leptospirosis-detection-rf

June 23, 2024

1 Leptospirosis Detection

1.1 Load train dataset

[1]:
```python
import pandas as pd
import numpy as np

train_csv = pd.read_csv('train.csv').drop('ID', axis = 1)
train_data = pd.DataFrame(train_csv)
```

```
C:\Users\Lasani\AppData\Local\Temp\ipykernel_16700\2849540320.py:4:
DtypeWarning: Columns (494,597,599,600,601,603,604) have mixed types. Specify
dtype option on import or set low_memory=False.
  train_csv = pd.read_csv('train.csv').drop('ID', axis = 1)
```

[2]:
```python
'''#Adjusting display options in the console
pd.set_option('display.max_columns', None)
pd.set_option('display.max_rows', None)'''
```

[2]:
```
"#Adjusting display options in the console\npd.set_option('display.max_columns',
None)\npd.set_option('display.max_rows', None)"
```

1.2 Explore train data

[3]:
```python
#Get number of rows and columns
train_data.shape
```

[3]:
```
(1387, 805)
```

[4]:
```python
#Explore the first few rows of the dataset
train_data.head()
```

[4]:
```
   Year  Month  Hospital  Sample  ICU  OPD  Sex  Age  Ethnicity  Income  …  \
0  2018     11         7       1    2    2    2   53          1   35000  …
1  2018      1         7       1    2    2    1   17          1      99  …
2  2018      5         7       1    2    2    1   47          1   40000  …
3  2018      1         7       1    2    2    1   21          1   30000  …
4  2016      8         7       1    2    1    1   99          1      99  …
```

```
   FU_L.interrogansserovarMankarsostr.Mankarso  \
0                                          NaN   
1                                          NaN   
2                                          NaN   
3                                          NaN   
4                                          NaN   

   FU_L.santarosaiserovarGeorgiastr.LT117  \
0                                     NaN   
1                                     NaN   
2                                     NaN   
3                                     NaN   
4                                     NaN   

   FU_L.santarosaiserovarPyrogenesstr.Salinem  \
0                                         NaN   
1                                         NaN   
2                                         NaN   
3                                         NaN   
4                                         NaN   

   FU_L.interrogansserovarBataviaestr.VanTienan  \
0                                           NaN   
1                                           NaN   
2                                           NaN   
3                                           NaN   
4                                           NaN   

   FU_L.interrogansserovarAlexistr.616  \
0                                  NaN   
1                                  NaN   
2                                  NaN   
3                                  NaN   
4                                  NaN   

   FU_L.interrogansserovarAustralisstr.Ballico  \
0                                          NaN   
1                                          NaN   
2                                          NaN   
3                                          NaN   
4                                          NaN   

   FU_L.interrogansserovarwolfiistr.3705  FU_L.interrogansserovarWeerasinghe  \
0                                    NaN                                 NaN   
1                                    NaN                                 NaN   
2                                    NaN                                 NaN   
```

```
3                                     NaN                                  NaN
4                                     NaN                                  NaN

   FU_Patoc  Final
0       NaN      2
1       NaN      1
2       NaN      2
3       NaN      2
4       NaN      2

[5 rows x 805 columns]
```

[5]:

```
#Get data types of columns
train_data.dtypes
```

[5]:

```
Year                                                int64
Month                                               int64
Hospital                                            int64
Sample                                              int64
ICU                                                 int64
                                                  …
FU_L.interrogansserovarAustralisstr.Ballico       float64
FU_L.interrogansserovarwolfiistr.3705             float64
FU_L.interrogansserovarWeerasinghe                float64
FU_Patoc                                          float64
Final                                               int64
Length: 805, dtype: object
```

1.3 Handle duplicates

[6]:

```
#Check for duplicates
duplicates = train_data.duplicated().sum()
print("Number of duplicate rows: ", duplicates)
```

```
Number of duplicate rows:  82
```

[7]:

```
#Remove duplicates
train_data = train_data.drop_duplicates()
print('Records after removing duplicates: ', train_data.shape[0])
```

```
Records after removing duplicates:  1305
```

1.4 Drop unnecessary (repeated) columns

[8]:

```
```

```
train_data.drop(columns = columns_to_drop, inplace = True)
train_data.shape
```

```
[8]: (1305, 219)
```

1.5 Replace vague values of numerical columns

[9]:

```
#Replace values starting with 'fiel' or 'occ' with 99
train_data = train_data.map(lambda x: 99 if isinstance(x, str) and (x.lower().
 ↪startswith('fiel') or x.lower().startswith('occ')) else x)
print(train_data)
```

```
      Hospital  Sample  ICU  OPD  Sex  Age  Prophylactics  Pasttreatments  \
0            7       1    2    2    2   53              3               1
1            7       1    2    2    1   17              2               1
2            7       1    2    2    1   47              2               1
3            7       1    2    2    1   21              2               1
4            7       1    2    1    1   99              2               1
…        …     …  …  …  …  …            …             …
1382         4       2    2    2    1   62             99              99
1383         7       1    2    2    2   59              2               1
1384         5       1    2    1    1   56              2               1
1385         4       2    2    2    1   61             99              99
1386         8       1    2    2    1   36              2               1

      Pastantibiotics  Chronicillness  …  S.amylase10  S.phosphate10  ALP10  \
0                   1               2  …           99             99   99.0
1                   1               2  …           99             99   99.0
2                   2               2  …           99             99   99.0
3                   1               2  …           99             99   99.0
4                   3              99  …           99             99   99.0
…               …             …  …          …            …    …
1382               99              99  …           99             99   99.0
1383                1               2  …           99             99   99.0
1384                3               1  …           99             99   99.0
1385               99              99  …           99             99   99.0
1386                3               2  …           99             99   99.0

      WPqPCRDiagnosis  UrineqPCRDiagnosis  CultureqPCRDia  SerumqPCRDiagnosis  \
0                   3                  99              99                  99
1                   1                   3               3                  99
2                   3                   3               3                  99
3                   3                   3               3                  99
4                   3                   3              99                   3
…               …                 …             …                 …
1382                3                  99              99                  99
1383                3                  99              99                  99
```

```
1384                3                  99              99                  99
1385                3                  99              99                  99
1386                3                   2              99                  99

      UFqPCRDiag  Isolate  Final
0             99        2      2
1             99        2      1
2             99        2      2
3             99        2      2
4             99       98      2
…          …      …    …
1382          99       98      2
1383          99       98      2
1384          99       98      2
1385          99        2      2
1386           3        2      1

[1305 rows x 219 columns]
```

1.6 Drop missing values of more than 80%

[10]:

```
#Convert values called '99' to missing values as in the description
train_data.replace(99, pd.NA, inplace = True)
train_data.replace('99', pd.NA, inplace = True)

print(train_data.head())
```

```
   Hospital  Sample ICU OPD Sex   Age Prophylactics Pasttreatments  \
0         7       1   2   2   2    53             3              1
1         7       1   2   2   1    17             2              1
2         7       1   2   2   1    47             2              1
3         7       1   2   2   1    21             2              1
4         7       1   2   1   1  <NA>             2              1

  Pastantibiotics Chronicillness  … S.amylase10 S.phosphate10 ALP10  \
0               1              2  …        <NA>          <NA>  <NA>
1               1              2  …        <NA>          <NA>  <NA>
2               2              2  …        <NA>          <NA>  <NA>
3               1              2  …        <NA>          <NA>  <NA>
4               3           <NA>  …        <NA>          <NA>  <NA>

  WPqPCRDiagnosis UrineqPCRDiagnosis CultureqPCRDia SerumqPCRDiagnosis  \
0               3               <NA>           <NA>               <NA>
1               1                  3              3               <NA>
2               3                  3              3               <NA>
3               3                  3              3               <NA>
4               3                  3           <NA>                  3
```

```
  UFqPCRDiag Isolate Final
0       <NA>       2     2
1       <NA>       2     1
2       <NA>       2     2
3       <NA>       2     2
4       <NA>      98     2

[5 rows x 219 columns]
```

[11]:

```
#Identify missing value counts
missing_counts = train_data.isnull().sum()
print(missing_counts)
```

```
Hospital                 0
Sample                   0
ICU                     20
OPD                     20
Sex                     67
                      …
CultureqPCRDia        1040
SerumqPCRDiagnosis    1023
UFqPCRDiag            1147
Isolate                  0
Final                    0
Length: 219, dtype: int64
```

[12]:

```
#Drop columns with too many missing values
missing_percentages = missing_counts / len(train_data)
threshold = 0.85
columns_to_drop = missing_percentages[missing_percentages > threshold].index
train_data.drop(columns = columns_to_drop, inplace = True)

#Verification
train_data.shape
```

[12]:

```
(1305, 176)
```

1.7 Divide variables into categorical and numerical

[13]:

```
#Group variables into categorical and numerical by defining a threshold value␣
  ↪for number of unique values in each column
categorical_vars = []
numerical_vars = []
unique_threshold = 12

for column in train_data.columns:
    unique_count = train_data[column].nunique()
    if unique_count <= unique_threshold:
        categorical_vars.append(column)
    else:
        numerical_vars.append(column)
```

[14]:

```
#Adjust after manually going through variable data types
categorical_vars.remove('Puscells')
numerical_vars.append('Puscells')

print("After manual adjustment:")
print("Categorical variables:", categorical_vars, "\n")
print("Numerical variables:", numerical_vars)
```

```
After manual adjustment:
Categorical variables: ['Hospital', 'Sample', 'ICU', 'OPD', 'Sex',
'Prophylactics', 'Pasttreatments', 'Pastantibiotics', 'Chronicillness',
'Possibleexposure', 'Usualdrinkingwatersource', 'Usualbathingwatersource',
'Sourceofwaterforhousehold', 'Accumilationofrefusal',
'Availabilityofpublicgarbagecollectionprocedure',
'HomeStreamrivercanaloranyotherrunningwatersource',
'WorkplaceStreamrivercanaloranyotherrunningwatersource',
'Homepondlaketankoranyotherstagnantwatersource',
'WorkPlacepondlaketankoranyotherstagnantwatersource', 'Homemarshywetland',
'Workplacemarshywet', 'HomeBushes', 'Workplacebushes', 'Homeforest',
'Workplaceforest', 'Homeworkingpaddyfield', 'WorkPlaceworkingpaddyfield',
'Homeabondantpaddyfield', 'Workplaceabondantpaddyfield',
'Homeotheragricultural', 'workplaceotheragricultural', 'Homeanimalfarm',
'Workplaceanimalfarm', 'Homegarbageaccumilation', 'Homeblockeddrainage',
'Homesewer', 'Rathome', 'RatWorkplace', 'RatNeighbourhood', 'Cattlehome',
'CattleWorkplace', 'Urumeeyahome', 'Urumeeyaworkplace', 'UrimeeyaNeighbourhood',
'OtherrhodentsHome', 'Marshlandexposure', 'Wetsoilexposure', 'Floodexposure',
'Forestexposure', 'BushesExposure', 'Otheragriexposure',
'Naturalrunningwaterexposure', 'Stagnantwaterexposure',
'Manmaderunningwaterexposure', 'Drainsexposure', 'Paddyfieldexposure',
'Walkingbarefootoutdoor', 'CattleHandle', 'BuffaloHandle', 'Goathandle',
'Pighandle', 'Cathandle', 'Doghandle', 'Feveronset', 'Headacheonset',
'Musclepainonset', 'Cnsuffusiononset', 'Jaundiceonset', 'Skinrashonset',
'Oliguriaonset', 'Anuriaonset', 'SOBonset', 'Coughonset', 'Haemoptasisonset',
'Chestpainonset', 'Nauseaonset', 'Vomitingonset', 'Diarrhoeaonset',
'Bleedingonset', 'Mucosalrashonset', 'Prostrationonset', 'Rigorsonset',
'Photophobiaonset', 'Chillsonset', 'Muscletendernessonset',
'Psychoticsymptomsonset', 'Confusiononset', 'Feverad', 'Headachead', 'Chillsad',
'Rigorsad', 'Musclepainad', 'Muscletendernessad', 'Nauseaad',
'Vomitingadmission', 'Cnsuffusionad', 'Skinrashad', 'Mucosalrashad',
'Prostrationad', 'Diarrhoeaad', 'OliguriaAd', 'Anuriaad', 'Jaundicead',
'Hepatictendernessad', 'Hepatomegalyad', 'Spleenimegalyad', 'Lympadenopathyad',
'Photophobiaad', 'Neckstiffnessad', 'Psychoticsymptomsad', 'Confusionad',
'Coughad', 'Haemoptasisad', 'SOBadd', 'Chestpainad', 'Bleedingad', 'Headache10',
'Fever10', 'Chills10', 'Rigors10', 'Musclepain10', 'Mustender10', 'Nausea10',
'Vomiting10', 'Consuf10', 'Skinrash10', 'Mucorash10', 'Prostration10',
'diarrhea10', 'Oliguria10', 'Anuria10', 'Jaundice10', 'hepatictender10',
'hepatomegaly10', 'Spleenomegaly10', 'Lymphadenopathy10', 'Photophobia10',
'Neckstiffness10', 'Confusion10', 'Cough10', 'Haemoptysis10', 'SOB10',
'Chestpain10', 'Bleeding10', 'Albumin', 'WPqPCRDiagnosis', 'UrineqPCRDiagnosis',
'CultureqPCRDia', 'SerumqPCRDiagnosis', 'Isolate', 'Final']

Numerical variables: ['Age', 'PRad', 'SBPadd', 'DBPadd', 'WBCcount', 'Ncount',
'N', 'Lcount', 'L', 'Plateletcount', 'PCV', 'RBC', 'CRP', 'ESR', 'Redcells',
'Na', 'K', 'AST', 'ALT', 'T.Bilirubin', 'D.Bilirubin', 'S.creatinine', 'B.urea',
'ALP', 'Puscells']
```

[15]:

```python
#Adjust data types in numerical columns
train_data[numerical_vars] = train_data[numerical_vars].apply(pd.to_numeric,␣
 ↪errors = 'coerce')

#Verify data types
train_data.dtypes
```

[15]:

```
Hospital                 int64
Sample                   int64
ICU                     object
OPD                     object
Sex                     object
                         …
UrineqPCRDiagnosis      object
CultureqPCRDia          object
SerumqPCRDiagnosis      object
Isolate                  int64
Final                    int64
Length: 176, dtype: object
```

1.8 Drop highly correlated numerical columns

[16]:

```python
#Identify highly correlated numerical columns
corr_matrix = train_data[numerical_vars].corr()
#Apply a threshold to get the most correlated ones
threshold = 0.8
highly_correlated = corr_matrix.abs() > threshold
highly_correlated_columns = highly_correlated.any(axis = 0)

#Determine highly correlated pairs
correlated_pairs = []
for i in range(len(corr_matrix.columns)):
    for j in range(i + 1, len(corr_matrix.columns)):
        if abs(corr_matrix.iloc[i, j]) > threshold:
            correlated_pairs.append((corr_matrix.columns[i], corr_matrix.
↪columns[j]))

print("Highly correlated column pairs:")
print(correlated_pairs)
```

```
Highly correlated column pairs:
[('SBPadd', 'DBPadd'), ('AST', 'ALT'), ('T.Bilirubin', 'D.Bilirubin')]
```

[17]:

```
#Drop one of highly correlated variables from pairs to avoid multicolinearity
train_data = train_data.drop(columns = ['DBPadd', 'ALT', 'D.Bilirubin'])

numerical_vars.remove('DBPadd')
numerical_vars.remove('ALT')
numerical_vars.remove('D.Bilirubin')

train_data.shape
```

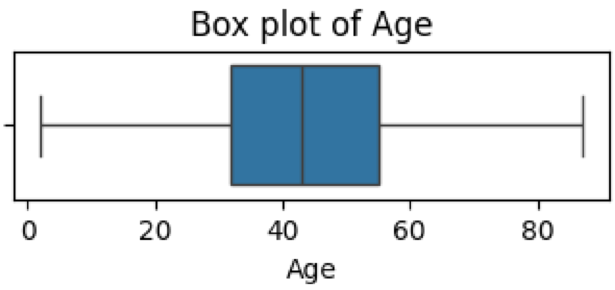
[17]:

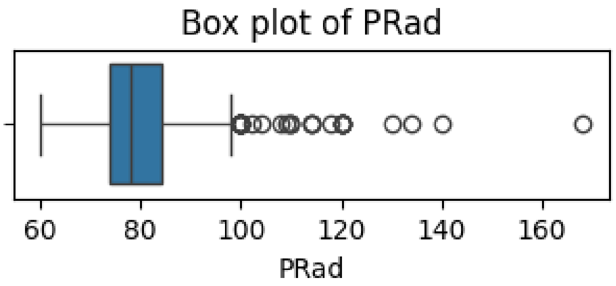
```
(1305, 173)
```

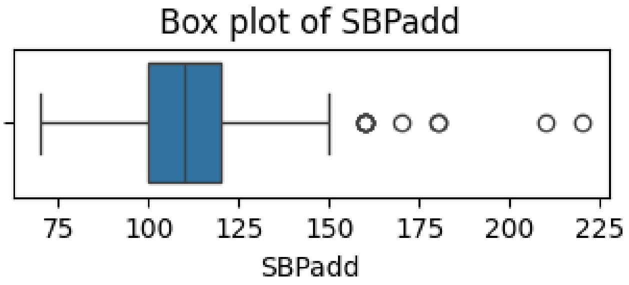
1.9 Check for outliers through boxplots in numerical data

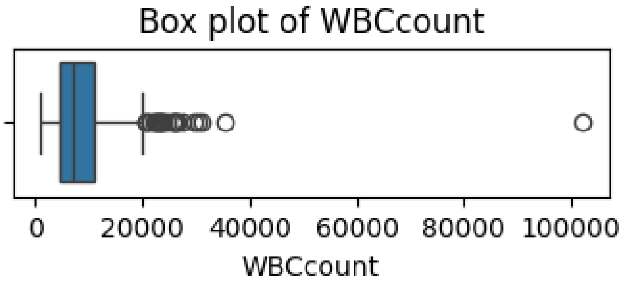
[18]:

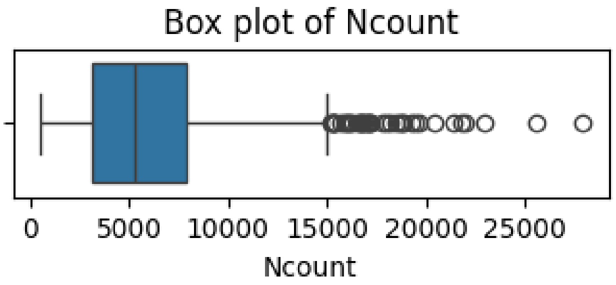
```
import matplotlib.pyplot as plt
import seaborn as sns

for col in numerical_vars:
    plt.figure(figsize = (4, 1))
    sns.boxplot(x = train_data[col])
    plt.title(f'Box plot of {col}')
    plt.xlabel(col)
    plt.show()

#Detecting heavy outliers in most of the columns
```

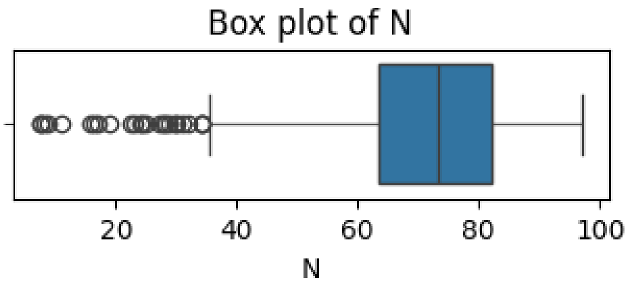


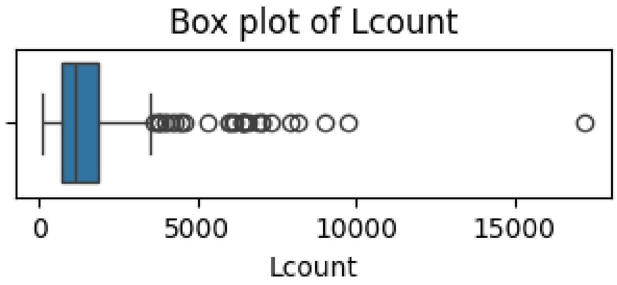

Box plot of PRad
60
80
100
120
140
160
PRad

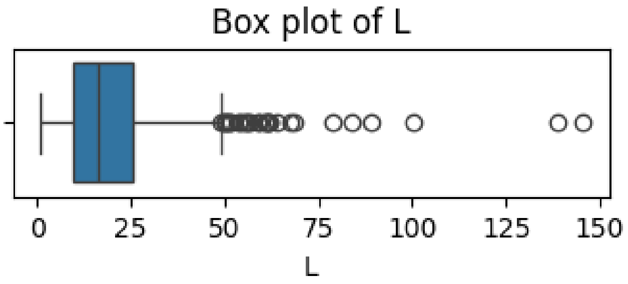

Box plot of SBPadd
75
100
125
150
175
200
225
SBPadd

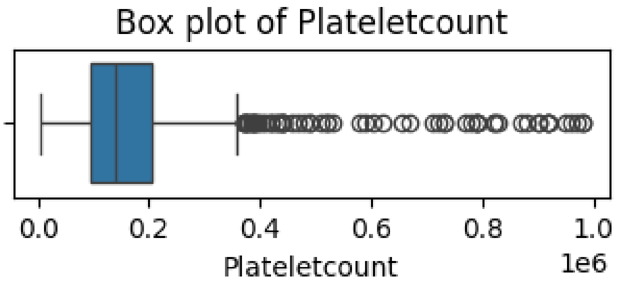

Box plot of WBCcount
0
20000
40000
60000
80000
100000
WBCcount

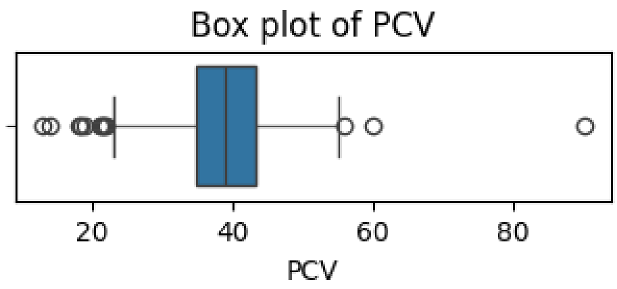

Box plot of Ncount
0
5000
10000
15000
20000
25000
Ncount

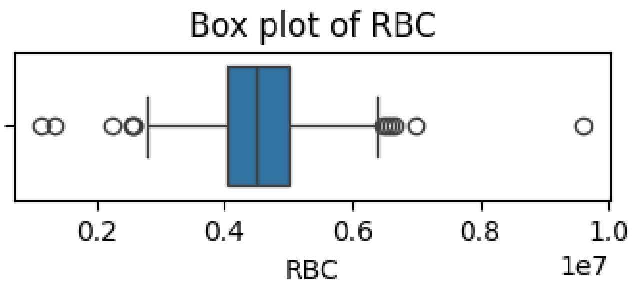

Box plot of N
20
40
60
80
100
N

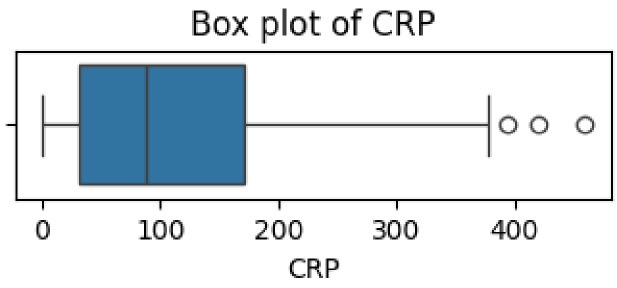

Box plot of Lcount
0
5000
10000
15000
Lcount

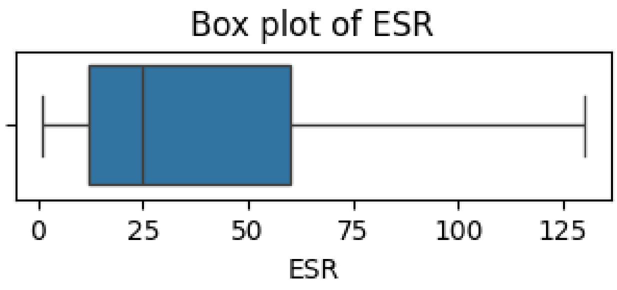

Box plot of L
0
25
50
75
100
125
150
L

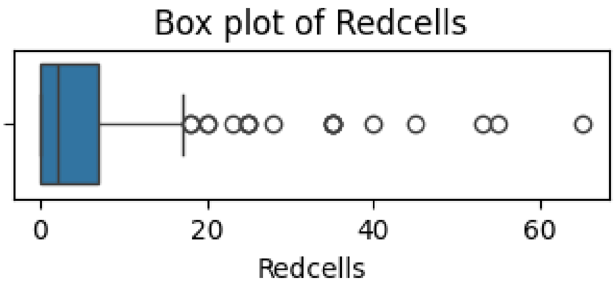

Box plot of Plateletcount
0.0
0.2
0.4
0.6
0.8
1.0
1e6
Plateletcount


Box plot of PCV
20
40
60
80
PCV

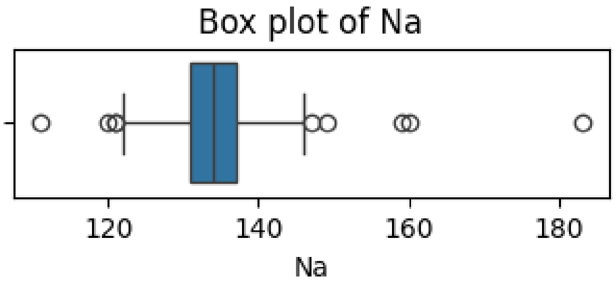

Box plot of RBC
0.2
0.4
0.6
0.8
1.0
1e7
RBC


Box plot of CRP
0
100
200
300
400
CRP

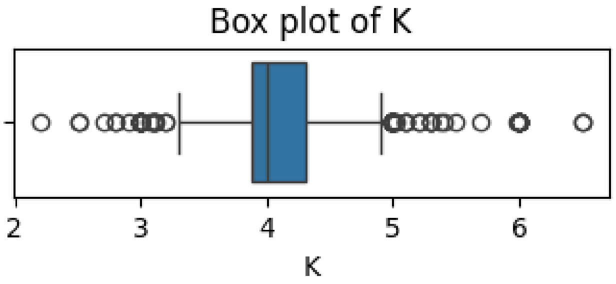

Box plot of ESR
0
25
50
75
100
125
ESR



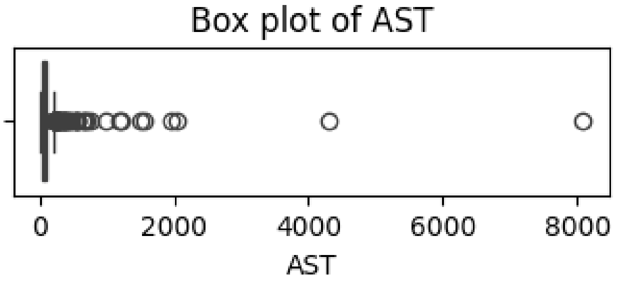
Box plot of Redcells



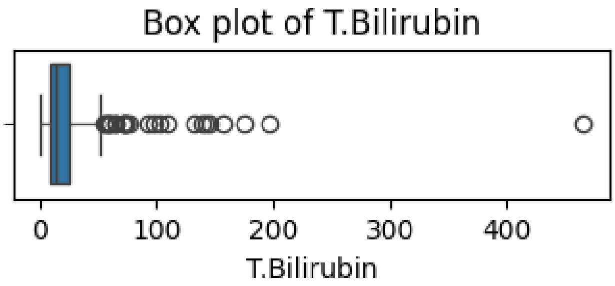
Box plot of Na

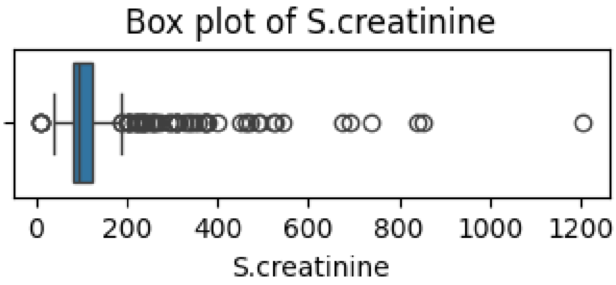


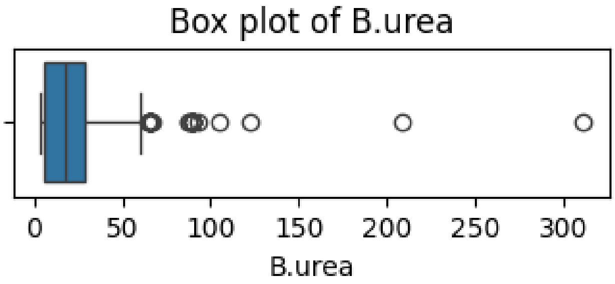
Box plot of K

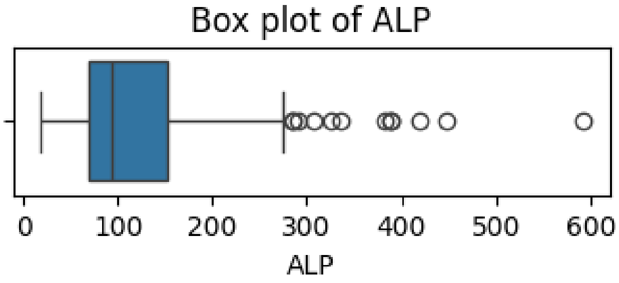


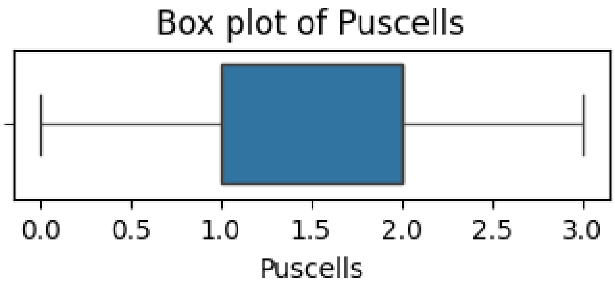
Box plot of AST


Box plot of T.Bilirubin
0
100
200
300
400
T.Bilirubin


Box plot of S.creatinine
0
200
400
600
800
1000
1200
S.creatinine


Box plot of B.urea
0
50
100
150
200
250
300
B.urea


Box plot of ALP
0
100
200
300
400
500
600
ALP



1.10 Impute numerical variables

[19]:

```
#With median
for col in numerical_vars:
    if train_data[col].isnull().sum() > 0:
        median_val = train_data[col].median()
        train_data[col].fillna(median_val, inplace = True)
```

1.11 Perform robust scaling on numerical data

[20]:

```
from sklearn.preprocessing import RobustScaler

scaler = RobustScaler()
train_data[numerical_vars] = scaler.fit_transform(train_data[numerical_vars])
train_data[numerical_vars] = pd.DataFrame(train_data[numerical_vars], columns =␣
  ↪numerical_vars)
train_data[numerical_vars]
```

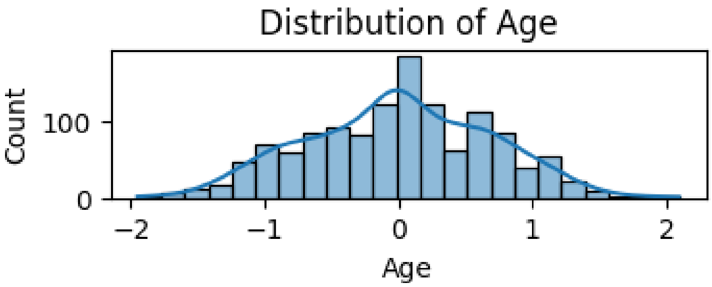
[20]:

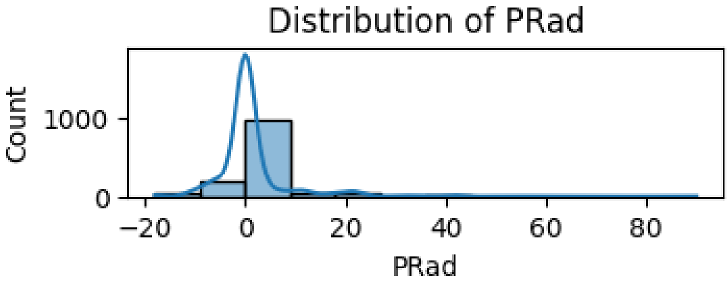
```
           Age  PRad  SBPadd  WBCcount    Ncount         N    Lcount  \
0     0.476190   8.0    10.0  1.670487  4.675926  1.201724  3.878505
1    -1.238095  -2.0     0.0 -1.289398  0.000000  0.000000  0.000000
2     0.190476  10.0   -10.0  0.226361  0.712963  0.453955  0.000000
3    -1.047619   0.0     0.0 -0.744986 -2.925926 -5.645010  4.018692
4     0.000000   0.0     0.0  0.000000  0.000000  0.000000  0.000000
…          …     …       …       …         …         …         …
1382  0.904762   0.0     0.0  0.000000  0.000000  0.000000  0.000000
1383  0.761905  22.0    -6.0 -0.309456  0.000000  0.000000  0.000000
1384  0.619048   0.0     0.0  0.000000  0.000000  0.000000  0.000000
1385  0.857143   0.0     0.0  0.000000  0.000000  0.000000  0.000000
1386 -0.333333   0.0    10.0 -0.243553  0.000000  1.960496 -2.196262

             L  Plateletcount   PCV  …  ESR  Redcells   Na    K  AST  \
0    -0.286085      -0.964286 -8.60  …  0.0       0.0 -1.0 -0.8  5.0
1     0.000000       0.000000  0.00  …  0.0      -1.0  0.0  0.0  0.0
```

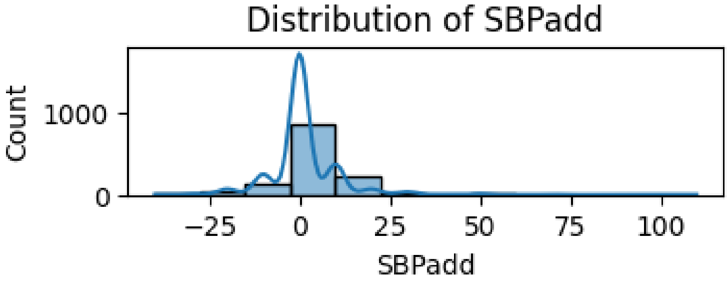
```
2    -0.469785      -1.250000 -1.70  …  0.0       0.0 -5.0  0.0  0.0
3     5.834799      -0.821429 -1.30  …  0.0       0.0  0.0  0.0  0.0
4     0.000000       0.000000  0.00  …  0.0       0.0  0.0  0.0  0.0
…        …            …   …  …  …       …  …  …  …
1382  0.000000       0.000000  0.00  …  0.0       0.0  0.0  0.0  0.0
1383  0.000000       0.000000  0.00  …  0.0       0.0  0.0  0.0  0.0
1384  0.000000       0.000000  0.00  …  0.0       0.0  0.0  0.0  0.0
1385  0.000000       0.000000  0.00  …  0.0       0.0  0.0  0.0  0.0
1386 -1.271963      -0.964286 -0.85  …  0.0       0.0  0.0  0.0  0.0

      T.Bilirubin  S.creatinine  B.urea    ALP  Puscells
0            25.3         197.0     4.2  114.0       0.0
1             0.0           0.0     0.0    0.0       0.0
2             0.0           0.0     0.0    0.0       0.0
3             0.0           0.0     0.0    0.0       0.0
4             0.0           0.0     0.0    0.0       0.0
…           …           …     …    …       …
1382          0.0           0.0     0.0    0.0       0.0
1383          0.0           0.0     0.0    0.0       0.0
1384          0.0           0.0     0.0    0.0       0.0
1385          0.0           0.0     0.0    0.0       0.0
1386          0.0           0.0     0.0    0.0       0.0

[1305 rows x 22 columns]
```

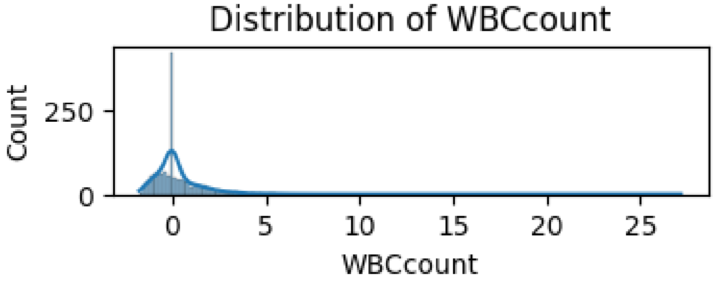
1.12 EDA on numerical data

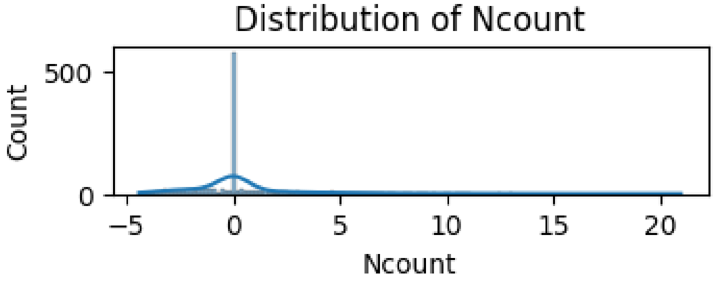
```
[21]: for column in train_data[numerical_vars]:
          plt.figure(figsize = (4, 1))
          sns.histplot(train_data[column], kde = True)
          plt.title(f'Distribution of {column}')
          plt.show()
```

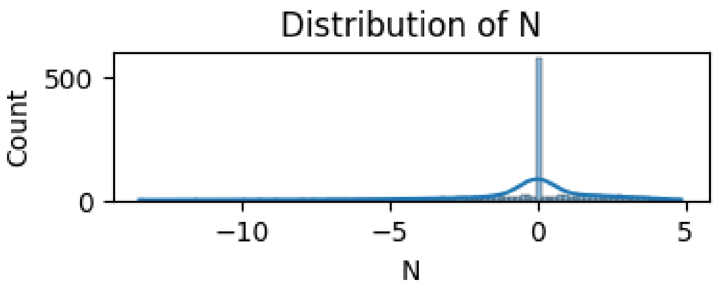


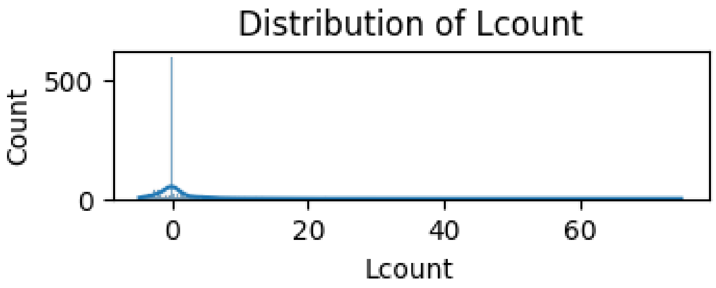

Distribution of PRad
Count
1000
0
−20
0
20
40
60
80
PRad

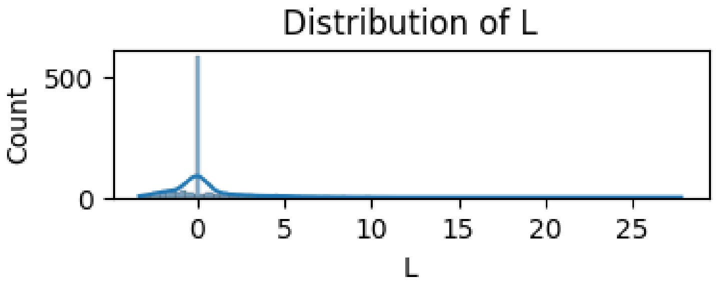

Distribution of SBPadd
Count
1000
0
−25
0
25
50
75
100
SBPadd

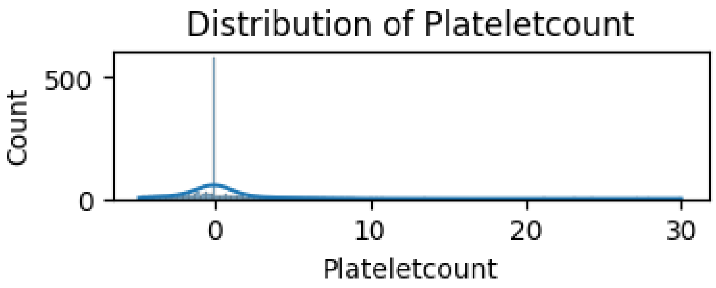

Distribution of WBCcount
Count
250
0
0
5
10
15
20
25
WBCcount

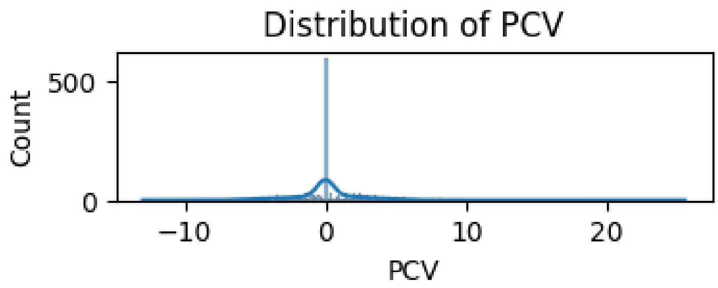

Distribution of Ncount
Count
500
0
−5
0
5
10
15
20
Ncount

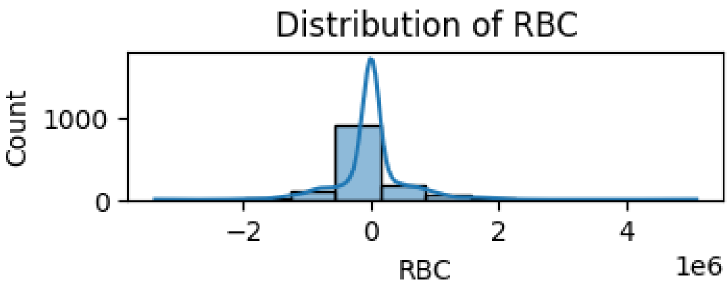

Distribution of N
Count
500
0
−10
−5
0
5
N

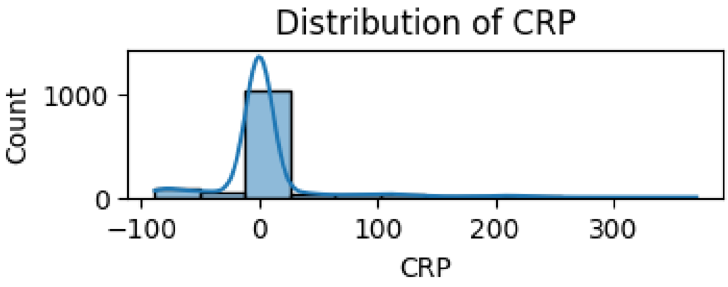

Distribution of Lcount
Count
500
0
0
20
40
60
Lcount

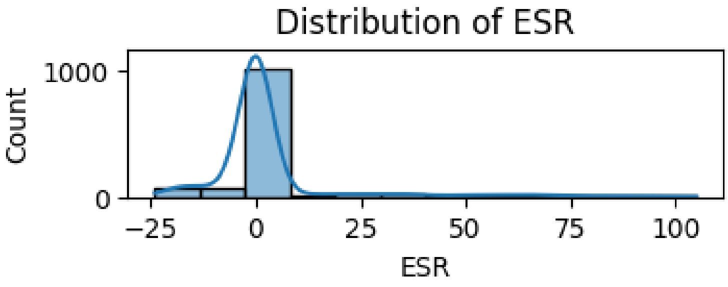

Distribution of L
Count
500
0
0
5
10
15
20
25
L

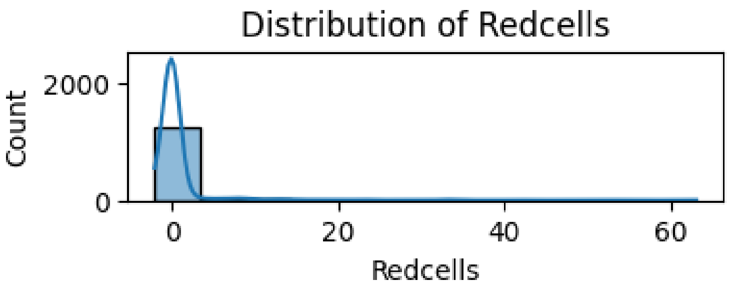

Distribution of Plateletcount
Count
500
0
0
10
20
30
Plateletcount

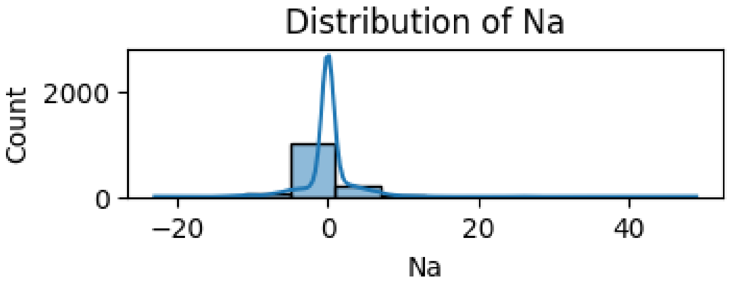

Distribution of PCV
500
0
Count
−10
0
10
20
PCV

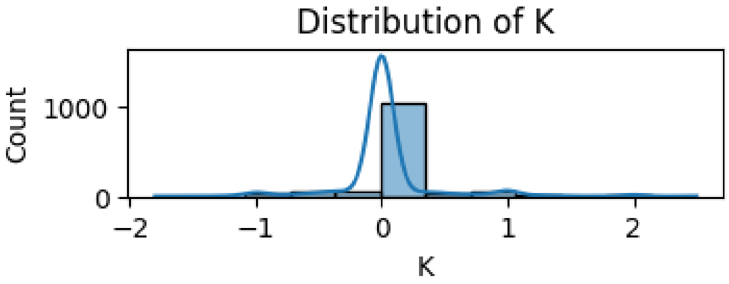

Distribution of RBC
1000
0
Count
−2
0
2
4
1e6
RBC

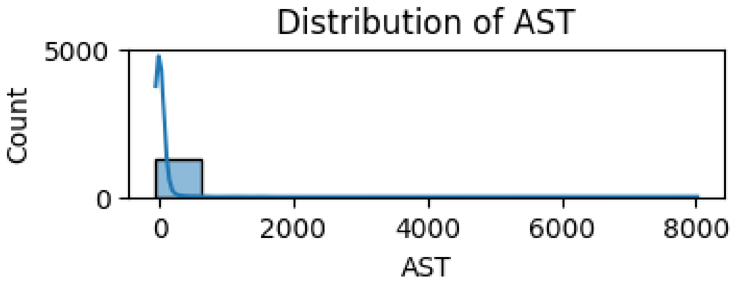

Distribution of CRP
1000
0
Count
−100
0
100
200
300
CRP

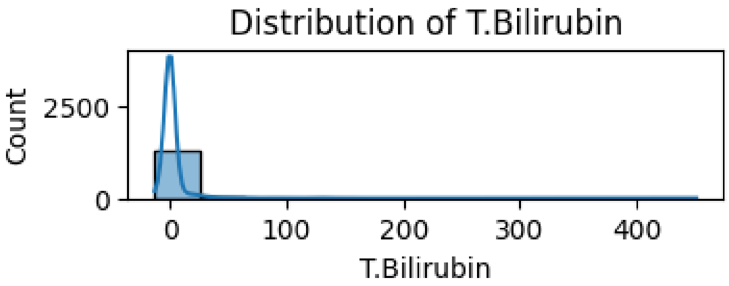

Distribution of ESR
1000
0
Count
−25
0
25
50
75
100
ESR

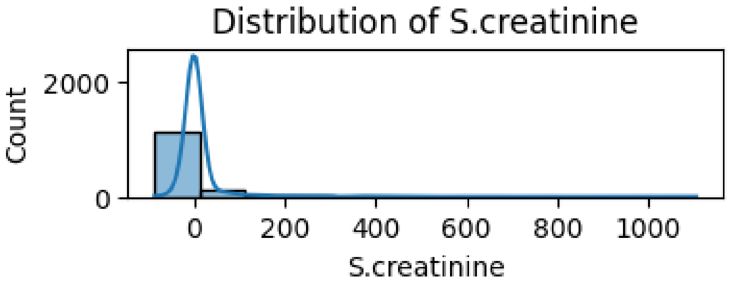

Distribution of Redcells
Count
2000
0
0
20
40
60
Redcells

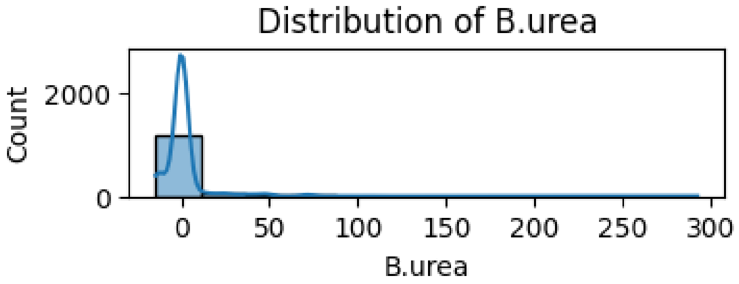

Distribution of Na
Count
2000
0
−20
0
20
40
Na

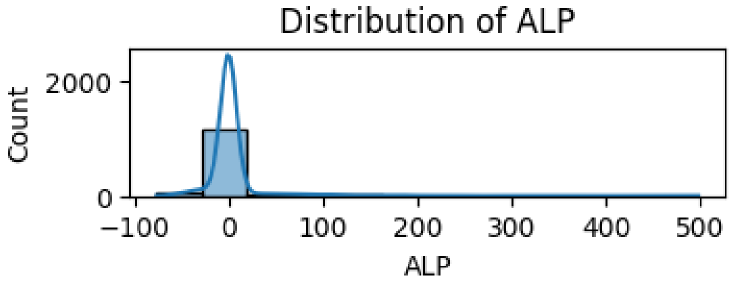

Distribution of K
Count
1000
0
−2
−1
0
1
2
K

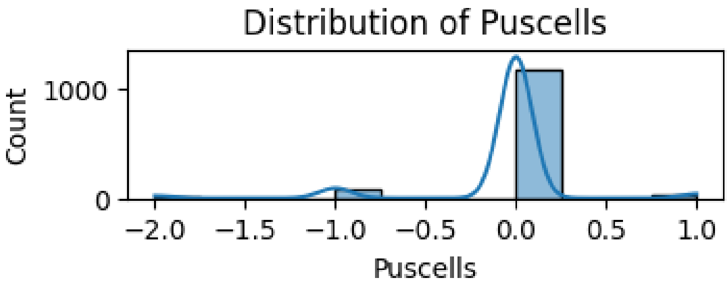

Distribution of AST
Count
5000
0
0
2000
4000
6000
8000
AST


Distribution of T.Bilirubin
Count
2500
0
0
100
200
300
400
T.Bilirubin


Distribution of S.creatinine
Count
2000
0
0
200
400
600
800
1000
S.creatinine


Distribution of B.urea
Count
2000
0
0
50
100
150
200
250
300
B.urea


Distribution of ALP
Count
2000
0
−100
0
100
200
300
400
500
ALP



1.13 Impute categorical variables

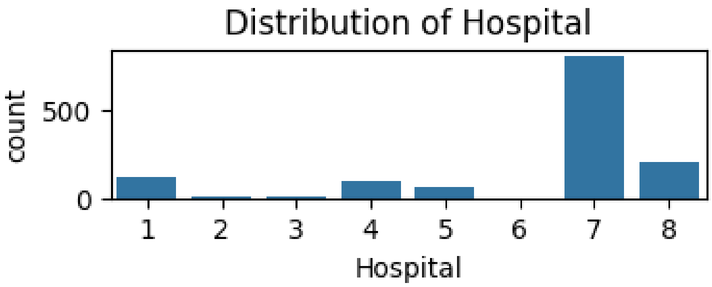
```
[22]: #With mode
      for col in categorical_vars:
          train_data[col].fillna(train_data[col].mode()[0], inplace = True)
```

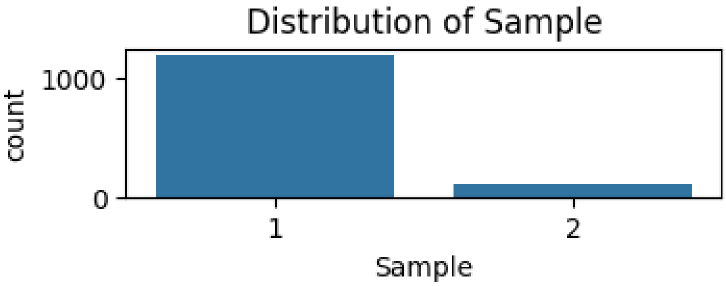
```
[23]: #Verification
      print(train_data.isnull().sum())
```

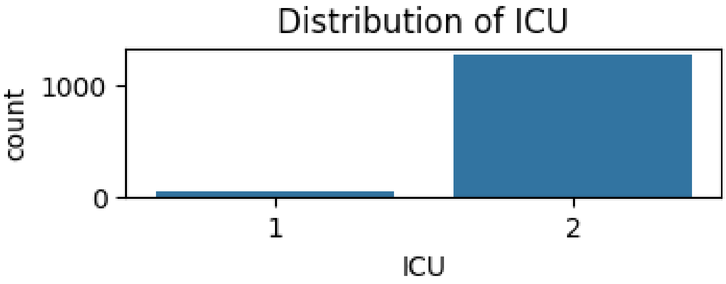
```
Hospital              0
Sample                0
ICU                   0
OPD                   0
Sex                   0
                     ..
UrineqPCRDiagnosis    0
CultureqPCRDia        0
SerumqPCRDiagnosis    0
Isolate               0
Final                 0
Length: 173, dtype: int64
```

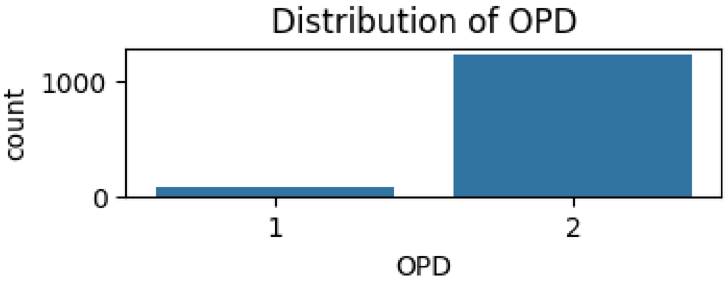
1.14 EDA on categorical data

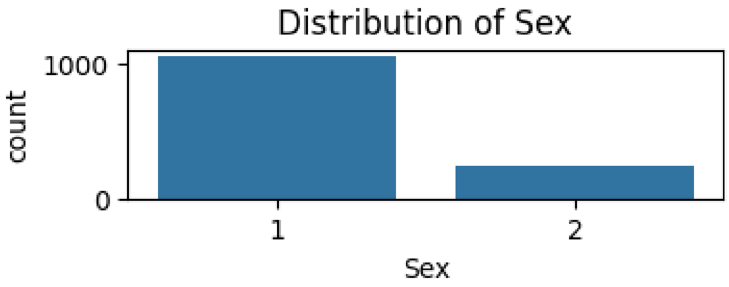
```
[24]: for column in categorical_vars:
          plt.figure(figsize = (4, 1))
          sns.countplot(x = train_data[column])
          plt.title(f'Distribution of {column}')
          plt.show()
```

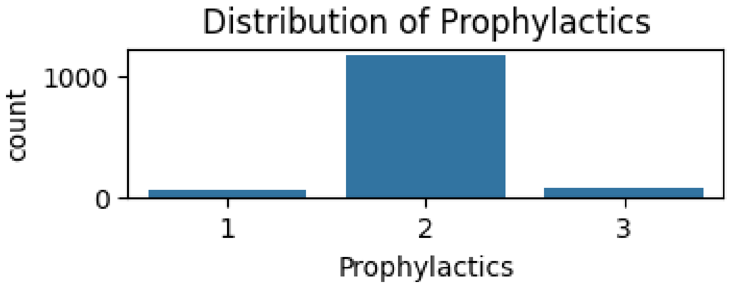

Distribution of Hospital
count
500
0
1
2
3
4
5
6
7
8
Hospital

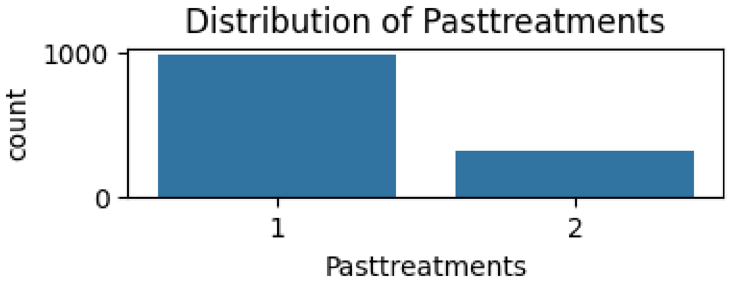

Distribution of Sample
count
1000
0
1
2
Sample

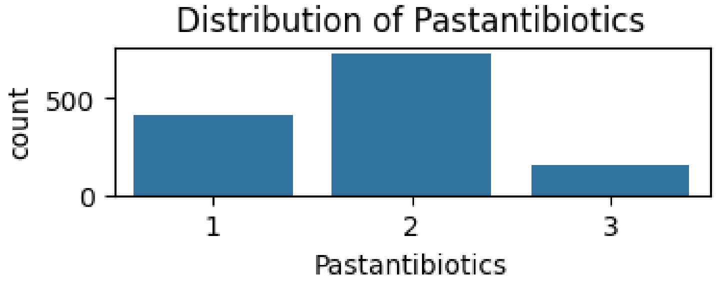

Distribution of ICU
count
1000
0
1
2
ICU

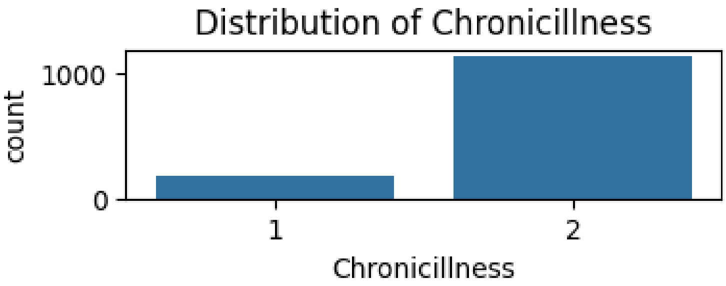

Distribution of OPD
count
1000
0
1
2
OPD

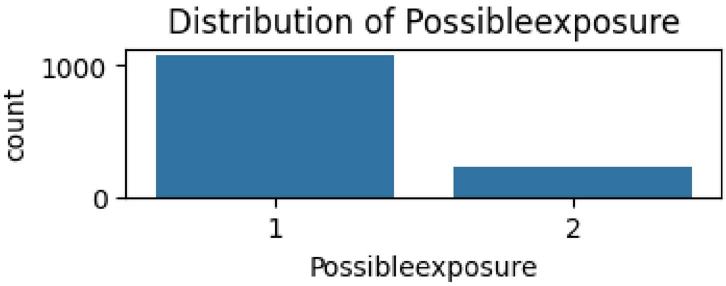

Distribution of Sex
count
1000
0
1
2
Sex

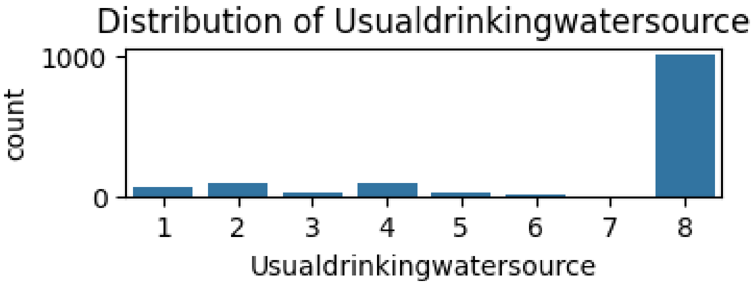

Distribution of Prophylactics
count
1000
0
1
2
3
Prophylactics

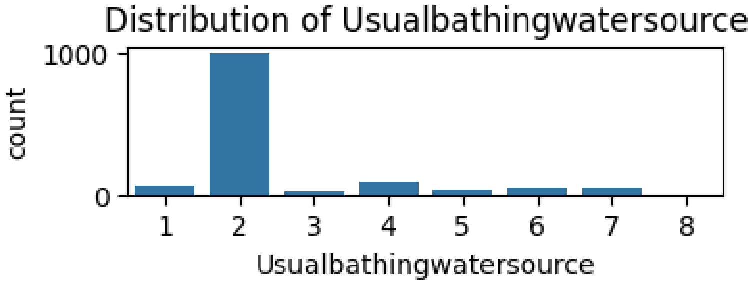

Distribution of Pasttreatments
count
1000
0
1
2
Pasttreatments

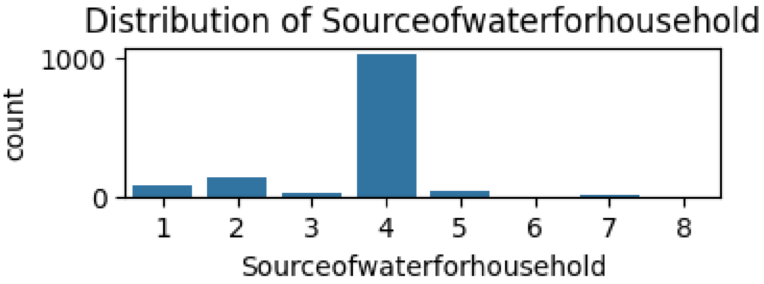

Distribution of Pastantibiotics
count
500
0
1
2
3
Pastantibiotics

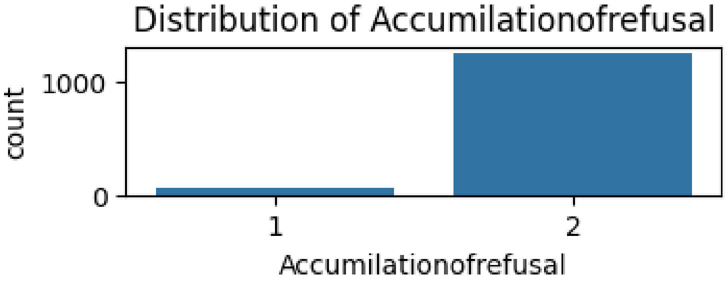

Distribution of Chronicillness
count
1000
0
1
2
Chronicillness

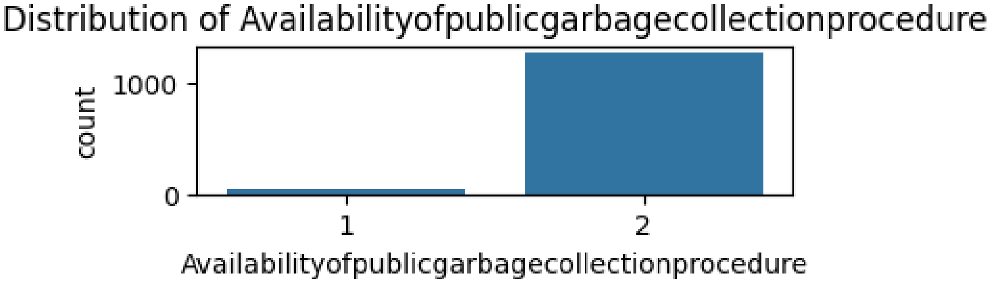

Distribution of Possibleexposure
count
1000
0
1
2
Possibleexposure

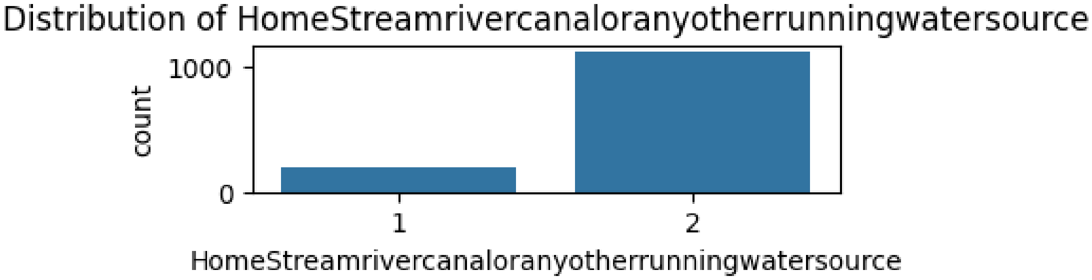

Distribution of Usualdrinkingwatersource
count
1000
0
1
2
3
4
5
6
7
8
Usualdrinkingwatersource

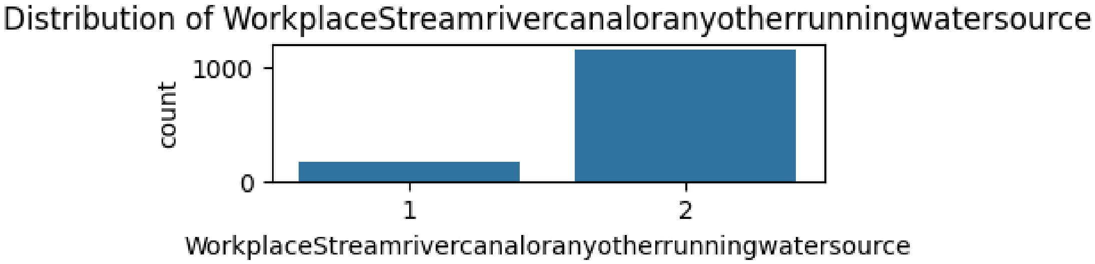

Distribution of Usualbathingwatersource
count
1000
0
1
2
3
4
5
6
7
8
Usualbathingwatersource

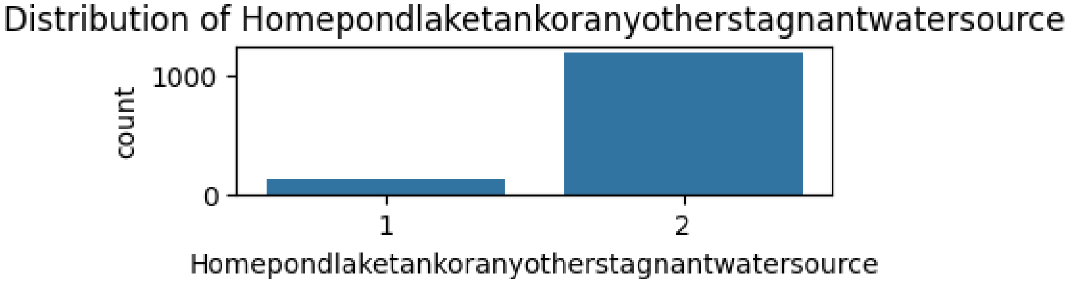

Distribution of Sourceofwaterforhousehold
count
1000
0
1
2
3
4
5
6
7
8
Sourceofwaterforhousehold

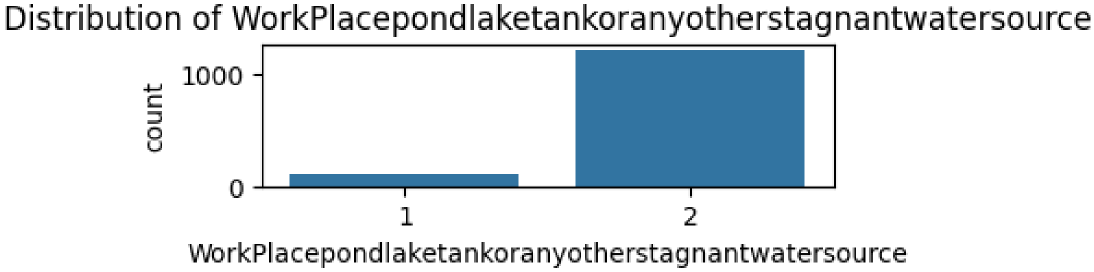

Distribution of Accumilationofrefusal
count
1000
0
1
2
Accumilationofrefusal

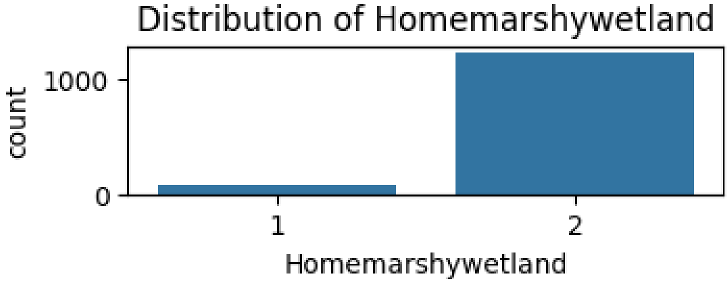

Distribution of Availabilityofpublicgarbagecollectionprocedure
count
1000
0
1
2
Availabilityofpublicgarbagecollectionprocedure

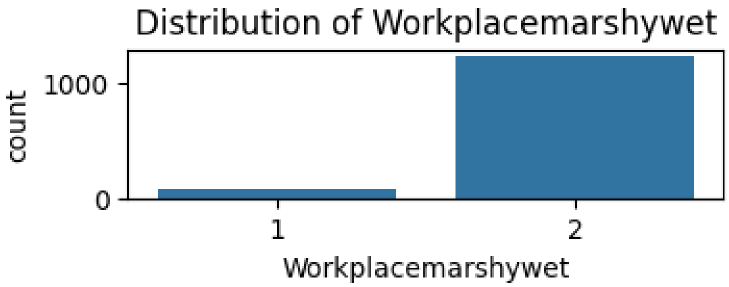

Distribution of HomeStreamrivercanaloranyotherrunningwatersource
count
1000
0
1
2
HomeStreamrivercanaloranyotherrunningwatersource

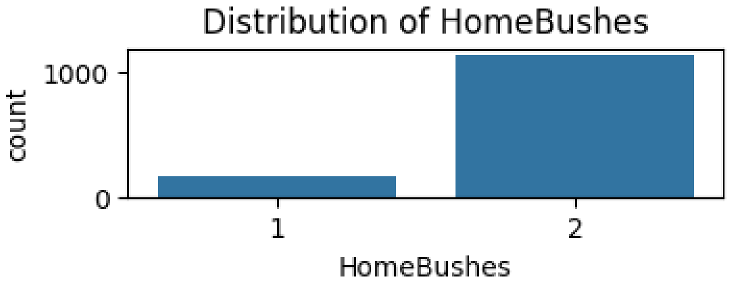

Distribution of WorkplaceStreamrivercanaloranyotherrunningwatersource
count
1000
0
1
2
WorkplaceStreamrivercanaloranyotherrunningwatersource

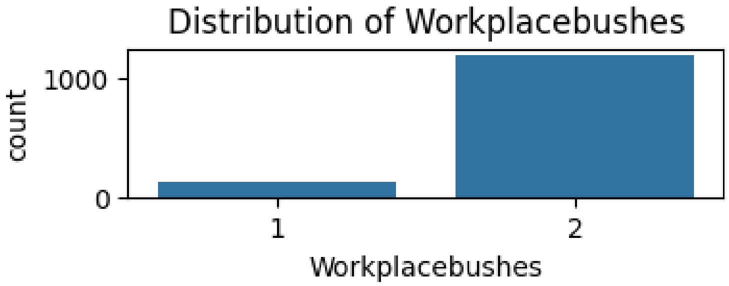

Distribution of Homepondlaketankoranyotherstagnantwatersource
count
1000
0
1
2
Homepondlaketankoranyotherstagnantwatersource

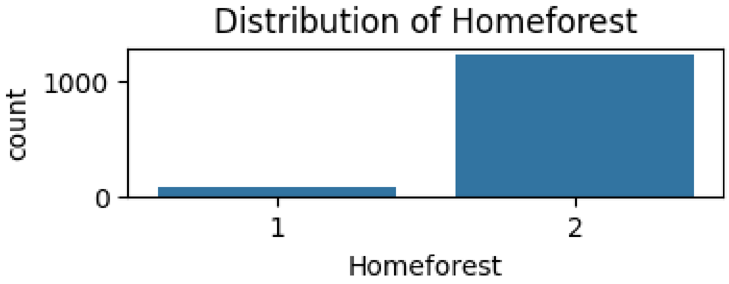

Distribution of WorkPlacepondlaketankoranyotherstagnantwatersource
count
1000
0
1
2
WorkPlacepondlaketankoranyotherstagnantwatersource

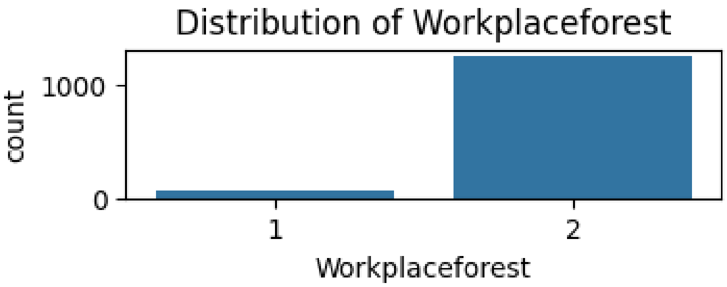

Distribution of Homemarshywetland
count
1000
0
1
2
Homemarshywetland

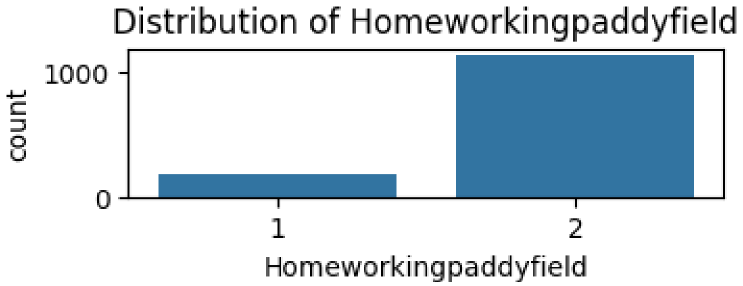

Distribution of Workplacemarshywet
count
1000
0
1
2
Workplacemarshywet

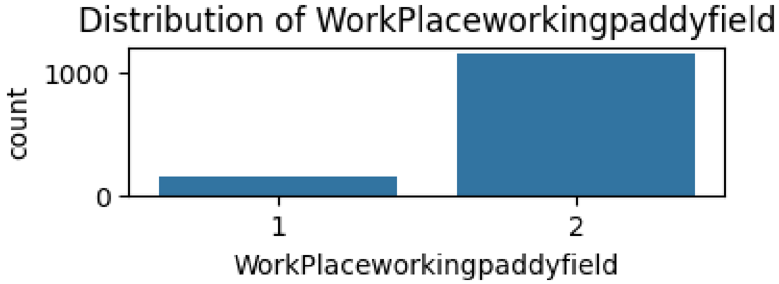

Distribution of HomeBushes
count
1000
0
1
2
HomeBushes

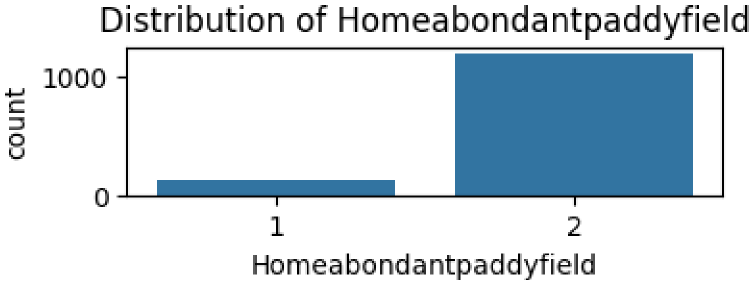

Distribution of Workplacebushes
count
1000
0
1
2
Workplacebushes

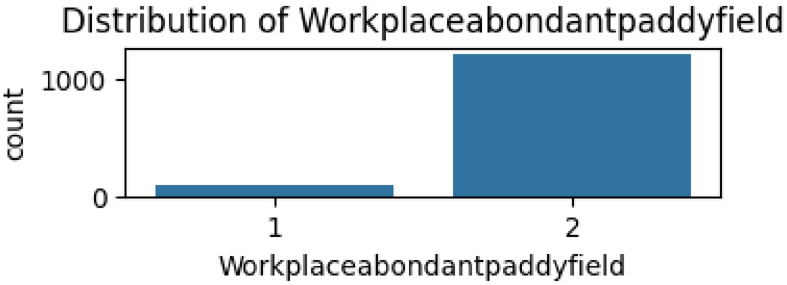

Distribution of Homeforest
count
1000
0
1
2
Homeforest

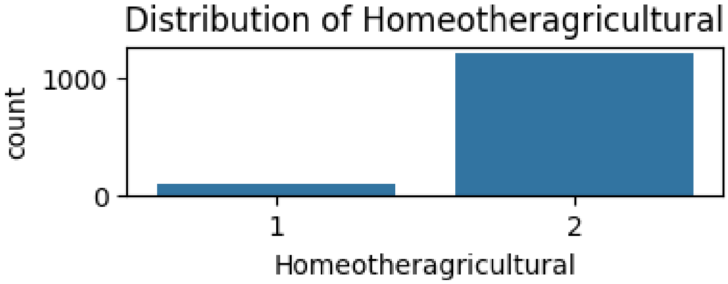

Distribution of Workplaceforest
count
1000
0
1
2
Workplaceforest

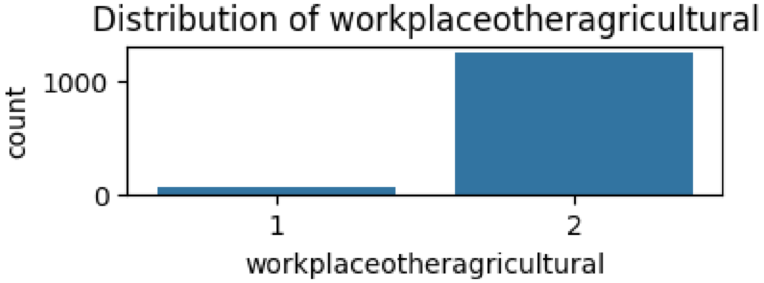

Distribution of Homeworkingpaddyfield
count
1000
0
1
2
Homeworkingpaddyfield

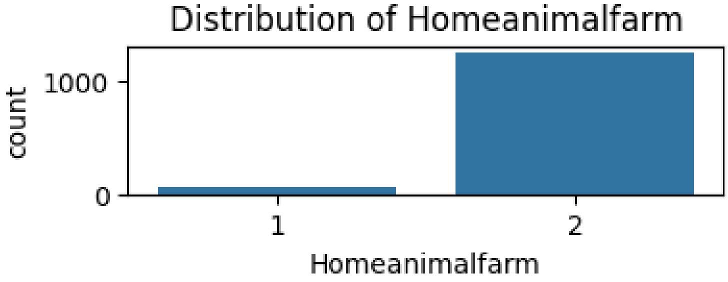

Distribution of WorkPlaceworkingpaddyfield
count
1000
0
1
2
WorkPlaceworkingpaddyfield

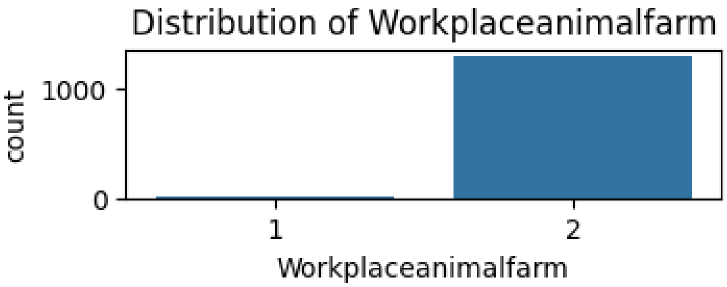

Distribution of Homeabondantpaddyfield
count
1000
0
1
2
Homeabondantpaddyfield

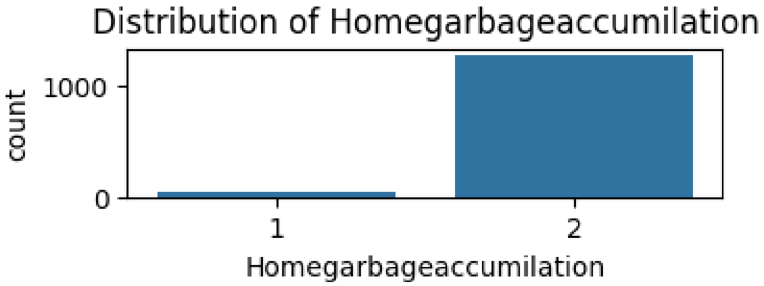

Distribution of Workplaceabondantpaddyfield
count
1000
0
1
2
Workplaceabondantpaddyfield

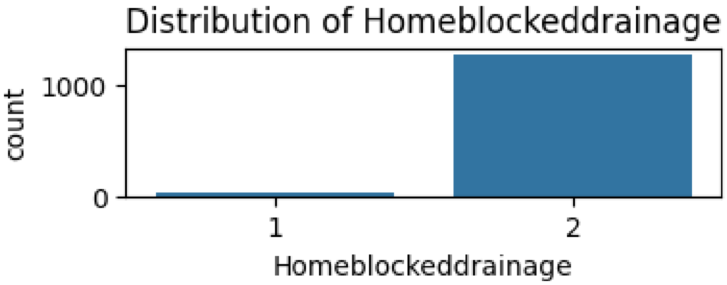

Distribution of Homeotheragricultural
count
1000
0
1
2
Homeotheragricultural

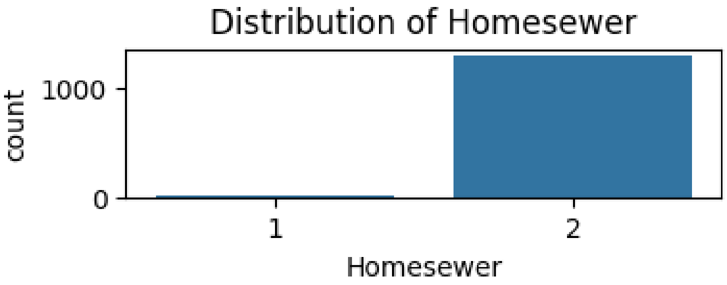

Distribution of workplaceotheragricultural
count
1000
0
1
2
workplaceotheragricultural

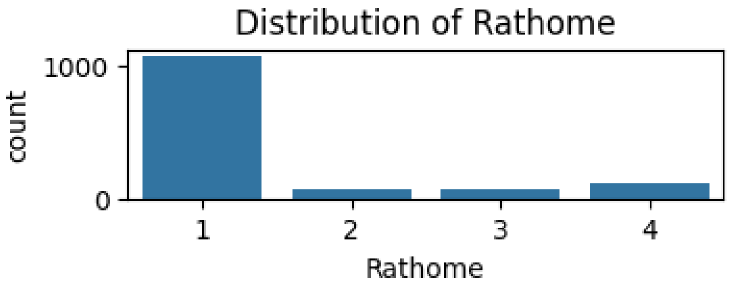

Distribution of Homeanimalfarm
count
1000
0
1
2
Homeanimalfarm

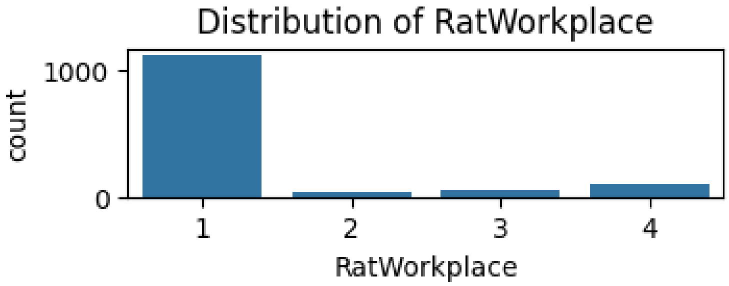

Distribution of Workplaceanimalfarm
count
1000
0
1
2
Workplaceanimalfarm

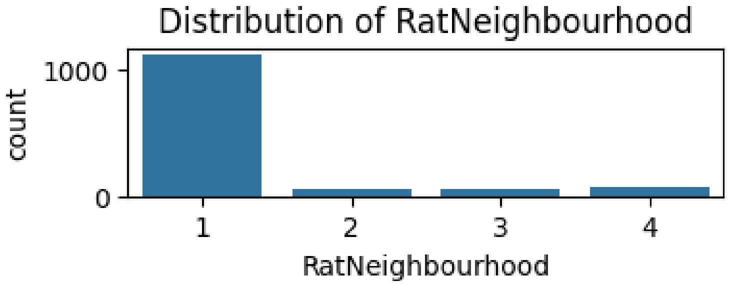

Distribution of Homegarbageaccumilation
count
1000
0
1
2
Homegarbageaccumilation

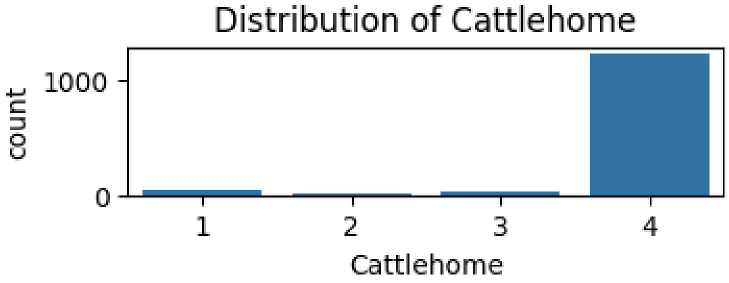

Distribution of Homeblockeddrainage
count
1000
0
1
2
Homeblockeddrainage

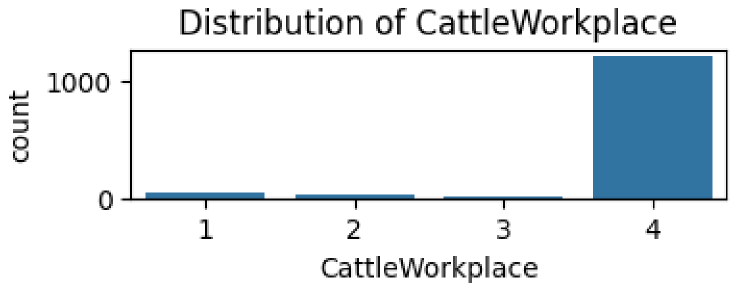

Distribution of Homesewer
count
1000
0
1
2
Homesewer

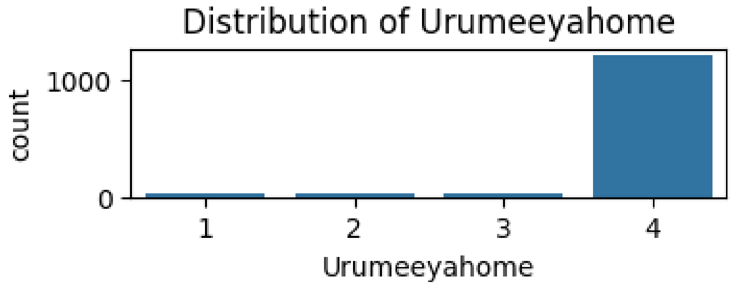

Distribution of Rathome
count
1000
0
1
2
3
4
Rathome

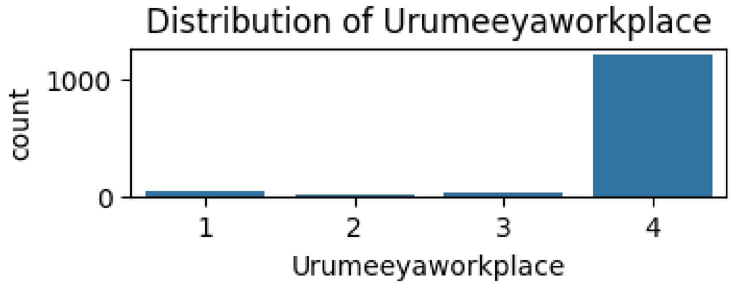

Distribution of RatWorkplace
count
1000
0
1
2
3
4
RatWorkplace

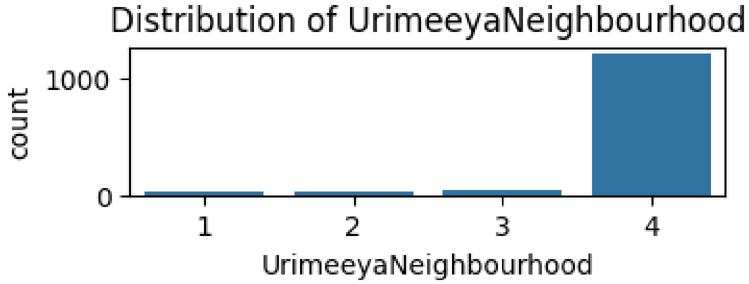

Distribution of RatNeighbourhood
count
1000
0
1
2
3
4
RatNeighbourhood

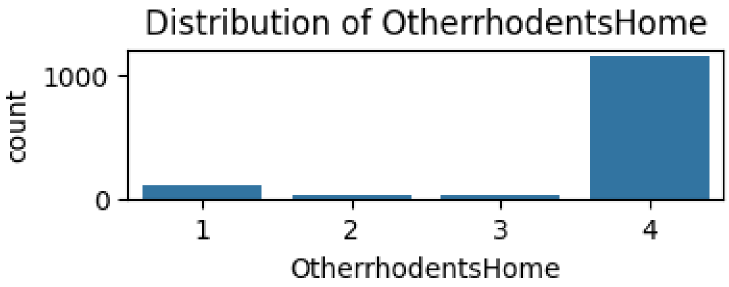

Distribution of Cattlehome
count
1000
0
1
2
3
4
Cattlehome

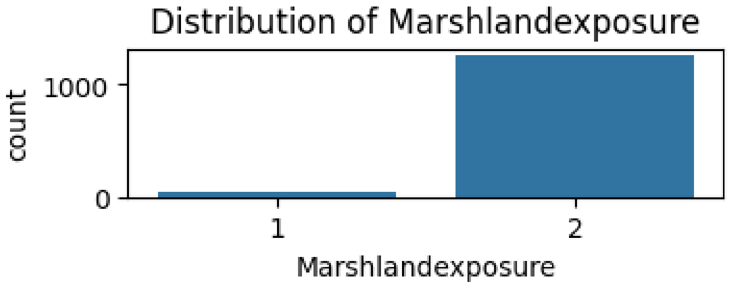

Distribution of CattleWorkplace
count
1000
0
1
2
3
4
CattleWorkplace

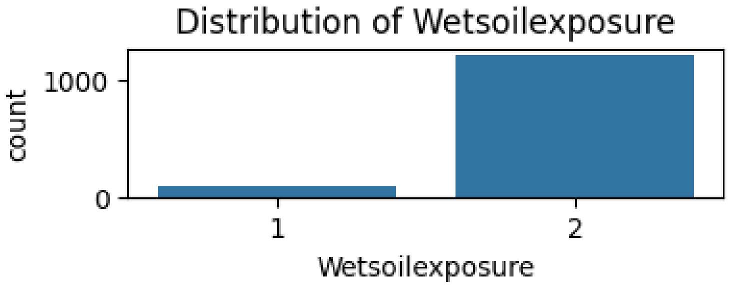

Distribution of Urumeeyahome
count
1000
0
1
2
3
4
Urumeeyahome

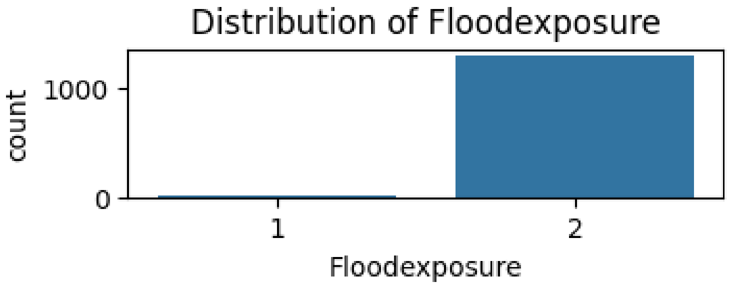

Distribution of Urumeeyaworkplace
count
1000
0
1
2
3
4
Urumeeyaworkplace

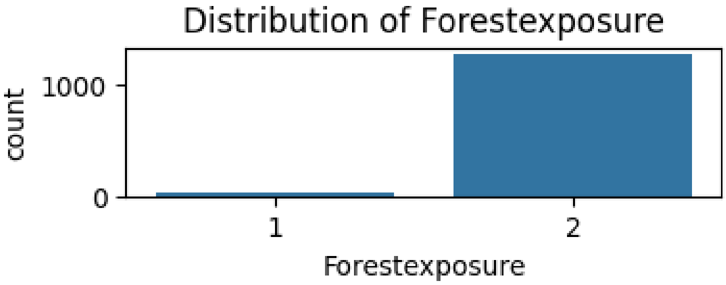

Distribution of UrimeeyaNeighbourhood
count
1000
0
1
2
3
4
UrimeeyaNeighbourhood

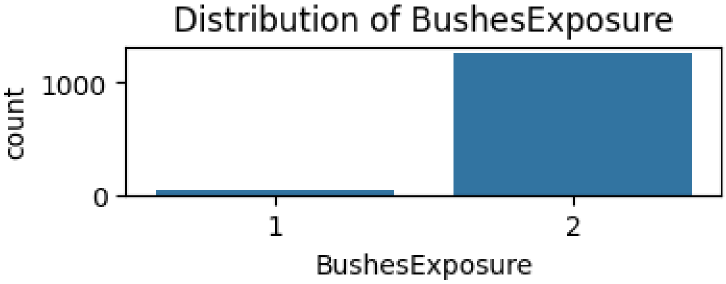

Distribution of OtherrhodentsHome
count
1000
0
1
2
3
4
OtherrhodentsHome

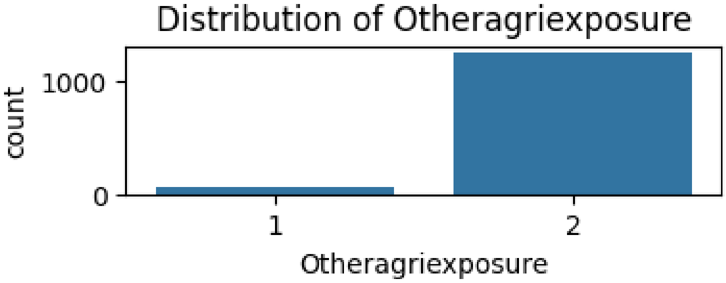

Distribution of Marshlandexposure
count
1000
0
1
2
Marshlandexposure

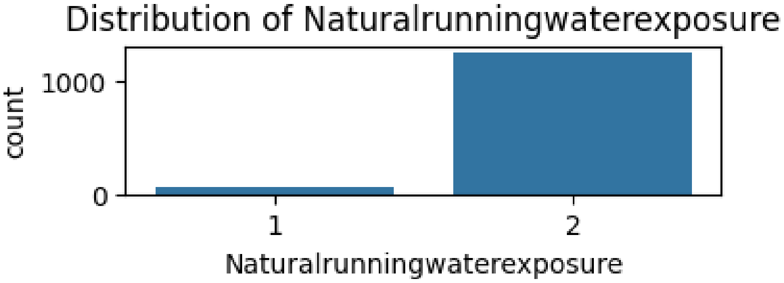

Distribution of Wetsoilexposure
count
1000
0
1
2
Wetsoilexposure

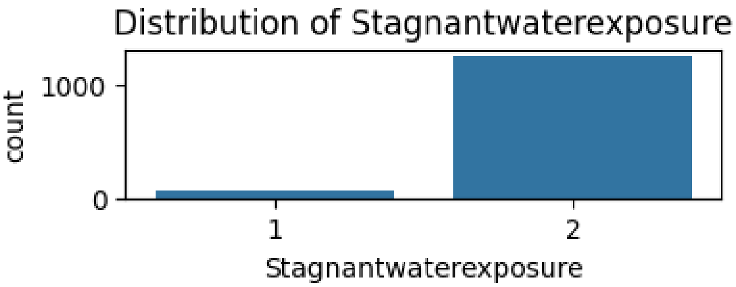

Distribution of Floodexposure
count
1000
0
1
2
Floodexposure

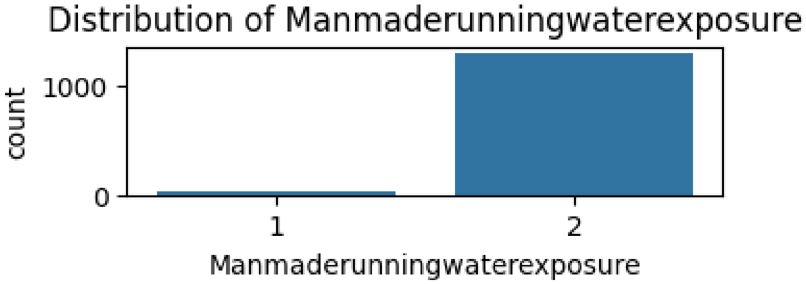

Distribution of Forestexposure
count
1000
0
1
2
Forestexposure

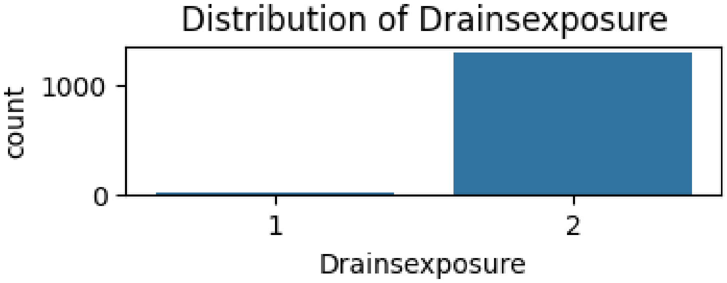

Distribution of BushesExposure
count
1000
0
1
2
BushesExposure

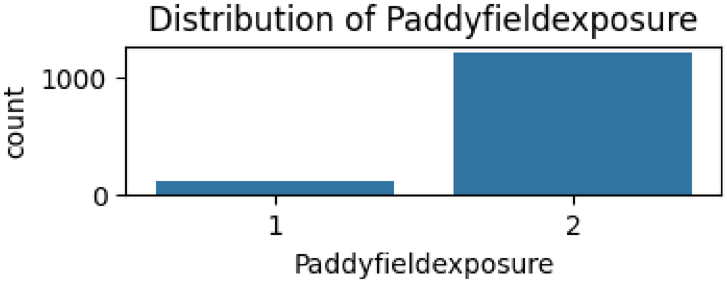

Distribution of Otheragriexposure
count
1000
0
1
2
Otheragriexposure

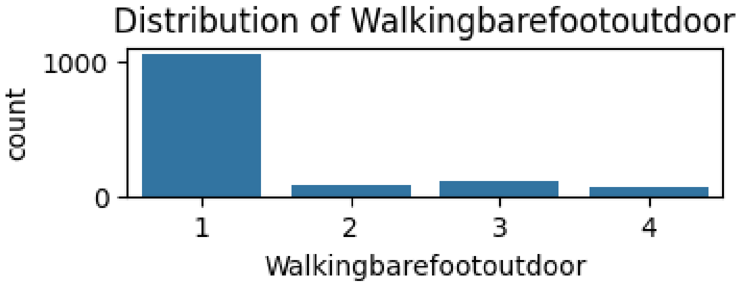

Distribution of Naturalrunningwaterexposure
count
1000
0
1
2
Naturalrunningwaterexposure

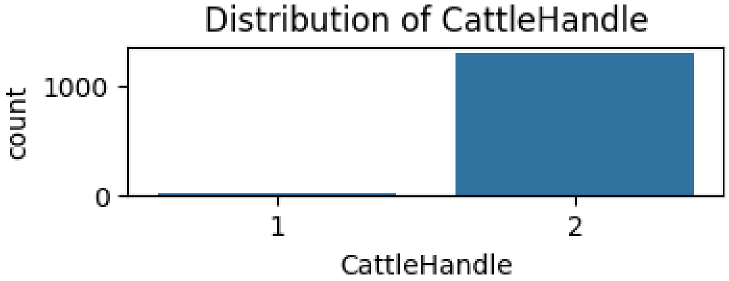

Distribution of Stagnantwaterexposure
count
1000
0
1
2
Stagnantwaterexposure

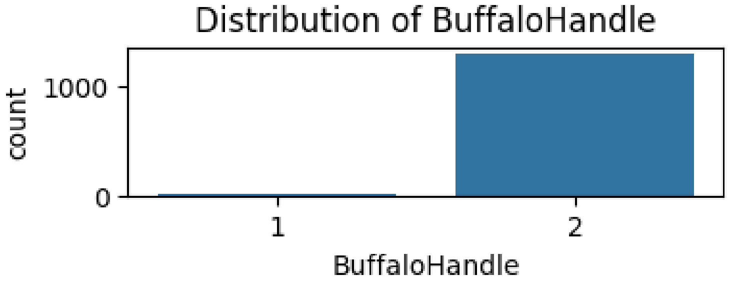

Distribution of Manmaderunningwaterexposure
count
1000
0
1
2
Manmaderunningwaterexposure

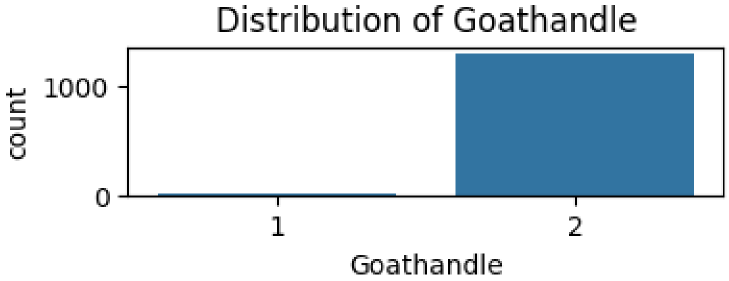

Distribution of Drainsexposure
count
1000
0
1
2
Drainsexposure

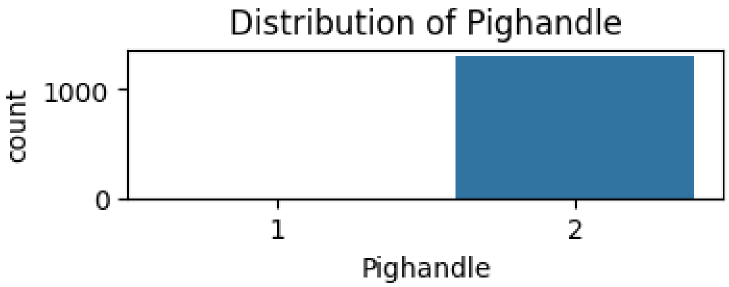

Distribution of Paddyfieldexposure
count
1000
0
1
2
Paddyfieldexposure

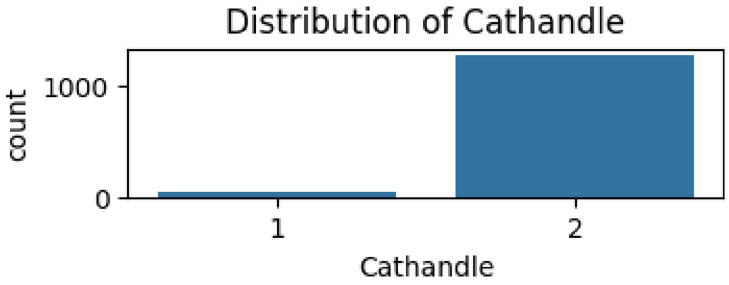

Distribution of Walkingbarefootoutdoor
count
1000
0
1
2
3
4
Walkingbarefootoutdoor

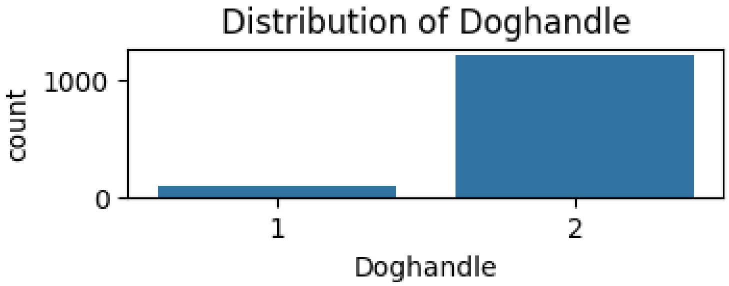

Distribution of CattleHandle
count
1000
0
1
2
CattleHandle

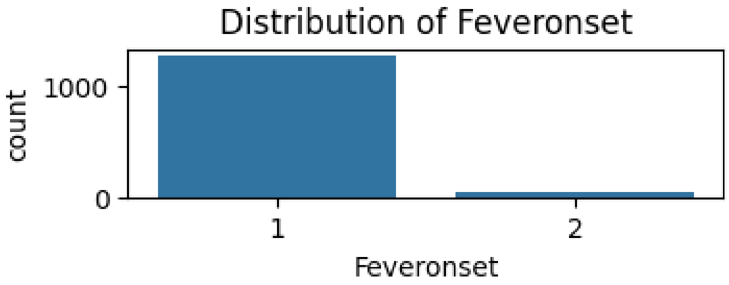

Distribution of BuffaloHandle
count
1000
0
1
2
BuffaloHandle

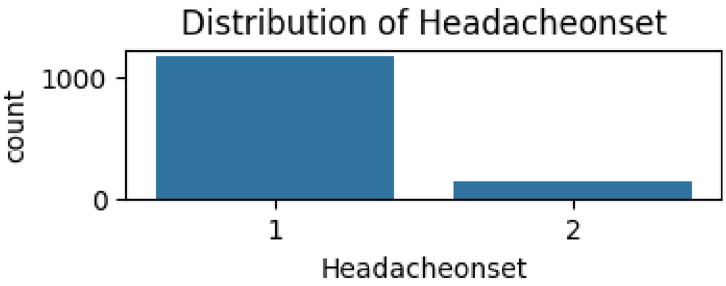

Distribution of Goathandle
count
1000
0
1
2
Goathandle

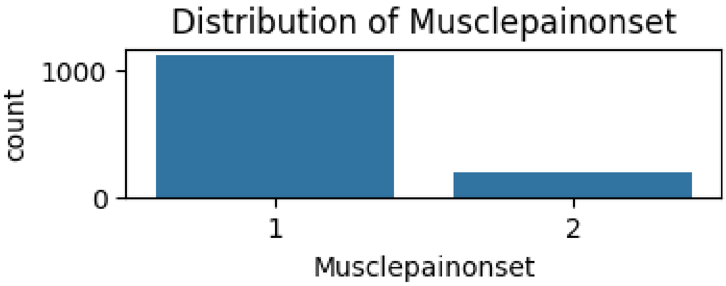

Distribution of Pighandle
count
1000
0
1
2
Pighandle

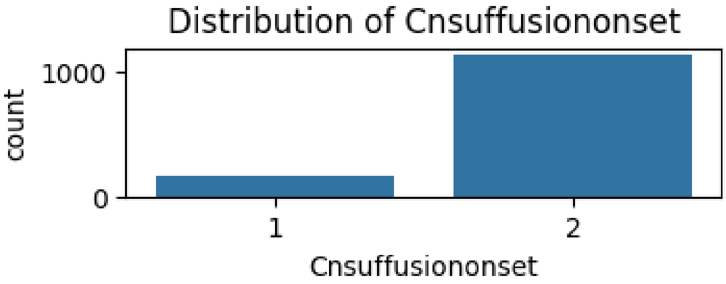

Distribution of Cathandle
count
1000
0
1
2
Cathandle

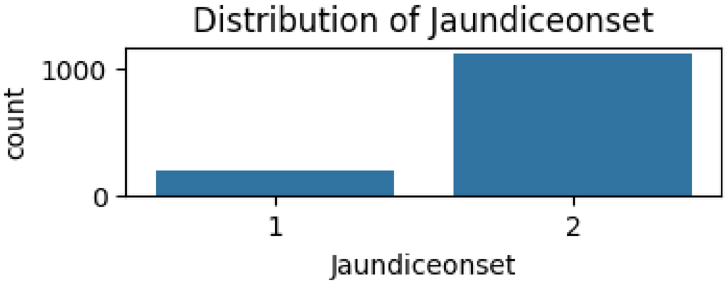

Distribution of Doghandle
count
1000
0
1
2
Doghandle

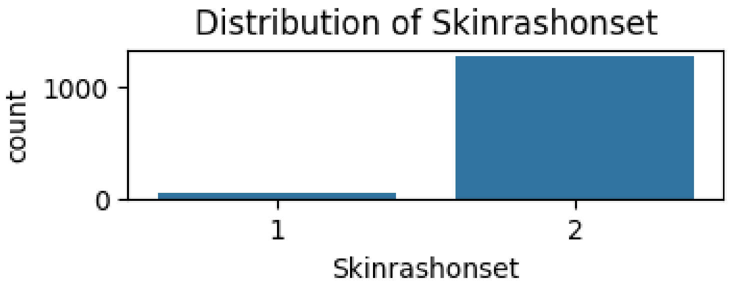

Distribution of Feveronset
count
1000
0
1
2
Feveronset

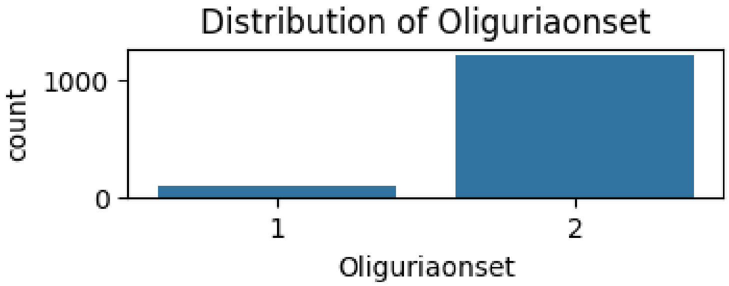

Distribution of Headacheonset
count
1000
0
1
2
Headacheonset

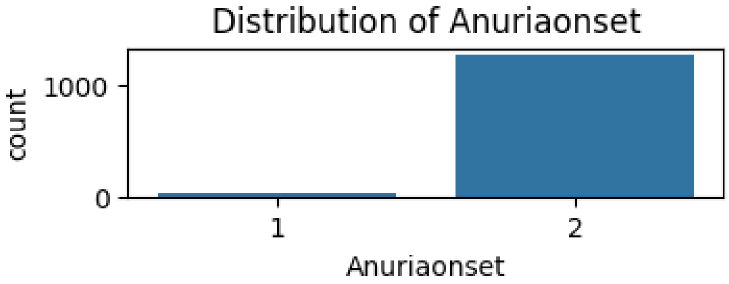

Distribution of Musclepainonset
count
1000
0
1
2
Musclepainonset

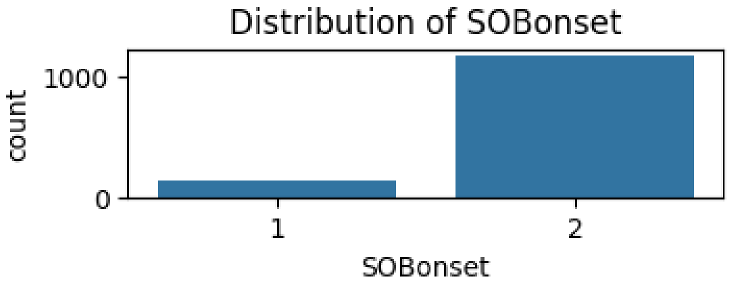

Distribution of Cnsuffusiononset
count
1000
0
1
2
Cnsuffusiononset

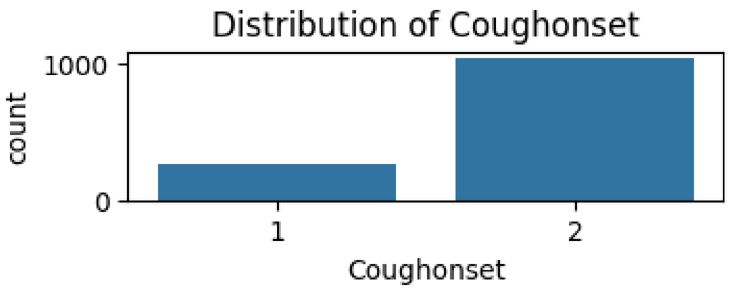

Distribution of Jaundiceonset
count
1000
0
1
2
Jaundiceonset

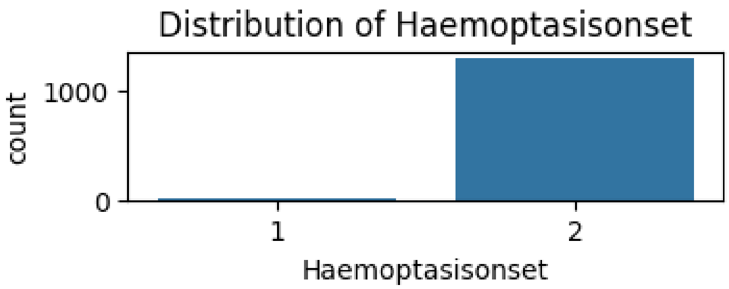

Distribution of Skinrashonset

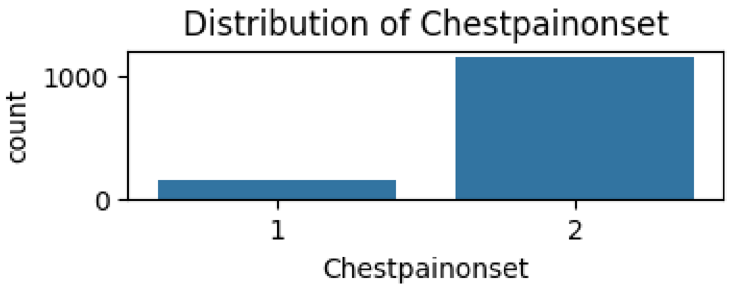

Distribution of Oliguriaonset

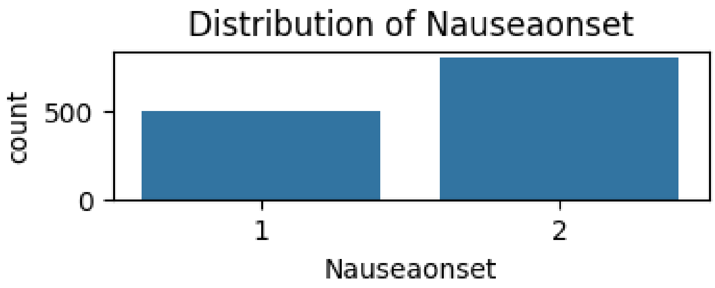

Distribution of Anuriaonset

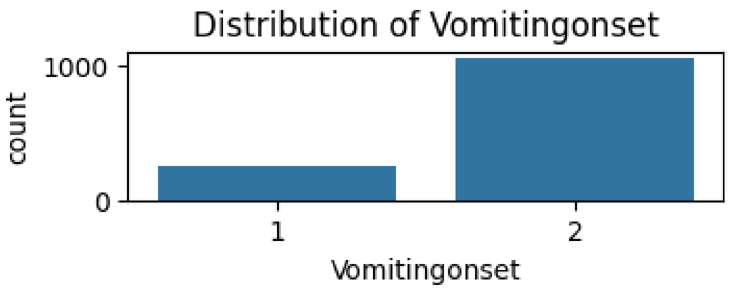

Distribution of SOBonset

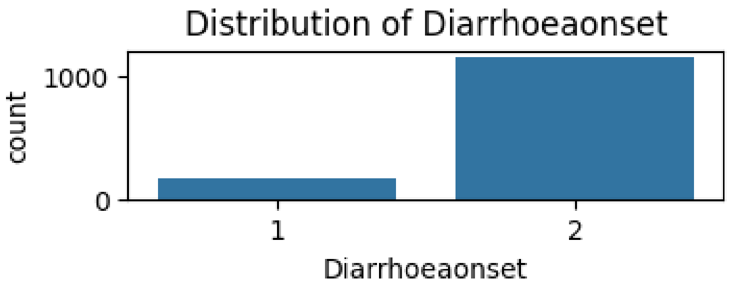

Distribution of Coughonset
1000
0
count
1
2
Coughonset

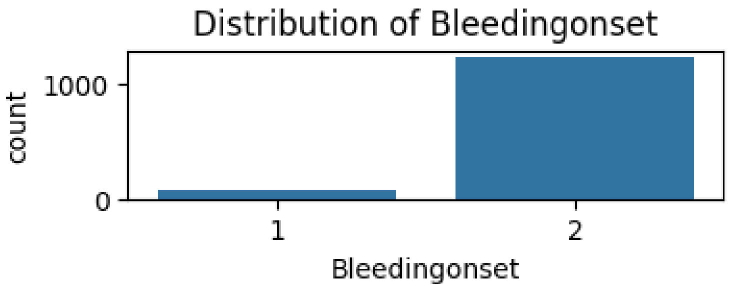

Distribution of Haemoptasisonset
1000
0
count
1
2
Haemoptasisonset

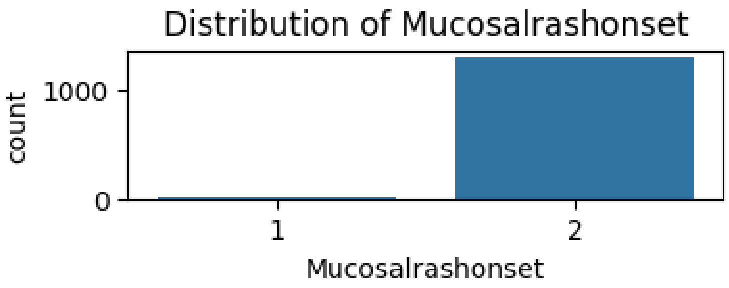

Distribution of Chestpainonset
1000
0
count
1
2
Chestpainonset

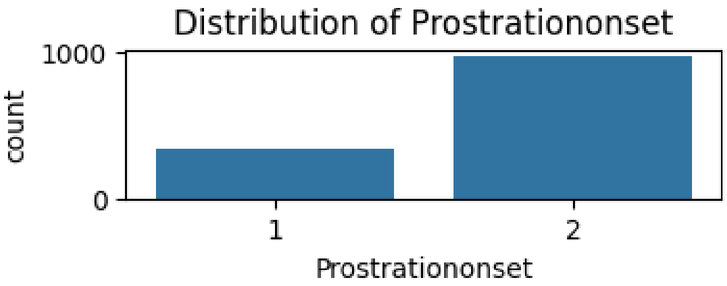

Distribution of Nauseaonset
500
0
count
1
2
Nauseaonset

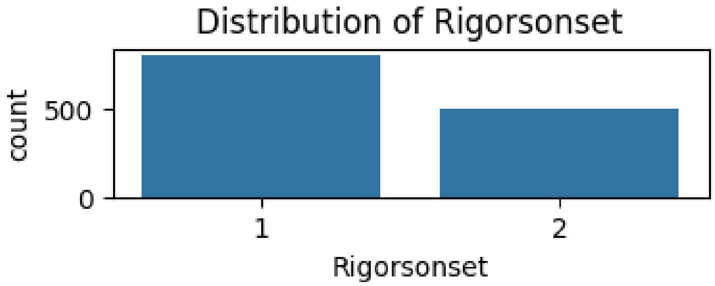

Distribution of Vomitingonset
count
1000
0
1
2
Vomitingonset

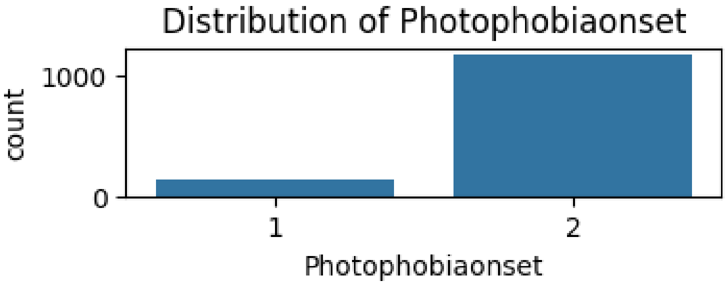

Distribution of Diarrhoeaonset
count
1000
0
1
2
Diarrhoeaonset

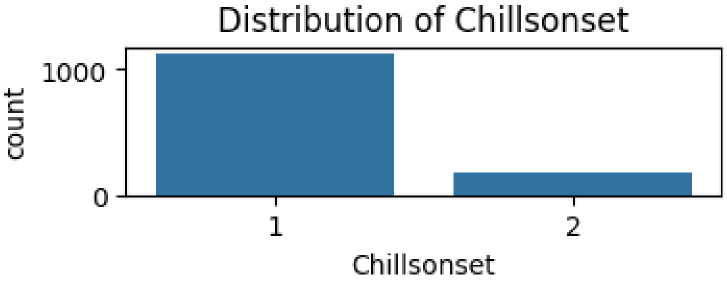

Distribution of Bleedingonset
count
1000
0
1
2
Bleedingonset

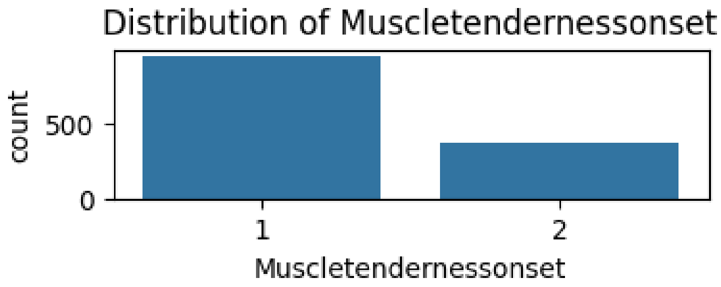

Distribution of Mucosalrashonset
count
1000
0
1
2
Mucosalrashonset

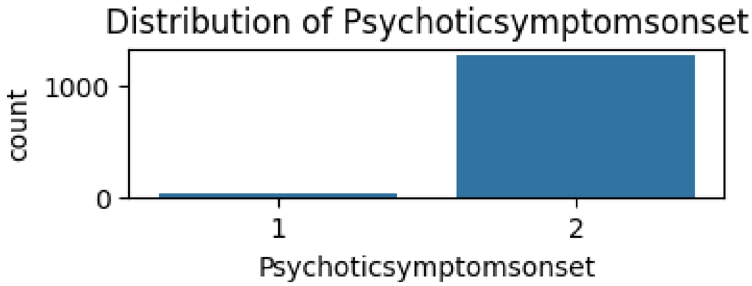

Distribution of Prostrationonset
1000
0
count
1
2
Prostrationonset

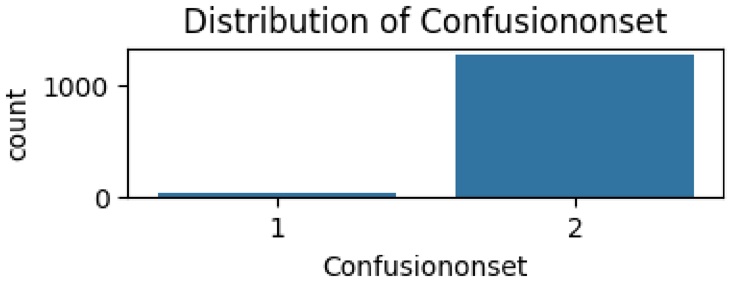

Distribution of Rigorsonset
500
0
count
1
2
Rigorsonset

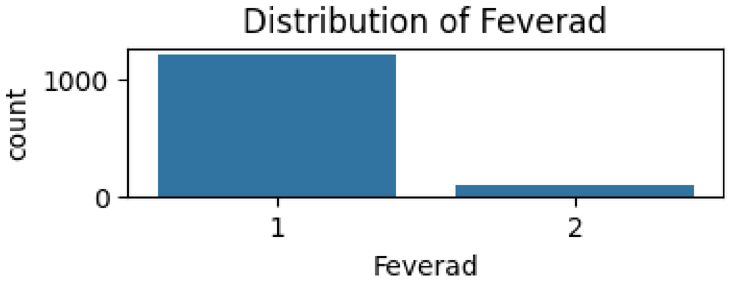

Distribution of Photophobiaonset
1000
0
count
1
2
Photophobiaonset

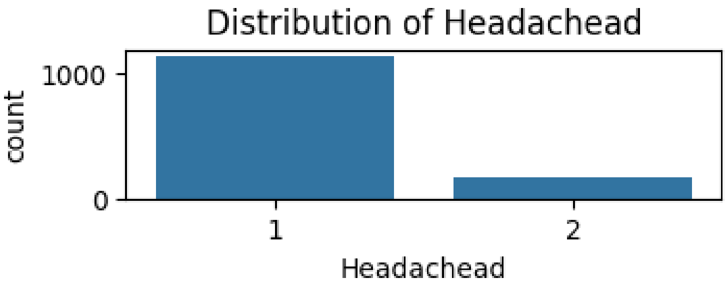

Distribution of Chillsonset
1000
0
count
1
2
Chillsonset

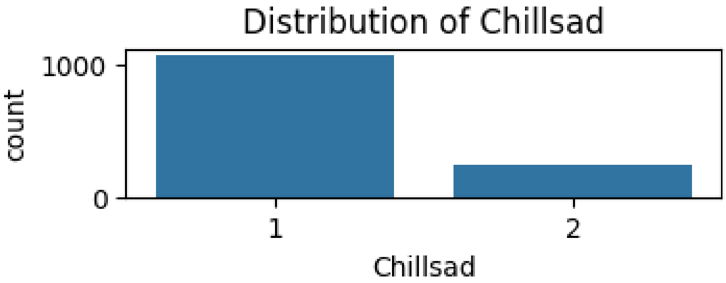

Distribution of Muscletendernessonset
count
500
0
1
2
Muscletendernessonset

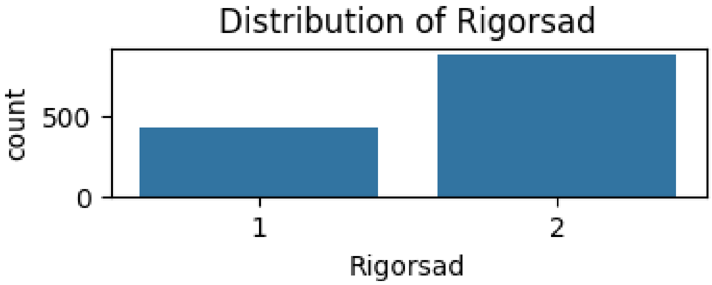

Distribution of Psychoticsymptomsonset
count
1000
0
1
2
Psychoticsymptomsonset

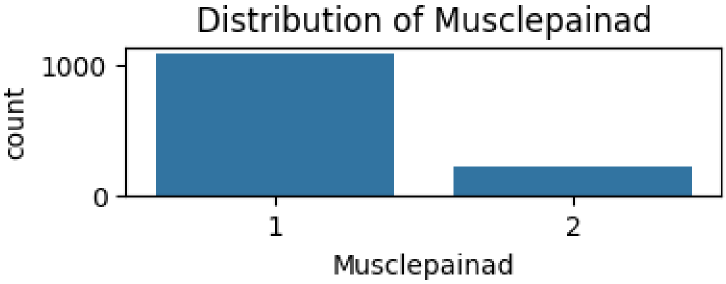

Distribution of Confusiononset
count
1000
0
1
2
Confusiononset

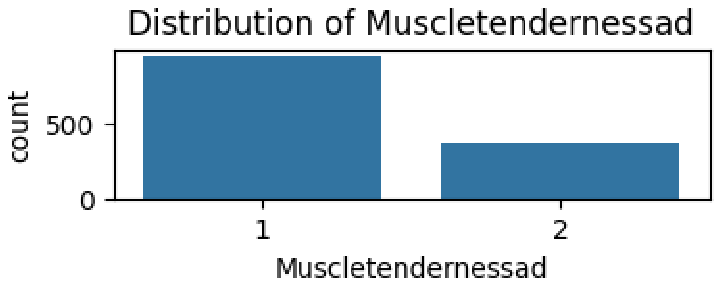

Distribution of Feverad
count
1000
0
1
2
Feverad

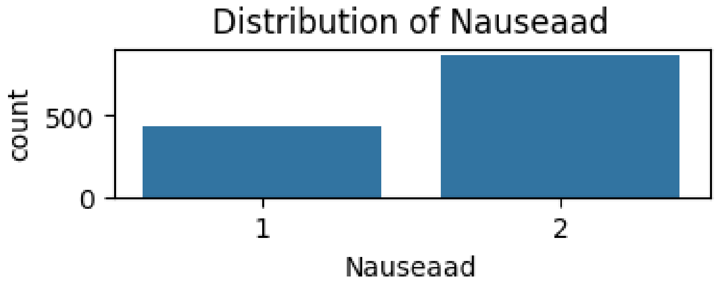

Distribution of Headachead
count
1000
0
1
2
Headachead

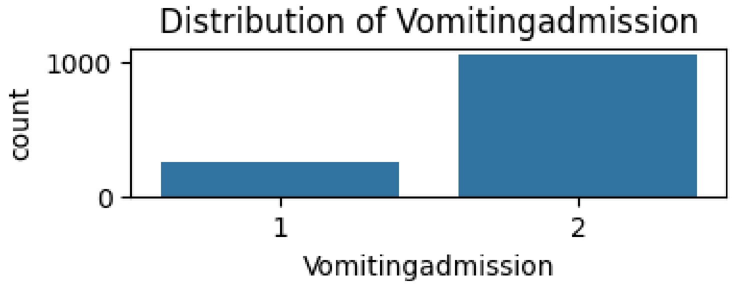

Distribution of Chillsad
count
1000
0
1
2
Chillsad

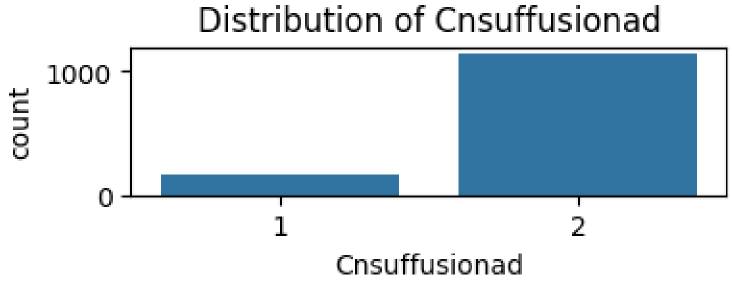

Distribution of Rigorsad
count
500
0
1
2
Rigorsad

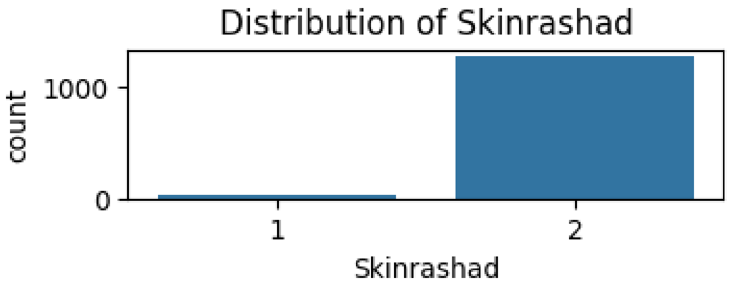

Distribution of Musclepainad
count
1000
0
1
2
Musclepainad

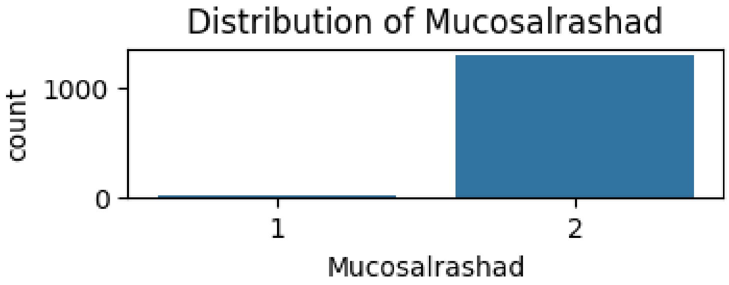

Distribution of Muscletendernessad

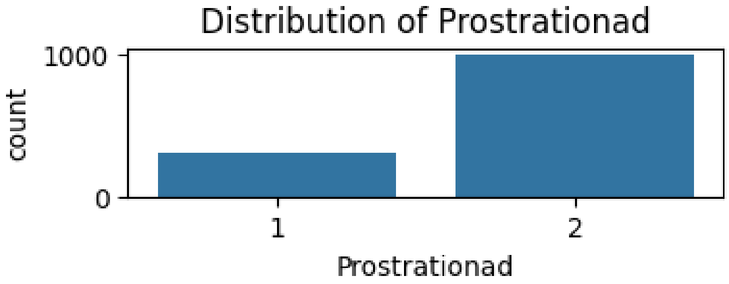

Distribution of Nauseaad

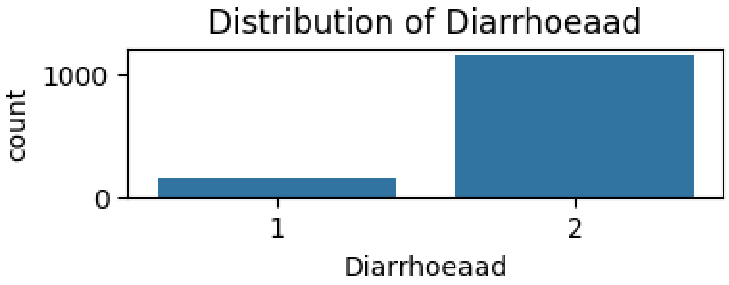

Distribution of Vomitingadmission

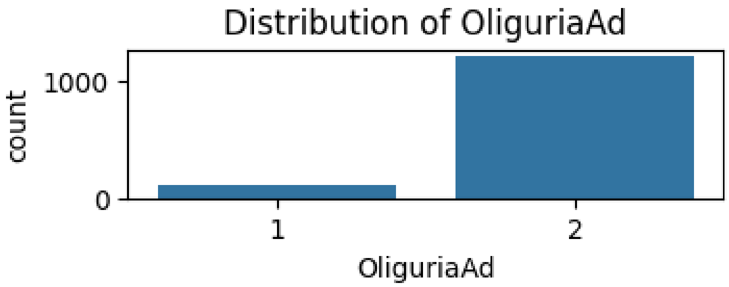

Distribution of Cnsuffusionad

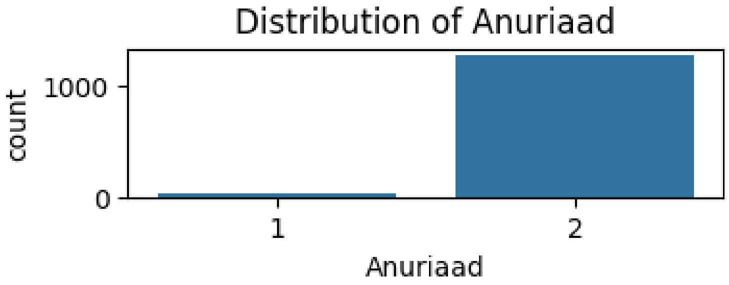

Distribution of Skinrashad
count
1000
0
1
2
Skinrashad

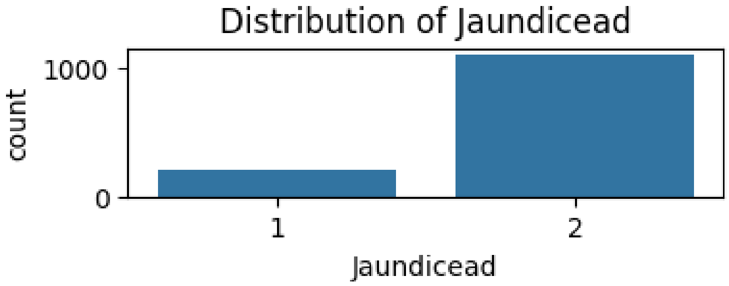

Distribution of Mucosalrashad
count
1000
0
1
2
Mucosalrashad

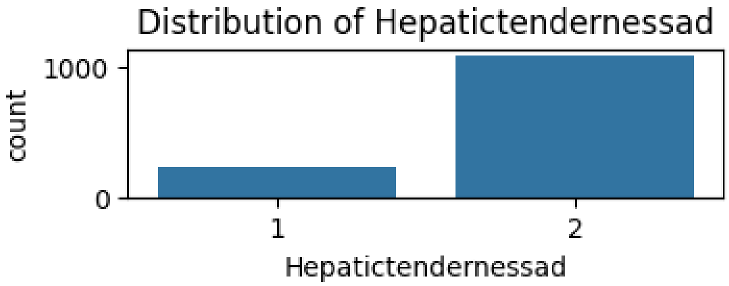

Distribution of Prostrationad
count
1000
0
1
2
Prostrationad

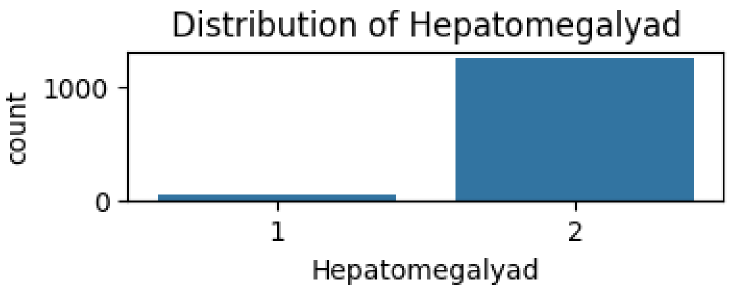

Distribution of Diarrhoeaad
count
1000
0
1
2
Diarrhoeaad

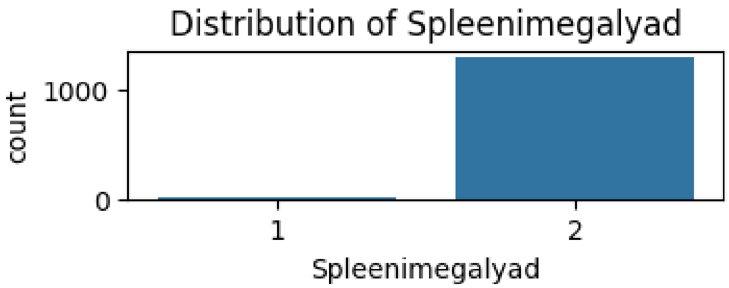

Distribution of OliguriaAd
count
1000
0
1
2
OliguriaAd

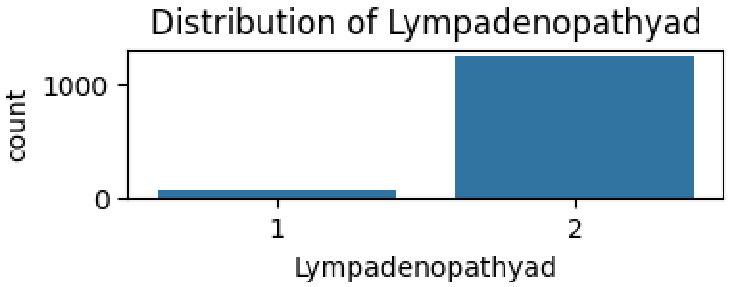

Distribution of Anuriaad
count
1000
0
1
2
Anuriaad

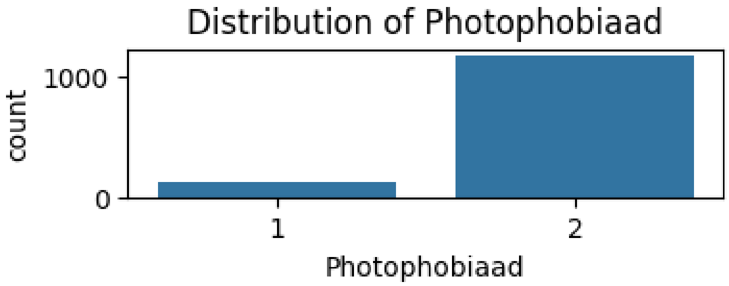

Distribution of Jaundicead
count
1000
0
1
2
Jaundicead

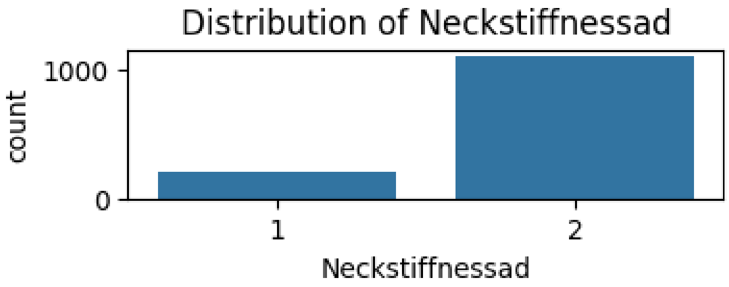

Distribution of Hepatictendernessad
count
1000
0
1
2
Hepatictendernessad

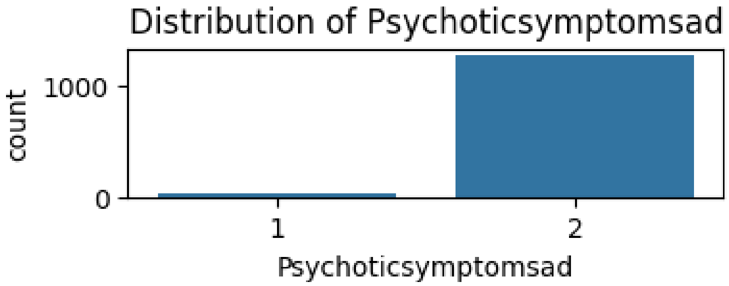

Distribution of Hepatomegalyad
count
1000
0
1
2
Hepatomegalyad

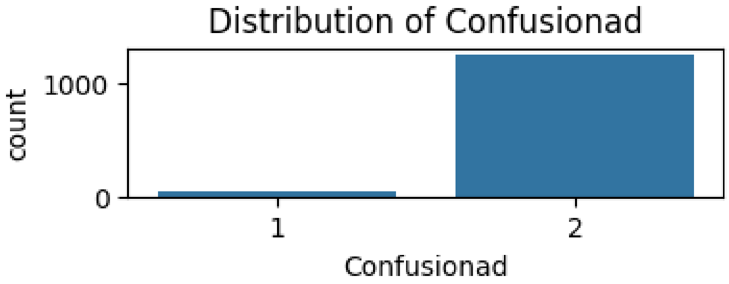

Distribution of Spleenimegalyad
count
1000
0
1
2
Spleenimegalyad

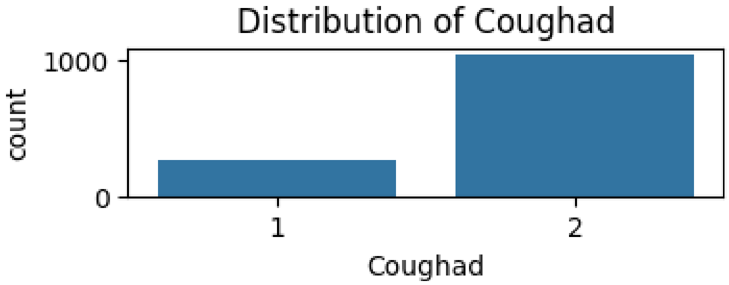

Distribution of Lympadenopathyad
count
1000
0
1
2
Lympadenopathyad

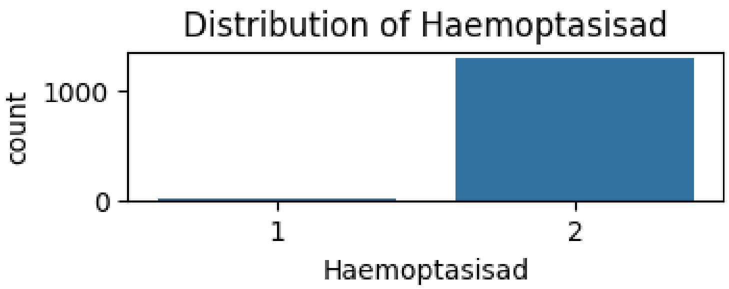

Distribution of Photophobiaad
count
1000
0
1
2
Photophobiaad

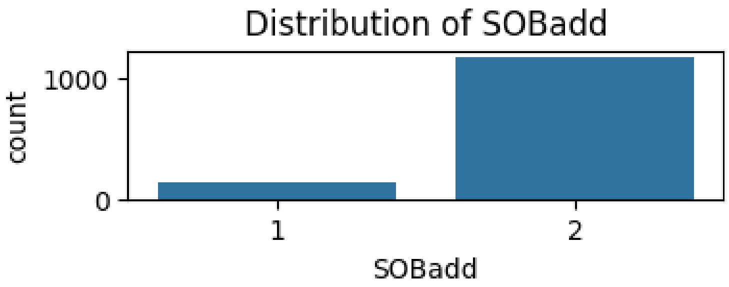

Distribution of Neckstiffnessad

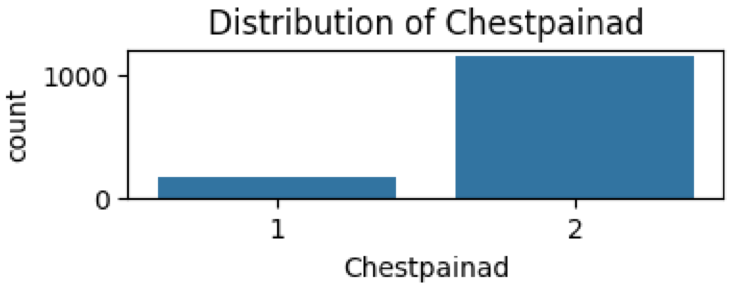

Distribution of Psychoticsymptomsad

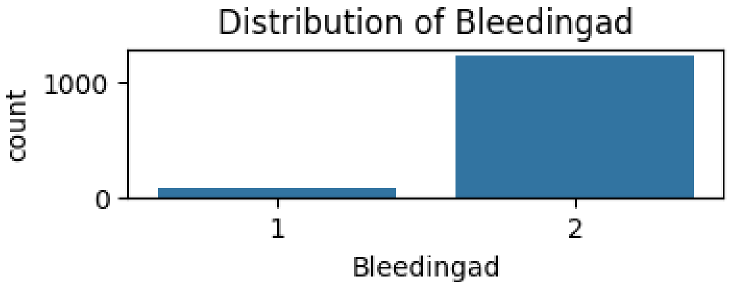

Distribution of Confusionad

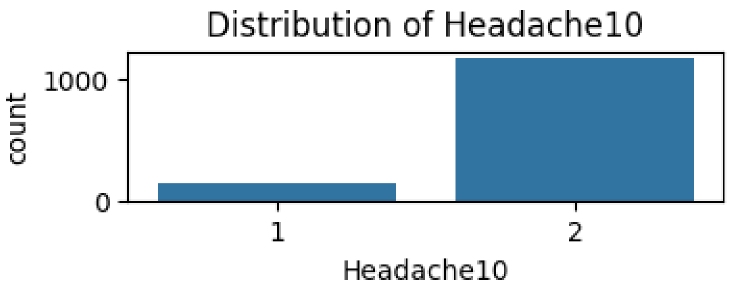

Distribution of Coughad


Distribution of Haemoptasisad
count
1000
0
1
2
Haemoptasisad

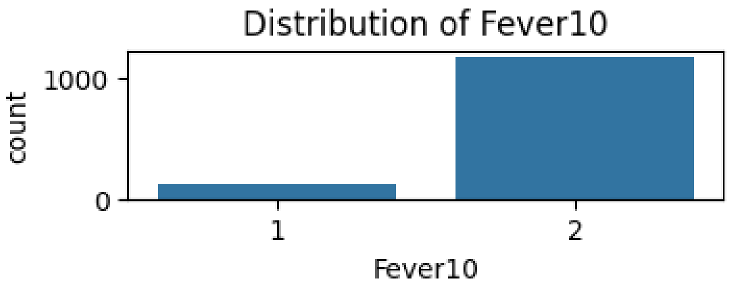

Distribution of SOBadd
count
1000
0
1
2
SOBadd


Distribution of Chestpainad
count
1000
0
1
2
Chestpainad

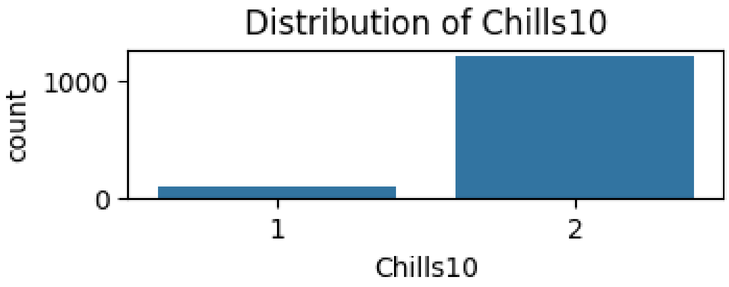

Distribution of Bleedingad
count
1000
0
1
2
Bleedingad



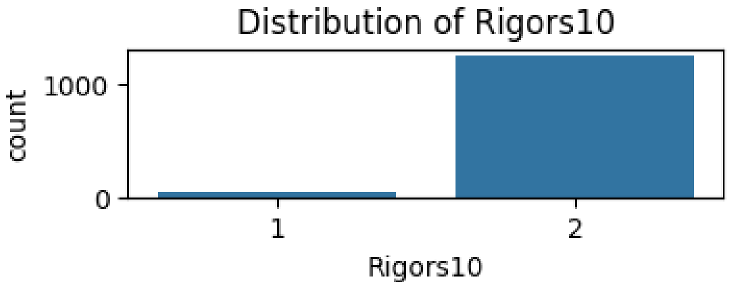
Distribution of Headache10



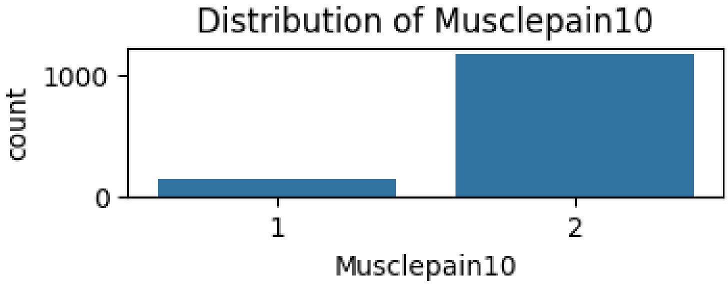
Distribution of Fever10

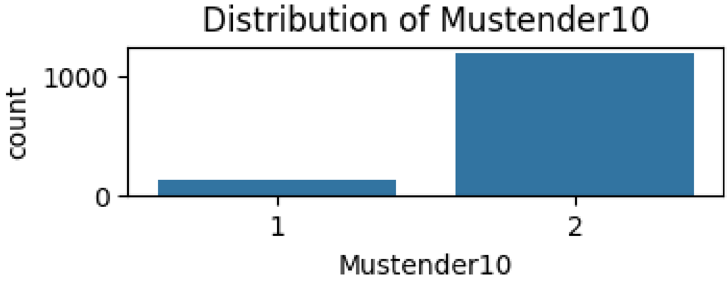


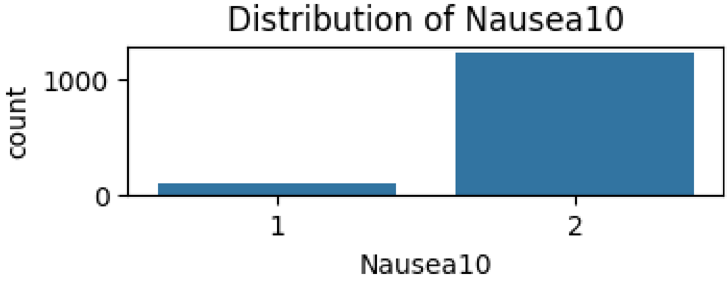
Distribution of Chills10

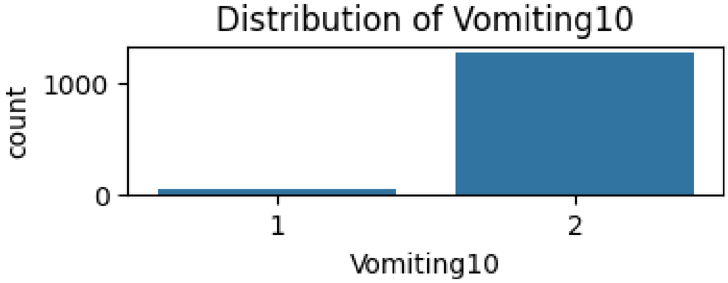


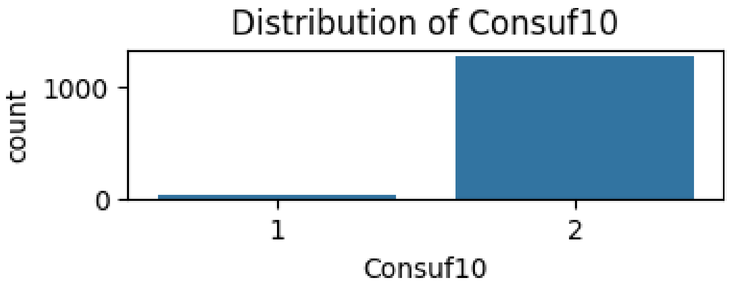
Distribution of Rigors10

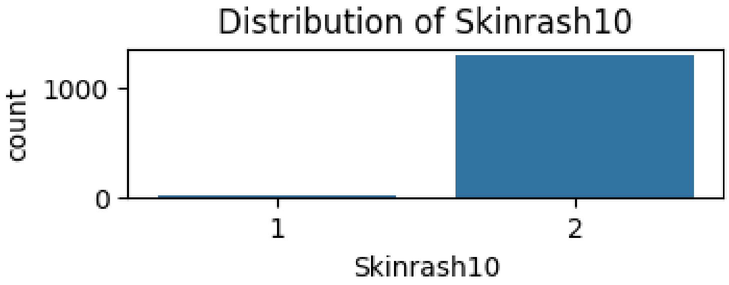

Distribution of Musclepain10
count
1000
0
1
2
Musclepain10

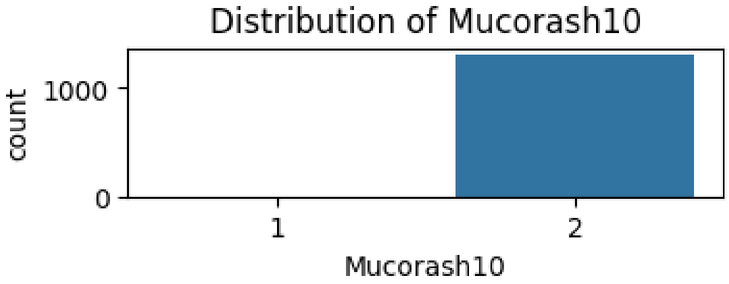

Distribution of Mustender10
count
1000
0
1
2
Mustender10

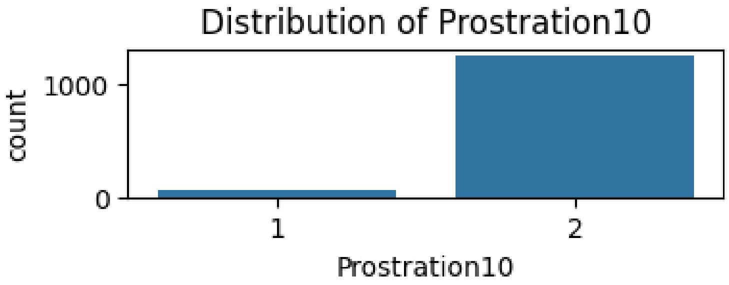

Distribution of Nausea10
count
1000
0
1
2
Nausea10

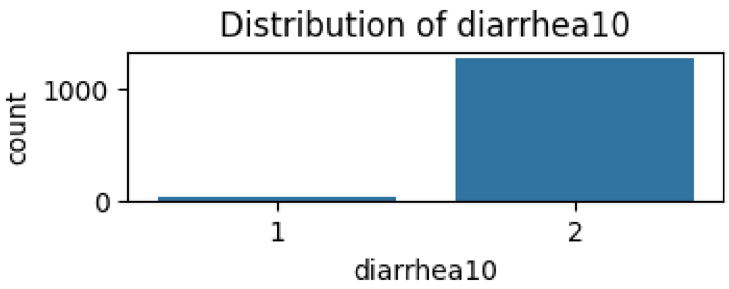

Distribution of Vomiting10
count
1000
0
1
2
Vomiting10

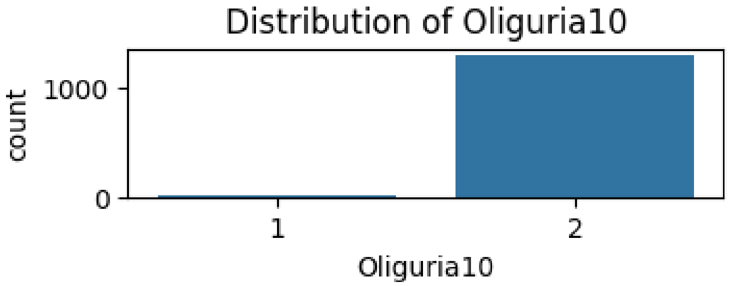

Distribution of Consuf10
count
1000
0
1
2
Consuf10

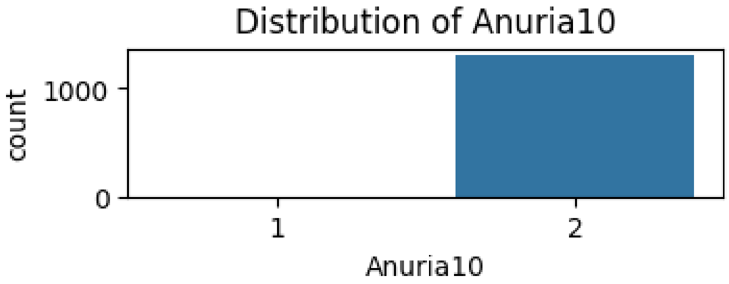

Distribution of Skinrash10
count
1000
0
1
2
Skinrash10

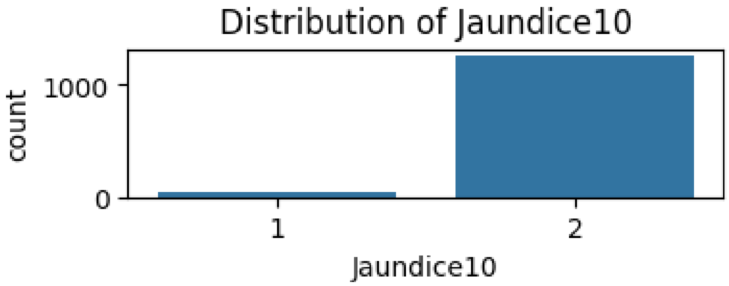

Distribution of Mucorash10
count
1000
0
1
2
Mucorash10

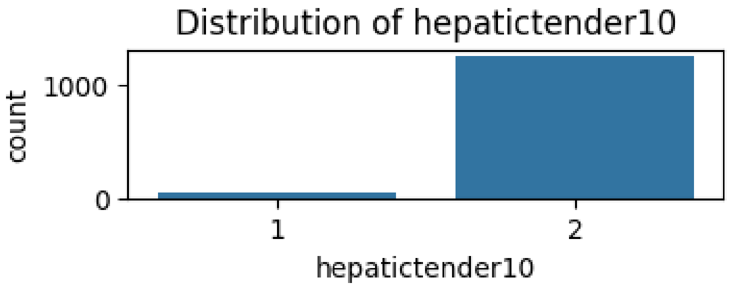

Distribution of Prostration10
count
1000
0
1
2
Prostration10

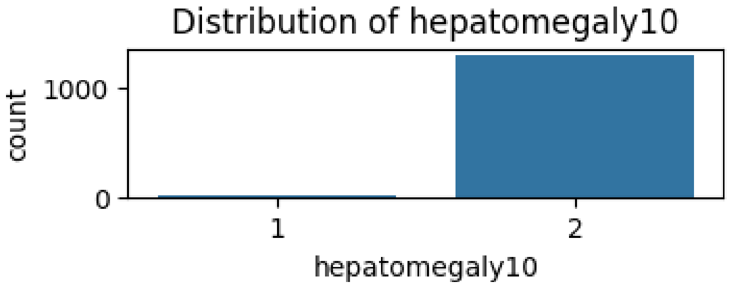

Distribution of diarrhea10
count
1000
0
1
2
diarrhea10

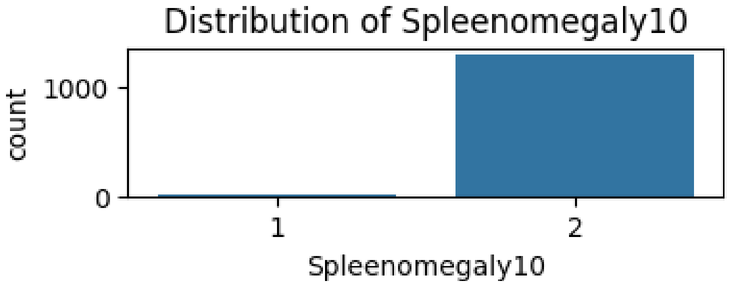

Distribution of Oliguria10
count
1000
0
1
2
Oliguria10

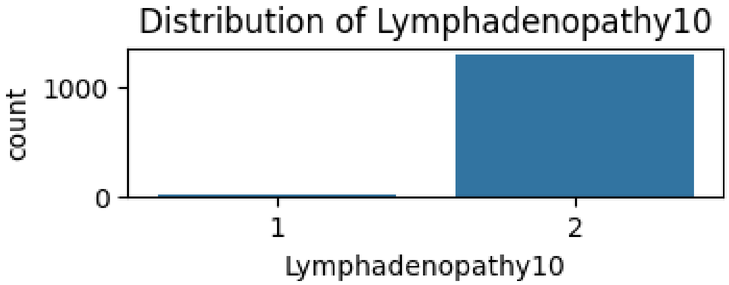

Distribution of Anuria10
count
1000
0
1
2
Anuria10

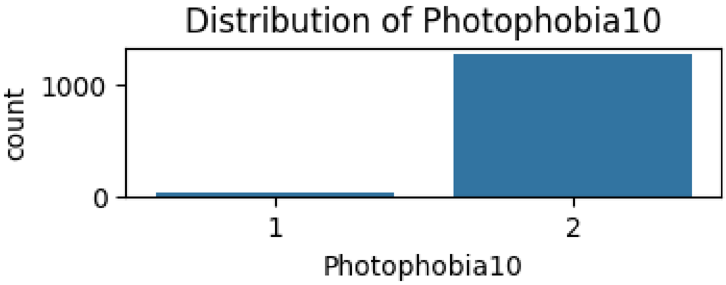

Distribution of Jaundice10
count
1000
0
1
2
Jaundice10

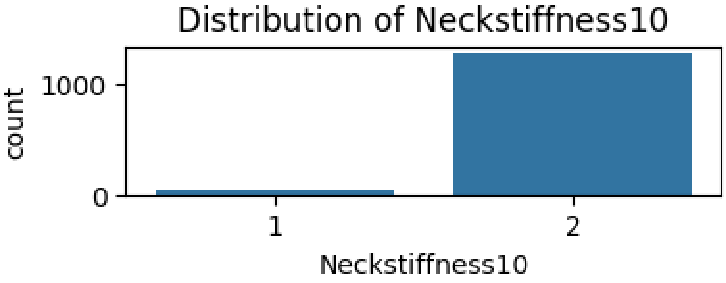

Distribution of hepatictender10
count
1000
0
1
2
hepatictender10

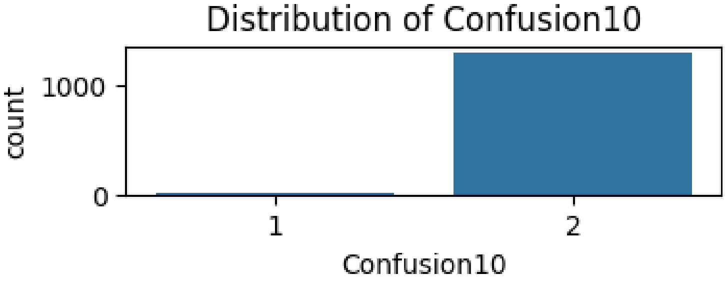

Distribution of hepatomegaly10
count
1000
0
1
2
hepatomegaly10

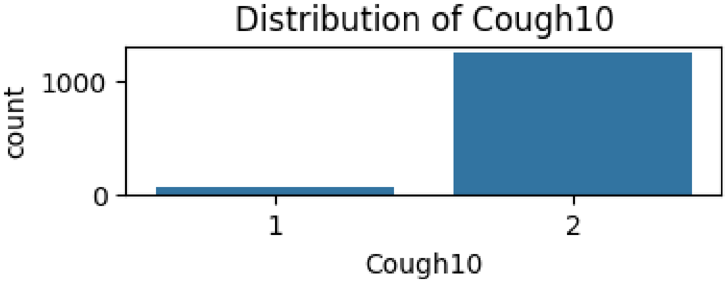

Distribution of Spleenomegaly10
count
1000
0
1
2
Spleenomegaly10

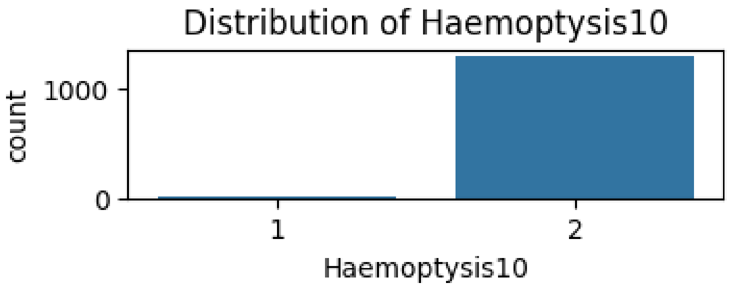

Distribution of Lymphadenopathy10
count
1000
0
1
2
Lymphadenopathy10

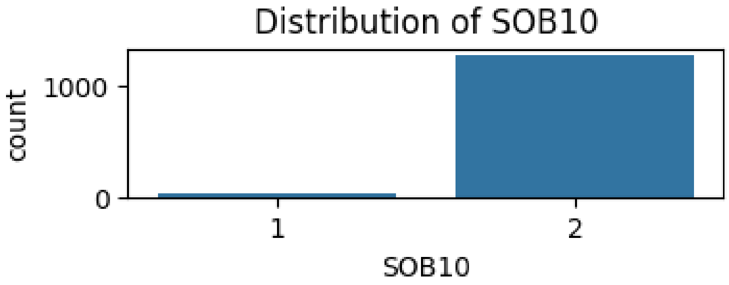

Distribution of Photophobia10
count
1000
0
1
2
Photophobia10

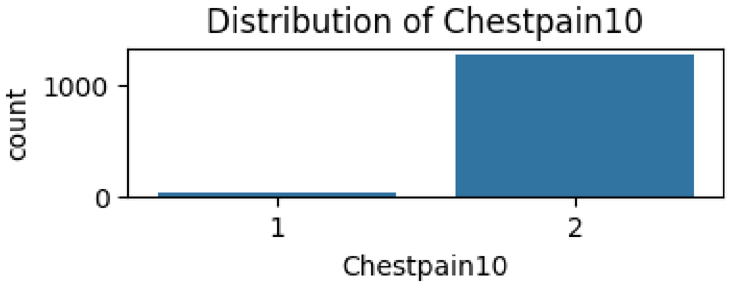

Distribution of Neckstiffness10
count
1000
0
1
2
Neckstiffness10

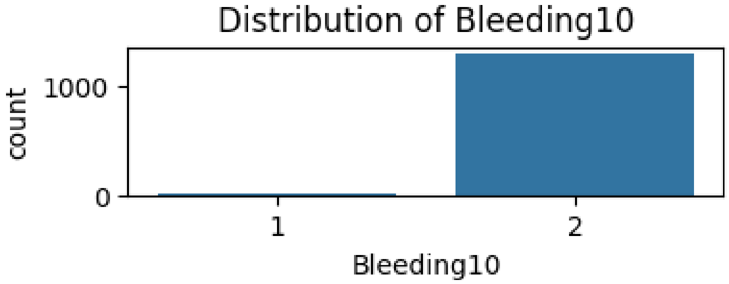

Distribution of Confusion10
count
1000
0
1
2
Confusion10

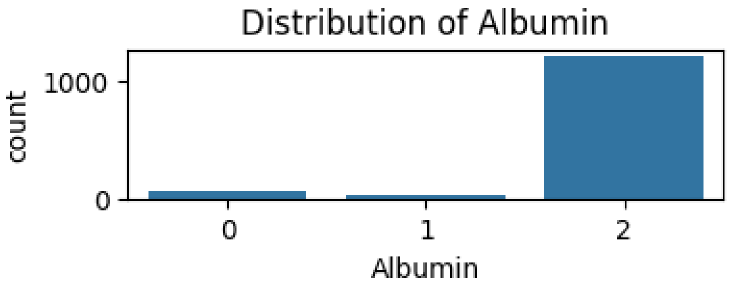

Distribution of Cough10
count
1000
0
1
2
Cough10

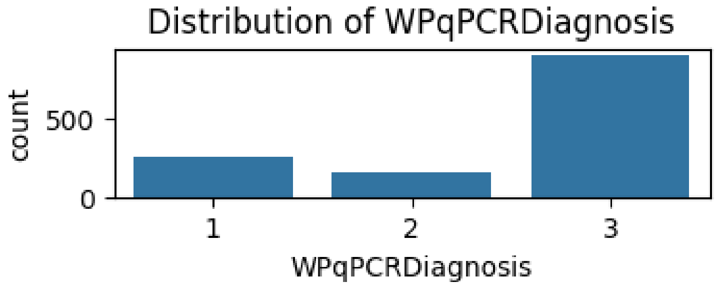

Distribution of Haemoptysis10
count
1000
0
1
2
Haemoptysis10

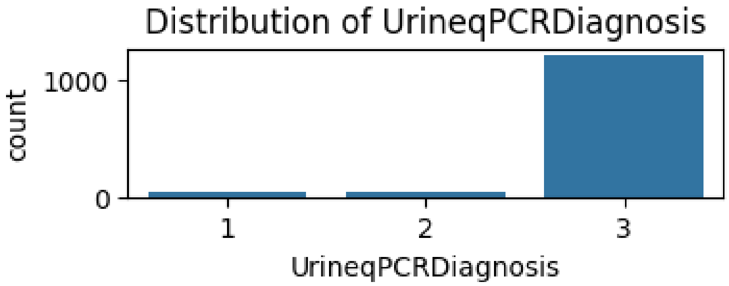

Distribution of SOB10
count
1000
0
1
2
SOB10

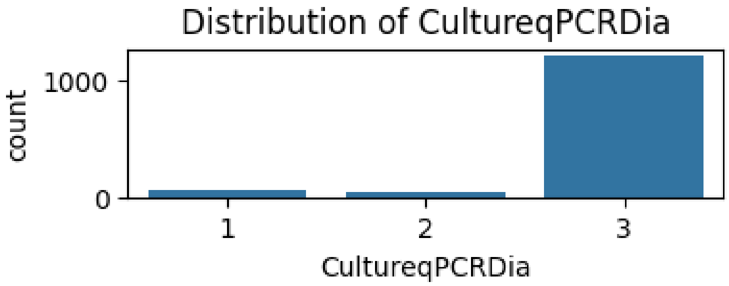

Distribution of Chestpain10
count
1000
0
1
2
Chestpain10

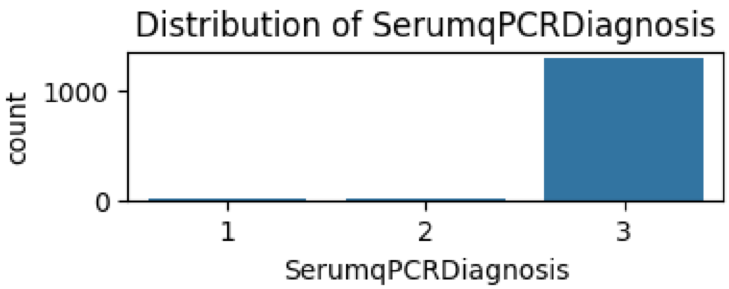

Distribution of Bleeding10
count
1000
0
1
2
Bleeding10

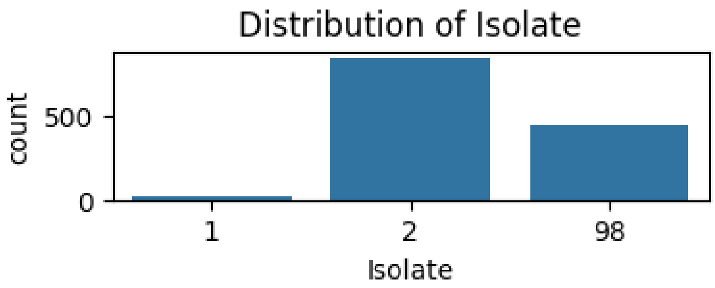

Distribution of Albumin
count
1000
0
0
1
2
Albumin

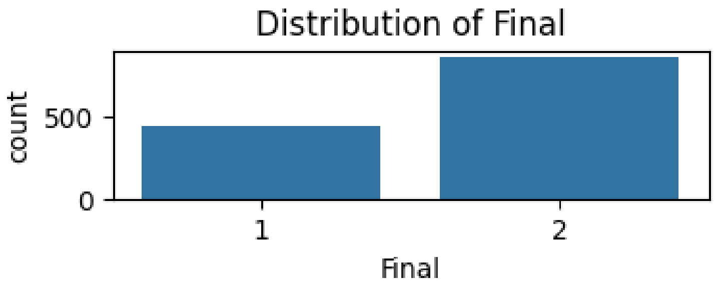

Distribution of WPqPCRDiagnosis
count
500
0
1
2
3
WPqPCRDiagnosis


Distribution of UrineqPCRDiagnosis
count
1000
0
1
2
3
UrineqPCRDiagnosis


Distribution of CultureqPCRDia
count
1000
0
1
2
3
CultureqPCRDia







1.15 Perform SMOTE on 'Final' variable

[25]:

```python
from imblearn.over_sampling import SMOTE
from collections import Counter

#Split train data into X and y
X_train = train_data.drop('Final', axis = 1)
y_train = train_data['Final']

smote = SMOTE(random_state = 42)
X_train, y_train = smote.fit_resample(X_train, y_train)
```

```
print("SMOTE class distribution:", Counter(y_train))
```

```
SMOTE class distribution: Counter({2: 861, 1: 861})
```

1.16 Train Random Forest Classifier model

[26]:

```
from sklearn.ensemble import RandomForestClassifier

rf = RandomForestClassifier(random_state = 42)
rf.fit(X_train, y_train)
```

[26]:

```
RandomForestClassifier(random_state=42)
```

1.17 Perform hyperparameter tuning with cross-validation

[27]:

```
from sklearn.model_selection import GridSearchCV

#Define hyperparameters
param_grid = {
    'n_estimators': [173, 174, 175],
    'max_depth': [22, 23, 24],
    'min_samples_split': [3, 4, 5],
    'min_samples_leaf': [1, 2]
}

#Perform GridSearchCV
grid_search = GridSearchCV(rf, param_grid, cv = 10, n_jobs = -1, scoring =␣
 ↪'accuracy')
grid_search.fit(X_train, y_train)

best_score = grid_search.best_score_
best_params = grid_search.best_params_
best_model = grid_search.best_estimator_

print("Best Score:", best_score)
print("Best Parameters:", best_params)
```

```
Best Score: 0.9251713940045704
Best Parameters: {'max_depth': 23, 'min_samples_leaf': 1, 'min_samples_split':
4, 'n_estimators': 174}
```

1.18 Predict model on train data

[28]:

```
y_pred_train = best_model.predict(X_train)
```

1.19 Check accuracy for train data predictions

[29]:
```python
from sklearn.metrics import accuracy_score, confusion_matrix, classification_report

accuracy_train = accuracy_score(y_train, y_pred_train)
print("Accuracy: ", accuracy_train)

conf_matrix_train = confusion_matrix(y_train, y_pred_train)
print("Confusion Matrix: \n", conf_matrix_train)

class_report_train = classification_report(y_train, y_pred_train)
print("Classification Report: \n", class_report_train)
```

```
Accuracy:  0.9814169570267132
Confusion Matrix:
 [[829  32]
 [  0 861]]
Classification Report:
               precision    recall  f1-score   support

           1       1.00      0.96      0.98       861
           2       0.96      1.00      0.98       861

    accuracy                           0.98      1722
   macro avg       0.98      0.98      0.98      1722
weighted avg       0.98      0.98      0.98      1722
```

1.20 Load test dataset

[30]:
```python
test_data_whole = pd.read_csv('test.csv').drop('ID', axis = 1)

#Get train dataset categorical columns without 'Final' variable
categorical_vars_filtered = [col for col in categorical_vars if col != 'Final']

#Get columns for test data that are included in train data after preprocessing
test_data = test_data_whole[categorical_vars_filtered + numerical_vars]
print(test_data.shape)
```

```
(347, 172)
```

1.21 Preprocess test data into train data format

[31]:
```python
#Handle duplicates
test_data = test_data.drop_duplicates()
```

[32]:

```python
#Replace values starting with 'fiel' or 'occ' with 99
test_data = test_data.map(lambda x: 99 if isinstance(x, str) and (x.lower().
 ↪startswith('fiel') or x.lower().startswith('occ')) else x)
print(test_data)
```

```
     Hospital  Sample  ICU  OPD  Sex  Prophylactics  Pasttreatments  \
0           1       1    2    2    1              2               2
1           1       1    2    2    1              2               1
2           1       1    2    2    1              1               1
3           1       1    2    2    2              2               1
4           1       1    2    1    1             99              99
..        …     …  …  …  …            …             …
342         8       1    2    2    1              2               1
343         8       1    2    2    1              2               2
344         8       1    2    2    1              2               2
345         8       1    2    2    1              2               2
346         8       1    1    2    2              2               2

     Pastantibiotics  Chronicillness  Possibleexposure  …   ESR  Redcells  \
0                 99               2                 1  …  99.0        99
1                  3               2                 2  …  99.0        99
2                  1               2                 1  …  99.0        99
3                  1               2                 1  …  99.0        99
4                 99              99                99  …  99.0        99
..               …             …               …  …   …       …
342                1               2                 1  …  99.0        99
343                2               2                 1  …  99.0        99
344                2               2                 1  …  99.0        99
345                2               2                 1  …  99.0        12
346                2               2                 1  …  99.0        99

      Na      K    AST  T.Bilirubin  S.creatinine  B.urea   ALP  Puscells
0     99  99.00   99.0         99.0          99.0    99.0    99        99
1     99  99.00  177.0         99.0          88.4     8.0    99        99
2     99  99.00   99.0         99.0          99.0    99.0    99        99
3     99  99.00   99.0         99.0          99.0    99.0    99        99
4     99  99.00   99.0         99.0          99.0    99.0    99        99
..   …    …    …          …           …     …   …       …
342  143   3.40   23.7          8.2          65.0    12.0    99        99
343  135   4.01   99.0         60.0         161.0    90.0  1111        99
344  137   3.90   30.0         21.0          89.0    12.0    99        99
345   99  99.00   53.0         99.0          99.0    99.0    99         1
346  141   4.60   83.6         34.3          71.5     5.6    99        99

[328 rows x 172 columns]
```

[33]:
```
#Convert values called '99' to missing values
test_data.replace(99, pd.NA, inplace = True)
test_data.replace('99', pd.NA, inplace = True)
test_data.isnull().sum()
```

[33]:
```
Hospital          0
Sample            0
ICU               7
OPD               7
Sex              17
                ...
T.Bilirubin     245
S.creatinine    205
B.urea          214
ALP             265
Puscells        266
Length: 172, dtype: int64
```

[34]:
```
#Adjust data types in test data
test_data[numerical_vars] = test_data[numerical_vars].apply(pd.to_numeric,␣
 ↪errors = 'coerce')
```

[35]:
```
#Impute numerical variables with median
for col in numerical_vars:
    if test_data[col].isnull().sum() > 0:
        median_val = test_data[col].median()
        test_data[col].fillna(median_val, inplace = True)
```

[36]:
```
#Perform robust scaling on numerical data
from sklearn.preprocessing import RobustScaler

scaler = RobustScaler()
test_data[numerical_vars] = scaler.fit_transform(test_data[numerical_vars])
test_data[numerical_vars] = pd.DataFrame(test_data[numerical_vars], columns =␣
 ↪numerical_vars)
test_data[numerical_vars]
```

[36]:
```
          Age  PRad  SBPadd  WBCcount     Ncount          N     Lcount  \
0    0.166667   0.0     0.0  2.889064  17.862857   2.879831  11.000000
1    0.055556   0.0     0.0 -1.973249  -8.556190  -6.815778 -15.333333
2    0.277778   0.0     0.0  0.000000   0.000000   0.000000   0.000000
3   -0.500000   0.0     0.0  1.117231   8.986667   3.381831  -0.333333
4    0.000000   0.0     0.0  0.000000   0.000000   0.000000   0.000000
..        …   …     …       …        …        …        …
342 -1.055556   6.0     0.0  2.077105  -7.769524 -18.755004  25.666667
343  1.722222   2.0   -30.0  0.084972   3.196190   2.878263  -5.666667
344 -0.500000 -18.0     0.0  0.361920   3.900952   1.665318  -6.000000
```

```
345 -0.777778  -8.0   -10.0 -0.242329   0.000000   0.000000   0.000000
346  0.444444  32.0   -40.0 -0.484658   0.262857   2.985140 -10.666667

            L  Plateletcount   PCV  …  ESR  Redcells   Na     K    AST  \
0   -2.442451      -5.534884  -0.8  …  0.0       0.0  0.0  0.00    0.0
1    8.526969      26.930233  -0.8  …  0.0       0.0  0.0  0.00  127.0
2    0.000000       0.000000   0.0  …  0.0       0.0  0.0  0.00    0.0
3   -2.095642       5.441860   2.2  …  0.0       0.0  0.0  0.00    0.0
4    0.000000       0.000000   0.0  …  0.0       0.0  0.0  0.00    0.0
..        …            …   …  …  …       …  …   …    …
342 -0.726531     -10.186047   3.2  …  0.0       0.0  8.0 -0.60  -26.3
343 -1.487197      -9.720930  -4.8  …  0.0       0.0  0.0  0.01    0.0
344 -1.922303      -0.790698   2.7  …  0.0       0.0  2.0 -0.10  -20.0
345  0.000000       0.000000   0.0  …  0.0      10.0  0.0  0.00    3.0
346 -1.256950      -6.558140 -14.0  …  0.0       0.0  6.0  0.60   33.6

     T.Bilirubin  S.creatinine  B.urea     ALP  Puscells
0            0.0           0.0     0.0     0.0       0.0
1            0.0         -13.6    -4.0     0.0       0.0
2            0.0           0.0     0.0     0.0       0.0
3            0.0           0.0     0.0     0.0       0.0
4            0.0           0.0     0.0     0.0       0.0
..           …           …     …     …       …
342         -7.0         -37.0     0.0     0.0       0.0
343         44.8          59.0    78.0  1030.0       0.0
344          5.8         -13.0     0.0     0.0       0.0
345          0.0           0.0     0.0     0.0      -1.0
346         19.1         -30.5    -6.4     0.0       0.0

[328 rows x 22 columns]
```

```
[37]: #Impute categorical variables with mode
      for col in categorical_vars_filtered:
          test_data[col].fillna(test_data[col].mode()[0], inplace = True)
```

```
[38]: #Verification
      test_data.isnull().sum()
```

```
[38]: Hospital        0
      Sample          0
      ICU             0
      OPD             0
      Sex             0
                     ..
      T.Bilirubin     0
      S.creatinine    0
      B.urea          0
```

```
ALP              0
Puscells         0
Length: 172, dtype: int64
```

```
[39]: #Create a new csv after test data preprocessing if needed
      test_data.to_csv('Preprocessed_test_RF.csv' , index = False)
      test_data.shape
```

```
[39]: (328, 172)
```

1.22 Handle column discrepency between train and test data

```
[40]: #Check if both train and test data have the same columns
      train_Final_dropped = train_data.columns.drop('Final')
      missing_cols_test = set(train_Final_dropped) - set(test_data.columns)
      print("Columns in train but not in test:", missing_cols_test)
```

```
Columns in train but not in test: set()
```

```
[41]: #Ensure the column order is the same as in the train data
      test_data = test_data[train_Final_dropped]
```

1.23 Predict test data

```
[42]: y_pred = best_model.predict(test_data)
      print(y_pred.astype(int))
```

```
[1 2 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 1
 2 2 2 2 2 1 1 1 2 2 2 2 1 2 2 1 1 1 2 2 2 2 1 2 2 1 2 2 2 2 2 1 2 2 2 2 2
 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 1 2 2 1 2 1 2 2 2 2 1 2 2 1 2 2 1
 2 2 2 2 2 2 2 2 2 2 2 2 1 2 2 1 2 1 2 2 2 1 1 1 1 2 1 1 1 1 2 2 2 2 2 2 2
 2 2 2 2 1 1 1 1 1 1 2 1 2 1 1 1 1 2 2 1 2 2 2 2 2 2 1 1 1 1 1 2 2 1 1 1 2
 1 2 1 2 1 1 1 1 1 1 1 1 1 1 1 2 2 2 2 2 1 2 2 1 2 2 1 2 2 2 1 2 2 2 1 1 1
 1 1 1 1 2 2 2 2 2 2 2 2 1 2 1 1 1 2 2 2 1 2 2 1 1 2 1 1 1 2 2 2 2 2 1 2 2
 1 2 1 1 1 2 2 1 1 2 1 2 2 2 2 2 2 2 2 1 2 1 2 1 2 1 1 2 2 2 2 2 1 1 2 2 2
 2 2 2 2 2 2 2 1 1 1 1 1 1 1 1 1 1 2 1 2 2 1 2 2 2 2 2 1 2 2 1 2]
```

```
[43]: #Preparing submission file - Logistic Regression
      submission = pd.DataFrame({'ID': range(1, len(y_pred) + 1), 'Final': y_pred})
      submission.to_csv('Predictions_RF.csv', index = False)
```