In [1]:

```python
# Importing the necessary libraries
import numpy as np
import matplotlib.pyplot as plt
import pandas as pd
import seaborn as sns
```

In [2]:

```python
# Loading the dataset
df = pd.read_csv('med dataset.csv')
```

In [3]:

```python
df.head()
```

Out[3]:

	id	age	year	sex	glang	part	job	stud_h	health	psyt	jspe	qcae_cog	qcae_aff	amsp	erec_mean	c
0	2	18	1	1	120	1	0	56	3	0	88	62	27	17	0.738095	
1	4	26	4	1	1	1	0	20	4	0	109	55	37	22	0.690476	
2	9	21	3	2	1	0	0	36	3	0	106	64	39	17	0.690476	
3	10	21	2	2	1	0	1	51	5	0	101	52	33	18	0.833333	
4	13	21	3	1	1	1	0	22	4	0	102	58	28	21	0.690476	

In [4]:

```python
# column types
df.dtypes
```

Out[4]:

```
id              int64
age             int64
year            int64
sex             int64
glang           int64
part            int64
job             int64
stud_h          int64
health          int64
psyt            int64
jspe            int64
qcae_cog        int64
qcae_aff        int64
amsp            int64
erec_mean     float64
cesd            int64
stai_t          int64
mbi_ex          int64
mbi_cy          int64
mbi_ea          int64
dtype: object
```

In [5]:

```python
# checking for missing values
df.isnull().sum() # no missing values
```

Out[5]:

```
id           0
age          0
year         0
sex          0
glang        0
part         0
job          0
stud_h       0
health       0
psyt         0
jspe         0
qcae_cog     0
qcae_aff     0
```

```
amsp          0
erec_mean     0
cesd          0
stai_t        0
mbi_ex        0
mbi_cy        0
mbi_ea        0
dtype: int64
```

In [6]:
```
# removing the 'id' column
df.drop(['id'], axis=1, inplace=True)
```

In [7]:
```
# check for duplicates
df.duplicated().sum() # no duplicates
```

Out[7]:
```
0
```

In [8]:
```
# separate the data into two groups: categorical and numerical
df_cat = df[['sex', 'year', 'part', 'glang', 'job', 'stud_h', 'health', 'psyt']]
df_num = df[['age', 'jspe', 'qcae_aff', 'amsp', 'erec_mean', 'cesd', 'stai_t', 'mbi_ex',
```

In [9]:
```
# Categorical Data
# Description
df_cat.head(20)
```

Out[9]:

	sex	year	part	glang	job	stud_h	health	psyt
0	1	1	1	120	0	56	3	0
1	1	4	1	1	0	20	4	0
2	2	3	0	1	0	36	3	0
3	2	2	0	1	1	51	5	0
4	1	3	1	1	0	22	4	0
5	2	5	1	1	1	10	2	0
6	2	5	1	1	0	15	3	0
7	1	4	1	1	1	8	4	0
8	2	4	1	1	1	20	2	0
9	2	2	1	1	0	20	5	0
10	1	1	0	1	0	20	4	0
11	2	1	0	1	1	9	5	1
12	2	5	0	90	0	25	5	0
13	2	2	1	1	0	51	2	1
14	2	2	1	1	0	42	3	0
15	1	2	1	1	0	40	4	0
16	1	1	1	90	0	9	4	0
17	1	4	1	1	0	10	4	0
18	2	5	0	1	0	38	4	0
19	2	3	1	1	0	15	4	0

In [10]:
```
# Descriptive Statistics
df_cat.describe(include="all")
```

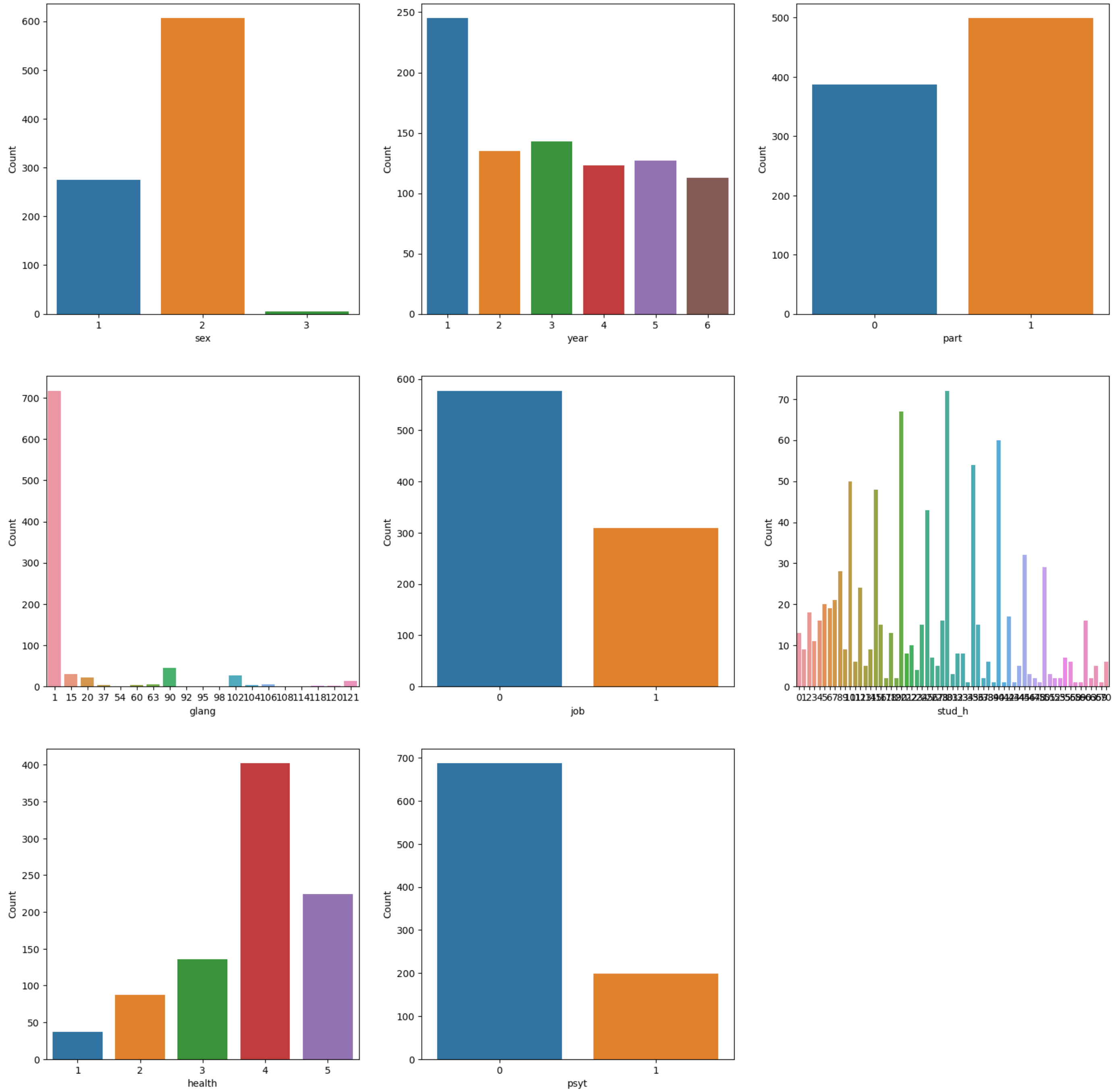
	sex	year	part	glang	job	stud_h	health	psyt

Out[10]:

count	886.000000	886.000000	886.000000	886.000000	886.000000	886.000000	886.000000	886.000000
mean	1.695260	3.102709	0.563205	14.327314	0.348758	25.288939	3.777652	0.224605
std	0.472665	1.763937	0.496269	32.366389	0.476847	15.927875	1.061497	0.417558
min	1.000000	1.000000	0.000000	1.000000	0.000000	0.000000	1.000000	0.000000
25%	1.000000	1.000000	0.000000	1.000000	0.000000	12.000000	3.000000	0.000000
50%	2.000000	3.000000	1.000000	1.000000	0.000000	25.000000	4.000000	0.000000
75%	2.000000	5.000000	1.000000	1.000000	1.000000	36.000000	5.000000	0.000000
max	3.000000	6.000000	1.000000	121.000000	1.000000	70.000000	5.000000	1.000000

In [11]:

```
# Plotting the count of each category for each feature using Seaborn

# Set the figure size
plt.figure(figsize=(20, 20))

# Plot the count of each category for each feature
for i, col in enumerate(df_cat.columns):
    plt.subplot(3, 3, i+1)
    sns.countplot(x=col, data=df_cat)
    plt.xlabel(col)
    plt.ylabel('Count')
```



In [12]:

```python
# Finding relationships between categorical variables using Chi-Square test
from scipy.stats import chi2_contingency
# create an empty list to store the results
chi2_results = []

#Loop through each pair of categorical columns and perform Chi-Square test
for i, col1 in enumerate(df_cat.columns):
    for j, col2 in enumerate(df_cat.columns):
        if i < j:
            chi2, p, dof, ex = chi2_contingency(pd.crosstab(df_cat[col1], df_cat[col2]))
            chi2_results.append({'Variable 1': col1, 'Variable 2': col2, 'Chi-Square': c

# Create a DataFrame from the results list
chi2_table = pd.DataFrame(chi2_results)

# Display the resulting DataFrame
print(chi2_table)
```

```
   Variable 1 Variable 2   Chi-Square       p-value
0         sex       year    12.769894  2.368234e-01
1         sex       part     6.787509  3.358236e-02
2         sex      glang    54.444023  2.496473e-02
```

```
3        sex       job    0.399311  8.190127e-01
4        sex    stud_h  102.535577  8.736027e-01
5        sex    health   21.975553  4.961357e-03
6        sex      psyt   23.484975  7.948815e-06
7       year      part   27.375938  4.818767e-05
8       year     glang  109.823807  7.634917e-02
9       year       job   72.560233  3.002212e-14
10      year    stud_h  608.992141  3.320205e-23
11      year    health   21.604790  3.623350e-01
12      year      psyt    4.315674  5.049176e-01
13      part     glang   22.638009  2.048861e-01
14      part       job    1.811389  1.783416e-01
15      part    stud_h   65.031867  3.058703e-01
16      part    health    7.025088  1.345683e-01
17      part      psyt    0.515159  4.729141e-01
18     glang       job   19.719717  3.488184e-01
19     glang    stud_h 1113.757550  2.317115e-01
20     glang    health   84.094422  1.559493e-01
21     glang      psyt    7.207154  9.882601e-01
22       job    stud_h   81.825491  3.207564e-02
23       job    health    5.115215  2.756787e-01
24       job      psyt    2.909025  8.808513e-02
25    stud_h    health  293.764489  1.013227e-02
26    stud_h      psyt   42.095944  9.616637e-01
27    health      psyt   27.583952  1.514423e-05
```

In [13]:

```python
# Keep only the pairs of variables that are related (p-value < 0.05) and sort them by p-
chi2_table = chi2_table[chi2_table['p-value'] < 0.05].sort_values(by='p-value')
chi2_table
#from the results, we can conclude that:
# sex and health are both related to psychoterapy in the last year
# sex and health are related
# how long students study is related to their health
```

Out[13]:

	Variable 1	Variable 2	Chi-Square	p-value
10	year	stud_h	608.992141	3.320205e-23
9	year	job	72.560233	3.002212e-14
6	sex	psyt	23.484975	7.948815e-06
27	health	psyt	27.583952	1.514423e-05
7	year	part	27.375938	4.818767e-05
5	sex	health	21.975553	4.961357e-03
25	stud_h	health	293.764489	1.013227e-02
2	sex	glang	54.444023	2.496473e-02
22	job	stud_h	81.825491	3.207564e-02
1	sex	part	6.787509	3.358236e-02

In [14]:

```python
# Percentage of each category for each pair of variables in chi2_table
for i, row in chi2_table.iterrows():
    var1 = row['Variable 1']
    var2 = row['Variable 2']
    print(var1 + " and " + var2)
    print(pd.crosstab(index=df[var1], columns=df[var2], normalize=True))
    print('-----------------')
```

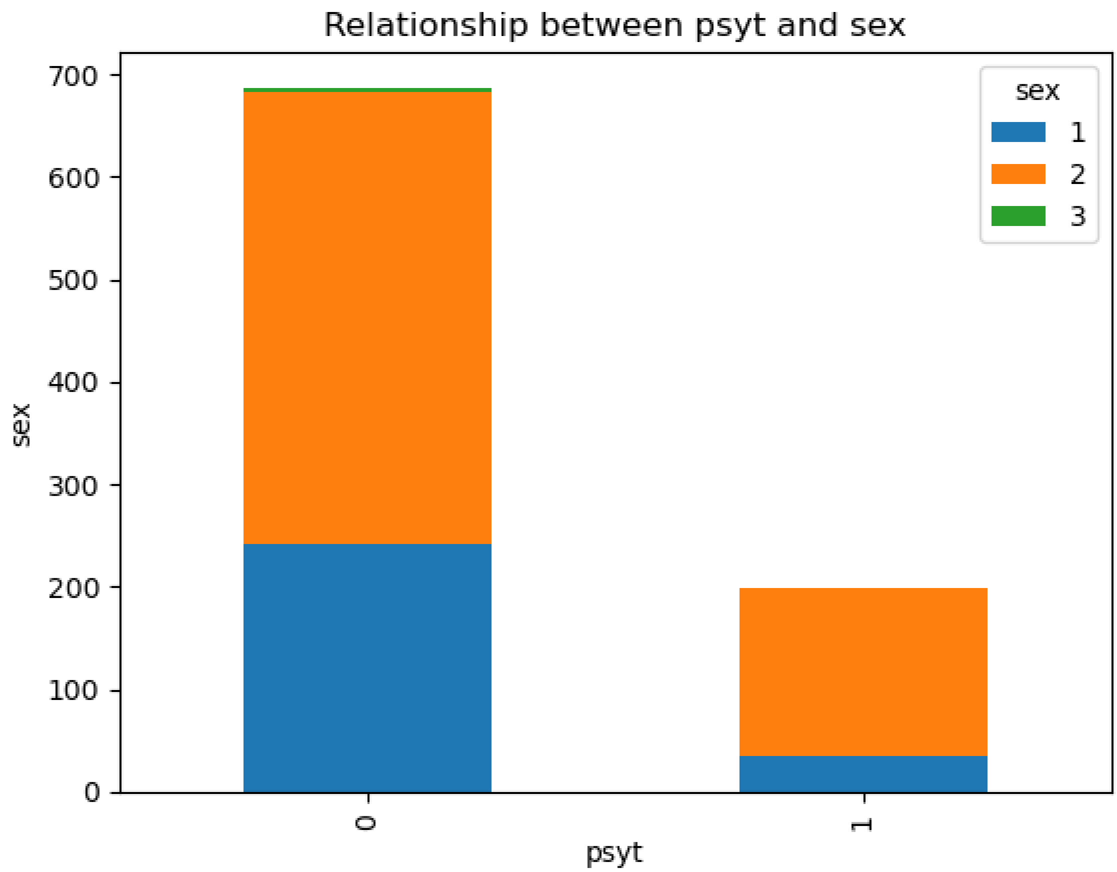
```
year and stud_h
stud_h         0         1         2         3         4         5         6  \
year
1       0.001129  0.000000  0.000000  0.000000  0.001129  0.001129  0.006772
```

```
2       0.000000  0.000000  0.000000  0.000000  0.001129  0.000000  0.001129
3       0.002257  0.000000  0.002257  0.001129  0.000000  0.004515  0.001129
4       0.001129  0.001129  0.001129  0.002257  0.004515  0.005643  0.003386
5       0.002257  0.000000  0.003386  0.001129  0.001129  0.005643  0.001129
6       0.007901  0.009029  0.013544  0.007901  0.010158  0.005643  0.007901

stud_h        7         8         9   ...        53        55        56  \
year                                  ...
1       0.009029  0.006772  0.004515  ...  0.001129  0.005643  0.005643
2       0.002257  0.001129  0.000000  ...  0.001129  0.002257  0.001129
3       0.003386  0.004515  0.000000  ...  0.000000  0.000000  0.000000
4       0.006772  0.004515  0.002257  ...  0.000000  0.000000  0.000000
5       0.001129  0.006772  0.001129  ...  0.000000  0.000000  0.000000
6       0.001129  0.007901  0.002257  ...  0.000000  0.000000  0.000000

stud_h        58        59        60        63        65        69        70
year
1       0.001129  0.001129  0.010158  0.002257  0.003386  0.001129  0.005643
2       0.000000  0.000000  0.004515  0.000000  0.001129  0.000000  0.001129
3       0.000000  0.000000  0.001129  0.000000  0.000000  0.000000  0.000000
4       0.000000  0.000000  0.000000  0.000000  0.001129  0.000000  0.000000
5       0.000000  0.000000  0.002257  0.000000  0.000000  0.000000  0.000000
6       0.000000  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000

[6 rows x 61 columns]
-----------------
year and job
job          0         1
year
1     0.223476  0.053047
2     0.118510  0.033860
3     0.092551  0.068849
4     0.064334  0.074492
5     0.071106  0.072235
6     0.081264  0.046275
-----------------
sex and psyt
psyt         0         1
sex
1     0.272009  0.038375
2     0.498871  0.185102
3     0.004515  0.001129
-----------------
health and psyt
psyt           0         1
health
1       0.033860  0.007901
2       0.060948  0.037246
3       0.106095  0.047404
4       0.356659  0.097065
5       0.217833  0.034989
-----------------
year and part
part         0         1
year
1     0.151242  0.125282
2     0.069977  0.082393
3     0.064334  0.097065
4     0.049661  0.089165
5     0.065463  0.077878
6     0.036117  0.091422
-----------------
sex and health
health         1         2         3         4         5
sex
1       0.014673  0.025959  0.034989  0.132054  0.102709
```

```
2       0.025959  0.072235  0.116253  0.320542  0.148984
3       0.001129  0.000000  0.002257  0.001129  0.001129
-----------------
stud_h and health
health         1         2         3         4         5
stud_h
0       0.002257  0.003386  0.001129  0.004515  0.003386
1       0.000000  0.001129  0.000000  0.003386  0.005643
2       0.000000  0.005643  0.001129  0.009029  0.004515
3       0.000000  0.000000  0.000000  0.009029  0.003386
4       0.002257  0.001129  0.001129  0.005643  0.007901
...          ...       ...       ...       ...       ...
60      0.001129  0.002257  0.006772  0.002257  0.005643
63      0.000000  0.000000  0.001129  0.000000  0.001129
65      0.000000  0.001129  0.000000  0.002257  0.002257
69      0.000000  0.000000  0.001129  0.000000  0.000000
70      0.000000  0.002257  0.000000  0.001129  0.003386

[61 rows x 5 columns]
-----------------
sex and glang
glang       1         15        20        37        54        60        63   \
sex
1      0.251693  0.010158  0.007901  0.000000  0.000000  0.000000  0.002257
2      0.554176  0.024831  0.016930  0.003386  0.001129  0.003386  0.002257
3      0.003386  0.000000  0.000000  0.000000  0.000000  0.000000  0.001129

glang       90        92        95        98        102       104       106  \
sex
1      0.022573  0.001129  0.000000  0.000000  0.005643  0.001129  0.001129
2      0.027088  0.000000  0.001129  0.001129  0.024831  0.003386  0.005643
3      0.001129  0.000000  0.000000  0.000000  0.000000  0.000000  0.000000

glang       108       114       118       120       121
sex
1      0.001129  0.000000  0.000000  0.001129  0.004515
2      0.000000  0.001129  0.002257  0.001129  0.010158
3      0.000000  0.000000  0.000000  0.000000  0.000000
-----------------
job and stud_h
stud_h        0         1         2         3         4         5         6   \
job
0       0.010158  0.004515  0.010158  0.007901  0.010158  0.009029  0.012415
1       0.004515  0.005643  0.010158  0.004515  0.007901  0.013544  0.009029

stud_h        7         8         9   ...        53        55        56  \
job                                   ...
0       0.014673  0.014673  0.006772  ...  0.001129  0.007901  0.006772
1       0.009029  0.016930  0.003386  ...  0.001129  0.000000  0.000000

stud_h        58        59        60        63        65        69        70
job
0       0.001129  0.001129  0.015801  0.002257  0.004515  0.001129  0.004515
1       0.000000  0.000000  0.002257  0.000000  0.001129  0.000000  0.002257

[2 rows x 61 columns]
-----------------
sex and part
part         0         1
sex
1     0.138826  0.171558
2     0.292325  0.391648
3     0.005643  0.000000
-----------------
```

In [15]:
```
# relationships between psyt and sex
var1 = "psyt"
var2 = "sex"

# create a cross-tabulation table
ctab = pd.crosstab(df[var1], df[var2])
```

In [16]:
```
# plot the cross-tabulation table
ctab.plot(kind='bar', stacked = True)
plt.title("Relationship between " + var1 + " and " +var2)
plt.xlabel(var1)
plt.ylabel(var2)
plt.show()
```



In [17]:
```
# let's see what sex visited a psychoterapist the most in the last year

# create a new data frame
df_psyt = pd.DataFrame(data = {'psyt' : df_cat['psyt'], 'sex' : df_cat['sex']})

#group the data by psychoterapy and sex
df_psyt = df_psyt.groupby(['psyt', 'sex']).size().reset_index(name='count')

# calculate the male, female and non binary in each health category
total = df_psyt['count'].sum()
df_psyt['percentage'] = df_psyt['count']/total *100
df_psyt['sex'] = df_psyt['sex'].map({1: 'Male', 2: 'Female', 3: 'Non-binary'})
```

In [18]:
```
df_psyt # females tend to visit the psychoterapist more than males or non-binary people
```

Out[18]:

	psyt	sex	count	percentage
0	0	Male	241	27.200903
1	0	Female	442	49.887133
2	0	Non-binary	4	0.451467

3	1	Male	34	3.837472
4	1	Female	164	18.510158
5	1	Non-binary	1	0.112867

In [19]:

```
# print each percentage for every pair of variables in chi2_table
for i, row in chi2_table.iterrows():
    var1 = row['Variable 1']
    var2 = row['Variable 2']
    print(f"{var1} and {var2}")

    # Create a temporary DataFrame with the pair of variables
    df_temp = pd.DataFrame(data={var1: df_cat[var1], var2: df_cat[var2]})
    df_temp = df_temp.groupby([var1, var2]).size().reset_index(name='count')
    total = df_temp['count'].sum()
    df_temp['percentage'] = df_temp['count'] / total * 100
    # Append the sum of numeric columns
    sum_row = df_temp.sum(numeric_only=True)
    sum_row[var1] = 'Total'
    sum_row[var2] = ''
    df_temp = pd.concat([df_temp, pd.DataFrame(sum_row).T], ignore_index=True)

    print(df_temp)
    print('-----------------')
```

```
year and stud_h
      year stud_h  count percentage
0        1      0      1   0.112867
1        1      4      1   0.112867
2        1      5      1   0.112867
3        1      6      6   0.677201
4        1      7      8   0.902935
..     ...    ...    ...        ...
218      6     36      2   0.225734
219      6     40      3     0.3386
220      6     45      1   0.112867
221      6     50      1   0.112867
222  Total         886.0      100.0

[223 rows x 4 columns]
-----------------
year and job
     year job  count percentage
0       1   0    198   22.34763
1       1   1     47    5.30474
2       2   0    105  11.851016
3       2   1     30   3.386005
4       3   0     82   9.255079
5       3   1     61   6.884876
6       4   0     57   6.433409
7       4   1     66    7.44921
8       5   0     63   7.110609
9       5   1     64   7.223476
10      6   0     72   8.126411
11      6   1     41    4.62754
12  Total      886.0      100.0
-----------------
sex and psyt
     sex psyt  count percentage
0      1    0    241  27.200903
1      1    1     34   3.837472
2      2    0    442  49.887133
3      2    1    164  18.510158
4      3    0      4   0.451467
```

```
5      3    1      1   0.112867
6  Total       886.0      100.0
-----------------
health and psyt
   health psyt  count percentage
0       1    0     30   3.386005
1       1    1      7   0.790068
2       2    0     54   6.094808
3       2    1     33   3.724605
4       3    0     94  10.609481
5       3    1     42   4.740406
6       4    0    316  35.665914
7       4    1     86   9.706546
8       5    0    193  21.783296
9       5    1     31   3.498871
10  Total       886.0      100.0
-----------------
year and part
     year part  count percentage
0       1    0    134  15.124153
1       1    1    111  12.528217
2       2    0     62   6.997743
3       2    1     73   8.239278
4       3    0     57   6.433409
5       3    1     86   9.706546
6       4    0     44    4.96614
7       4    1     79   8.916479
8       5    0     58   6.546275
9       5    1     69    7.78781
10      6    0     32   3.611738
11      6    1     81   9.142212
12  Total       886.0      100.0
-----------------
sex and health
      sex health  count percentage
0       1      1     13   1.467269
1       1      2     23   2.595937
2       1      3     31   3.498871
3       1      4    117  13.205418
4       1      5     91   10.27088
5       2      1     23   2.595937
6       2      2     64   7.223476
7       2      3    103  11.625282
8       2      4    284  32.054176
9       2      5    132   14.89842
10      3      1      1   0.112867
11      3      3      2   0.225734
12      3      4      1   0.112867
13      3      5      1   0.112867
14  Total          886.0      100.0
-----------------
stud_h and health
    stud_h health  count percentage
0        0      1      2   0.225734
1        0      2      3     0.3386
2        0      3      1   0.112867
3        0      4      4   0.451467
4        0      5      3     0.3386
..     ...    ...    ...        ...
189     69      3      1   0.112867
190     70      2      2   0.225734
191     70      4      1   0.112867
192     70      5      3     0.3386
193  Total          886.0      100.0

[194 rows x 4 columns]
```

```
-----------------
sex and glang
      sex glang  count percentage
0       1     1    223    25.1693
1       1    15      9   1.015801
2       1    20      7   0.790068
3       1    63      2   0.225734
4       1    90     20   2.257336
5       1    92      1   0.112867
6       1   102      5   0.564334
7       1   104      1   0.112867
8       1   106      1   0.112867
9       1   108      1   0.112867
10      1   120      1   0.112867
11      1   121      4   0.451467
12      2     1    491  55.417607
13      2    15     22    2.48307
14      2    20     15   1.693002
15      2    37      3     0.3386
16      2    54      1   0.112867
17      2    60      3     0.3386
18      2    63      2   0.225734
19      2    90     24   2.708804
20      2    95      1   0.112867
21      2    98      1   0.112867
22      2   102     22    2.48307
23      2   104      3     0.3386
24      2   106      5   0.564334
25      2   114      1   0.112867
26      2   118      2   0.225734
27      2   120      1   0.112867
28      2   121      9   1.015801
29      3     1      3     0.3386
30      3    63      1   0.112867
31      3    90      1   0.112867
32  Total        886.0      100.0
-----------------
job and stud_h
       job stud_h  count percentage
0        0      0      9   1.015801
1        0      1      4   0.451467
2        0      2      9   1.015801
3        0      3      7   0.790068
4        0      4      9   1.015801
..     ...    ...    ...        ...
101      1     53      1   0.112867
102      1     60      2   0.225734
103      1     65      1   0.112867
104      1     70      2   0.225734
105  Total         886.0      100.0

[106 rows x 4 columns]
-----------------
sex and part
     sex part  count percentage
0      1    0    123  13.882619
1      1    1    152  17.155756
2      2    0    259  29.232506
3      2    1    347  39.164786
4      3    0      5   0.564334
5  Total       886.0      100.0
-----------------
```

In [20]:

```
# Numerical variables
df_num.head()
```

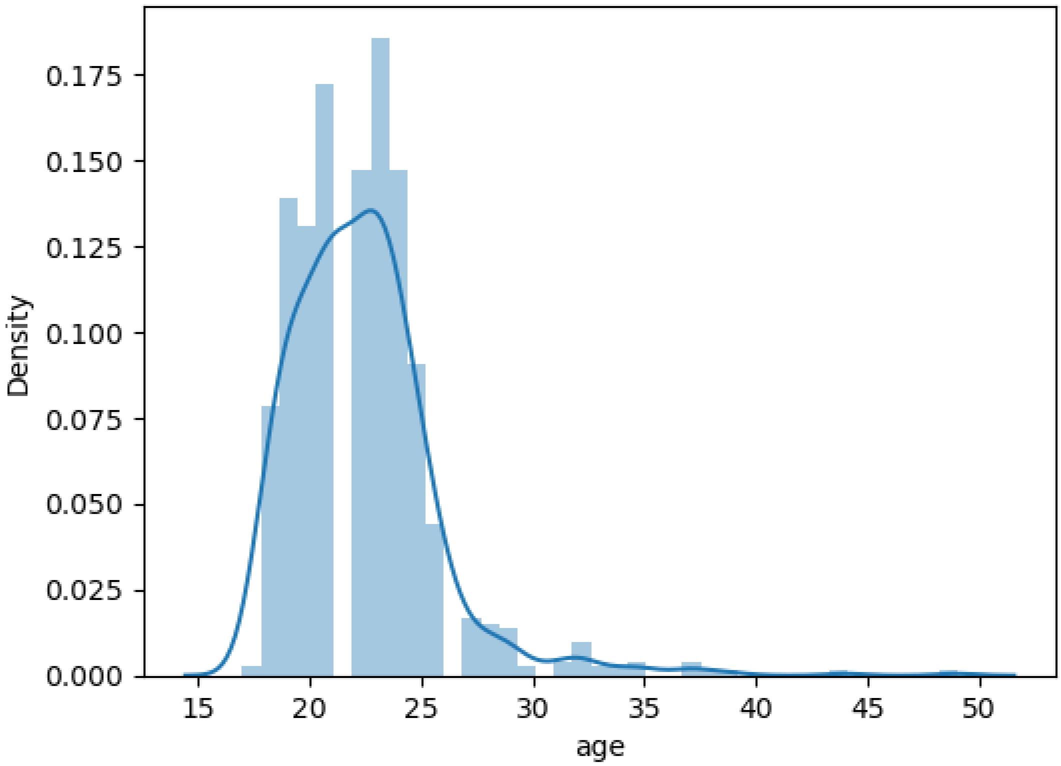
Out[20]:

	age	jspe	qcae_aff	amsp	erec_mean	cesd	stai_t	mbi_ex	mbi_cy	mbi_ea
0	18	88	27	17	0.738095	34	61	17	13	20
1	26	109	37	22	0.690476	7	33	14	11	26
2	21	106	39	17	0.690476	25	73	24	7	23
3	21	101	33	18	0.833333	17	48	16	10	21
4	21	102	28	21	0.690476	14	46	22	14	23

In [21]:

```
# Distribution of the numerical variables
plt.figure(figsize = (20,20))
for i, col in enumerate(df_num.columns):
    plt.subplot(4, 3, i+1)
    sns.distplot(df_num[col])
    plt.xlabel(col)
    plt.ylabel('Density')
    plt.show()
```

```
C:\Users\Oana\AppData\Local\Temp\ipykernel_15732\2063736890.py:5: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(df_num[col])
```




```
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```

```
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```

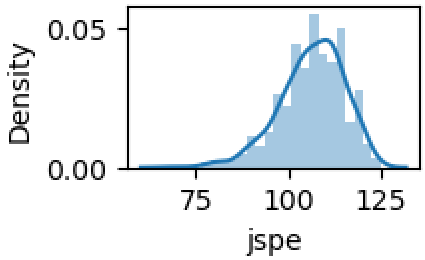


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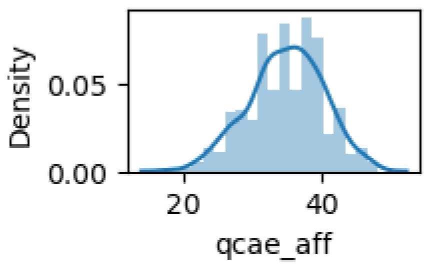
```




```
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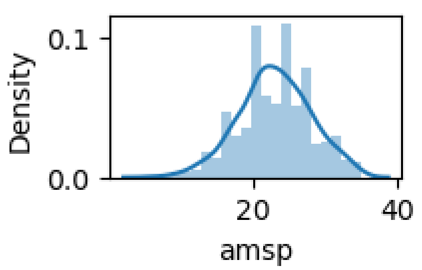
```




```
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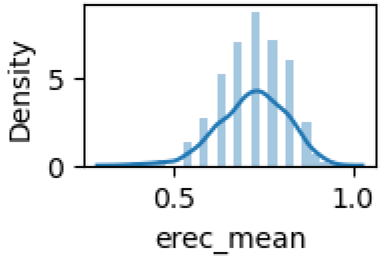


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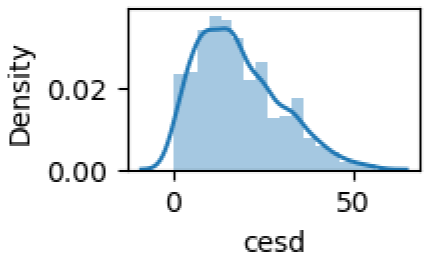


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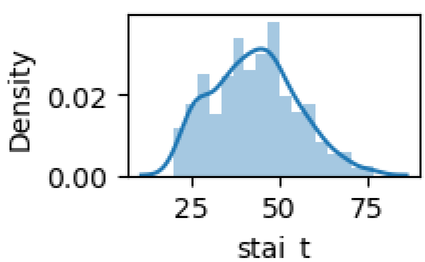


```
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```

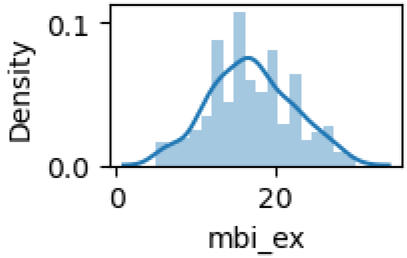


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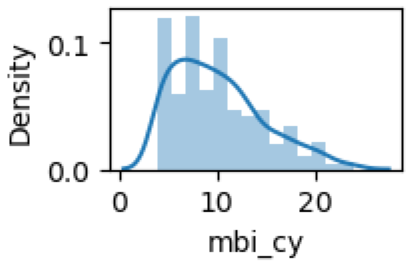
```




```
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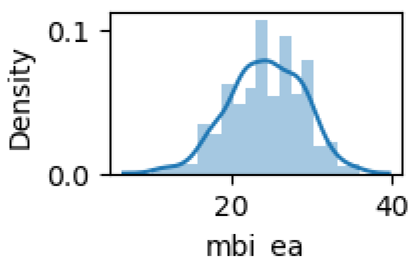
  sns.distplot(df_num[col])
```



In [22]:

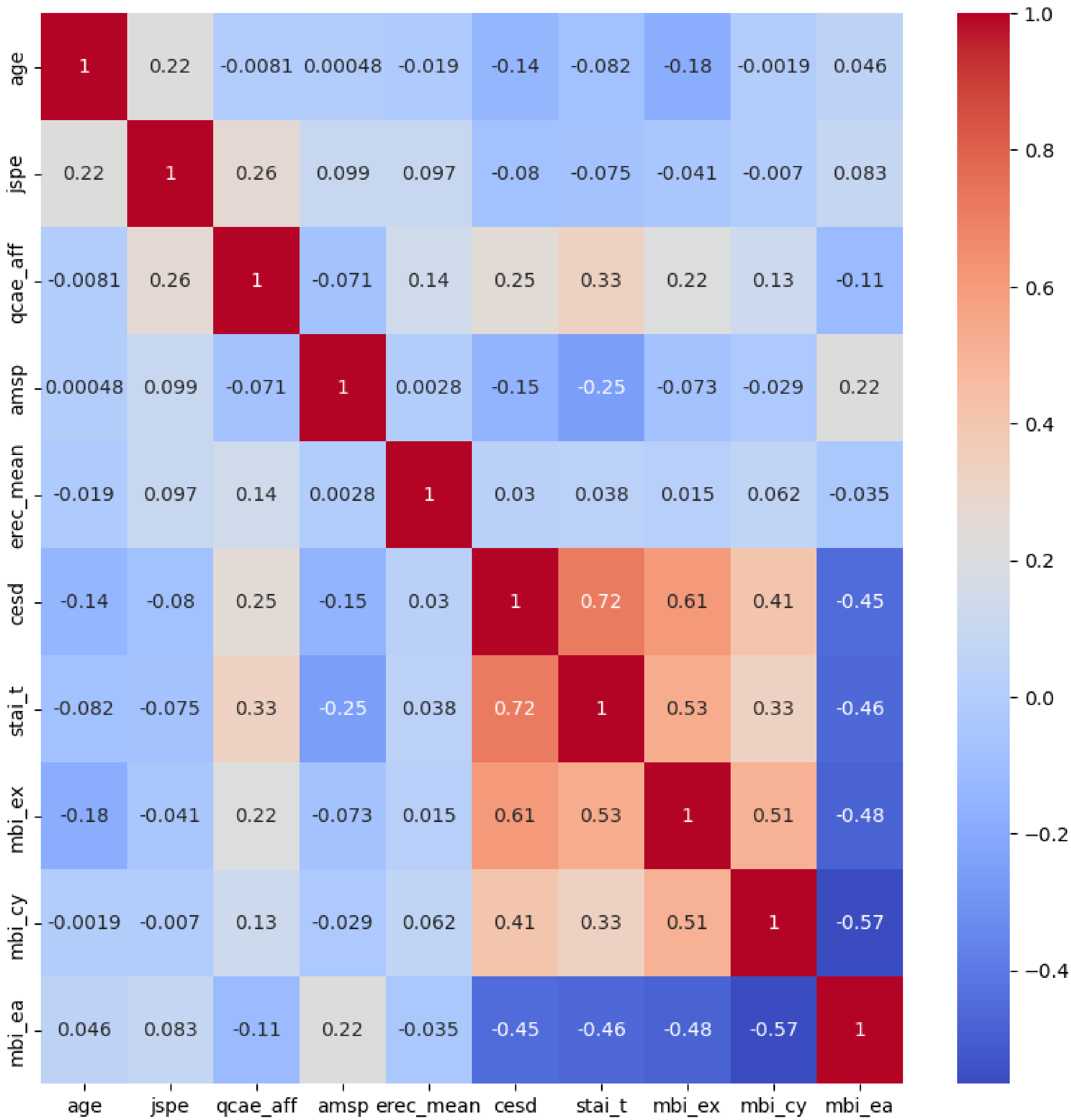
```
# Correlation matrix
corr_matrix = df_num.corr(method = 'pearson')
corr_matrix
```

Out[22]:

	age	jspe	qcae_aff	amsp	erec_mean	cesd	stai_t	mbi_ex	mbi_cy
age	1.000000	0.223221	-0.008130	0.000477	-0.018699	-0.139106	-0.081893	-0.182733	-0.001853
jspe	0.223221	1.000000	0.263384	0.099395	0.097062	-0.080058	-0.075036	-0.040542	-0.006981
qcae_aff	-0.008130	0.263384	1.000000	-0.071391	0.141379	0.250947	0.331350	0.215886	0.128488
amsp	0.000477	0.099395	-0.071391	1.000000	0.002780	-0.152052	-0.249231	-0.073011	-0.029343
erec_mean	-0.018699	0.097062	0.141379	0.002780	1.000000	0.029881	0.037688	0.015348	0.061965
cesd	-0.139106	-0.080058	0.250947	-0.152052	0.029881	1.000000	0.715728	0.605617	0.407727

stai_t	-0.081893	-0.075036	0.331350	-0.249231	0.037688	0.715728	1.000000	0.530486	0.331884
mbi_ex	-0.182733	-0.040542	0.215886	-0.073011	0.015348	0.605617	0.530486	1.000000	0.505200
mbi_cy	-0.001853	-0.006981	0.128488	-0.029343	0.061965	0.407727	0.331884	0.505200	1.000000
mbi_ea	0.046130	0.082508	-0.113891	0.220616	-0.034889	-0.453589	-0.462535	-0.480821	-0.565939

In [23]:
```
# heatmap of the correlation matrix
plt.figure(figsize = (10,10))
sns.heatmap(corr_matrix, annot = True, cmap = 'coolwarm')
plt.show()
```



In [24]:
```
# get a dataframe of the the most to least correlated variables
corr_matrix = corr_matrix.unstack().reset_index()
corr_matrix.columns = ['Variable 1', 'Variable 2', 'Correlation']
corr_matrix = corr_matrix[corr_matrix['Variable 1'] != corr_matrix['Variable 2']]
corr_matrix = corr_matrix.sort_values(by = 'Correlation', ascending = False)
corr_matrix
```

Out[24]:

	Variable 1	Variable 2	Correlation
65	stai_t	cesd	0.715728
56	cesd	stai_t	0.715728
75	mbi_ex	cesd	0.605617
57	cesd	mbi_ex	0.605617
67	stai_t	mbi_ex	0.530486
...	...	...	...
96	mbi_ea	stai_t	-0.462535
79	mbi_ex	mbi_ea	-0.480821
97	mbi_ea	mbi_ex	-0.480821
89	mbi_cy	mbi_ea	-0.565939
98	mbi_ea	mbi_cy	-0.565939

90 rows × 3 columns

In [25]:

```
# Principal Component Analysis (PCA)
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
```

In [26]:

```
# standardize the data
scaler = StandardScaler()
df_num_scaled = scaler.fit_transform(df_num)

# create a PCA instance
pca = PCA(n_components = 0.95)

# fit the PCA instance to the scaled samples
pca.fit(df_num_scaled)

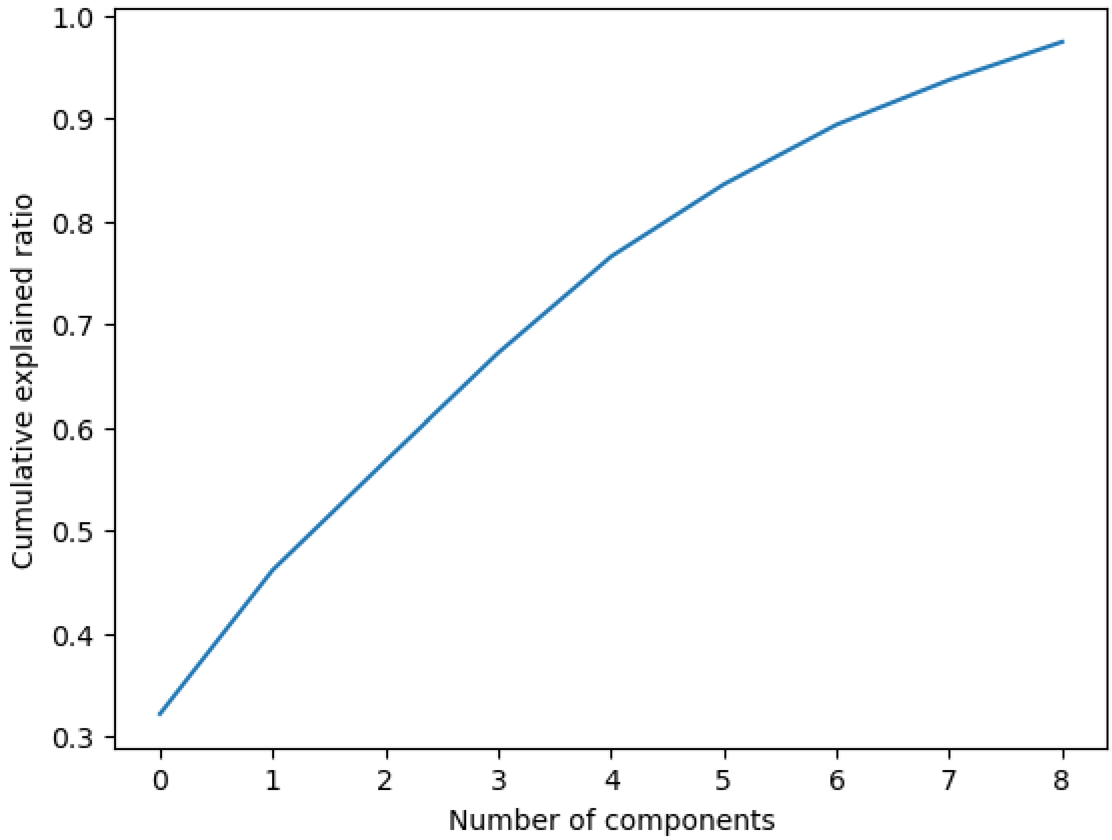
# transform the scaled samples
pca_features = pca.transform(df_num_scaled)

# print the shape of the pca features
print("The shape of the PCA is: ", pca_features.shape)
```

```
The shape of the PCA is:  (886, 9)
```

In [27]:

```
# plot the cumulative sum of the explained variance ratio
plt.plot(np.cumsum(pca.explained_variance_ratio_))
plt.xlabel('Number of components')
plt.ylabel('Cumulative explained ratio')
plt.show()
# the explained variance tells how much information can be attributed to each of the pri
```



In [28]:
```
# loadings = coefficients that describe how each variable contributes to the principal c
loadings = pd.DataFrame({'Feature' : df_num.columns, 'PC1' : pca.components_[0], 'PC2':
loadings
```

Out[28]:

	Feature	PC1	PC2	PC3	PC4
0	age	-0.096826	0.383863	0.700289	-0.143540
1	jspe	-0.046286	0.680183	0.093058	0.065010
2	qcae_aff	0.208184	0.509245	-0.318282	-0.204569
3	amsp	-0.151479	0.121522	-0.109618	0.827293
4	erec_mean	0.045743	0.326902	-0.455469	0.052569
5	cesd	0.461591	-0.028029	-0.079636	-0.026066
6	stai_t	0.450715	0.022358	-0.074328	-0.221556
7	mbi_ex	0.442653	-0.033443	-0.030296	0.220002
8	mbi_cy	0.373686	0.036472	0.299290	0.378758
9	mbi_ea	-0.410257	0.072821	-0.278935	-0.067228

In [29]:
```
# sort the loadings in descending order
loadings = loadings.sort_values(by = ['PC1', 'PC2', 'PC3', 'PC4'], ascending = False)
loadings.head(20)
# for the first pc, the variables with the highest absolute loadings are 'cesd', 'stai_t
# for the second pc, the variables with the highest absolute loadings is 'jspe'
# for the third pc - 'erec_mean'
# for the fourth pc - 'amsp'
```

Out[29]:

	Feature	PC1	PC2	PC3	PC4
5	cesd	0.461591	-0.028029	-0.079636	-0.026066
6	stai_t	0.450715	0.022358	-0.074328	-0.221556
7	mbi_ex	0.442653	-0.033443	-0.030296	0.220002

8	mbi_cy	0.373686	0.036472	0.299290	0.378758
2	qcae_aff	0.208184	0.509245	-0.318282	-0.204569
4	erec_mean	0.045743	0.326902	-0.455469	0.052569
1	jspe	-0.046286	0.680183	0.093058	0.065010
0	age	-0.096826	0.383863	0.700289	-0.143540
3	amsp	-0.151479	0.121522	-0.109618	0.827293
9	mbi_ea	-0.410257	0.072821	-0.278935	-0.067228

In [30]:

```
# Clustering
from sklearn.cluster import KMeans
```

In [32]:

```
# determine the optimal number of clusters
# create a list of inertia values for different k values
inertia = []
for k in range (1,10):
    # create a KMeans instance with k clusters
    model = KMeans(n_clusters = k)
    #fit model to samples
    model.fit(pca_features)
    #append the inertia to the list of inertias
    inertia.append(model.inertia_)

# plot the ks vs inertias
plt.plot(range(1,10), inertia, '-o')
plt.xlabel('Number of clusters, k')
plt.ylabel('Inertia')
plt.show()

# the  point where the inertia begins to decrease more slowly is a good choice for the n
```

```
C:\Users\Oana\anaconda3\lib\site-packages\sklearn\cluster\_kmeans.py:870: FutureWarning:
The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_
init` explicitly to suppress the warning
  warnings.warn(
C:\Users\Oana\anaconda3\lib\site-packages\sklearn\cluster\_kmeans.py:1382: UserWarning:
KMeans is known to have a memory leak on Windows with MKL, when there are less chunks th
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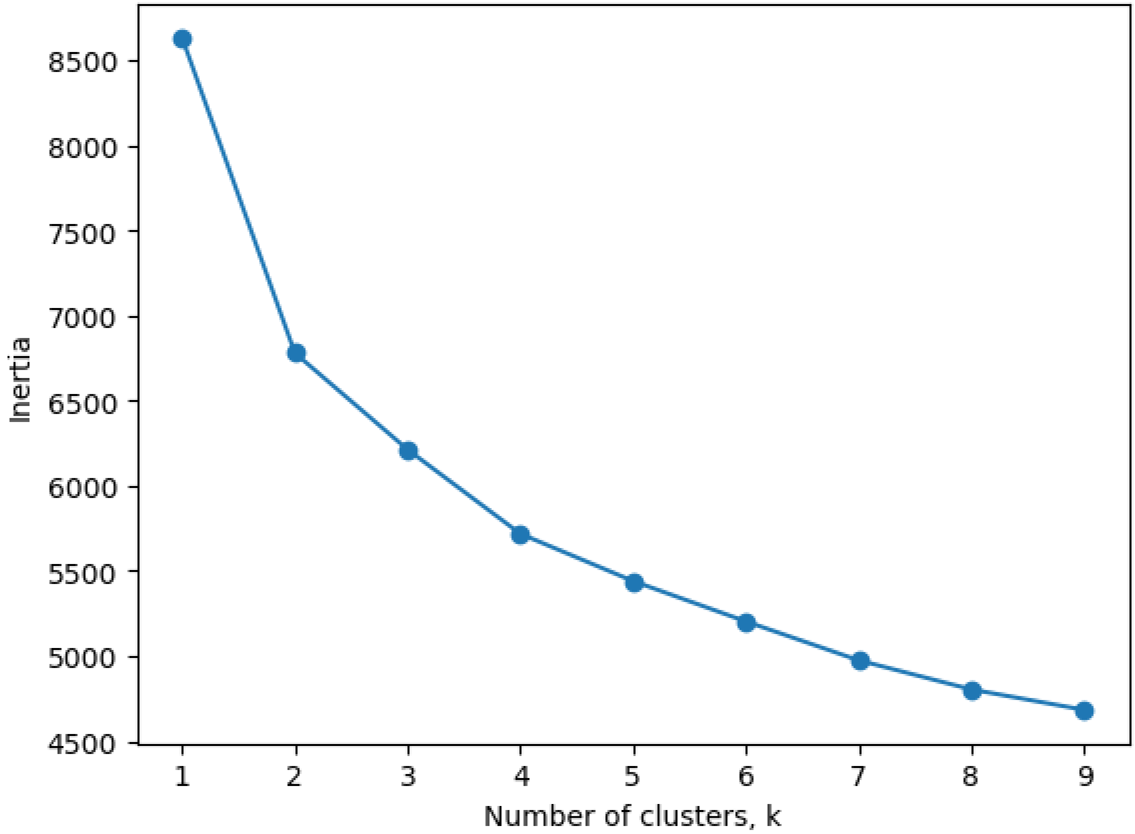

In [34]:
```
# we choose n=3 clusters
model = KMeans(n_clusters = 3)
clusters = model.fit_predict(pca_features)
```

```
C:\Users\Oana\anaconda3\lib\site-packages\sklearn\cluster\_kmeans.py:870: FutureWarning:
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an available threads. You can avoid it by setting the environment variable OMP_NUM_THREA
DS=4.
  warnings.warn(
```
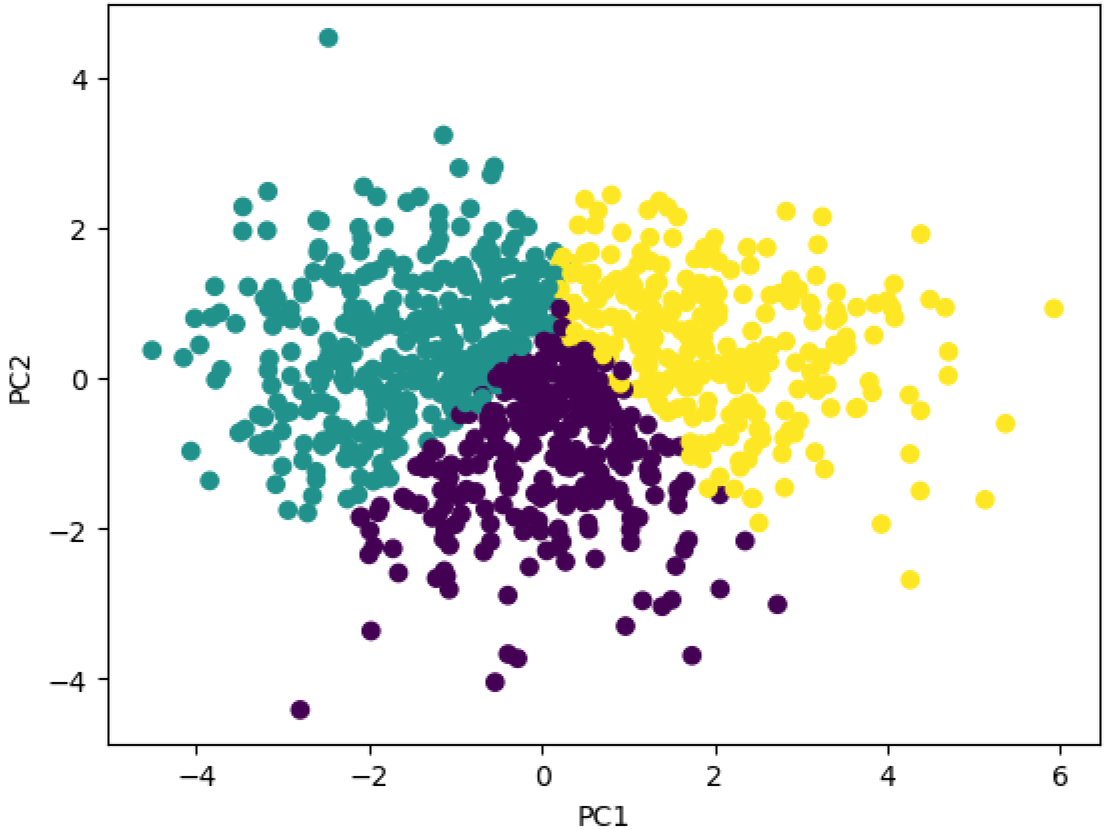

In [35]:
```
# create a scatter plot of the first two principal components
plt.scatter(pca_features[:, 0], pca_features[:, 1], c=clusters, cmap = 'viridis')
plt.xlabel('PC1')
plt.ylabel('PC2')
plt.show()
```



In [36]:
```
# extracting the cluster labels
clusters_labels  = model.labels_
```

In [37]:
```
# adding the cluster labels to the original data frame
df_clustered = df_num.copy()
df_clustered['Cluster'] = clusters_labels
df_clustered.head()
```

Out[37]:

	age	jspe	qcae_aff	amsp	erec_mean	cesd	stai_t	mbi_ex	mbi_cy	mbi_ea	Cluster
0	18	88	27	17	0.738095	34	61	17	13	20	0
1	26	109	37	22	0.690476	7	33	14	11	26	1
2	21	106	39	17	0.690476	25	73	24	7	23	2
3	21	101	33	18	0.833333	17	48	16	10	21	0
4	21	102	28	21	0.690476	14	46	22	14	23	0

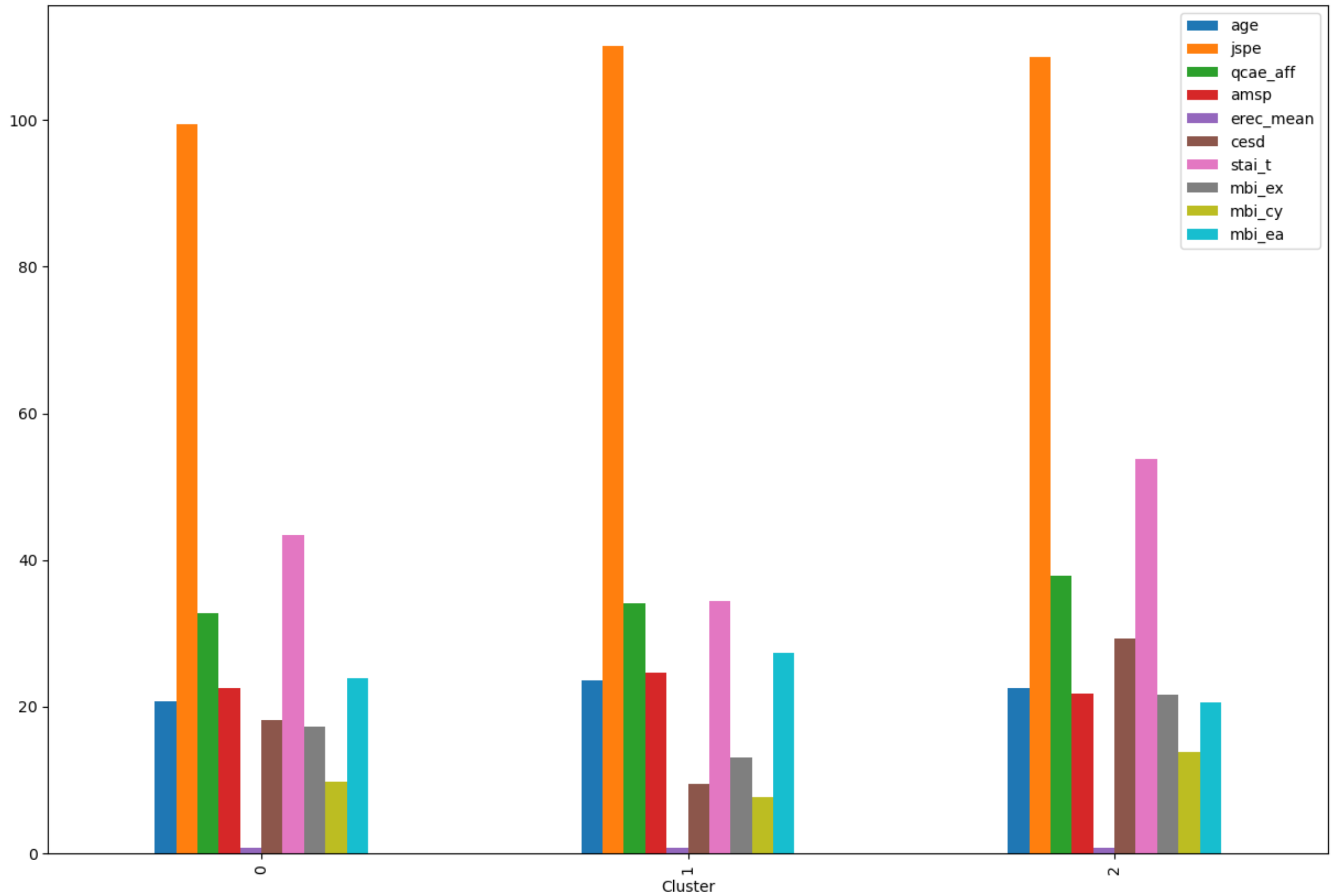
In [38]:
```
# grouping the data frame by cluster to get the properties of each cluster
cluster_grouped = df_clustered.groupby('Cluster')
cluster_properties = cluster_grouped.mean()
print(cluster_properties)
```

```
               age        jspe   qcae_aff       amsp   erec_mean       cesd  \
Cluster
0        20.737410   99.460432  32.798561  22.514388   0.691076  18.165468
1        23.639769  110.198847  34.106628  24.688761   0.723823   9.481268
2        22.467433  108.655172  37.800766  21.781609   0.746214  29.321839

            stai_t     mbi_ex     mbi_cy     mbi_ea
Cluster
0        43.348921  17.208633   9.708633  23.798561
1        34.354467  13.097983   7.593660  27.268012
2        53.777778  21.551724  13.777778  20.574713
```

In [39]:
```
cluster_grouped.size()
```

Out[39]:
```
Cluster
0    278
1    347
2    261
dtype: int64
```

In [41]:
```
# plotting the properties for each cluster
cluster_properties.plot(kind = 'bar', figsize = (15,10))
plt.show()

# Cluster 0 is the cluster with the lowest values of the variables; the patients in this
# Cluster 1 is the cluster with the intermediate values of the variables; the patients i
# Cluster 2 is the cluster with the highest values of the variables; the patients in thi
```



In [42]:
```
# Machine Learning
# Logistic Regression
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

In [44]:
```
# split the data into training and testing sets
X_train, X_test, y_train, y_test = train_test_split(pca_features, clusters_labels, test_
```

In [45]:
```
# create a logistic regression classifier
logreg = LogisticRegression()
```

In [46]:
```
# fit the classifier to the training data
logreg.fit(X_train, y_train)
```

Out[46]:
```
LogisticRegression
LogisticRegression()
```

In [47]:
```
# predict the labels of the test set
y_pred = logreg.predict(X_test)
```

In [49]:
```
# compute and print the accuracy
accuracy = accuracy_score(y_test, y_pred)
print("Accuracy: {}" .format(accuracy))
```

```
Accuracy: 0.9887640449438202
```

In [50]:
```
# Model evaluation
from sklearn.metrics import classification_report
from sklearn.metrics import confusion_matrix
```

In [51]:
```
print(classification_report(y_test, y_pred))
print(confusion_matrix(y_test, y_pred))
```

```
              precision    recall  f1-score   support

           0       1.00      0.97      0.98        58
           1       0.98      1.00      0.99        65
           2       0.98      1.00      0.99        55

    accuracy                           0.99       178
   macro avg       0.99      0.99      0.99       178
weighted avg       0.99      0.99      0.99       178

[[56  1  1]
 [ 0 65  0]
 [ 0  0 55]]
```

In [52]:
```
# precision is the ability of the classifier not to label a positive sample that is nega
# recall is the ability of the classifier to find all positive labels
# f1-score is the weighted average of the precision and recall
# support is the number of occurrences of each class in  y_test
```

In [ ]:
```
# CONCLUSION
# In this project, I used the chi-square test to determine the relationships between the
# For continuous variables, I used the Pearson correlation coefficient to determine the
# data set, and I used the K-Means clustering algorithm to cluster the patients into 3 g
# Regression model to predict the cluster labels of the patients based on the principal
# labels
```