Assignment 1

CS422 - Data Mining
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Recitation Exercises

Exercise 1: Data Mining Task: True or False

1.1. **False:** This is a simple data query task.
1.2. **False:** Since we do not predict some value ~ predictive task nor do we perform any descriptive task this is not a data mining task. This can be manually done by accounts.
1.3. **False:** Since we do not predict some value ~ predictive task nor do we perform any descriptive task this is not a data mining task. This can be manually done by accounts.
1.4. **False:** This is a simple data query task.
1.5. **False:** This can be done by calculating the probability from dice's possible outcomes since they are fair.
1.6. **True:** Since we do not predict some value ~ predictive task based on previous data records, this can be considered as a data mining task.
1.7. **True:** Since we perform a descriptive task (where we alert/notify on unusual pattern i.e. classification task ~ error detection) this is a data mining task.
1.8. **True:** Yes, in this we have to model a dataset of earthquakes and then retrieve important information like patterns. Since we are performing a descriptive task, it is data mining.
1.9. **False:** This is a signal processing task and not data mining.

Exercise 2.2: Classify as 'binary, discrete, or continuous' & 'qualitative (nominal or ordinal) or quantitative (interval or ratio)'.

1. Binary (AM/PM) , qualitative, ordinal (order of am/pm matters)
2. Continuous, quantitative, ratio (meters capture ratio based on unit standards)
3. Discrete, qualitative, ordinal
4. Continuous, quantitative, ratio (unit/scales)
5. Discrete, qualitative, ordinal (order of medal matters)
6. Continuous, quantitative, interval (there is no unit sea-leave, we just use interval)
7. Discrete, quantitative, ratio (units of individual patients)
8. Discrete, qualitative, nominal (order doesn't matter here)
9. Discrete, qualitative, ordinal (order of luminance matters)
10. Discrete, qualitative, ordinal (ranked order)
11. Continuous, quantitative, interval (no fixed unit distance for ratio)

12. Continuous, quantitative, ratio (measured in units)
13. Discrete, qualitative, nominal (order doesn’t matter here)

Exercise 2.7: Which of the following quantities is likely to show more temporal autocorrelation: daily rainfall or daily temperature? Why?

Daily temperature is a continuous data that is being recorded all the time, while daily rainfall is a discrete data that is only recorded when it rains. Because of this reason finding the correlation of daily rainfall is difficult as compared to daily temperature. Therefore daily temperature is mor likely to show more temporal autocorrelation.

Exercise 2.15: difference between the sampling schemes

The first sampling method selects samples based on the group and are proportional as groups themselves are proportional. The second method is random sampling, where n samples are selected from the population. The first strategy has the advantage that it can sample objects in groups which are unique / homogeneous i.e. they do not appear in other groups. Inclusion of these groups gives us an estimate of the parameters of that group. Another advantage first strategy has is that the variance of these samples is smaller as compared to random sampling.

Exercise 2.16:

(a) In the case that a term occurs in every document: the document frequency will be the same as total documents. Thus the log of their division will result in a 0 value.

In the case of occurrence in just one document, the frequency(tf_{ij}) will be multiplied by the log of total documents divided by number of appeared documents. For a large number of documents, the log part will be larger. Further if the frequency is high the log part will multiply giving us a weighted outcome.

(b) This transformation can be used to search for documents by using important keywords. This transformation will eliminate the trivial keywords that appear everywhere by bringing them down to or close to 0. This has an application in search engines where keyword based search is used.

Exercise 2.17:

(a) Since $x^* = x^{1/2}$, $(x^*)^2 = x$. And since (a,b) are linearly, the corresponding interval in terms of x would be: (a^2,b^2).

(b) We know that x* is having linear relation with y, so the stand equation is given as $y=m.x^*+c$. But since we have to relate this to y, we change x* with its x equivalent. The equation we get is: $y = m.x^{1/2} + c$.

Exercise 2.18:

1. $x=010\underline{1}01\underline{0}00\underline{1}$
   $y=010\underline{0}01\underline{1}00\underline{0}$

   Since three bits are different between x and y, hamming distance = 3.

   For Jaccard similarity 0-0 matches (5 frequency) are not considered in |x| and |y|. And 1-1 similar appears 2 times.

   Jaccard similarity = (1-1 frequency) / (|x| + |y| - (0-0 frequency)) = 2/(5+5-5) = ⅖ = 0.4

2. Jaccard similarity and cosine measure are similar as they both do not consider 0-0 matches. Hamming distance is similar to Simple Matching Coefficient as by definition SMI is the ratio of Hamming distance to the total bits in a vector.

3. Jaccard is useful to compare similarity between two organisms as it finds the intersection between the classes. It can be represented as,
   Jaccard = (species 1 ∩ species 2) / (species 1 + species 2 - (species 1 ∩ species 2)).

4. In this case we should be looking for EXOR differences i.e. Hamming distance. Since the genes will be matching for most parts, getting hamming distance will give us more meaningful information.

Exercise 2.19:

1. x=(1, 1, 1, 1)
   y=(2, 2, 2, 2)

   Cosine = (x.y) / (norm(x) * norm(y))
   x.y = (1x2)+(1x2)+(1x2)+(1x2) = 8
   norm(x) = $(1^2 + 1^2 + 1^2 + 1^2)^{1/2} = 2$
   norm(y) = $(2^2 + 2^2 + 2^2 + 2^2)^{1/2} = 4$
   Cosine = 8 / (2*4) = 1

Correlation = covariance / [std dev(x) * std dev(y)]
XMean = 1; YMean = 2
Covariance = 0 (Since values are equal to mean)
Std dev(x) = Std dev(y) = 0 (Since values are equal to mean)
Correlation = 0/0 = undefined

Euclidean Distance = $((1-2)^2 + (1-2)^2 + (1-2)^2 + (1-2)^2)^{½} = 2$

2. x=(0, 1, 0, 1)
   y=(1, 0, 1, 0)

   Cosine = 0

   Correlation = covariance / [std dev(x) * std dev(y)]
   XMean = ½ ; YMean = ½
   Covariance = 1/[(4-1) * ((0-½)(1-½) + (1-½)(0-½) +(0-½)(1-½) +(1-½)(0-½))] = -⅓
   Std dev(x) = Std dev(y) = $((⅓) * ((1-½)^2 + (0-½)^2 + (1-½)^2 + (0-½)^2))^{½} = (⅓)^{½}$
   Correlation = $(-⅓) / ((⅓)^{½} * (⅓)^{½}) = -1$

   Euclidean Distance = 2

   Jaccard Distance = 0 / (2+2-0) = 0

3. x=(0, −1, 0, 1)
   y=(1, 0, −1, 0)

   Cosine = 0 (same as 2, just vectors in different direction)

   Correlation = covariance / [std dev(x) * std dev(y)]
   XMean = 0 ; YMean = 0
   Covariance = 1/ [(4-1) * ((0-0)(1-0) + (1-0)(0-0) +(0-0)(1-0) +(1-0)(0-0))] = 0
   Std dev(x) = Std dev(y) = $(1 / (4-1) * ((1-0)^2 + (0-0)^2 + (1-0)^2 + (0-0)^2))^{½} = (⅔)^{½}$
   Correlation = 0 / (⅔) = 0

   Euclidean Distance = 2

4. x = (1, 1, 0, 1, 0, 1)
   y = (1, 1, 1, 0, 0, 1)

   Cosine = (x.y) / (norm(x) * norm(y))
   x.y = 1*1 + 1*1 + 0*1 + 1*0 + 0*0 + 1*1 = 3
   norm(x) = $(1^2 + 1^2 + 0^2 + 1^2 + 0^2 + 1^2)^{½} = 2$
   norm(y) = $(1^2 + 1^2 + 1^2 + 0^2 + 0^2 + 1^2)^{½} = 2$
   Cosine = 3 / (2*2) = ¾ = 0.75

Correlation = covariance / [std dev(x) * std dev(y)]
XMean = $\frac{2}{3}$; YMean = $\frac{2}{3}$
Covariance = $\frac{1}{5}$ * ($(1-\frac{2}{3})(1-\frac{2}{3})$ + $(1-\frac{2}{3})(1-\frac{2}{3})$ + $(0-\frac{2}{3})(1-\frac{2}{3})$ + $(1-\frac{2}{3})(0-\frac{2}{3})$ + $(0-\frac{2}{3})(0-\frac{2}{3})$ + $(1-\frac{2}{3})(1-\frac{2}{3})$) = 1/15
Std dev(x) = Std dev(y) = ($(\frac{1}{5})$ * $((1-\frac{2}{3})^2 + (1-\frac{2}{3})^2 + (1-\frac{2}{3})^2 + (1-\frac{2}{3})^2 + (0-\frac{2}{3})^2 + (0-\frac{2}{3})^2)$)$^{\frac{1}{2}}$ = $(4/15)^{\frac{1}{2}}$
Correlation = 1/15 / ($(4/15)^{\frac{1}{2}}$ * $(4/15)^{\frac{1}{2}}$) =(1/15) / (4/15) = ¼ = 0.25

Jaccard Distance = 3 / (4+4-3) = 0.6

5. x = (2, −1, 0, 2, 0, −3)
   y = (−1, 1, −1, 0, 0, −1)

   Cosine = (x.y) / (norm(x) * norm(y))
   x.y = 2*-1 + -1*1 + 0*-1 + 2*0 + 0*0 + -3*-1 = 0
   norm(x) = $(2^2 + -1^2 + 0^2 + 2^2 + 0^2 + -3^2)^{\frac{1}{2}} = 18^{\frac{1}{2}}$
   norm(y) = $(-1^2 + 1^2 + -1^2 + 0^2 + 0^2 + -1^2)^{\frac{1}{2}} = 2$
   Cosine = 0 / ($18^{\frac{1}{2}}$ * 2) = 0

   Correlation = covariance / [std dev(x) * std dev(y)]
   XMean = 0 ; YMean = $-\frac{1}{6}$
   Covariance = 0 (as one of the means is 0)
   Correlation = 0

Practicum Problems

In [1]:
```
import seaborn as sns
import pandas as pd
import numpy as np
from sklearn.impute import SimpleImputer
from sklearn.decomposition import PCA
from sklearn.preprocessing import StandardScaler
from sklearn.datasets import load_iris
from scipy.spatial.distance import cosine
import matplotlib.pyplot as plt
```

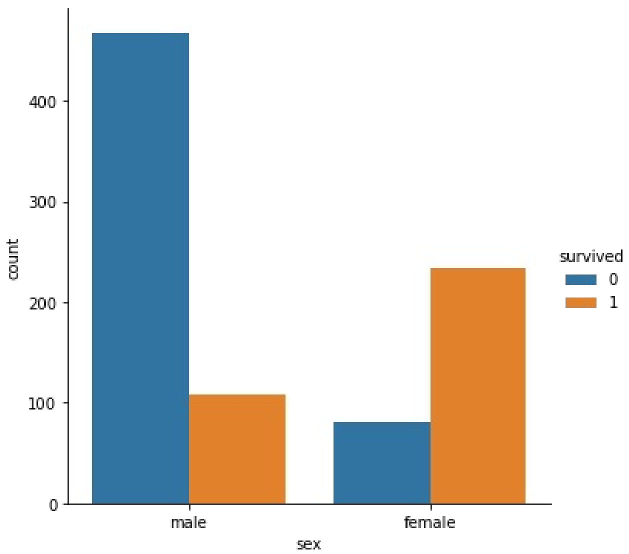
Problem 1

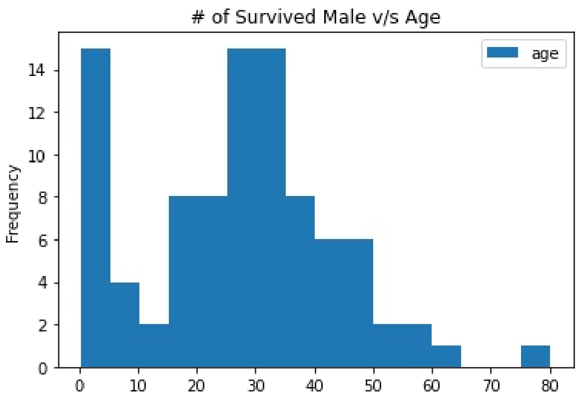
(visualize and analyze titanic dataset)

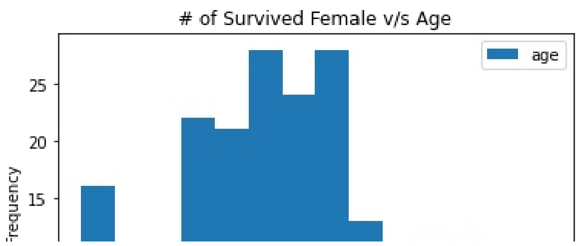
In [2]:
```
# import and group specific feature wise
titanic = sns.load_dataset("titanic")
survived_male = titanic[ (titanic['survived'] == 1) & (titanic['sex'] == 'male') ]
survived_female = titanic[ (titanic['survived'] == 1) & (titanic['sex'] == 'female') ]
dead_male = titanic[ (titanic['survived'] == 0) & (titanic['sex'] == 'male') ]
dead_female = titanic[ (titanic['survived'] == 0) & (titanic['sex'] == 'female') ]
```

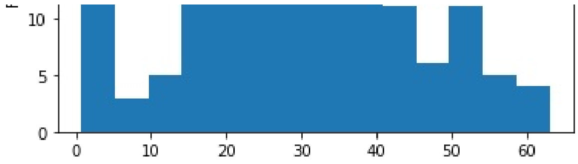
In [3]:
```
# plot histogram for the groups
sns.catplot(x="sex", hue="survived", kind="count", data=titanic)
survived_male[['age']].plot(kind='hist',bins=16,title='# of Survived Male v/s Age')
survived_female[['age']].plot(kind='hist',bins=14,title='# of Survived Female v/s Age')
dead_male[['age']].plot(kind='hist',bins=15,title='# of Dead Male v/s Age')
dead_female[['age']].plot(kind='hist',bins=12,title='# of Dead Female v/s Age')
```

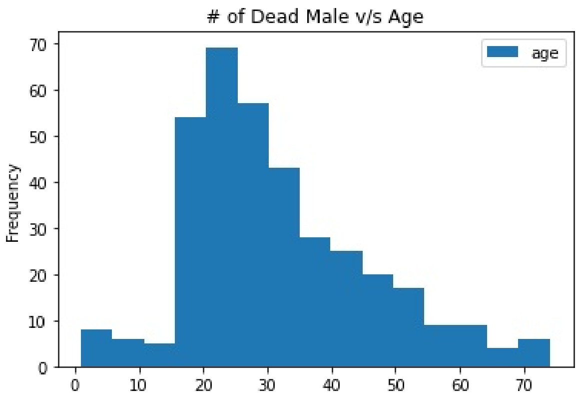
Out[3]:
```
<AxesSubplot:title={'center':'# of Dead Female v/s Age'}, ylabel='Frequency'>
```

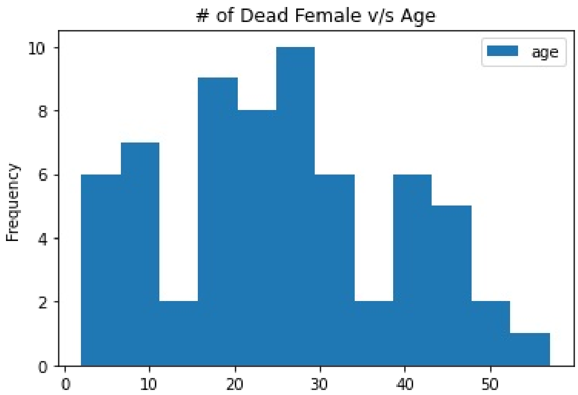












conclusion:

From a visual inspection it can be observed that the ratio of male:female population is approximately 1.75 ~ 7:4. From the 'Sex v/s Survived' plot it can be observed that the number of females who survived is more than double then that of females who have died. On the other hand in males, the number of males who have died is approximately five time the number of males who have survived.

Looking at the histgram with respect to survival & Sex against age, it can be observed that chances of survival for males between ages 20-50 were the least and the most deaths were from this area. But it can also be observed that the changes of survival for male who were kids or old were high. Other the other hand, in females, the death plot seems to be balanced. These observations are because (in reality) priority was given to woman, children and old people when the life boats were being loaded.

Problem 2

(Load auto_mpg dataset -> replace '?' in horsepower feature to NaN -> find variance when imputer with mean, median and mode)

In [4]:

```
# load and prepare data
auto_mpg = pd.read_csv("./data/auto-mpg.data", delim_whitespace=True, header=None)
columns = ['mpg','cylinders','displacement','horsepower','weight','acceleration','model year','origin','car name'
auto_mpg.columns=columns
auto_mpg["horsepower"].replace(to_replace={"?":np.nan}, inplace=True)
auto_mpg["horsepower"] = pd.to_numeric(auto_mpg["horsepower"])

# Explore Data
print(auto_mpg.describe())
print(f'\nVariance of horsepower = {auto_mpg["horsepower"].var()}')
print(f'Mode of horsepower = {auto_mpg["horsepower"].mode()}')
```

```
              mpg   cylinders  displacement  horsepower       weight  \
count  398.000000  398.000000    398.000000  392.000000   398.000000
mean    23.514573    5.454774    193.425879  104.469388  2970.424623
std      7.815984    1.701004    104.269838   38.491160   846.841774
min      9.000000    3.000000     68.000000   46.000000  1613.000000
25%     17.500000    4.000000    104.250000   75.000000  2223.750000
50%     23.000000    4.000000    148.500000   93.500000  2803.500000
75%     29.000000    8.000000    262.000000  126.000000  3608.000000
max     46.600000    8.000000    455.000000  230.000000  5140.000000
```

```
       acceleration  model year      origin
count    398.000000  398.000000  398.000000
mean      15.568090   76.010050    1.572864
std        2.757689    3.697627    0.802055
min        8.000000   70.000000    1.000000
25%       13.825000   73.000000    1.000000
50%       15.500000   76.000000    1.000000
75%       17.175000   79.000000    2.000000
max       24.800000   82.000000    3.000000

Variance of horsepower = 1481.5693929745862
Mode of horsepower = 0    150.0
dtype: float64
```

In [5]:
```
# mean imputation
imp_mean = SimpleImputer()
imp_mean = pd.DataFrame(imp_mean.fit_transform(auto_mpg.iloc[:, :-1]))
imp_mean.columns = columns[:-1]
imp_mean.index = auto_mpg.index
```

In [6]:
```
# median imputation
imp_median = SimpleImputer(strategy='median')
imp_median = pd.DataFrame(imp_median.fit_transform(auto_mpg.iloc[:, :-1]))
imp_median.columns = columns[:-1]
imp_median.index = auto_mpg.index
```

In [7]:
```
# mode imputation
imp_mode = SimpleImputer(strategy='most_frequent')
imp_mode = pd.DataFrame(imp_mode.fit_transform(auto_mpg.iloc[:, :-1]))
imp_mode.columns = columns[:-1]
imp_mode.index = auto_mpg.index
```

In [8]:
```
# Results
print(f'Variance of horsepower (mean imputation) =   {imp_mean["horsepower"].var()}')
print(f'Variance of horsepower (median imputation) = {imp_median["horsepower"].var()}')
print(f'Variance of horsepower (mode imputation) =   {imp_mode["horsepower"].var()}')
```

```
Variance of horsepower (mean imputation) =   1459.1779160026776
Variance of horsepower (median imputation) = 1460.96905180816
Variance of horsepower (mode imputation) =   1490.0361252104324
```

Conclusion:

Mean Imputation results into lowest variance. This is because of the way variance is calculated i.e. we take the sum of the difference of values from their mean and then divide that by the total number of values. But in our case since we are increasing the total number of values which are equal to mean, their contribution to the sum of the difference is 0. This ultimately results in a reduced varience.

The other method of imputing values that would match the distribution more accurately is using Multiple Imputation. In multiple imputations we calculate several different imputations, create several version of the same data with different imputations and then combine them to get the best values. This helps reduce bias and at the same time retain useful information that can be helpful to find co-variance and such. (source)

Problem 3

(find PCA and compare with original variance percent)

In [9]:
```
# Import Data
iris = load_iris()
iris_col = iris.feature_names
iris_df = pd.DataFrame(iris.data, columns=iris_col)

# Percent Variance
sep_len_var, sep_wid_var, pet_len_var, pet_wid_var = iris_df.var()
total_iris_var= sum(iris_df.var())
sep_len_var_per, sep_wid_var_per, pet_len_var_per, pet_wid_var_per = sep_len_var/total_iris_var,sep_wid_var/total

# Standardize
sc = StandardScaler()
iris_df_std = pd.DataFrame(sc.fit_transform(iris_df))
```

In [10]:
```
# PCA Decomposition
pca = PCA(n_components=4, svd_solver="full")
pca_df = pd.DataFrame(pca.fit_transform(iris_df_std.iloc[:,0:4]))
pca_var = pca.explained_variance_ratio_
pc1_var,pc2_var,pc3_var,pc4_var = pca_var[0],pca_var[1],pca_var[2],pca_var[3]
```

In [11]:
```
# Compare Variance of Original Feature and Principal components
print(f'{"Feature":<17}{"Variance (*100 = %)":<23}| {"Principal Comp.":<17}Variance (*100 = %)')
print(f'{"Sepal Length":<17}{sep_len_var_per:<23}| {"PC1":<17}{pc1_var}')
print(f'{"Sepal Width":<17}{sep_wid_var_per:<23}| {"PC2":<17}{pc2_var}')
print(f'{"Petal Length":<17}{pet_len_var_per:<23}| {"PC3":<17}{pc3_var}')
print(f'{"Petal width":<17}{pet_wid_var_per:<23}| {"PC4":<17}{pc4_var}')
```

```
Feature          Variance (*100 = %)    | Principal Comp.  Variance (*100 = %)
Sepal Length     0.14994532099467353    | PC1              0.7296244541329986
Sepal Width      0.04154410732328823    | PC2              0.22850761786701776
Petal Length     0.681457931997653      | PC3              0.03668921889282878
Petal width      0.12705263968438513    | PC4              0.005178709107154798
```

Observation:

Observing the variances from the original features, we realize that sepal width has the least variance i.e. the records do not spread much from the mean and are cluttered together. Petal length has the highest variance and it is useful for analysis.

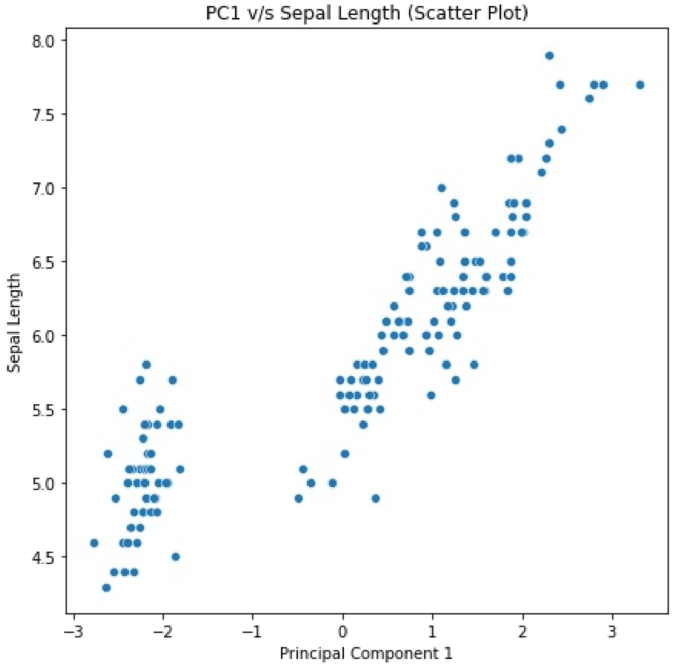
Observing the First Principal Component we understand that it gives us better variance percentage. This is because the principal components are eigenvectors of the data's covariance matrix. Principal component represents the direction of a best-fitting line which is the one that minimizes the average squared distance from the points to the line.

For our analysis we need data that contributes more towards our analysis. Since principal components are directions constituting orthonormal basis, different individual dimensions of the data are linearly uncorrelated to them. Thus we are preserving as much of the data's variation as possible.

Problem 4

In [12]:
```
# Plot Sepal Length vs PC1
plt.figure(figsize=(7,7))
sns.scatterplot(x=pca_df.iloc[:,0], y=iris_df.iloc[:,0])
plt.xlabel('Principal Component 1')
plt.ylabel('Sepal Length')
plt.title('PC1 v/s Sepal Length (Scatter Plot)')
print('PC1 v/s Sepal Length:')
print(f'Correlation Coefficient = {np.corrcoef(pca_df.iloc[:,0], iris_df.iloc[:,0])[1][0]}')
print(f'Cosine Similarity = {1 - cosine(pca_df.iloc[:,0],iris_df.iloc[:,0])}')
```

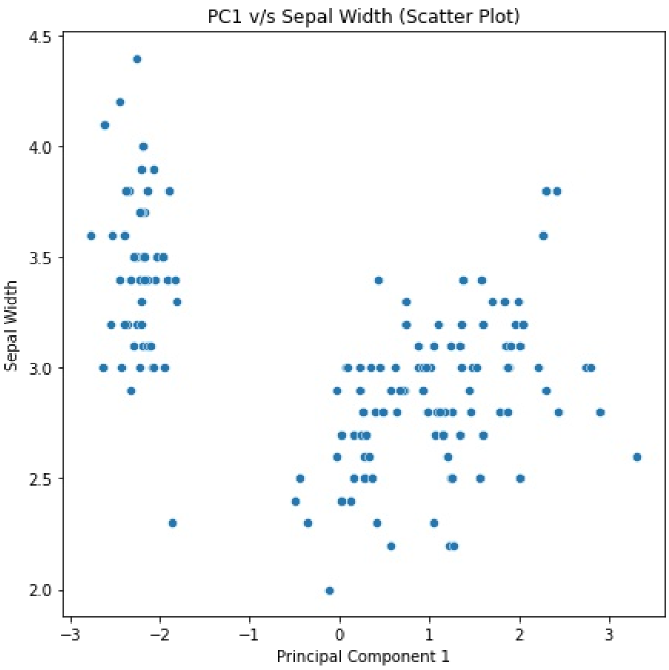
```
PC1 v/s Sepal Length:
Correlation Coefficient = 0.8901687648612951
Cosine Similarity = 0.12449019771928183
```



In [13]:
```
# Plot Sepal Width vs PC1
plt.figure(figsize=(7,7))
sns.scatterplot(x=pca_df.iloc[:,0], y=iris_df.iloc[:,1])
plt.xlabel('Principal Component 1')
plt.ylabel('Sepal Width')
plt.title('PC1 v/s Sepal Width (Scatter Plot)')
```

```
print('PC1 v/s Sepal Width:')
print(f'Correlation Coefficient = {np.corrcoef(pca_df.iloc[:,0], iris_df.iloc[:,1])[1][0]}')
print(f'Cosine Similarity = {1 - cosine(pca_df.iloc[:,0],iris_df.iloc[:,1])}')
```

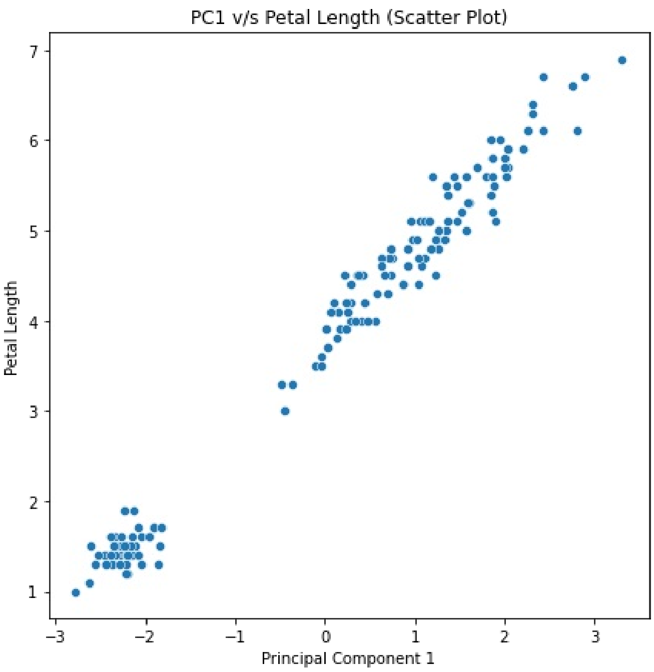
```
PC1 v/s Sepal Width:
Correlation Coefficient = -0.4601427064479081
Cosine Similarity = -0.06473068500170664
```



In [14]:

```
# Plot Petal Length vs PC1
plt.figure(figsize=(7,7))
sns.scatterplot(x=pca_df.iloc[:,0], y=iris_df.iloc[:,2])
plt.xlabel('Principal Component 1')
plt.ylabel('Petal Length')
plt.title('PC1 v/s Petal Length (Scatter Plot)')
print('PC1 v/s Petal Length:')
print(f'Correlation Coefficient = {np.corrcoef(pca_df.iloc[:,0], iris_df.iloc[:,2])[1][0]}')
print(f'Cosine Similarity = {1 - cosine(pca_df.iloc[:,0],iris_df.iloc[:,2])}')
```

```
PC1 v/s Petal Length:
Correlation Coefficient = 0.9915551834193603
Cosine Similarity = 0.4204266990041009
```

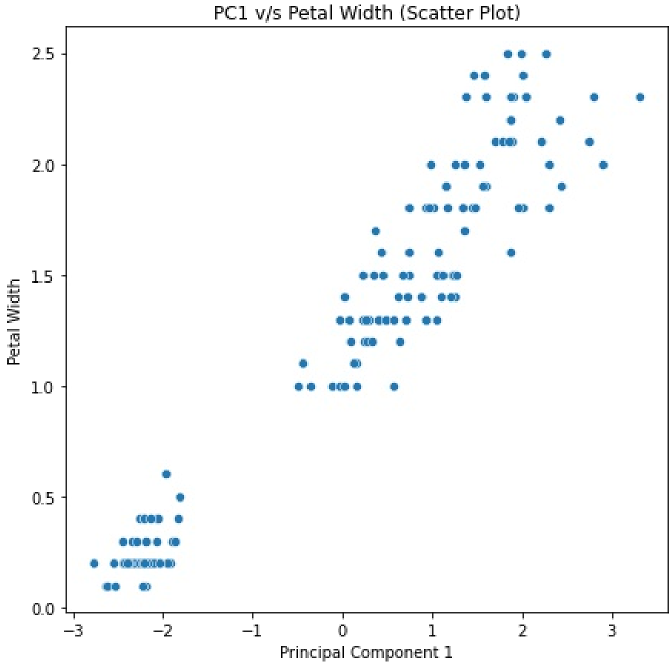


In [15]:

```
# Plot Petal Width vs PC1
plt.figure(figsize=(7,7))
sns.scatterplot(x=pca_df.iloc[:,0], y=iris_df.iloc[:,3])
plt.xlabel('Principal Component 1')
```

```
plt.ylabel('Petal Width')
plt.title('PC1 v/s Petal Width (Scatter Plot)')
print('PC1 v/s Petal Width:')
print(f'Correlation Coefficient = {np.corrcoef(pca_df.iloc[:,0], iris_df.iloc[:,3])[1][0]}')
print(f'Cosine Similarity = {1 - cosine(pca_df.iloc[:,0],iris_df.iloc[:,3])}')
```

```
PC1 v/s Petal Width:
Correlation Coefficient = 0.9649789606692489
Cosine Similarity = 0.5163697162322227
```



Conclusion:

It can be observed that features sepal length and sepal width when projected onto PC1 have a Correlation Coefficient less then that of petal length and petal width. Infact even their plots are quite scattered. This can be supported by the Cosine Similarity found between those two features and the PC1 which is ~0 i.e. it is at approximately right angle to the Principal Component and have no match.

On the other hand, petal length and petal width have much more visually definite graph and also have a higher Correlation Coefficient and their Cosine Similarity comes to be around ~0.45 which is at approximately 45 degrees from the PC1.

Problem 5

In [16]:

```
# Find total variance of PCA
pca_df_nonstd = pd.DataFrame(pca.fit_transform(iris_df.iloc[:,0:4]))
pca_nonstd_veriences = pca_df_nonstd.var()
pca_veriences = pca_df.var()
total_pca_var = sum(pca_veriences)
total_nonstd_pca_var = sum(pca_nonstd_veriences)


# Find cumulative percents of PCA to find >95% threshold point
print(f'Cumulitive Percents-> {np.cumsum(pca_var)}')
```

```
Cumulitive Percents-> [0.72962445 0.95813207 0.99482129 1.        ]
```

In [17]:

```
# Compare total varience of PCA and Features
print(f'{"Total varience of features:":<38}{total_iris_var}')
print(f'{"Total varience of PCA(standardized):":<38}{total_pca_var}')
print(f'{"Total varience of PCA:":<38}{total_nonstd_pca_var}')
```

```
Total varience of features:           4.572957046979867
Total varience of PCA(standardized):  4.026845637583895
Total varience of PCA:                4.572957046979873
```

Conclusion:

It can be observed that variance of the PCA and Original Features remains the same. Although the variance slightly reduces in PCA if the values are standardized, this is because the values get centered when standardization is performed but the PCA is performed better as data is centered.

If we wish to capture more then 95% of the variance of the original data, we need to select first 2 Principal Components as they combined cover 95.81% variance. This way we can reduce the dimensions from 4 to 2. Since PCA are the eigenvectors of the correlation matrix, we are capturing the vectors(PC) in directions that can include majority of the records.