Lets import the libraries

In [1]:
```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
```

Lets import the data

In [2]:
```
human_data = pd.read_table(r'C:\Users\SHREE\Downloads\Python CODES\DNA Sequencing using NI
human_data.head()
```

Out[2]:

	sequence	class
0	ATGCCCCAACTAAATACTACCGTATGGCCCACCATAATTACCCCCA...	4
1	ATGAACGAAAATCTGTTCGCTTCATTCATTGCCCCCACAATCCTAG...	4
2	ATGTGTGGCATTTGGGCGCTGTTTGGCAGTGATGATTGCCTTTCTG...	3
3	ATGTGTGGCATTTGGGCGCTGTTTGGCAGTGATGATTGCCTTTCTG...	3
4	ATGCAACAGCATTTTGAATTTGAATACCAGACCAAAGTGGATGGTG...	3

We have some data for human DNA sequence coding regions and a class label.

Let's define a function to collect all possible overlapping k-mers of a specified length from any sequence string.

In [3]:
```
# function to convert sequence strings into k-mer words, default size = 6 (hexamer words)
def getKmers(sequence, size=6):
    return [sequence[x:x+size].lower() for x in range(len(sequence) - size + 1)]
```

Now we can convert our training data sequences into short overlapping k-mers of legth 6. Lets do that for each species of data we have using our getKmers function.

In [4]:
```
human_data['words'] = human_data.apply(lambda x: getKmers(x['sequence']), axis=1)
human_data = human_data.drop('sequence', axis=1)
```

Now, our coding sequence data is changed to lowercase, split up into all possible k-mer words of length 6 and ready for the next step. Let's take a look.

In [5]:
```
human_data.head()
```

Out[5]:

	class	words
0	4	[atgccc, tgcccc, gcccca, ccccaa, cccaac, ccaac...
1	4	[atgaac, tgaacg, gaacga, aacgaa, acgaaa, cgaaa...
2	3	[atgtgt, tgtgtg, gtgtgg, tgtggc, gtggca, tggca...
3	3	[atgtgt, tgtgtg, gtgtgg, tgtggc, gtggca, tggca...
4	3	[atgcaa, tgcaac, gcaaca, caacag, aacagc, acagc...

Since we are going to use scikit-learn natural language processing tools to do the k-mer counting, we need to now convert the lists of k-mers for each gene into string sentences of words that the count vectorizer can use.

We can also make a y variable to hold the class labels. Let's do that now.

In [6]:

```python
human_texts = list(human_data['words'])
for item in range(len(human_texts)):
    human_texts[item] = ' '.join(human_texts[item])
y_data = human_data.iloc[:, 0].values
print(human_texts[2])
```

```
atgtgt tgtgtg gtgtgg tgtggc gtggca tggcat ggcatt gcattt catttg atttgg tttggg ttgggc tgggcg
gggcgc ggcgct gcgctg cgctgt gctgtt ctgttt tgtttg gtttgg tttggc ttggca tggcag ggcagt gcagtg
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caatgg aatggt atggtg tggtga ggtgaa gtgaaa tgaaat gaaatc aaatct aatcta atctac tctaca ctacaa
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gaattg aattga attgag ttgagc tgagca gagcaa agcaaa gcaaac caaaca aaacaa aacaat acaatt caattt
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```

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caagtc aagtca agtcag gtcagc tcagct cagctg agctgt gctgtc ctgtca tgtcaa gtcaaa tcaaag caaagc
aaagct aagctt agctta gcttag
```

In [7]:

```
y_data
```

Out[7]:

```
array([4, 4, 3, ..., 6, 6, 6], dtype=int64)
```

We will perform the same steps for chimpanzee and dog

Now we will apply the BAG of WORDS using CountVectorizer using NLP

In [8]:

```
# Creating the Bag of Words model using CountVectorizer()
# This is equivalent to k-mer counting
# The n-gram size of 4 was previously determined by testing
from sklearn.feature_extraction.text import CountVectorizer
cv = CountVectorizer(ngram_range=(4,4))
X = cv.fit_transform(human_texts)
print(X.shape)
```

```
(4380, 232414)
```

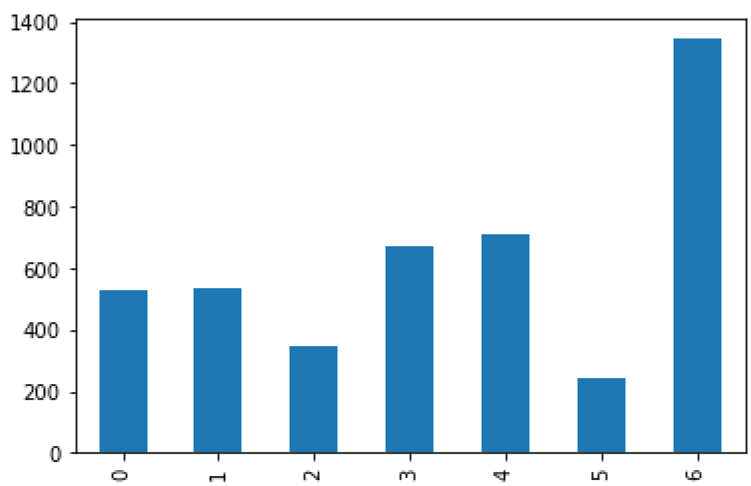
If we have a look at class balance we can see we have relatively balanced data set.

In [9]:

```
human_data['class'].value_counts().sort_index().plot.bar()
```

Out[9]:

```
<AxesSubplot:>
```



Splitting the human data set into the training set and test set

In [10]:

```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X,
                                                    y_data,
                                                    test_size = 0.20,
                                                    random_state=42)
print(X_train.shape)
print(X_test.shape)
```

```
(3504, 232414)
(876, 232414)
```

A multinomial naive Bayes classifier will be created. I previously did some parameter tuning and found the ngram size of 4 (reflected in the Countvectorizer() instance) and a model alpha of 0.1 did the best.

In [11]:

```
# The alpha parameter was determined by grid search previously
from sklearn.naive_bayes import MultinomialNB
classifier = MultinomialNB(alpha=0.1)
classifier.fit(X_train, y_train)
```

Out[11]:

```
▾     MultinomialNB
MultinomialNB(alpha=0.1)
```

In [12]:

```
y_pred = classifier.predict(X_test)
```

Let's look at some model performance metrics like the confusion matrix, accuracy, precision, recall and f1 score.

In [13]:

```
from sklearn.metrics import accuracy_score, f1_score, precision_score, recall_score
print("Confusion matrix\n")
print(pd.crosstab(pd.Series(y_test, name='Actual'), pd.Series(y_pred, name='Predicted')))
def get_metrics(y_test, y_predicted):
    accuracy = accuracy_score(y_test, y_predicted)
    precision = precision_score(y_test, y_predicted, average='weighted')
    recall = recall_score(y_test, y_predicted, average='weighted')
    f1 = f1_score(y_test, y_predicted, average='weighted')
    return accuracy, precision, recall, f1
accuracy, precision, recall, f1 = get_metrics(y_test, y_pred)
print("accuracy = %.3f \nprecision = %.3f \nrecall = %.3f \nf1 = %.3f" % (accuracy, precis
```

```
Confusion matrix

Predicted   0    1   2    3    4   5    6
Actual
0          99    0   0    0    1   0    2
1           0  104   0    0    0   0    2
2           0    0  78    0    0   0    0
3           0    0   0  124    0   0    1
4           1    0   0    0  143   0    5
5           0    0   0    0    0  51    0
6           1    0   0    1    0   0  263
accuracy = 0.984
precision = 0.984
recall = 0.984
f1 = 0.984
```

We are getting really good results on our unseen data, so it looks like our model did not overfit to the training data.