Please follow the steps below to complete your assignment:

1. You need to download 'breast cancer wisconsin' data using the library Scikit learn; ref is given below. [2]
2. Remove the missing/infinite values using the mean strategy if required. [3]
3. Visualize the data in 2-D scatter plot and write the inferences, How the data look like. [5]
4. Make a boxplot for each feature and highlight the outlier, if any, then remove the outlier, make again box plot to show the outlier effect and write the inferences. [5]
5. Normalized the data if required, and write a note for what, why and how you performed normalization.[5] Ref:
6. https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html#sklearn.datasets.load_brea (https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html#sklearn.datasets.load_brea

In [1]:

```
# importing necessary libraries

import pandas as pd
import numpy as np
import sklearn
from scipy import stats
import pyforest
from sklearn.datasets import load_breast_cancer
from sklearn import preprocessing
from sklearn.preprocessing import MinMaxScaler
from scipy import stats
```

1. You need to download 'breast cancer wisconsin' data using the library Scikit learn; ref is given below.

https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html#sklearn.datasets.load_breast_c (https://scikit-learn.org/stable/modules/generated/sklearn.datasets.load_breast_cancer.html#sklearn.datasets.load_breast_c

In [2]:

```
# Loading the breast cancer dataset from sklearn

df = load_breast_cancer()
df1 = pd.DataFrame(df.data, columns=df.feature_names)
df2 = pd.DataFrame(df.target, columns=["Result"])
df3 = pd.concat([df1,df2], axis = 1)
df3.head()
```

Out[2]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	mean concavity	mean concave points	m symme
0	17.99	10.38	122.80	1001.0	0.11840	0.27760	0.3001	0.14710	0.2
1	20.57	17.77	132.90	1326.0	0.08474	0.07864	0.0869	0.07017	0.1
2	19.69	21.25	130.00	1203.0	0.10960	0.15990	0.1974	0.12790	0.2
3	11.42	20.38	77.58	386.1	0.14250	0.28390	0.2414	0.10520	0.2
4	20.29	14.34	135.10	1297.0	0.10030	0.13280	0.1980	0.10430	0.1

5 rows × 31 columns

To check the count of malignant & benign cases.

In [3]:

```
df3["Result"].value_counts()
```

Out[3]:

```
1    357
0    212
Name: Result, dtype: int64
```

In [4]:

```
# checking datatype of columns before plotting

df3.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
mean radius                569 non-null float64
mean texture               569 non-null float64
mean perimeter             569 non-null float64
mean area                  569 non-null float64
mean smoothness            569 non-null float64
mean compactness           569 non-null float64
mean concavity             569 non-null float64
mean concave points        569 non-null float64
mean symmetry              569 non-null float64
mean fractal dimension     569 non-null float64
radius error               569 non-null float64
texture error              569 non-null float64
perimeter error            569 non-null float64
area error                 569 non-null float64
smoothness error           569 non-null float64
compactness error          569 non-null float64
concavity error            569 non-null float64
concave points error       569 non-null float64
symmetry error             569 non-null float64
fractal dimension error    569 non-null float64
worst radius               569 non-null float64
worst texture              569 non-null float64
worst perimeter            569 non-null float64
worst area                 569 non-null float64
worst smoothness           569 non-null float64
worst compactness          569 non-null float64
worst concavity            569 non-null float64
worst concave points       569 non-null float64
worst symmetry             569 non-null float64
worst fractal dimension    569 non-null float64
Result                     569 non-null int32
dtypes: float64(30), int32(1)
memory usage: 135.7 KB
```

In [5]:

```
# As we observed the dtype for column Result was int, we converted it to float with bel
ow code
# just so as to bring the dataframe into a common datatype

df3 = df3.astype(float)
df3.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 569 entries, 0 to 568
Data columns (total 31 columns):
mean radius                569 non-null float64
mean texture               569 non-null float64
mean perimeter             569 non-null float64
mean area                  569 non-null float64
mean smoothness            569 non-null float64
mean compactness           569 non-null float64
mean concavity             569 non-null float64
mean concave points        569 non-null float64
mean symmetry              569 non-null float64
mean fractal dimension     569 non-null float64
radius error               569 non-null float64
texture error              569 non-null float64
perimeter error            569 non-null float64
area error                 569 non-null float64
smoothness error           569 non-null float64
compactness error          569 non-null float64
concavity error            569 non-null float64
concave points error       569 non-null float64
symmetry error             569 non-null float64
fractal dimension error    569 non-null float64
worst radius               569 non-null float64
worst texture              569 non-null float64
worst perimeter            569 non-null float64
worst area                 569 non-null float64
worst smoothness           569 non-null float64
worst compactness          569 non-null float64
worst concavity            569 non-null float64
worst concave points       569 non-null float64
worst symmetry             569 non-null float64
worst fractal dimension    569 non-null float64
Result                     569 non-null float64
dtypes: float64(31)
memory usage: 137.9 KB
```

2. Remove the missing/infinite values using the mean strategy if required. [3]

In [6]:

```
# checking the dataset

df3.describe()
```

Out[6]:

	mean radius	mean texture	mean perimeter	mean area	mean smoothness	mean compactness	me concav
count	569.000000	569.000000	569.000000	569.000000	569.000000	569.000000	569.0000
mean	14.127292	19.289649	91.969033	654.889104	0.096360	0.104341	0.0887
std	3.524049	4.301036	24.298981	351.914129	0.014064	0.052813	0.0797
min	6.981000	9.710000	43.790000	143.500000	0.052630	0.019380	0.0000
25%	11.700000	16.170000	75.170000	420.300000	0.086370	0.064920	0.0295
50%	13.370000	18.840000	86.240000	551.100000	0.095870	0.092630	0.0615
75%	15.780000	21.800000	104.100000	782.700000	0.105300	0.130400	0.1307
max	28.110000	39.280000	188.500000	2501.000000	0.163400	0.345400	0.4268

8 rows × 31 columns

In [7]:

```
# Checking if nan values are present

df3.isna().sum()
```

Out[7]:

```
mean radius                0
mean texture               0
mean perimeter             0
mean area                  0
mean smoothness            0
mean compactness           0
mean concavity             0
mean concave points        0
mean symmetry              0
mean fractal dimension     0
radius error               0
texture error              0
perimeter error            0
area error                 0
smoothness error           0
compactness error          0
concavity error            0
concave points error       0
symmetry error             0
fractal dimension error    0
worst radius               0
worst texture              0
worst perimeter            0
worst area                 0
worst smoothness           0
worst compactness          0
worst concavity            0
worst concave points       0
worst symmetry             0
worst fractal dimension    0
Result                     0
dtype: int64
```

There seems to be no missing value. So we don't need to do any missing value imputation.

3. Visualize the data in 2-D scatter plot and write the inferences, How the data look like. [5]

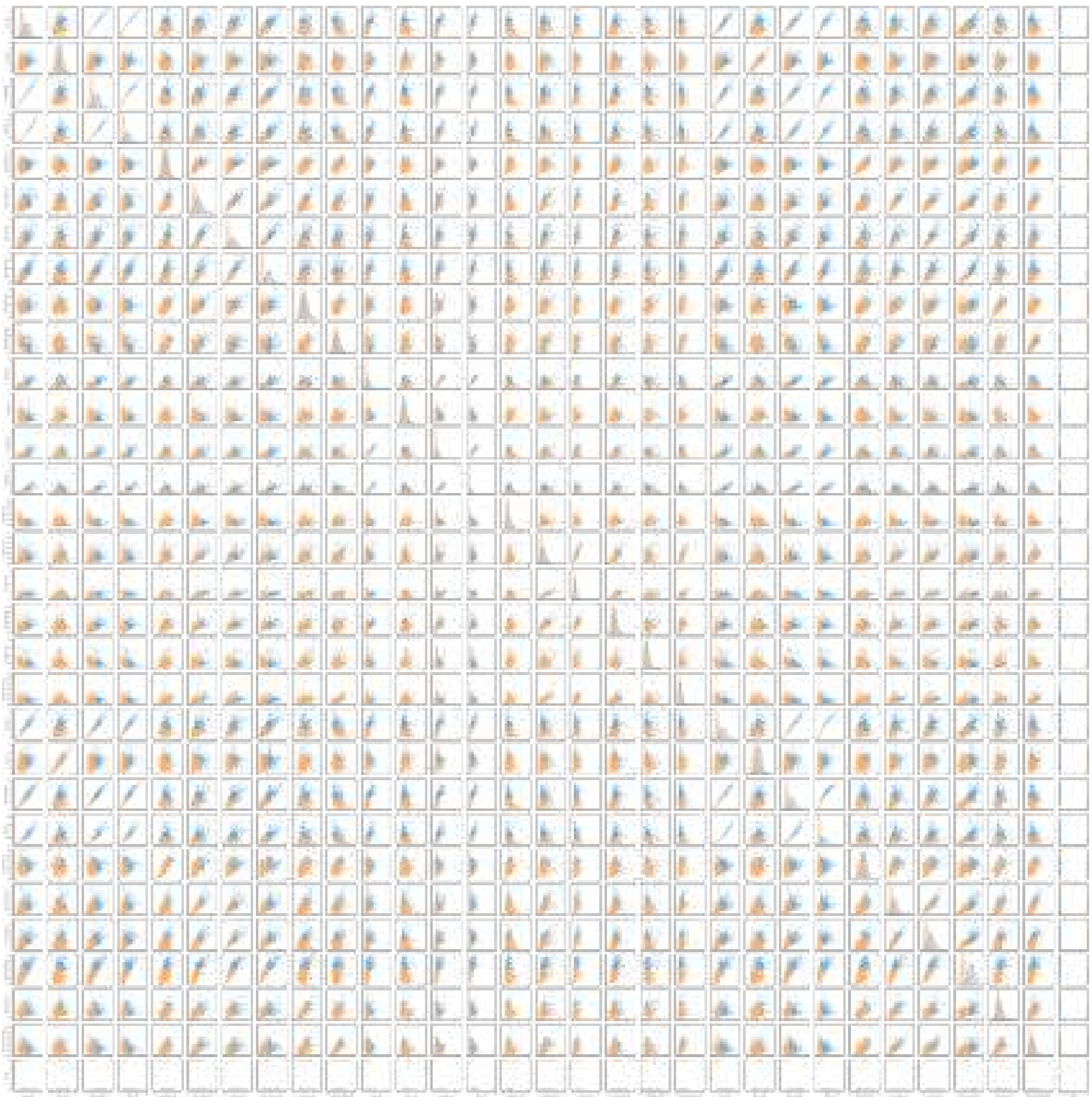
In [9]:

```
# This plot shows scatter plots between all columns in terms of bi-variate analysis

sns.pairplot(df3, hue="Result")
```

```
C:\Users\kumar\Anaconda3\lib\site-packages\statsmodels\nonparametric\kde.p
y:487: RuntimeWarning: invalid value encountered in true_divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
C:\Users\kumar\Anaconda3\lib\site-packages\statsmodels\nonparametric\kdeto
ols.py:34: RuntimeWarning: invalid value encountered in double_scalars
  FAC1 = 2*(np.pi*bw/RANGE)**2
C:\Users\kumar\Anaconda3\lib\site-packages\statsmodels\nonparametric\kde.p
y:487: RuntimeWarning: invalid value encountered in true_divide
  binned = fast_linbin(X, a, b, gridsize) / (delta * nobs)
C:\Users\kumar\Anaconda3\lib\site-packages\statsmodels\nonparametric\kdeto
ols.py:34: RuntimeWarning: invalid value encountered in double_scalars
  FAC1 = 2*(np.pi*bw/RANGE)**2
```

Out[9]:

```
<seaborn.axisgrid.PairGrid at 0x22559d01c48>
```



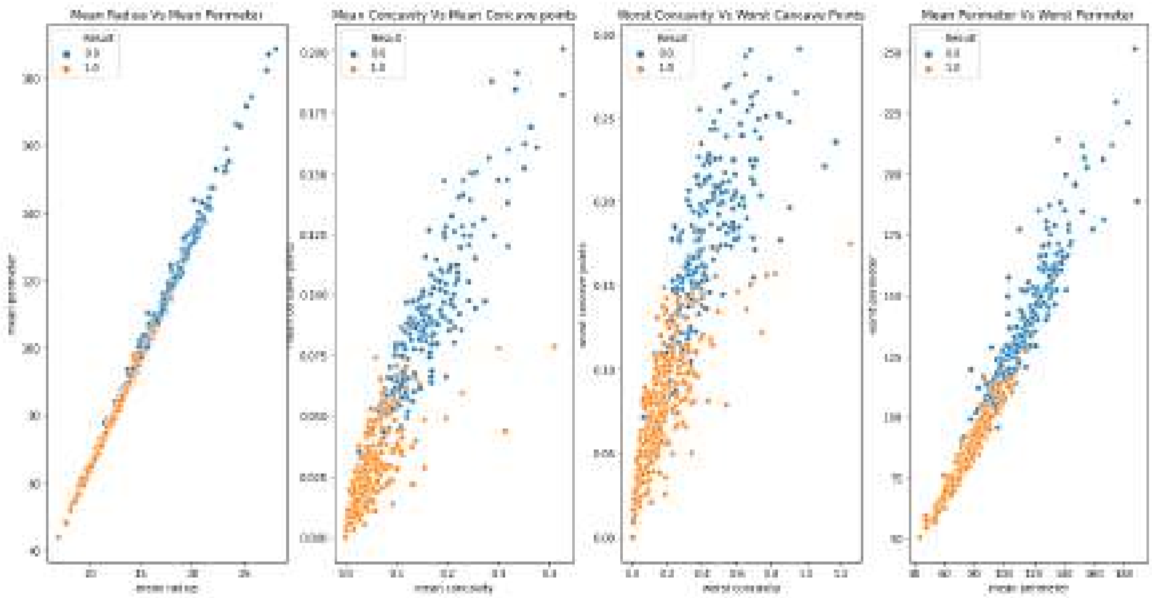
As we see, plot of all the features appears difficult to comprehend and very time consuming as well. So we will pick a few features which appear to show certain relation between the picked features.

In [11]:

```
fig, (ax1,ax2, ax3, ax4) = plt.subplots(1,4, figsize=(20,10))

ax1.set_title('Mean Radius Vs Mean Perimeter')
sns.scatterplot(x=df3['mean radius'], y=df3['mean perimeter'], data=df3, ax=ax1, hue="Result")

ax2.set_title('Mean Concavity Vs Mean Concave points')
sns.scatterplot(x=df3['mean concavity'], y=df3['mean concave points'], data=df3, ax=ax2,hue="Result")


ax3.set_title('Worst Concavity Vs Worst Cancave Points')
sns.scatterplot(x=df3['worst concavity'], y=df3['worst concave points'], data=df3, ax=ax3,hue="Result")


ax4.set_title('Mean Perimeter Vs Worst Perimeter')
sns.scatterplot(x=df3['mean perimeter'], y=df3['worst perimeter'], data=df3, ax=ax4,hue="Result")
```

Out[11]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x22510b20a88>
```



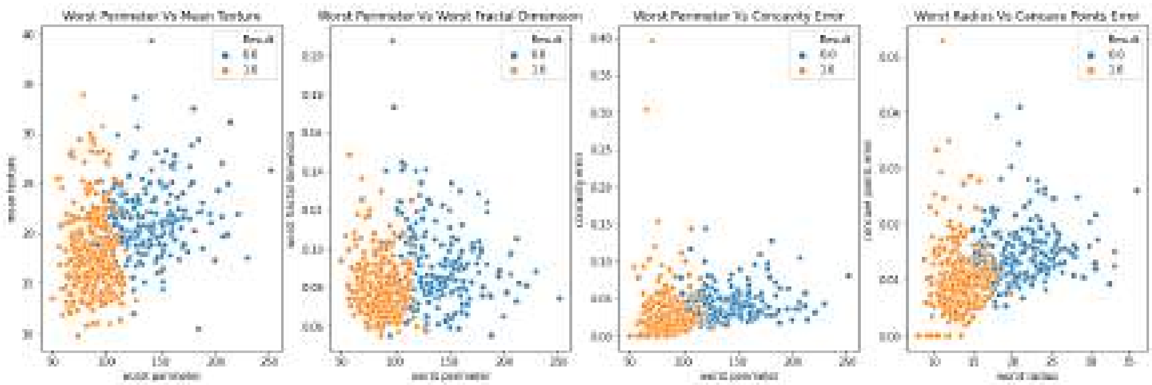
From the above 4 plots we could see that the two features under consideration in every plot are positively corelated and exhibit a relation that is directly proportional. For example, with rise in value of mean radius there is a proportional rise in mean perimeter. From this we get an idea that these features exhibit similar behaviour.

In [12]:

```
fig, (ax1,ax2, ax3, ax4) = plt.subplots(1,4, figsize=(20,6))

ax1.set_title('Worst Perimeter Vs Mean Texture')
sns.scatterplot(x=df3['worst perimeter'], y=df3['mean texture'], data=df3, ax=ax1, hue=
"Result")

ax2.set_title('Worst Perimeter Vs Worst Fractal Dimension')
sns.scatterplot(x=df3['worst perimeter'], y=df3['worst fractal dimension'], data=df3, a
x=ax2,hue="Result")


ax3.set_title('Worst Perimeter Vs Concavity Error')
sns.scatterplot(x=df3['worst perimeter'], y=df3['concavity error'], data=df3, ax=ax3,hu
e="Result")


ax4.set_title('Worst Radius Vs Cancave Points Error')
sns.scatterplot(x=df3['worst radius'], y=df3['concave points error'], data=df3, ax=ax4,
hue="Result")
```

Out[12]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x22511e37a48>
```



Here is another 2D scatter plot among a few features plotted against one another. Here we could see that there appears to be a distinction between benign and malignant cases. Just by observing the plots we can say with a great confidence that cases with mean texture beyond 10 and worst perimeter beyond 120 are malignant i.e. 0. Similar is the case for plot 2, 3 & 4. We can roughly draw a line to separate out benign from malignant.

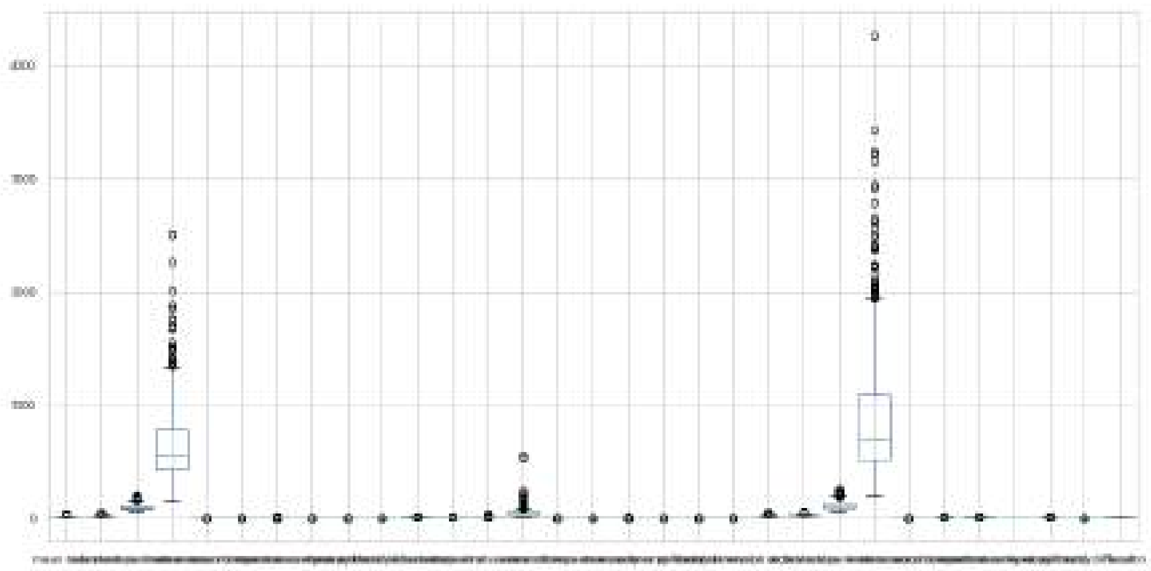
4. Make a boxplot for each feature and highlight the outlier, if any, then remove the outlier, make again box plot to show the outlier effect and write the inferences. [5]

In [13]:

```
# To plot a set of boxplot on the entire dataframe

sns.set(rc={'figure.figsize':(16,8)}, font_scale=0.9, style='whitegrid')
df3.boxplot(widths = 0.9)
```

Out[13]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x22511ea1548>
```

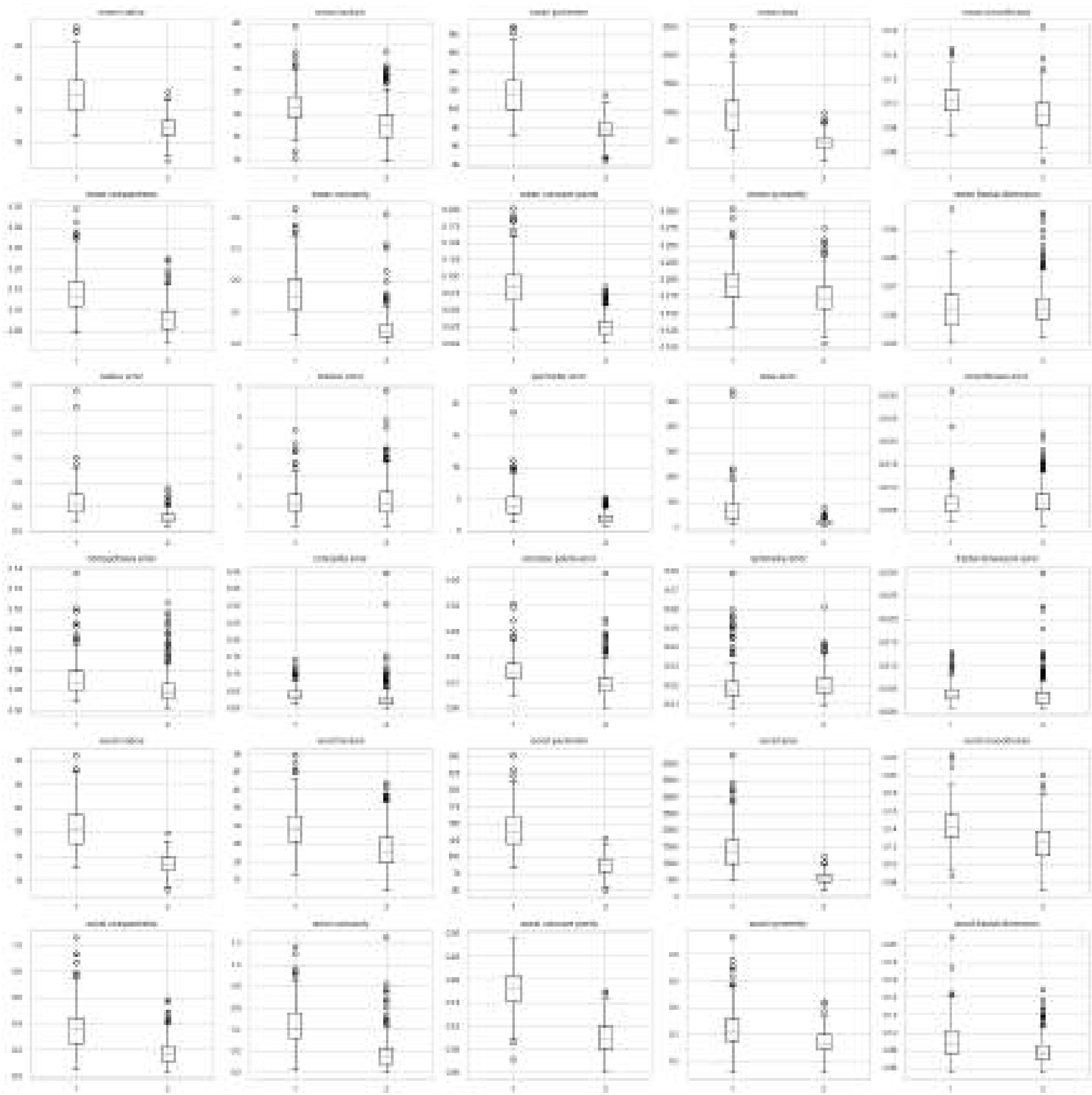


The above boxplot though gives us an overall picture, is not very readable. Hence we will need to plot the features one by one as follows.

In [14]:

```
global new_df # declaring it as global so as to be able to
              #use this var within local scopes of functions in future
new_df = df3.copy() # Making a copy of the original dataframe for ease

df_0 = new_df[new_df['Result'] == 0]
df_1 = new_df[new_df['Result'] == 1]
fig = plt.figure(figsize=(20,20))

#
for i,b in enumerate(list(new_df.columns[0:30])):

    i +=1
    ax = fig.add_subplot(6,5,i)
    ax.boxplot([df_0[b], df_1[b]])

    ax.set_title(b)

sns.set_style("whitegrid")
plt.tight_layout()
plt.legend()
plt.show()
```

```
No handles with labels found to put in legend.
```



This plot above gives a nice distinct view of boxplots for all the features at hand. We could see there exists outliers in all the features. Hence we will attempt removing outiers in the further cells using IQR method.

Using IQR (Inter Quartile Range) method for outlier removal

In [15]:

```python
def IQR_OutlierRemoval(new_df):  # Creating a function for outlier removal using IQR me
thod
    Q1 = new_df.quantile(0.25)
    Q3 = new_df.quantile(0.75)
    IQR = Q3 - Q1

    new_df = new_df[~((new_df < (Q1 - 1.5 * IQR)) |(new_df > (Q3 + 1.5 * IQR))).any(axi
s=1)]

    return new_df
```

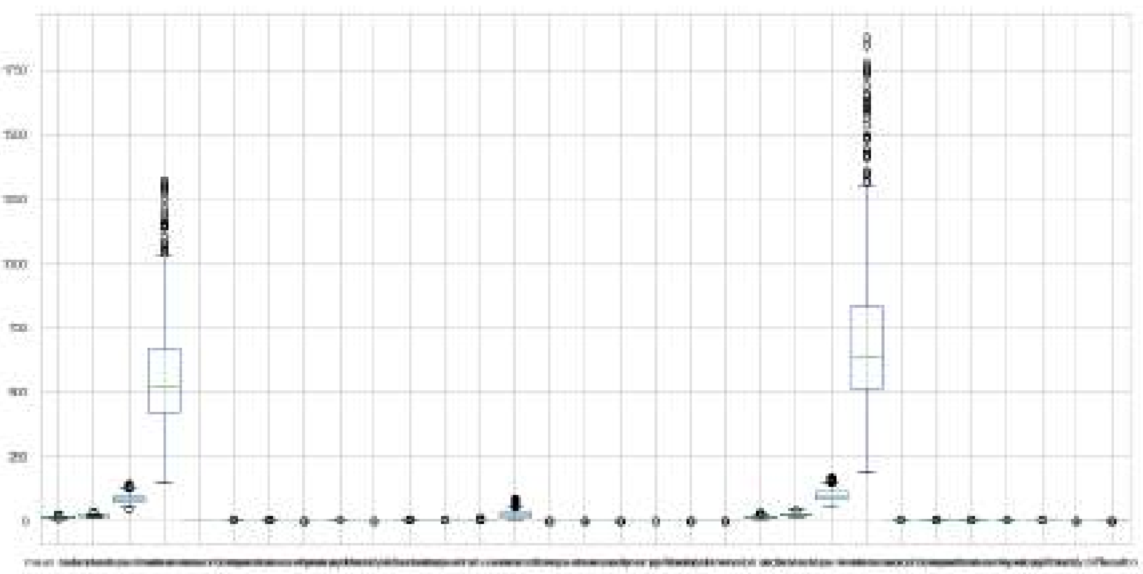
In [16]:

```
# Removing outliers using the function we created before

new_df = IQR_OutlierRemoval(new_df)

print("Shape of the dataframe before outlier removal: ", df3.shape)

print("Shape of the dataframe after outlier removal: ", new_df.shape)

# Plotting a set of boxplot over the entire dataset again post outlier removal

sns.set(rc={'figure.figsize':(16,8)}, font_scale=0.9, style='whitegrid')
new_df.boxplot(widths = 0.9)
```

```
Shape of the dataframe before outlier removal:  (569, 31)
Shape of the dataframe after outlier removal:  (398, 31)
```

Out[16]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x22512436708>
```



We performed outlier removal using Inter Quartile Range method and plotted box plot before outlier removal as well as after outlier removal. We observed that post removing outliers, we end up with a reduces sized dataframe. From a size of 569 rows we arrive at a row size of 398.

This, given we dropped the outlier rows as we asked in the question, could be dealt with better, had we imputed the outlier values with median values of their respective feature columns.

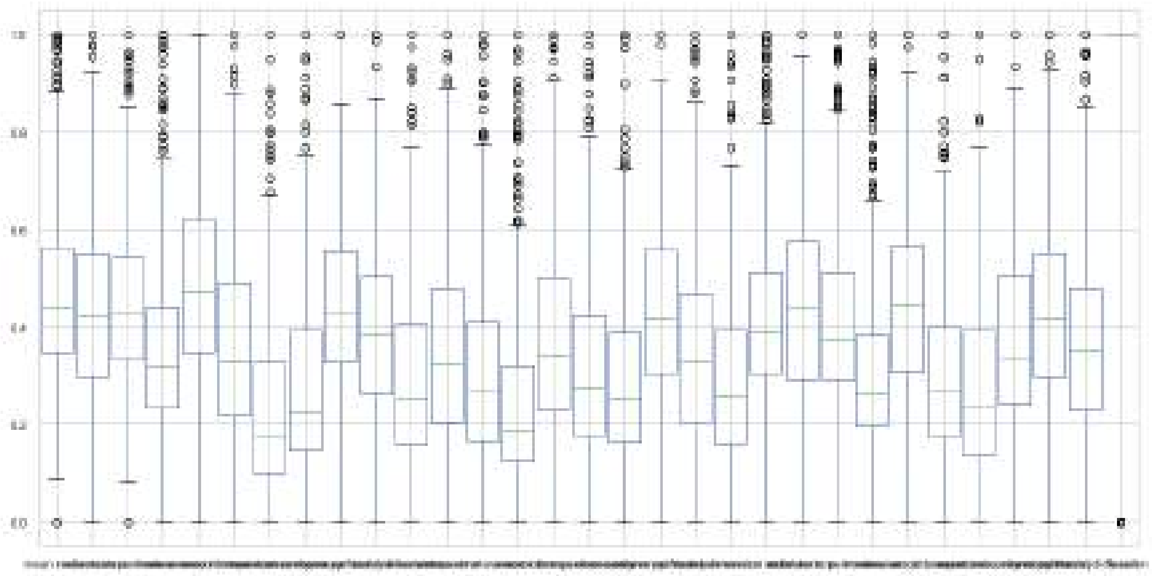
5. Normalized the data if required, and write a note for what, why and how you performed normalization.[5]

In [17]:

```
# Using MinMaxScaler to perform normalization
scaler = MinMaxScaler()
scaled_values = scaler.fit_transform(new_df)
new_df.loc[:,:] = scaled_values

sns.set(rc={'figure.figsize':(16,8)}, font_scale=0.9, style='whitegrid')
new_df.boxplot(widths = 0.9)
```

Out[17]:

```
<matplotlib.axes._subplots.AxesSubplot at 0x22592257ac8>
```



As all the features are of varied ranges, we applied MinMaxScaler here to scale it within 0 & 1. This makes analysis easier as all features now appear to vary within the same range.

In [ ]: