Working with the ADNI PatData data and creating a Random Forest model for predicting Alzheimer's status.

1) Opening the file location and loading libraries

Importing all necessary libraries to create our models

```
# Data cleaning and wrangling packages
import pandas as pd
import numpy as np
from sklearn.model_selection import train_test_split
from sklearn.preprocessing import OneHotEncoder
from sklearn.compose import make_column_transformer

# Machine learning model building packages and evaluating their performance
from sklearn.ensemble import RandomForestClassifier
from sklearn import metrics

# Plots and graphs packages
import matplotlib.pyplot as plt
from sklearn.metrics import ConfusionMatrixDisplay
import seaborn as sns

# packages to save your work in google colab
from google.colab import files
```

Here you will read in data from a file called PatData.csv. I (Pleuni Pennings) created that file as a summary of a larger file called "TADPOLE_D1_D2.csv." This has electronic health record data for every patient and this dataset contains all the variables mentioned in our course text plus the other ones and it is measured across several timepoint. **PatData.csv** is a summary, with just one time point per patient and this is the dataset we will be working on in notebook.

```
url = "https://raw.githubusercontent.com/pleunipennings/CSC508Data/main/PatData.csv"
data = pd.read_csv(url)
```

2) Having a first look at the data

As usual we should get into the practice of taking a look at how your data is structured, what is the dimention of our data, which variables are our features and which is a label. For the purpose of this notebook, it is important for us to check what variables we would need to one-hot encode.

```
# Checking how big is our data
data.shape
```

```
(1737, 16)
```

```
# Looking at each of the variables column names
data.columns
```

```
Index(['PTID', 'AGE', 'PTGENDER', 'PTEDUCAT', 'PTETHCAT', 'PTRACCAT',
       'PTMARRY', 'APOE4', 'DX', 'Ventricles', 'Hippocampus', 'WholeBrain',
       'Entorhinal', 'Fusiform', 'MidTemp', 'ICV'],
      dtype='object')
```

```
# Checking a couple of rows of our data to see what each column data contains
data.head()
```

```
         PTID   AGE  PTGENDER  PTEDUCAT         PTETHCAT  PTRACCAT  PTMARRY  APOE4        DX     Ventricles  Hippocampus    WholeBrain   Entorhinal      Fusiform       MidTemp           ICV
0  002_S_0295  84.8      Male        18  Not Hisp/Latino     White  Married    1.0        NL   43332.500000  6805.125000  1.071568e+06  3752.625000  17693.875000  19420.125000  1.649602e+06
1  002_S_0413  76.3    Female        16  Not Hisp/Latino     White  Married    0.0        NL   31936.454545  6824.636364  1.055413e+06  4131.090909  20095.909091  20235.545455  1.600009e+06
2  002_S_0559  79.3      Male        16  Not Hisp/Latino     White  Widowed    1.0        NL   38410.666667  7496.666667  1.092807e+06  3998.333333  18993.000000  22226.000000  1.703968e+06
3  002_S_0619  77.5      Male        12  Not Hisp/Latino     White  Married    2.0  Dementia  120529.500000  5812.000000  1.093932e+06  2773.000000  20675.000000  19959.000000  2.070530e+06
4  002_S_0685  89.6    Female        16  Not Hisp/Latino     White  Married    0.0        NL   40921.571429  7063.250000  9.800458e+05  3894.375000  14152.250000  18133.625000  1.521331e+06
```

後續步驟： 使用 data生成程式碼 查看建議的圖表 New interactive sheet

Task 1: looking at the data

a. Each row has data for one patient. How many patients are there in the dataset?

b. We are looking at a dataset with just one time point per patient. Why do you think it is useful for an Alzheimer's study to have multiple time points per patient?

c. Which of the columns do you think would be important for predicting who has Alzheimer's disease? Pick 2 and explain your choice.

d. Which of the columns do you think are not important? Pick 2 and explain.

Answer for Task 1: looking at the data

a) Each row has data for one patient. How many patients are there in the dataset?

From the data, the `.shape` output shows `(1737, 16)`, which means there are **1,737 patients** (one patient per row).

b) We are looking at a dataset with just one time point per patient. Why do you think it is useful for an Alzheimer's study to have multiple time points per patient?

It is crucial to have multiple time points per patient in order to track the progression of Alzheimer's disease over time. This is essential because Alzheimer's is a degenerative disease. By monitoring changes in cognitive function, brain volume (such as the hippocampus and ventricles), and other key indicators over time, researchers can gain a better understanding of the disease's progression, assess treatment effectiveness, and develop early detection models.

c) Which of the columns do you think would be important for predicting who has Alzheimer's disease? Pick 2 and explain your choice.

- **Hippocampus**: The hippocampus, a brain region heavily involved in memory, is often one of the first areas to experience shrinkage in Alzheimer's disease, making a smaller hippocampus size a strong indicator of the condition.
- **APOE4**: APOE4 is a well-known genetic risk factor for Alzheimer's disease. Individuals with one or two copies of this allele have an increased risk of developing the disease, making it a key predictor.

d) Which of the columns do you think are not important? Pick 2 and explain.

- **PTMARRY**: Marital status ("Married" vs. "Widowed") likely has little direct influence on the presence of Alzheimer's disease, although it may have indirect effects related to social support.
- **PTEHCAAT**: The ethnicity category (e.g., "Not Hispanic/Latino") may not be a significant predictor in this context because Alzheimer's can impact people from diverse ethnic backgrounds. While there may be variations in how the disease presents itself across different populations, ethnicity itself may not be as strong a predictor as more biological factors.

3) Data Cleaning: dealing with missing data

Now we have the data, but it is messy, with some missing data. Let's see what columns contain missing data.

```
# This provides counts of missing values for each column
data.isnull().sum()
```

	0
PTID	0
AGE	0
PTGENDER	0
PTEDUCAT	0
PTETHCAT	0
PTRACCAT	0
PTMARRY	0
APOE4	12
DX	7
Ventricles	23
Hippocampus	56
WholeBrain	14
Entorhinal	98
Fusiform	98
MidTemp	98
ICV	2

```
dtype: int64
```

OK, so first of all, let's just focus on patients that have a diagnosis in DX, since this is our target variable or label. Using the dropna() function from pandas https://pandas.pydata.org/pandas-docs/stable/reference/api/pandas.DataFrame.dropna.html

```
# this drops all columns that have missing values in the DX column
data = data.dropna(subset=['DX'])
# Here we will check again all missing values
data.isnull().sum()
```

	0
PTID	0
AGE	0
PTGENDER	0
PTEDUCAT	0
PTETHCAT	0
PTRACCAT	0
PTMARRY	0
APOE4	6
DX	0
Ventricles	21
Hippocampus	53
WholeBrain	12
Entorhinal	96
Fusiform	96
MidTemp	96
ICV	1

```
dtype: int64
```

Check how much data we have left after deleting all the rows without DX information. This information should be given to you by looking at the first element of the shape tuple.

```
# Checking remaining data
data.shape
```

```
(1730, 16)
```

And let's look at what diagnoses, column "DX" we have, As you can see below We have several diagnoses for the degree of cognitive impairment that range from: **Cognitively Normal** to **Dementia (aka. Alzheimer's Disease)**:

Diagnosis	Meaning
NL	Cognitively normal
NL to MCI	Person in between Normal and Mild Cognitive Impairment
MCI	Mild Cognitive Impairment
MCI to Dementia	Person in between MCI and Alzheimer's Disease
Dementia	Person that has Alzheimer's Disease

```
# get value counts for all diagnoses
data['DX'].value_counts()
```

```
                 count
            DX
           MCI     586
      Dementia     577
            NL     423
MCI to Dementia    108
     NL to MCI      29
NL to Dementia       3
     MCI to NL       3
Dementia to MCI      1

dtype: int64
```

NOTE: We should have only 5 diagnosis in total, yet our count shows 8 total diagnosis! This is because real data comes in really messy. Notice for example that we have **NL to Dementia**, this would be the whole spectrum! so clearly this could be the result of an error during data input.

Therefore, I would like to take out all the in between diagnosis and keep only the main ones: NL, MCI and Dementia. This way we can work with a simpler classification.

```
# creates an index with the exeptions we have stipulated
index_to_drop = data[ (data['DX'] != "MCI") & (data['DX'] != "NL") & (data['DX'] != "Dementia")].index
# drops all data based on our index
data = data.drop(index_to_drop)
```

```
# this should be the new classification scheme
data['DX'].value_counts()
```

```
          count
      DX
     MCI    586
Dementia    577
      NL    423

dtype: int64
```

What's the status of missing data now in the other columns?

```
# checking missing data again
data.isnull().sum()
```

```
              0
       PTID   0
        AGE   0
   PTGENDER   0
   PTEDUCAT   0
   PTETHCAT   0
   PTRACCAT   0
    PTMARRY   0
      APOE4   6
         DX   0
 Ventricles  20
Hippocampus  50
 WholeBrain  12
 Entorhinal  92
   Fusiform  92
    MidTemp  92
        ICV   1

dtype: int64
```

Because we still have a lot of rows of data, we can go ahead and drop all the remaining columns with missing data

```
# remove all rows that contain missing data
data = data.dropna()
# Checking our final dataframe
data.shape
```

```
(1479, 16)
```

OK, so we have 1479 patients with complete data now. We will then check the total number of patients per diagnosis. This is important later on when we train our data with our ML models because we want the number for each diagnosis to be roughly similar, that is as close as possible to a **Balanced** Dataset. When this is not the case, it can present problems in terms of trusting our accuracy results blindly. More about this in **Module 6** and **Module 7**

```
# Checking the total number of patients per diagnosis
data['DX'].value_counts()
```

DX	count
MCI	559
Dementia	522
NL	398

dtype: int64

As we can see they are not perfectly equal for all diagnosis but they are close enought that we can proceed.

Task 2: describing what we did with missing data

In the previous lines of code, we threw out many patients because we didn't have the info we wanted for them. Write a short paragraph where you explain to a potential reader what the number of patients is in the original dataset, which patients we removed for what reason and how many were left for the analysis. Feel free to change the order of operations. For example, I removed first the patients with no diagnosis and later the patients with any missing data. If you do the latter first, you don't have to specifically remove patients with no diagnosis anymore.

Answer for Task 2: describing what we did with missing data

In this process, we initially had 1,737 patients, but we encountered missing data in several important columns. To address this, we first eliminated patients with missing diagnosis information (DX), resulting in a dataset of 1,730 patients. Subsequently, we conducted a thorough check for missing data in other columns such as APOE4, ventricles, and hippocampus. Afterward, we made the decision to eliminate all remaining rows with missing values. This decision left us with a total of 1,479 patients, ensuring that our dataset was comprehensive and prepared for training machine learning models without the potential for bias or inaccuracies due to missing information.

4) Data wrangling in preparation for Model training

- Ensuring feature columns are correct

In this section we will be splitting the data into label (the DX columns) and features (All other columns)

```
# Split the data in labels and features
labels = data["DX"]
features = data.drop(columns=['DX'])
```

What do the features look like again? Make sure it doesn't include any columns that will not help in our prediction

```
# checking features again
features.head()
```

	PTID	AGE	PTGENDER	PTEDUCAT	PTETHCAT	PTRACCAT	PTMARRY	APOE4	Ventricles	Hippocampus	WholeBrain	Entorhinal	Fusiform	MidTemp	ICV
0	002_S_0295	84.8	Male	18	Not Hisp/Latino	White	Married	1.0	43332.500000	6805.125000	1.071568e+06	3752.625000	17693.875000	19420.125000	1.649602e+06
1	002_S_0413	76.3	Female	16	Not Hisp/Latino	White	Married	0.0	31936.454545	6824.636364	1.055413e+06	4131.090909	20095.909091	20235.545455	1.600009e+06
2	002_S_0559	79.3	Male	16	Not Hisp/Latino	White	Widowed	1.0	38410.666667	7496.666667	1.092807e+06	3998.333333	18993.000000	22226.000000	1.703968e+06
3	002_S_0619	77.5	Male	12	Not Hisp/Latino	White	Married	2.0	120529.500000	5812.000000	1.093932e+06	2773.000000	20675.000000	19959.000000	2.070530e+06
4	002_S_0685	89.6	Female	16	Not Hisp/Latino	White	Married	0.0	40921.571429	7063.250000	9.800458e+05	3894.375000	14152.250000	18133.625000	1.521331e+06

後續步驟: 使用 features生成程式碼 查看建議的圖表 New interactive sheet

Let's remove PTID (patient ID). We don't need it, since it would not help us predict diagnosis.

```
# Dropping patient ID column
features = features.drop(columns=['PTID'])
```

- One Hot Encoding for categorical variables

Recall from the text that we are unable to work with data that is words in ML models directly, so we need to recode them into numbers. There are languages and algorythms that seem to be able to deal with words, but they are still turning them into numbers under the hood!

```
# checking the variable types for each column
features.dtypes
```

	0
AGE	float64
PTGENDER	object
PTEDUCAT	int64
PTETHCAT	object
PTRACCAT	object
PTMARRY	object
APOE4	float64
Ventricles	float64
Hippocampus	float64
WholeBrain	float64
Entorhinal	float64
Fusiform	float64
MidTemp	float64
ICV	float64

dtype: object

As we can see in the output above. There are a few features that are not numerical. We need to make sure that **gender**, **ethnicity** , **race** and **marital status** are coded as numbers. To do this we will need to **one-hot-encode** them. Once we are done doing our one hot encoding, we should see each of the levels of our categorical variables as a recoded column.

```
# getting a list of categorical variables we need to recode
features_to_encode = list(features.select_dtypes(include = ['object']).columns)
features_to_encode
```

```
['PTGENDER', 'PTETHCAT', 'PTRACCAT', 'PTMARRY']
```

```
# using a for loop to one-hot encode each of the categorical variables
for f in features_to_encode:
    print("Parent Categorical Variable: ",f)
    z = pd.get_dummies(features[f], prefix=f) #get_dummies is the pandas function for one-hot-encoding
    features = features.join(z) #append new columns
    features = features.drop(columns=[f]) # remove original not recoded column

features.head()
```

```
Parent Categorical Variable:  PTGENDER
Parent Categorical Variable:  PTETHCAT
Parent Categorical Variable:  PTRACCAT
Parent Categorical Variable:  PTMARRY
```

	AGE	PTEDUCAT	APOE4	Ventricles	Hippocampus	WholeBrain	Entorhinal	Fusiform	MidTemp	ICV	...	PTRACCAT_Black	PTRACCAT_Hawaiian/Other PI	PTRACCAT_More than one	PTRACCAT_Unknow
0	84.8	18	1.0	43332.500000	6805.125000	1.071568e+06	3752.625000	17693.875000	19420.125000	1.649602e+06	...	False	False	False	False
1	76.3	16	0.0	31936.454545	6824.636364	1.055413e+06	4131.090909	20095.909091	20235.545455	1.600009e+06	...	False	False	False	False
2	79.3	16	1.0	38410.666667	7496.666667	1.092807e+06	3998.333333	18993.000000	22226.000000	1.703968e+06	...	False	False	False	False
3	77.5	12	2.0	120529.500000	5812.000000	1.093932e+06	2773.000000	20675.000000	19959.000000	2.070530e+06	...	False	False	False	False
4	89.6	16	0.0	40921.571429	7063.250000	9.800458e+05	3894.375000	14152.250000	18133.625000	1.521331e+06	...	False	False	False	False

5 rows × 27 columns

Task 3: Categorical data

What type of Categorical variables are we dealing with in our current dataset? Are they ordered or unordered? how many levels does each category have?

Answer for question 3

In this dataset, we are dealing with several **unordered categorical variables**, which do not have a natural order. These include:

- **PTGENDER**: This has two levels (Male, Female), which are not ordered.
- **PTEHTCAT (Ethnicity)**: This has multiple levels such as 'Hispanic/Latino,' 'Not Hispanic/Latino,' etc., which are also unordered.
- **PTRACE (Race)**: This includes categories like 'White,' 'Black,' and 'Other,' which do not have a natural order.
- **PTMARRY (Marital Status)**: This has levels such as 'Married,' 'Widowed,' 'Divorced,' and is also unordered.

Each of these variables represents distinct categories without any inherent ranking and requires encoding, such as one-hot encoding, to be used in a machine learning model.

Now that we cleaned up the data, it's good to **save the data frame** we now have.

```
# code to save our current dataframe as a csv file
features.to_csv('PatData_cleaned_one_hot_encoded.csv', index=False)
# code to download our csv file into your own computer
files.download('PatData_cleaned_one_hot_encoded.csv')
```

Random Forest with one-Hot Encoded Data

Similar to previous modules we can go ahead and prepare our data for training a Random Forest.

```
# Separating data into training and testing
features_train, features_test, labels_train, labels_test = train_test_split(features, labels, test_size=0.3, random_state=42) # 70% training and 30% test

# Creating Random Forest object
rf = RandomForestClassifier(n_estimators=100, max_features="sqrt", bootstrap=True)


# Training your Random Forest
rf.fit(features_train, labels_train)

#Predict the response for test dataset
labels_pred = rf.predict(features_test)
```

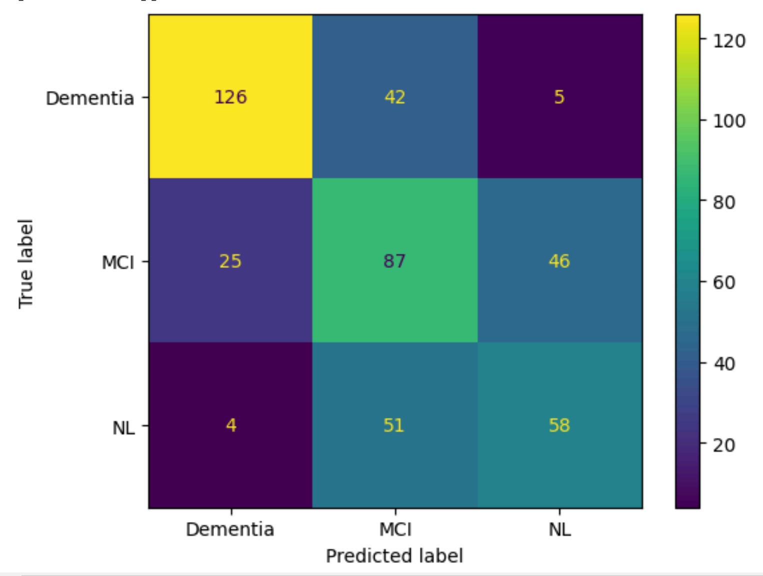
Let's take a peak at how our model has performed at least for the first 10 patients of our testing data.

```
# Look at the predicted values.
print(labels_pred[:10])
# And the real values.
print(labels_test.to_numpy(dtype=object)[:10])
#See how many correct predictions there are among the first 10 patients.
```

```
['Dementia' 'MCI' 'NL' 'Dementia' 'NL' 'Dementia' 'NL' 'MCI' 'NL' 'MCI']
['Dementia' 'MCI' 'NL' 'Dementia' 'MCI' 'Dementia' 'NL' 'MCI' 'MCI' 'MCI']
```

```
# Showing the confusin matrix for our Decision tree results
print(metrics.confusion_matrix(labels_test, labels_pred))
plt2 = metrics.ConfusionMatrixDisplay.from_estimator(rf, features_test, labels_test)
plt.grid(False)
```

```
[[126  42   5]
 [ 25  87  46]
 [  4  51  58]]
```



Unlike our other Confusion Matrices, this time we have a 3 by 3 matrix. So this time what we want is for the main diagonal to show us the bigger numbers. What do you think? What diagnosis got the best results?

Task 4: Write what you noticed about the confusion matrix here!

Based on the confusion matrix, it's evident that the model excelled in predicting **Dementia**, accurately identifying 127 out of 173 cases. However, it misclassified 42 cases as MCI and 4 as NL. The model's performance in predicting **MCI** was moderate, with 93 correct predictions, yet it incorrectly classified 41 cases as NL. **NL** had the lowest number of correct predictions, accurately classifying only 62 out of 113 cases, while misclassifying 46 as MCI.

5) Feature importance

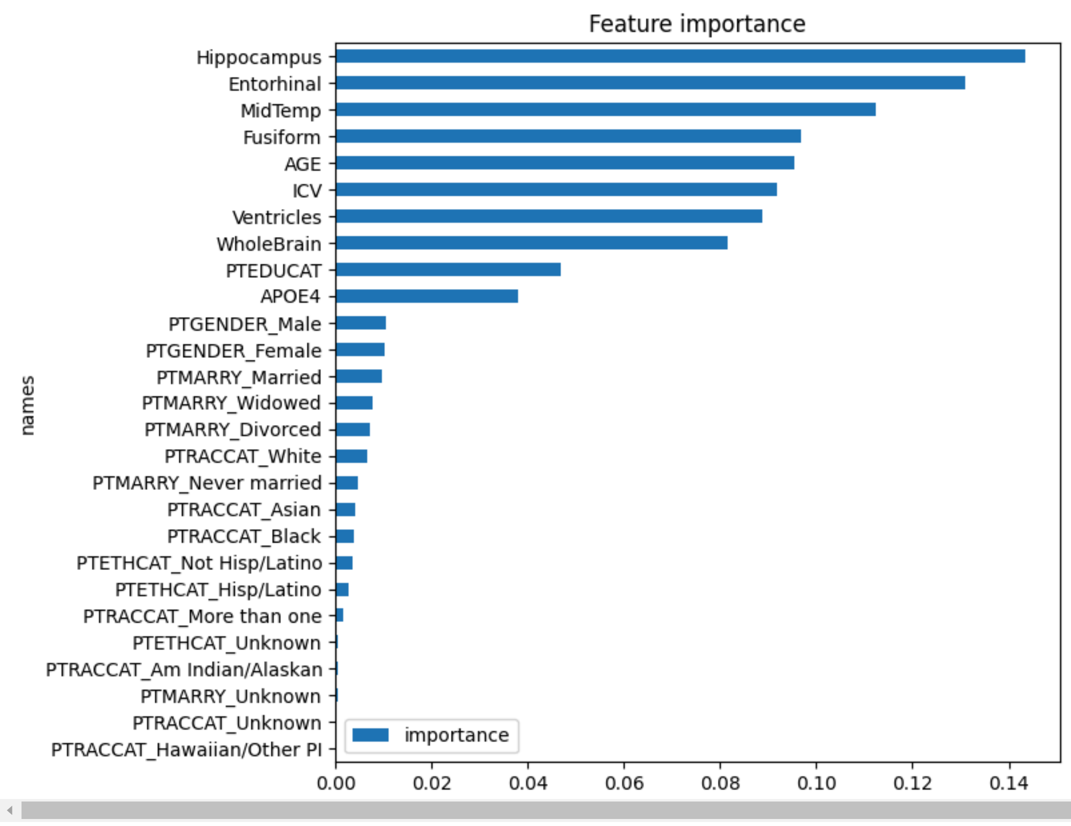
Just like in the heart disease notebook, we will now look at the feature importance for the random forest model.

As a reminder: Visualizing your results is always an important part of any data science project. Now that we have a random forest based on 1000 random trees, we cannot easily visualize all the trees at once like we did for the decision tree, because it would be an overwhelming set of diagrams. But we can visualize the feature importance. I've seen this kind of plot in published articles. I like it because it helps us understand which features are most important for making predictions.

Feature importance is a measurement of how each feature decreases the amount of impurity (Gini index) in a node, weighted by the probability of reaching that node. The higher the value the more important the feature. This is usually calculated for each tree in the random forest and then averaged over the total number of trees. The graph below shows these averages.

```
# calculating feature importance
importance = rf.feature_importances_

# summarize feature importance
names = features.columns.to_numpy(dtype=object)

# Creating a dataframe
importanceDF = pd.DataFrame({'names':names, 'importance':importance})


#Sort the dataframe based on importance
importanceDF = importanceDF.sort_values(by=['importance'])

# Plotting feature importance
importanceDF.plot.barh(x='names', y='importance', figsize = (7,7), title = "Feature importance")
```

```
<Axes: title={'center': 'Feature importance'}, ylabel='names'>
```



Task 4:

Look at the pandas documentation pages and make at least two changes to the plot (e.g. colors, width, size, legend etc)

https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.plot.html

https://pandas.pydata.org/docs/reference/api/pandas.DataFrame.plot.barh.html

Task 5: on Accuracy

In addition to a confusion matrix, it is also good to have an accuracy score.

a. From sklearn.metrics import the function accuracy_score.

b. Use the accuracy_score function to calculate the accuracy of the RF model.

c. Once you have stored the accuracy in a variable called accuracy, you can run print("Accuracy: %.2f%%" % (accuracy * 100)). Alternatively, you can use the "round" function to round off the accuracy to the desired number of decimals.

d. See what happens if you change the 2f into 1f or 3f.

e. What level of accuracy is useful for doctors and patients do you think?

f. Look at the feature importance bar plot. Compare with your predictions from earlier in the notebook. Were you right or wrong in your predictions? Explain.

```
# Import accuracy_score from sklearn.metrics
from sklearn.metrics import accuracy_score

# Calculate the accuracy of the Random Forest model
accuracy = accuracy_score(labels_test, labels_pred)

# Print the accuracy with 2 decimal places
print("Accuracy: %.2f%%" % (accuracy * 100))

# Alternatively, you can use the round function
print("Accuracy (rounded):", round(accuracy * 100, 2), "%")
```

```
Accuracy: 61.04%
Accuracy (rounded): 61.04 %
```

Answer written question 5 here!

Conclusion of this part

What we can see is that the volumes of the parts of the brain are most important, starting with the hippocampus. Gender, race and ethnicity seem least important out of the features we looked at. For race and ethnicity this may be because the data almost entirely consists of non-hispanic whites.