MileStone_4_Prashant_Raghuwanshi_DSC550

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Assignment: 8.3 Project Milestone 1 ,2, 3, & 4

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Course: DSC550-T301 Data Mining (2221-1)

Analyze data to predict the traits to detect Autistics disease amoung the toddlers Data Source : https://www.kaggle.com/fabdelja/autism-screening-for-toddlers?select=Toddler+Autism+dataset+July+2018.csv

Description about Dataset:

The dataset was developed by Dr Fadi Fayez Thabtah (fadifayez.com) using a mobile app called ASDTests (ASDtests.com) to screen autism in toddlers.we can use it to estimate the predictive power of machine learning techniques in detecting autistic traits

Abstract: Autistic Spectrum Disorder (ASD) is a neurodevelopmental condition associated with significant healthcare costs, and early diagnosis can significantly reduce these. Unfortunately, waiting times for an ASD diagnosis are lengthy and procedures are not cost effective. The economic impact of autism and the increase in the number of ASD cases across the world reveals an urgent need for the development of easily implemented and effective screening methods. Therefore, a time-efficient and accessible ASD screening is imminent to help health professionals and inform individuals whether they should pursue formal clinical diagnosis. The rapid growth in the number of ASD cases worldwide necessitates datasets related to behaviour traits

[1]:
```python
# Import library
import pandas as pd
import yellowbrick
import matplotlib.pyplot as plt
import numpy as np
```

```
C:\ProgramData\Anaconda3\lib\site-packages\sklearn\utils\deprecation.py:143:
FutureWarning: The sklearn.metrics.classification module is  deprecated in
version 0.22 and will be removed in version 0.24. The corresponding classes /
functions should instead be imported from sklearn.metrics. Anything that cannot
be imported from sklearn.metrics is now part of the private API.
  warnings.warn(message, FutureWarning)
```

Columns Details : Features collected and their descriptions Feature Type Description Variable in Dataset Corresponding Q-chat-10-Toddler Features A1 Does your child look at you when you call his/her name? A2 How easy is it for you to get eye contact with your child? A3 Does your child point to indicate that s/he wants something? (e.g. a toy that is out of reach) A4 Does your child point to share interest with you? (e.g. poin9ng at an interes9ng sight) A5 Does your child pretend? (e.g. care for dolls, talk on a toy phone) A6 Does your child follow where you're looking? A7 If you or someone else in the family is visibly upset, does your child show signs of wan9ng to comfort them? (e.g. stroking hair, hugging them) A8 Would you describe your child's first words as: A9 Does your child use simple gestures? (e.g. wave goodbye) A10 Does your child stare at nothing with no apparent purpose? Age Number Toddlers (months) Score by Q-chat-10 Number 1-10 (Less that or equal 3 no ASD traits; > 3 ASD traits Sex Character Male or Female Ethnicity String List of common ethnicities in text format Born with jaundice Boolean (yes or no) Whether the case was born with jaundice Family member with ASD history Boolean (yes or no) Whether any immediate family member has a PDD Who is completing the test String Parent, self, caregiver, medical staff, clinician ,etc. Why_are_you_taken_the_screening String Use input textbox Class variable String ASD traits or No ASD traits (automatically assigned by the ASDTests app). (Yes / No)

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[2]:
```
# 1.Load the data from the "Toddler Autism dataset July 2018.csv" file into a␣
↪DataFrame.
addr1 = "D:/MS_DataScience/DSC550/Milestone-1/Toddler Autism dataset July 2018.
↪csv"
df_todd = pd.read_csv(addr1)
df_todd.head()
```

[2]:
```
   Case_No  A1  A2  A3  A4  A5  A6  A7  A8  A9  A10  Age_Mons  Qchat-10-Score  \
0        1   0   0   0   0   0   0   1   1   0    1        28               3
1        2   1   1   0   0   0   1   1   0   0    0        36               4
2        3   1   0   0   0   0   0   1   1   0    1        36               4
3        4   1   1   1   1   1   1   1   1   1    1        24              10
4        5   1   1   0   1   1   1   1   1   1    1        20               9

  Sex       Ethnicity Jaundice Family_mem_with_ASD Who completed the test  \
0   f  middle eastern      yes                  no          family member
1   m  White European      yes                  no          family member
2   m  middle eastern      yes                  no          family member
3   m        Hispanic       no                  no          family member
4   f  White European       no                 yes          family member

  ASD_Traits
0         No
1        Yes
2        Yes
3        Yes
4        Yes
```

[3]:
```
df_todd.info() # find out the datatype for each columns
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1054 entries, 0 to 1053
Data columns (total 19 columns):
 #   Column                  Non-Null Count  Dtype
---  ------                  --------------  -----
 0   Case_No                 1054 non-null   int64
 1   A1                      1054 non-null   int64
 2   A2                      1054 non-null   int64
 3   A3                      1054 non-null   int64
 4   A4                      1054 non-null   int64
 5   A5                      1054 non-null   int64
 6   A6                      1054 non-null   int64
 7   A7                      1054 non-null   int64
 8   A8                      1054 non-null   int64
 9   A9                      1054 non-null   int64
 10  A10                     1054 non-null   int64
 11  Age_Mons                1054 non-null   int64
 12  Qchat-10-Score          1054 non-null   int64
 13  Sex                     1054 non-null   object
 14  Ethnicity               1054 non-null   object
 15  Jaundice                1054 non-null   object
 16  Family_mem_with_ASD     1054 non-null   object
 17  Who completed the test  1054 non-null   object
 18  ASD_Traits              1054 non-null   object
dtypes: int64(13), object(6)
memory usage: 156.6+ KB
```

[4]:

```
#5.        Look at summary information about your data (total, mean, min, max,
↪freq, unique, etc.)  Does this present any more questions for you?  Does it
↪lead you to a conclusion yet?
print("\nDescribe Data\n")
print(df_todd.describe())
```

```
Describe Data

          Case_No           A1           A2           A3           A4  \
count  1054.000000  1054.000000  1054.000000  1054.000000  1054.000000
mean    527.500000     0.563567     0.448767     0.401328     0.512334
std     304.407895     0.496178     0.497604     0.490400     0.500085
min       1.000000     0.000000     0.000000     0.000000     0.000000
25%     264.250000     0.000000     0.000000     0.000000     0.000000
50%     527.500000     1.000000     0.000000     0.000000     1.000000
75%     790.750000     1.000000     1.000000     1.000000     1.000000
max    1054.000000     1.000000     1.000000     1.000000     1.000000

               A5           A6           A7           A8           A9  \
count  1054.000000  1054.000000  1054.000000  1054.000000  1054.000000
```

```
mean      0.524668     0.576850     0.649905     0.459203     0.489564
std       0.499628     0.494293     0.477226     0.498569     0.500128
min       0.000000     0.000000     0.000000     0.000000     0.000000
25%       0.000000     0.000000     0.000000     0.000000     0.000000
50%       1.000000     1.000000     1.000000     0.000000     0.000000
75%       1.000000     1.000000     1.000000     1.000000     1.000000
max       1.000000     1.000000     1.000000     1.000000     1.000000

               A10      Age_Mons  Qchat-10-Score
count  1054.000000  1054.000000     1054.000000
mean      0.586338    27.867173        5.212524
std       0.492723     7.980354        2.907304
min       0.000000    12.000000        0.000000
25%       0.000000    23.000000        3.000000
50%       1.000000    30.000000        5.000000
75%       1.000000    36.000000        8.000000
max       1.000000    36.000000       10.000000
```

[5]:

```python
print("\nSummarized Data\n")
print(df_todd.describe(include=['O']))
```

```
Summarized Data

         Sex       Ethnicity Jaundice Family_mem_with_ASD  \
count   1054            1054     1054                1054
unique     2              11        2                   2
top        m  White European       no                  no
freq     735             334      766                 884

       Who completed the test ASD_Traits
count                    1054       1054
unique                      5          2
top             family member        Yes
freq                     1018        728
```

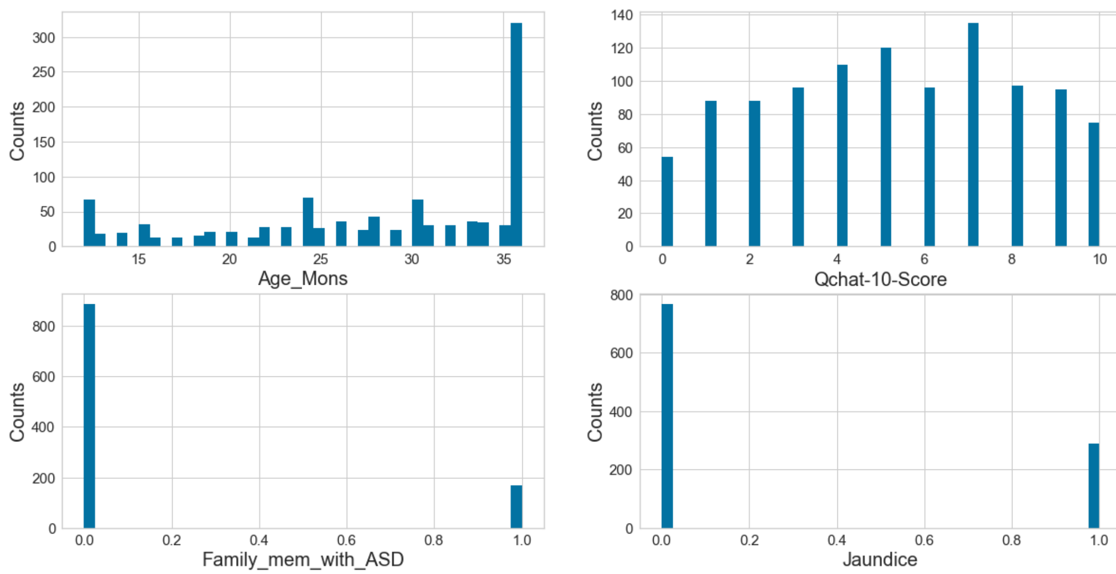
[6]:

```python
# converting categorical data to numbers
df_todd['ASD_Traits'] = df_todd['ASD_Traits'].replace(['Yes', 'No'],[1, 0])
df_todd['Jaundice'] = df_todd['Jaundice'].replace(['yes', 'no'],[1, 0])
df_todd['Family_mem_with_ASD'] = df_todd['Family_mem_with_ASD'].replace(['yes',␣
 ↪'no'],[1, 0])
```

[7]:

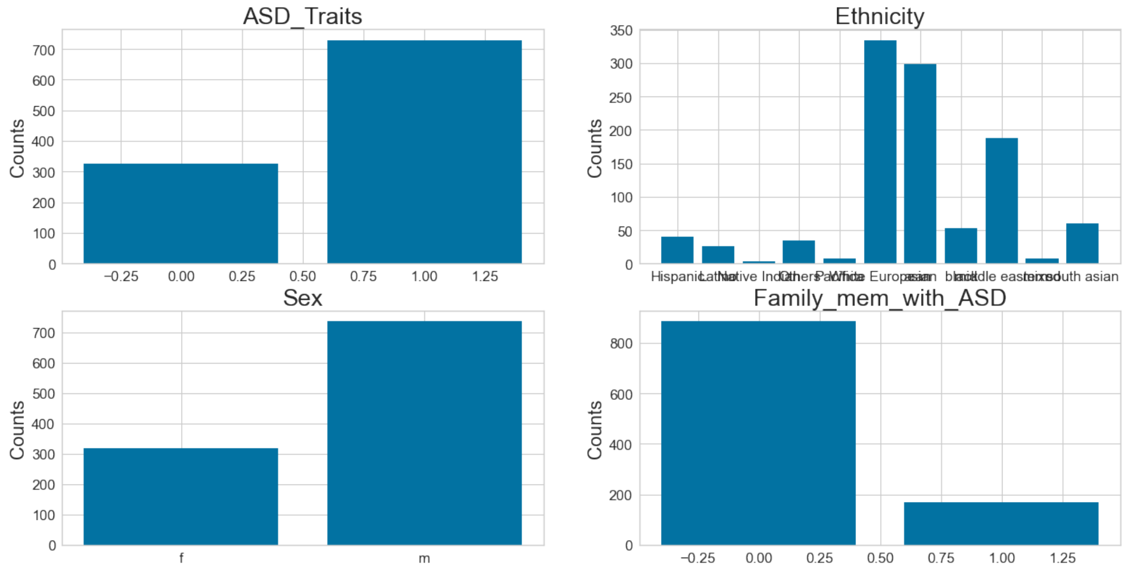
```python
#6.        Make some histograms of your data ("A picture is worth a thousand␣
 ↪words!")
# Specify the features of interest
num_features = ['Age_Mons', 'Qchat-10-Score', 'Family_mem_with_ASD', 'Jaundice']
xaxes = num_features
yaxes = ['Counts', 'Counts', 'Counts', 'Counts']
```

```
# set up the figure size
plt.rcParams['figure.figsize'] = (20, 10)
# make subplots
fig, axes = plt.subplots(nrows = 2, ncols = 2)
# draw histograms
axes = axes.ravel()
for idx, ax in enumerate(axes):
    ax.hist(df_todd[num_features[idx]].dropna(), bins=40)
    ax.set_xlabel(xaxes[idx], fontsize=20)
    ax.set_ylabel(yaxes[idx], fontsize=20)
    ax.tick_params(axis='both', labelsize=15)
plt.show()
```

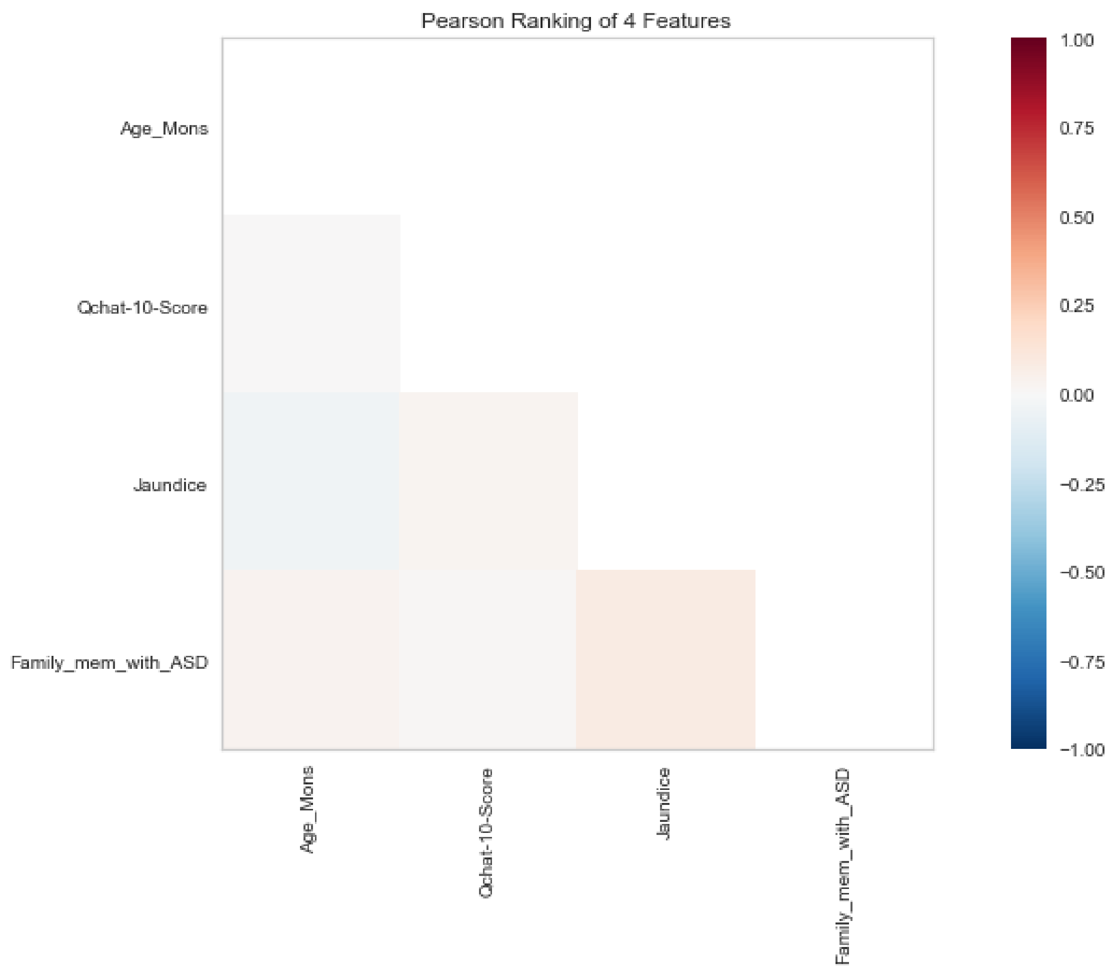


[8]:
```
#7:  Barcharts: set up the figure size
%matplotlib inline
plt.rcParams['figure.figsize'] = (20, 10)

# make subplots
fig, axes = plt.subplots(nrows = 2, ncols = 2)

# make the data read to feed into the visulizer
X_ASD_Traits = df_todd.groupby('ASD_Traits').size().
↪reset_index(name='Counts')['ASD_Traits']
Y_ASD_Traits = df_todd.groupby('ASD_Traits').size().
↪reset_index(name='Counts')['Counts']
# make the bar plot
axes[0, 0].bar(X_ASD_Traits, Y_ASD_Traits)
axes[0, 0].set_title('ASD_Traits', fontsize=25)
```

```
axes[0, 0].set_ylabel('Counts', fontsize=20)
axes[0, 0].tick_params(axis='both', labelsize=15)

# make the data read to feed into the visulizer
X_Ethnicity = df_todd.groupby('Ethnicity').size().
 ↪reset_index(name='Counts')['Ethnicity']
Y_Ethnicity = df_todd.groupby('Ethnicity').size().
 ↪reset_index(name='Counts')['Counts']
# make the bar plot
axes[0, 1].bar(X_Ethnicity, Y_Ethnicity)
axes[0, 1].set_title('Ethnicity', fontsize=25)
axes[0, 1].set_ylabel('Counts', fontsize=20)
axes[0, 1].tick_params(axis='both', labelsize=15)

# make the data read to feed into the visulizer
X_Sex = df_todd.groupby('Sex').size().reset_index(name='Counts')['Sex']
Y_Sex = df_todd.groupby('Sex').size().reset_index(name='Counts')['Counts']
# make the bar plot
axes[1, 0].bar(X_Sex, Y_Sex)
axes[1, 0].set_title('Sex', fontsize=25)
axes[1, 0].set_ylabel('Counts', fontsize=20)
axes[1, 0].tick_params(axis='both', labelsize=15)

# make the data read to feed into the visualizer
X_Family_mem_with_ASD = df_todd.groupby('Family_mem_with_ASD').size().
 ↪reset_index(name='Counts')['Family_mem_with_ASD']
Y_Family_mem_with_ASD = df_todd.groupby('Family_mem_with_ASD').size().
 ↪reset_index(name='Counts')['Counts']
# make the bar plot
axes[1, 1].bar(X_Family_mem_with_ASD, Y_Family_mem_with_ASD)
axes[1, 1].set_title('Family_mem_with_ASD', fontsize=25)
axes[1, 1].set_ylabel('Counts', fontsize=20)
axes[1, 1].tick_params(axis='both', labelsize=15)
plt.show()
```

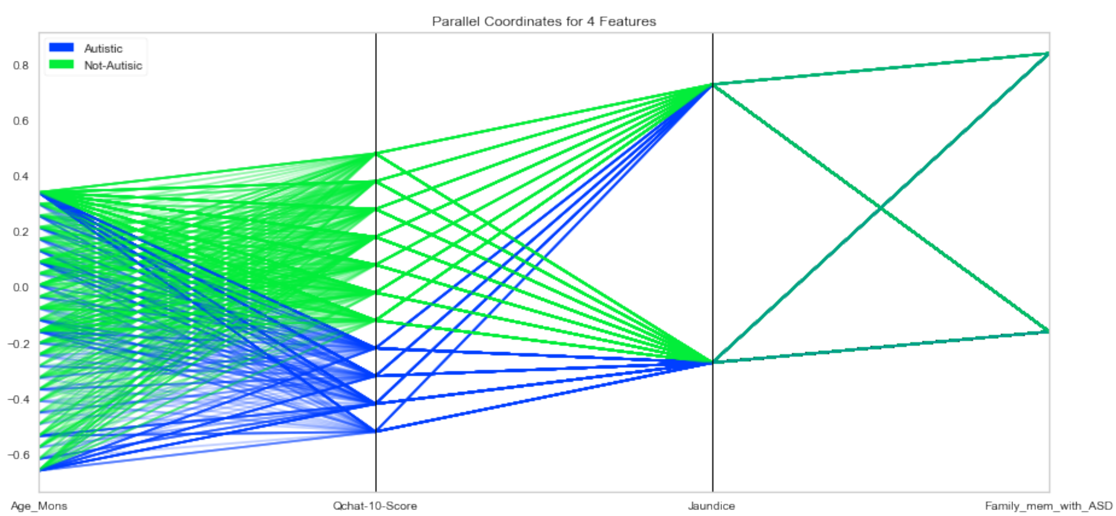


[9]:
```python
# The correlation between the variables is low (1 or -1 is high positive or high negative, 0 is low or no correlation)
# These results show there is  positive correlation between 'ASD_Traits' & 'Qchat-10-Score', but it's not a high correlation amoung other variables.

#Step 8: Pearson Ranking
#set up the figure size
#%matplotlib inline
plt.rcParams['figure.figsize'] = (15, 7)

# import the package for visulization of the correlation
from yellowbrick.features import Rank2D
num_features = ['Age_Mons', 'Qchat-10-Score', 'Jaundice', 'Family_mem_with_ASD']
# Define features to test for correlation
# extract the numpy arrays from the data frame
X = df_todd[num_features].to_numpy()

# instantiate the visualizer with the Covariance ranking algorithm
visualizer = Rank2D(features=num_features, algorithm='pearson')
visualizer.fit(X)                 # Fit the data to the visualizer
visualizer.transform(X)              # Transform the data
visualizer.poof(outpath="pcoords1.png") # Draw/show/poof the data
plt.show()
```



[10]:
```
# Use Parallel Coordinates visualization to compare the distributions of␣
↪numerical variables between
# In a Parallel Coordinates Plot, each variable is given its own axis and all␣
↪the axes are placed in parallel to each other.
# Values are plotted as a series of lines that connected across all the axes.␣
↪This means that each line is a collection of points placed on each axis,␣
↪that have all been connected together.
# Parallel Coordinates Plots are ideal for comparing many variables together␣
↪and seeing the relationships between them.
plt.rcParams['figure.figsize'] = (15, 7)
plt.rcParams['font.size'] = 50
# setup the color for yellowbrick visulizer
from yellowbrick.style import set_palette
set_palette('sns_bright')

# import packages
```

```
from yellowbrick.features import ParallelCoordinates
# Specify the features of interest and the classes of the target
classes = ['Autistic', 'Not-Autisic']
num_features = ['Age_Mons', 'Qchat-10-Score', 'Jaundice', 'Family_mem_with_ASD']
# copy data to a new dataframe
data_norm = df_todd.copy()
# Each axis can have a different scale, as each variable works off a different␣
↪unit of measurement,
# or all the axes can be normalised to keep all the scales uniform..
# normalize data to 0-1 range
for feature in num_features:
    data_norm[feature] = (df_todd[feature] - df_todd[feature].
↪mean(skipna=True)) / (df_todd[feature].max(skipna=True) - df_todd[feature].
↪min(skipna=True))

# Extract the numpy arrays from the data frame
X = data_norm[num_features].to_numpy()
y = df_todd.ASD_Traits.to_numpy()

# Instantiate the visualizer

visualizer = ParallelCoordinates(classes=classes, features=num_features)
visualizer.fit(X, y)      # Fit the data to the visualizer
visualizer.transform(X)   # Transform the data
visualizer.poof(outpath="d://pcoords2.png") # Draw/show/poof the data
plt.show();
```



Parallel cordinate for 4 features shows below information

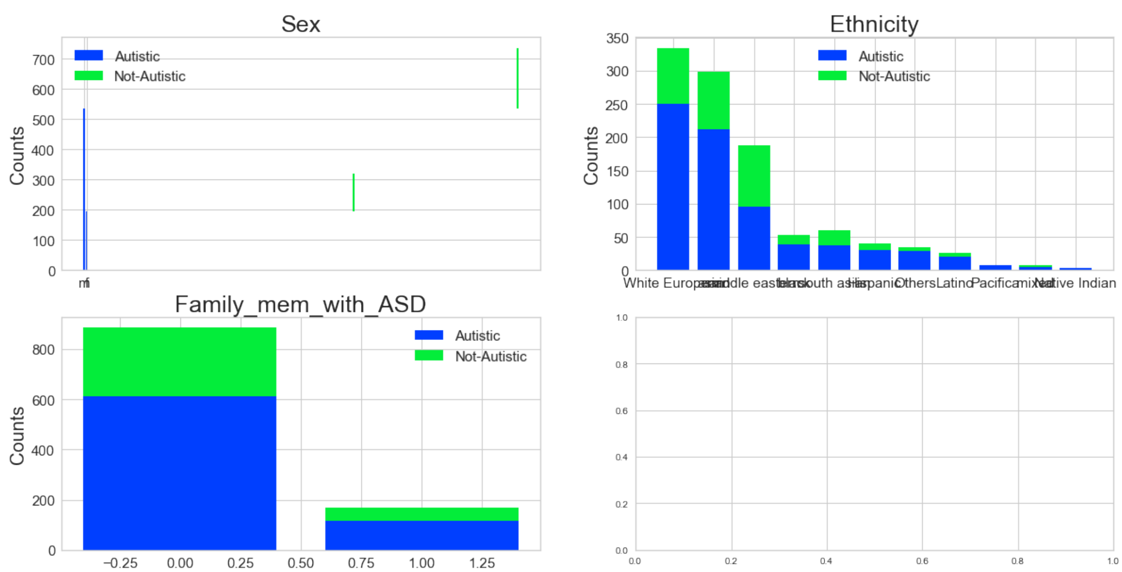
as per the graph fro autistic patients,we have a seen relationship between age ,score and jaundice variables,how ever family men with ads feature is not having any relation with other features

for non austics, we have seens relationship beteen all listed 4 features

[11]:
```
# Use Stack Bar Charts to compare toddlers who is having ASD &  who didn't have␣
↪ASD based on the other variables.

# Step 10 - stacked bar charts to compare autistic/not autistic
#set up the figure size
#%matplotlib inline
plt.rcParams['figure.figsize'] = (20, 10)

# make subplots
fig, axes = plt.subplots(nrows = 2, ncols = 2)

# make the data read to feed into the visulizer
Sex_autism = df_todd[df_todd['ASD_Traits']==1]['Sex'].value_counts()
Sex_not_autism = df_todd[df_todd['ASD_Traits']==0]['Sex'].value_counts()
Sex_not_autism = Sex_not_autism.reindex(index = Sex_autism.index)
# make the bar plot
p1 = axes[0, 0].bar(Sex_autism.index, Sex_autism.values)
p2 = axes[0, 0].bar(Sex_not_autism, Sex_not_autism.values, bottom=Sex_autism.
↪values)
axes[0, 0].set_title('Sex', fontsize=25)
axes[0, 0].set_ylabel('Counts', fontsize=20)
axes[0, 0].tick_params(axis='both', labelsize=15)
axes[0, 0].legend((p1[0], p2[0]), ('Autistic', 'Not-Autistic'), fontsize = 15)

# make the data read to feed into the visualizer
ethnicity_autism = df_todd[df_todd['ASD_Traits']==1]['Ethnicity'].value_counts()
ethnicity_not_autism = df_todd[df_todd['ASD_Traits']==0]['Ethnicity'].
↪value_counts()
ethnicity_not_autism = ethnicity_not_autism.reindex(index = ethnicity_autism.
↪index)
# make the bar plot
p3 = axes[0, 1].bar(ethnicity_autism.index, ethnicity_autism.values)
p4 = axes[0, 1].bar(ethnicity_not_autism.index, ethnicity_not_autism.values,␣
↪bottom=ethnicity_autism.values)
axes[0, 1].set_title('Ethnicity', fontsize=25)
axes[0, 1].set_ylabel('Counts', fontsize=20)
axes[0, 1].tick_params(axis='both', labelsize=15)
axes[0, 1].legend((p3[0], p4[0]), ('Autistic', 'Not-Autistic'), fontsize = 15)

# make the data read to feed into the visualizer
ASD_autism = df_todd[df_todd['ASD_Traits']==1]['Family_mem_with_ASD'].
↪value_counts()
```

```
ASD_not_autism = df_todd[df_todd['ASD_Traits']==0]['Family_mem_with_ASD'].
 ↪value_counts()
ASD_not_autism = ASD_not_autism.reindex(index = ASD_autism.index)

# make the bar plot
p5 = axes[1, 0].bar(ASD_autism.index, ASD_autism.values)
p6 = axes[1, 0].bar(ASD_not_autism.index, ASD_not_autism.values,␣
 ↪bottom=ASD_autism.values)
axes[1, 0].set_title('Family_mem_with_ASD', fontsize=25)
axes[1, 0].set_ylabel('Counts', fontsize=20)
axes[1, 0].tick_params(axis='both', labelsize=15)
axes[1, 0].legend((p5[0], p6[0]), ('Autistic', 'Not-Autistic'), fontsize = 15)
```

[11]: <matplotlib.legend.Legend at 0x216ae3b0dc0>



less females have ASD as compared to MEN, white europian is having more rate for insfaction from ASD,

Family with ASD history and with Non ASD history, in both toddlers have ASD

Milestone 2

1) drop any features that are not useful for your model building. You should explain and justify why the feature dropped is not useful

2) address any missing data issues.

3) Build any new features that you need for your model, e.g., create dummy variables for categorical features if necessary. Explain your process at each step. You can use any methods/tools you think are most appropriate.

[12]:
```
#fill the missing data with median value
# num_features = ['Age_Mons', 'Qchat-10-Score', 'Jaundice',␣
↪'Family_mem_with_ASD']
def fill_na_median(df_todd, inplace=True):
    return df_todd.fillna(df_todd.median(), inplace=inplace)

fill_na_median(df_todd['Qchat-10-Score'])

# check the result
print(df_todd['Qchat-10-Score'].describe())
```

```
count    1054.000000
mean        5.212524
std         2.907304
min         0.000000
25%         3.000000
50%         5.000000
75%         8.000000
max        10.000000
Name: Qchat-10-Score, dtype: float64
```

[13]:
```
# fill with the most represented value
def fill_na_most(df_todd, inplace=True):
    return df_todd.fillna('family member', inplace=inplace)

fill_na_most(df_todd['Who completed the test'])

# check the result
print(df_todd['Who completed the test'].describe())
```

```
count              1054
unique                5
top       family member
freq               1018
Name: Who completed the test, dtype: object
```

[14]:
```
np.unique(df_todd['Who completed the test'])
```

[14]:
```
array(['Health Care Professional', 'Health care professional', 'Others',
       'Self', 'family member'], dtype=object)
```

found data quality issue in one of the variable value of df_todd['Who completed the test'] . so replace the values

[15]:
```
df_todd['Who completed the test'] = df_todd['Who completed the test'].
↪replace(['Health Care Professional'],'Health care professional')
```

[16]:
```
np.unique(df_todd['Who completed the test'])
```

[16]:
```
array(['Health care professional', 'Others', 'Self', 'family member'],
      dtype=object)
```

[17]:
```
# check the result
print(df_todd['Who completed the test'].describe())
```

```
count              1054
unique                4
top       family member
freq               1018
Name: Who completed the test, dtype: object
```

[18]:
```
# fill with the most represented value
def fill_na_most(df_todd, inplace=True):
    return df_todd.fillna('White European', inplace=inplace)

fill_na_most(df_todd['Ethnicity'])

# check the result
print(df_todd['Ethnicity'].describe())
```

```
count               1054
unique                11
top       White European
freq                 334
Name: Ethnicity, dtype: object
```

[19]:
```
# import package
import numpy as np

# log-transformation
def log_transformation(df_todd):
    return df_todd.apply(np.log1p)

df_todd['Qchat-10-Score_log'] = log_transformation(df_todd['Qchat-10-Score'])

# check the data
print(df_todd.describe())
```

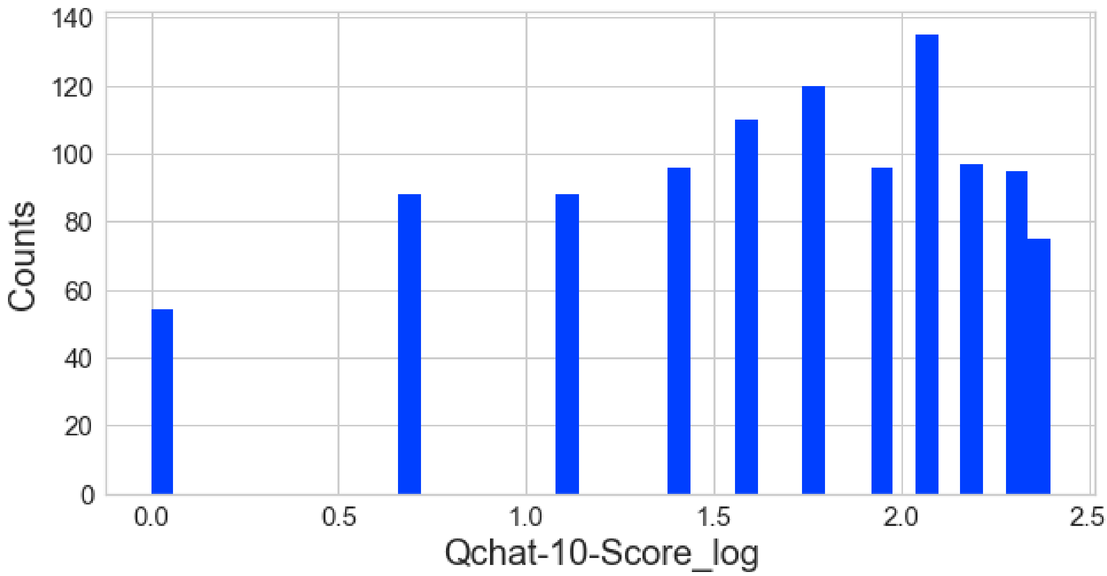
```
           Case_No           A1           A2           A3           A4  \
count  1054.000000  1054.000000  1054.000000  1054.000000  1054.000000
mean    527.500000     0.563567     0.448767     0.401328     0.512334
std     304.407895     0.496178     0.497604     0.490400     0.500085
min       1.000000     0.000000     0.000000     0.000000     0.000000
25%     264.250000     0.000000     0.000000     0.000000     0.000000
50%     527.500000     1.000000     0.000000     0.000000     1.000000
75%     790.750000     1.000000     1.000000     1.000000     1.000000
```

```
max     1054.000000      1.000000      1.000000      1.000000      1.000000

                 A5            A6            A7            A8            A9  \
count  1054.000000   1054.000000   1054.000000   1054.000000   1054.000000
mean      0.524668      0.576850      0.649905      0.459203      0.489564
std       0.499628      0.494293      0.477226      0.498569      0.500128
min       0.000000      0.000000      0.000000      0.000000      0.000000
25%       0.000000      0.000000      0.000000      0.000000      0.000000
50%       1.000000      1.000000      1.000000      0.000000      0.000000
75%       1.000000      1.000000      1.000000      1.000000      1.000000
max       1.000000      1.000000      1.000000      1.000000      1.000000

                A10     Age_Mons  Qchat-10-Score     Jaundice  \
count  1054.000000  1054.000000     1054.000000  1054.000000
mean      0.586338    27.867173        5.212524     0.273245
std       0.492723     7.980354        2.907304     0.445837
min       0.000000    12.000000        0.000000     0.000000
25%       0.000000    23.000000        3.000000     0.000000
50%       1.000000    30.000000        5.000000     0.000000
75%       1.000000    36.000000        8.000000     1.000000
max       1.000000    36.000000       10.000000     1.000000

       Family_mem_with_ASD   ASD_Traits  Qchat-10-Score_log
count          1054.000000  1054.000000         1054.000000
mean              0.161290     0.690702            1.671783
std               0.367973     0.462424            0.622364
min               0.000000     0.000000            0.000000
25%               0.000000     0.000000            1.386294
50%               0.000000     1.000000            1.791759
75%               0.000000     1.000000            2.197225
max               1.000000     1.000000            2.397895
```

above results shows the new feature qchart-1-score_log columns which contains Log Transformed values for highly skewed data

[20]:

```python
# Log Transformation is a good method to use on highly skewed data.
#check the distribution using histogram
# set up the figure size
#adjust skewed data (result)

plt.rcParams['figure.figsize'] = (10, 5)

plt.hist(df_todd['Qchat-10-Score_log'], bins=40)
plt.xlabel('Qchat-10-Score_log', fontsize=20)
plt.ylabel('Counts', fontsize=20)
plt.tick_params(axis='both', labelsize=15)
plt.show()
```



log transformed high skewed values & its counts are showing in historgram

[21]:
```
# convert categorical data to numbers
#get the categorical data
cat_features = ['Who completed the test', 'Sex']
data_cat = df_todd[cat_features]
# One Hot Encoding
data_cat_dummies = pd.get_dummies(data_cat)
# check the data
print(data_cat_dummies.head(8))
```

```
   Who completed the test_Health care professional  \
0                                                0
1                                                0
2                                                0
3                                                0
4                                                0
5                                                0
6                                                0
7                                                0

   Who completed the test_Others  Who completed the test_Self  \
0                              0                            0
1                              0                            0
2                              0                            0
3                              0                            0
4                              0                            0
5                              0                            0
6                              0                            0
```

```
7                              0                            0

   Who completed the test_family member  Sex_f  Sex_m
0                                     1      1      0
1                                     1      0      1
2                                     1      0      1
3                                     1      0      1
4                                     1      1      0
5                                     1      0      1
6                                     1      0      1
7                                     1      0      1
```

created new dummy variables , Who completed the test__Health Care Professional, Who completed the test__Others, Who completed the test__Self, Who completed the test__family member,Sex__f,Sex__m Milestone 3

[22]:
```
# In Milestone 3, you should build and evaluate at least one model.
# You can use any methods/tools you think are most appropriate, but you should␣
 ↪explain/justify why you are choosing the model(s) and evaluation metric(s)␣
 ↪you choose.
# It is important to think about what type of model and metric makes sense for␣
 ↪the context of your problem.
# If you are familiar with hyperparameter tuning, this would also be a great␣
 ↪addition to your project.
# Again, keep in mind that this may look very different from what is done in␣
 ↪the Titanic tutorial case study.
# You should do what makes sense for your project.
# Write a short overview/conclusion of the insights gained from your model␣
 ↪building/evaluation
```

[23]:
```
df_todd.head()
```

[23]:
```
   Case_No  A1  A2  A3  A4  A5  A6  A7  A8  A9  A10  Age_Mons  Qchat-10-Score  \
0        1   0   0   0   0   0   0   1   1   0    1        28               3
1        2   1   1   0   0   0   1   1   0   0    0        36               4
2        3   1   0   0   0   0   0   1   1   0    1        36               4
3        4   1   1   1   1   1   1   1   1   1    1        24              10
4        5   1   1   0   1   1   1   1   1   1    1        20               9

  Sex       Ethnicity  Jaundice  Family_mem_with_ASD Who completed the test  \
0   f  middle eastern         1                    0          family member
1   m  White European         1                    0          family member
2   m  middle eastern         1                    0          family member
3   m        Hispanic         0                    0          family member
4   f  White European         0                    1          family member

  ASD_Traits  Qchat-10-Score_log
```

```
0          0          1.386294
1          1          1.609438
2          1          1.609438
3          1          2.397895
4          1          2.302585
```

[24]:
```
#create a whole features dataset that can be used for train and validation data␣
↪splitting
# here we will combine the numerical features and the dummie features together
features_model = ['Jaundice', 'Age_Mons', 'Qchat-10-Score_log']
data_model_X = pd.concat([df_todd[features_model], data_cat_dummies], axis=1)
```

[25]:
```
# create a whole target dataset that can be used for train and validation data␣
↪splitting
#data_model_y = df_todd.replace({'autism': {1: 'Autistic', 0:␣
↪'Not_Autistic'}})['ASD_Traits']
data_model_y = df_todd['ASD_Traits']
# separate data into training and validation and check the details of the␣
↪datasets
# import packages
from sklearn.model_selection import train_test_split

# split the data
X_train, X_val, y_train, y_val = train_test_split(data_model_X, data_model_y,␣
↪test_size =0.3, random_state=11)
```

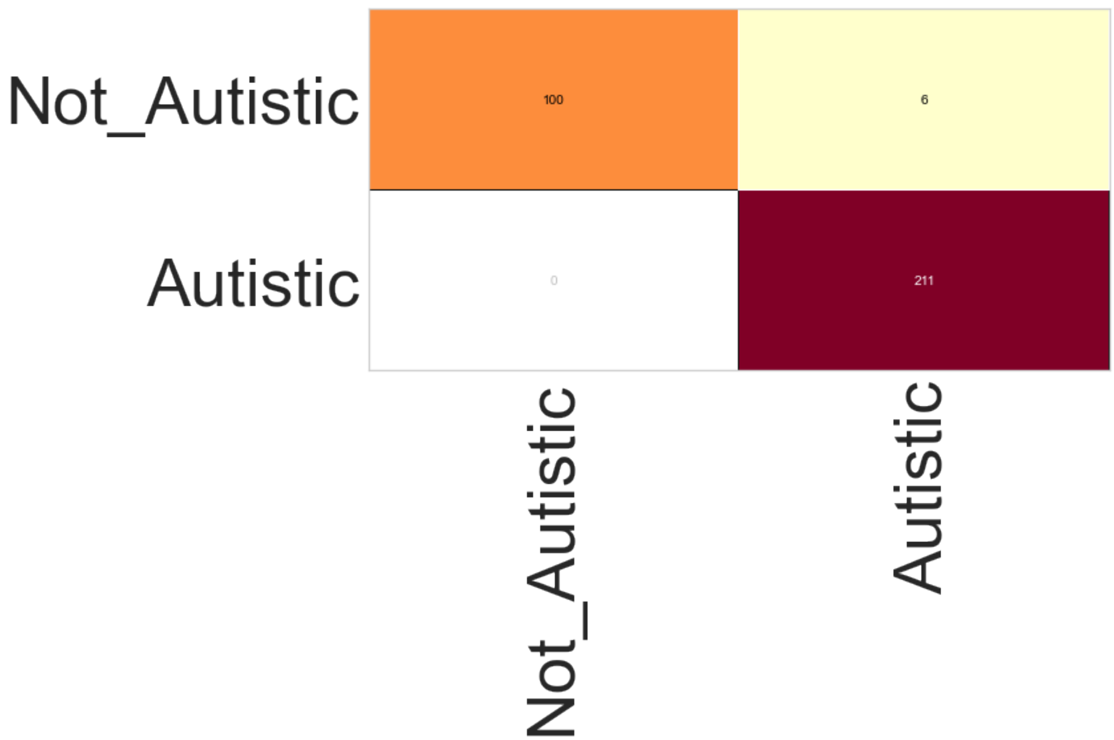
[26]:
```
# number of samples in each set
print("No. of samples in training set: ", X_train.shape[0])
print("No. of samples in validation set:", X_val.shape[0])

# Autistic and not-autistic
print('\n')
print('No. of autistic and not-autistic in the training set:')
print(y_train.value_counts())

print('\n')
print('No. of autistic and not-autistic in the validation set:')
print(y_val.value_counts())
```

```
No. of samples in training set:  737
No. of samples in validation set: 317


No. of autistic and not-autistic in the training set:
1    517
0    220
Name: ASD_Traits, dtype: int64
```

```
No. of autistic and not-autistic in the validation set:
1    211
0    106
Name: ASD_Traits, dtype: int64
```

[27]:
```
# Classification is a technique where we categorize data into a given number of␣
↪classes like 'Not_Autistic','Autistic'.
# The main goal of a classification problem is to identify the category/class␣
↪to which a new data will fall under.

# Eval Metrics  - ConfusionMatrix
from sklearn.linear_model import LogisticRegression
from yellowbrick.classifier import ConfusionMatrix
from yellowbrick.classifier import ClassificationReport
from yellowbrick.classifier import ROCAUC

# Instantiate the classification model
model = LogisticRegression(solver='liblinear')

#The ConfusionMatrix visualizer taxes a model

classes = ['Not_Autistic','Autistic']

cm = ConfusionMatrix(model, classes=classes,  label_encoder={0: "Not_Autistic",␣
↪1: "Autistic"}, percent=False)
#Fit fits the passed model. This is unnecessary if you pass the visualizer a␣
↪pre-fitted model
cm.fit(X_train, y_train)

#To create the ConfusionMatrix, we need some test data. Score runs predict() on␣
↪the data
#and then creates the confusion_matrix from scikit learn.
cm.score(X_val, y_val)

# change fontsize of the labels in the figure
for label in cm.ax.texts:
    label.set_size(10)
```

```
C:\ProgramData\Anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:193: FutureWarning: elementwise
comparison failed; returning scalar instead, but in the future will perform
elementwise comparison
  score = y_true == y_pred
```



There are two possible predicted classes: "Autistic" and "Not_Autistic". If we were predicting the presence of a disease, for example, "yes" would mean they have the disease, and "no" would mean they don't have the disease.

The classifier made a total of 317 predictions

Out of those 317 cases, the classifier predicted "yes" 217 times, and "no" 100 times.

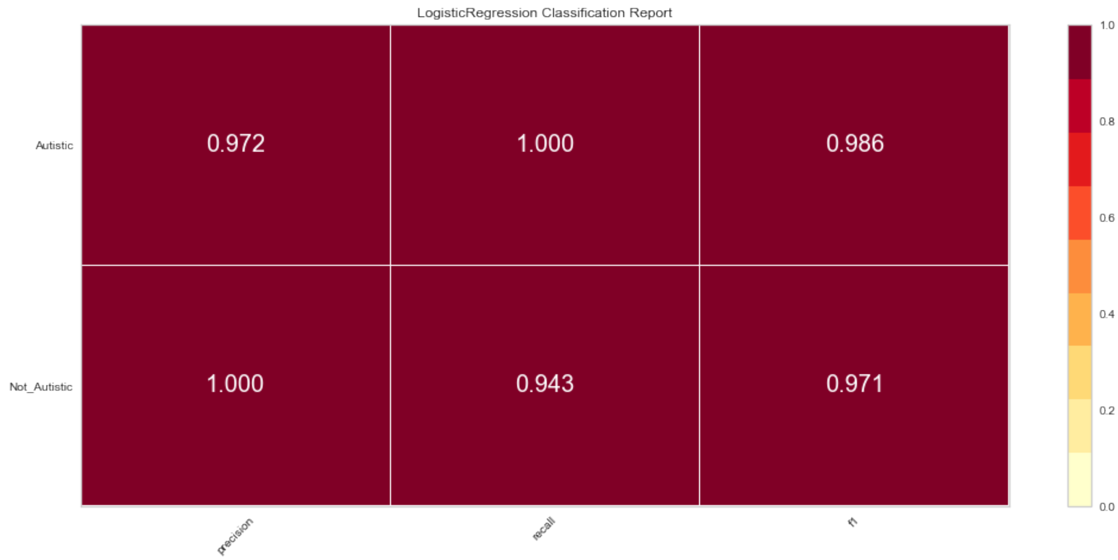
In reality, 211 patients in the sample have the disease, and 106 patients do not.

Accuracy: Overall, how often is the classifier correct?

(TP+TN)/total = (211+100)/317 = 0.98

[28]:
```
# ClassificationReport
#How did we do?
cm.poof()

# Precision, Recall, and F1 Score
# set the size of the figure and the font size
#%matplotlib inline
plt.rcParams['figure.figsize'] = (15, 7)
plt.rcParams['font.size'] = 20
```

```
# Instantiate the visualizer
visualizer = ClassificationReport(model, classes=classes)

visualizer.fit(X_train, y_train)  # Fit the training data to the visualizer
visualizer.score(X_val, y_val)  # Evaluate the model on the test data
g = visualizer.poof()
```

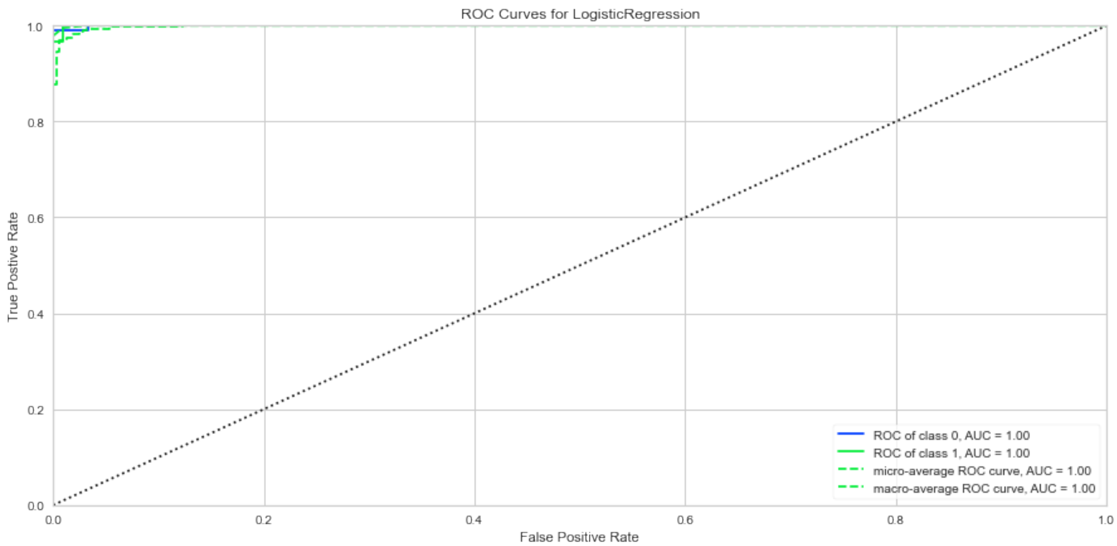


Precision – What percent of your predictions were correct? 97.2%

Recall – What percent of the positive cases did you catch? 100%

F1 score – What percent of positive predictions were correct? 98.6%

[29]:
```
# ROC and AUC
#Instantiate the visualizer
visualizer = ROCAUC(model, pos_label = 1)
visualizer.fit(X_train, y_train)  # Fit the training data to the visualizer
visualizer.score(X_val, y_val)  # Evaluate the model on the test data
g = visualizer.poof()
```



classifier that does a very good job separating the classes will have an ROC curve that hugs the upper left corner of the plot with accuracy rate of near 98%

[30]:
```
#MileStone 4- Implement the reveived review comments:

# Mile Stone 1- review comment, Document work , added some more steps comments
#Mile Stone 2 review comment-- Drop feature "Who completed the test" from data set,since test" is almost all one category "family member"
#Implemented the aobve comment in Milestone 3:
#please find below used features for my modle
#features_model = ['Jaundice', 'Age_Mons', 'Qchat-10-Score_log']
#Mile stone 3: do a bit of research to see if the features you are using are really fair to use for diagnosiging autism
# -- in mile stone three, i found the feature Qchat-10-Score_log is fiar to use in prediction ,
# but not sure how much it is fair to say other included features have similar impact.
# so under milestone 4 ia m going to train model with using other two feature('Jaundice', 'Age_Mons') and predict the accuracy of the model
```

[31]:
```
#create a whole features dataset that can be used for train and validation data splitting
# here we will combine the numerical features and the dummie features together
features_model = ['Jaundice', 'Age_Mons']
data_model_X = pd.concat([df_todd[features_model], data_cat_dummies], axis=1)
# create a whole target dataset that can be used for train and validation data splitting
```

```
#data_model_y = df_todd.replace({'autism': {1: 'Autistic', 0:␣
↪'Not_Autistic'}})['ASD_Traits']
data_model_y = df_todd['ASD_Traits']
# separate data into training and validation and check the details of the␣
↪datasets
# import packages
from sklearn.model_selection import train_test_split

# split the data
X_train, X_val, y_train, y_val = train_test_split(data_model_X, data_model_y,␣
↪test_size =0.3, random_state=11)
```

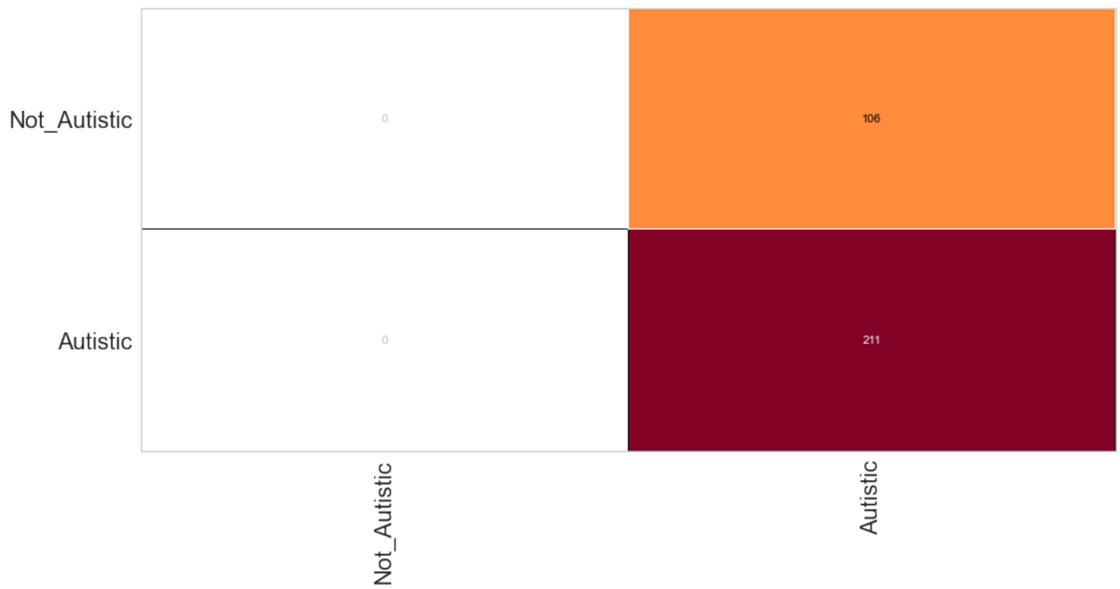
[32]:
```
# number of samples in each set
print("No. of samples in training set: ", X_train.shape[0])
print("No. of samples in validation set:", X_val.shape[0])

# Autistic and not-autistic
print('\n')
print('No. of autistic and not-autistic in the training set:')
print(y_train.value_counts())

print('\n')
print('No. of autistic and not-autistic in the validation set:')
print(y_val.value_counts())
```

```
No. of samples in training set:  737
No. of samples in validation set: 317


No. of autistic and not-autistic in the training set:
1    517
0    220
Name: ASD_Traits, dtype: int64


No. of autistic and not-autistic in the validation set:
1    211
0    106
Name: ASD_Traits, dtype: int64
```

[33]:
```
# Classification is a technique where we categorize data into a given number of␣
↪classes like 'Not_Autistic','Autistic'.
# The main goal of a classification problem is to identify the category/class␣
↪to which a new data will fall under.

# Eval Metrics  - ConfusionMatrix
from sklearn.linear_model import LogisticRegression
```

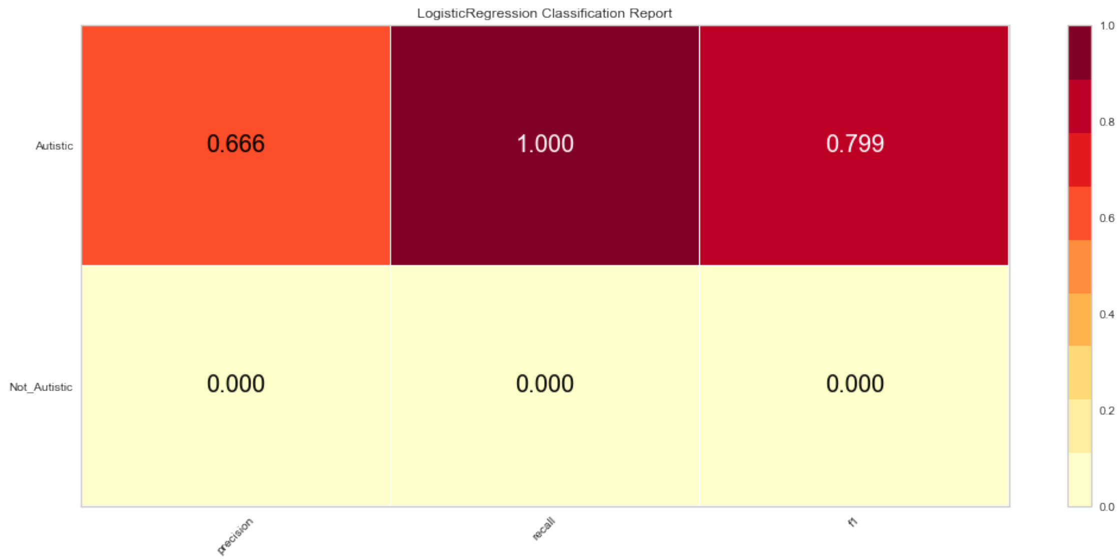
```python
from yellowbrick.classifier import ConfusionMatrix
from yellowbrick.classifier import ClassificationReport
from yellowbrick.classifier import ROCAUC

# Instantiate the classification model
model = LogisticRegression(solver='liblinear')

#The ConfusionMatrix visualizer taxes a model

classes = ['Not_Autistic','Autistic']

cm = ConfusionMatrix(model, classes=classes,  label_encoder={0: "Not_Autistic",␣
↪1: "Autistic"}, percent=False)
#Fit fits the passed model. This is unnecessary if you pass the visualizer a␣
↪pre-fitted model
cm.fit(X_train, y_train)

#To create the ConfusionMatrix, we need some test data. Score runs predict() on␣
↪the data
#and then creates the confusion_matrix from scikit learn.
cm.score(X_val, y_val)

# change fontsize of the labels in the figure
for label in cm.ax.texts:
    label.set_size(10)
```

```
C:\ProgramData\Anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:193: FutureWarning: elementwise
comparison failed; returning scalar instead, but in the future will perform
elementwise comparison
  score = y_true == y_pred
```




```
[34]: # ClassificationReport
#How did we do?
cm.poof()

# Precision, Recall, and F1 Score
# set the size of the figure and the font size
#%matplotlib inline
plt.rcParams['figure.figsize'] = (15, 7)
plt.rcParams['font.size'] = 20

# Instantiate the visualizer
visualizer = ClassificationReport(model, classes=classes)

visualizer.fit(X_train, y_train)  # Fit the training data to the visualizer
visualizer.score(X_val, y_val)  # Evaluate the model on the test data
g = visualizer.poof()
```

```
C:\ProgramData\Anaconda3\lib\site-
packages\sklearn\metrics\_classification.py:1221: UndefinedMetricWarning:
Precision and F-score are ill-defined and being set to 0.0 in labels with no
predicted samples. Use `zero_division` parameter to control this behavior.
  _warn_prf(average, modifier, msg_start, len(result))
```



Precision – What percent of your predictions were correct? 66.2% Recall – What percent of the positive cases did you catch? 100% F1 score – What percent of positive predictions were correct? .79% data is biased it is not all combination autistic and not autistic datas seems 'Jaundice', 'Age_Mons' are not good candidates as individuals predictors

[ ]:

```

```