-mammal']
error += tail_col.loc['False', 'mammal']
error_rate = error/tail_col.loc['All', 'All']
error_rate
```

```
0.5046728971962616
```

```
# domestic
domestic_col = pd.crosstab(index = X_train ["domestic"], columns = Y_train["ismammal"], margi
domestic_col
```

ismammal	mammal	non-mammal	All
domestic			
False	37	60	97
True	6	4	10
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the domestic attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the domestic rules

```
error = 0
error += domestic_col.loc['True', 'non-mammal']
error += domestic_col.loc['False', 'mammal']
```

```
error_rate = error/domestic_col.loc['All', 'All']
error_rate
```

```
0.28217757009345793
```

```
# catsize
catsize_col = pd.crosstab(index = X_train ["catsize"], columns = Y_train["ismammal"], margins
catsize_col
```

ismammal	mammal	non-mammal	All
catsize			
False	11	54	65
True	32	10	42
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the catsize attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the catsize rules

```
error = 0
error += catsize_col.loc['True', 'non-mammal']
error += catsize_col.loc['False', 'mammal']
error_rate = error/catsize_col.loc['All', 'All']
error_rate
```

```
0.19626168224299065
```

```
# degestation
degestation_col = pd.crosstab(index = X_train ["degestation"], columns = Y_train["ismammal"],
degestation_col
```

ismammal	mammal	non-mammal	All
degestation			
0.0	0	5	5
1.0	43	59	102
All	43	64	107

Based on the frequancy of mammal and non mammal count, we aould generate the following rule set for the degestation attribute

True - non-mammal

False- non-mammal

Now we detemine the error rate of the degestation rules

```
errors = 0
errors += degestation_col.loc[0,'mammal']
errors += degestation_col.loc[1,'mammal']
error_rate = errors/degestation_col.loc['All','All']

error_rate
```

```
0.40186915887850466
```

Evaluation:

TRUE - mammal

FALSE - non-mammal

```
#Determine the predicted values
prediction = pd.DataFrame(X_test['milk'])
prediction = prediction.rename(columns={'milk':'prediction'})
prediction[prediction['prediction']=='True']='mammal'
prediction[prediction['prediction']=='False']='non-mammal'
Y_test
```

	ismammal
125	non-mammal
47	mammal
74	non-mammal
91	mammal
105	non-mammal
54	mammal
124	mammal
129	mammal
121	non-mammal
43	non-mammal

```
prediction['prediction']
```

```
125    non-mammal
47         mammal
74     non-mammal
91         mammal
105    non-mammal
54         mammal
124        mammal
129        mammal
121    non-mammal
43     non-mammal
92         mammal
52     non-mammal
109    non-mammal
36     non-mammal
45     non-mammal
123        mammal
75     non-mammal
107    non-mammal
128    non-mammal
Name: prediction, dtype: object
```

```
#confusion Matrix
cm = confusion_matrix(Y_test['ismammal'], prediction['prediction'])
print(cm)
```

```
[[ 7  0]
 [ 0 12]]
```

```
print("Accuracy Score: ")
print(accuracy_score(Y_test['ismammal'], prediction['prediction']))
print("\n")
```

```
print("Report: ")
print(classification_report(Y_test['ismammal'], prediction['prediction']))
```

```
Accuracy Score:
1.0


Report:
              precision    recall  f1-score   support

      mammal       1.00      1.00      1.00         7
  non-mammal       1.00      1.00      1.00        12

    accuracy                           1.00        19
   macro avg       1.00      1.00      1.00        19
weighted avg       1.00      1.00      1.00        19
```

After a successfull validation, we feel that the milk rules set would make a good model to determine wheather an animal is a mammal or non-mammal. the Milk rules set are as follows:

True - mammal False - non-mammal

References:

https://www.geeksforgeeks.org/confusion-matrix-machine-learning/

https://stackoverflow.com/questions/31511997/pandas-dataframe-replace-all-values-in-a-column-based-on-condition

Lecture Note: 1R Mushroom.

✓ 0s completed at 4:49 PM