In [1]:
```
# This Python 3 environment comes with many helpful analytics libraries i
# It is defined by the kaggle/python Docker image: https://github.com/kag
# For example, here's several helpful packages to load

import numpy as np # linear algebra
import pandas as pd # data processing, CSV file I/O (e.g. pd.read_csv)

# Input data files are available in the read-only "../input/" directory
# For example, running this (by clicking run or pressing Shift+Enter) wil

import os
for dirname, _, filenames in os.walk('/kaggle/input'):
    for filename in filenames:
        print(os.path.join(dirname, filename))

# You can write up to 20GB to the current directory (/kaggle/working/) th
# You can also write temporary files to /kaggle/temp/, but they won't be
```

```
/kaggle/input/acute-nephritis/diagnosis.csv
```

In [2]:
```
import os
print(os.listdir("../input"))
```

```
['acute-nephritis']
```

In [3]:
```
import numpy as np
import pandas as pd


name = ['Temperature of patient', 'Occurrence of nausea', 'Lumbar pain',
       'Burning of urethra, itch, swelling of urethra outlet ', 'decisior
       'decision: Nephritis of renal pelvis origin']


df = pd.read_csv('../input/acute-nephritis/diagnosis.csv', names = name,
df.head()
```

Out [3]:

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet	decision: Inflammation of urinary bladder	decision: Nephritis of renal pelvis origin
0	35.5	no	yes	no	no	no	no	no
1	35.9	no	no	yes	yes	yes	yes	no
2	35.9	no	yes	no	no	no	no	no
3	36.0	no	no	yes	yes	yes	yes	no

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet	decision: Inflammation of urinary bladder	decision: Nephritis of renal pelvis origin
4	36.0	no	yes	no	no	no	no	no

In [4]:
```
df.tail()
```

Out [4]:

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet	decision: Inflammation of urinary bladder	decision: Nephritis of renal pelvis origin
115	41.4	no	yes	yes	no	yes	no	yes
116	41.5	no	no	no	no	no	no	no
117	41.5	yes	yes	no	yes	no	no	yes
118	41.5	no	yes	yes	no	yes	no	yes
119	41.5	no	yes	yes	no	yes	no	yes

In [5]:
```
df.shape
```

Out [5]:
```
(120, 8)
```

In [6]:
```
df.describe()
```

Out [6]:

	Temperature of patient
count	120.000000
mean	38.724167
std	1.819132
min	35.500000
25%	37.100000
50%	37.950000
75%	40.600000
max	41.500000

In [7]:
```
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 120 entries, 0 to 119
Data columns (total 8 columns):
 #   Column                                                Non-Null Count  Dtype  
---  ------                                                --------------  -----  
 0   Temperature of patient                                120 non-null    float64
 1   Occurrence of nausea                                  120 non-null    object 
 2   Lumbar pain                                           120 non-null    object 
 3   Urine pushing                                         120 non-null    object 
 4   Micturition pains                                     120 non-null    object 
 5   Burning of urethra, itch, swelling of urethra outlet  120 non-null    object 
 6   decision: Inflammation of urinary bladder             120 non-null    object 
```

```
 7   decision: Nephritis of renal pelvis origin            120 non-null    object
dtypes: float64(1), object(7)
memory usage: 7.6+ KB
```

In [8]:
```
df.isnull().sum()
```

Out [8]:
```
Temperature of patient                                  0
Occurrence of nausea                                    0
Lumbar pain                                             0
Urine pushing                                           0
Micturition pains                                       0
Burning of urethra, itch, swelling of urethra outlet    0
decision: Inflammation of urinary bladder               0
decision: Nephritis of renal pelvis origin              0
dtype: int64
```

In [9]:
```
df['decision: Inflammation of urinary bladder'].value_counts()
```

Out [9]:
```
no     61
yes    59
Name: decision: Inflammation of urinary bladder, dtype: int64
```

In [10]:
```
df['decision: Nephritis of renal pelvis origin'].value_counts()
```

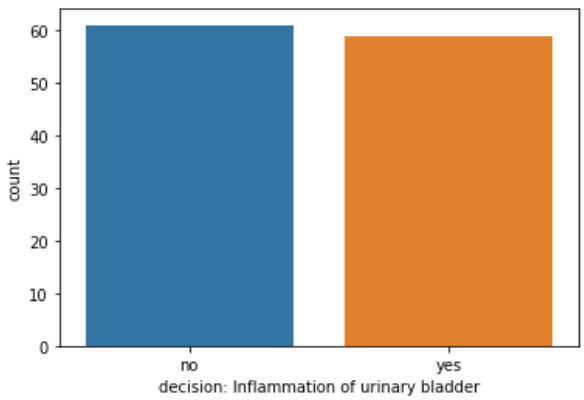
Out [10]:
```
no     70
yes    50
Name: decision: Nephritis of renal pelvis origin, dtype: int64
```

In [11]:
```
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline

sns.countplot(df['decision: Inflammation of urinary bladder'])
```

```
/opt/conda/lib/python3.7/site-packages/seaborn/_decorators.py:43: FutureWarning: Pass
the following variable as a keyword arg: x. From version 0.12, the only valid positional
argument will be `data`, and passing other arguments without an explicit keyword will
result in an error or misinterpretation.
  FutureWarning
```

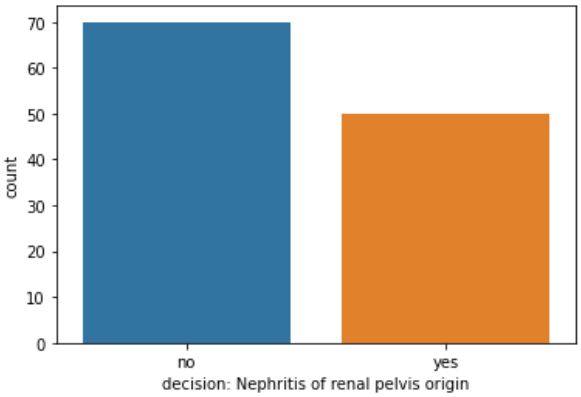
Out [11]:
```
<AxesSubplot:xlabel='decision: Inflammation of urinary bladder', ylabel='count'>
```



In [12]:
```
sns.countplot(df['decision: Nephritis of renal pelvis origin'])
```

```
/opt/conda/lib/python3.7/site-packages/seaborn/_decorators.py:43: FutureWarning: Pass
the following variable as a keyword arg: x. From version 0.12, the only valid positional
argument will be `data`, and passing other arguments without an explicit keyword will
result in an error or misinterpretation.
  FutureWarning
```

Out [12]:
```
<AxesSubplot:xlabel='decision: Nephritis of renal pelvis origin', ylabel='count'>
```



In [13]:
```
from sklearn.preprocessing import LabelEncoder

le = LabelEncoder()

for i in df.columns[0:] :
    df[i] = le.fit_transform(df[i])
```

In [14]:
```
df.head()
```

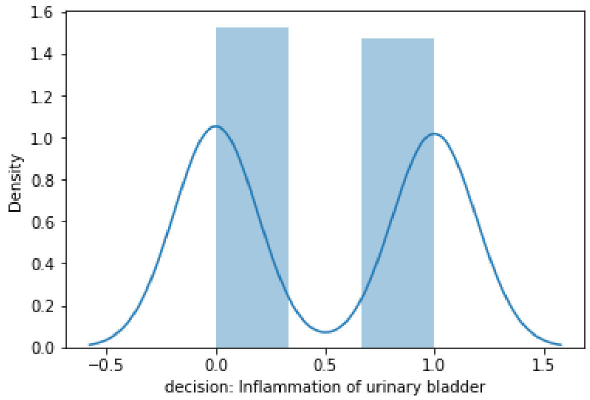
Out [14]:

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet	decision: Inflammation of urinary bladder	decision: Nephritis of renal pelvis origin
0	0	0	1	0	0	0	0	0
1	1	0	0	1	1	1	1	0
2	1	0	1	0	0	0	0	0
3	2	0	0	1	1	1	1	0
4	2	0	1	0	0	0	0	0

In [15]:
```
sns.distplot(df['decision: Inflammation of urinary bladder'])
```

```
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

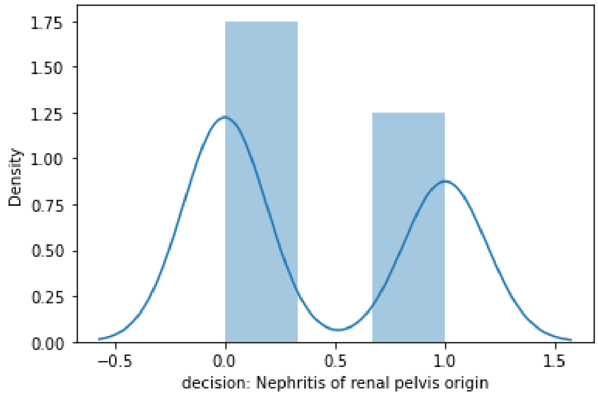
Out [15]: <AxesSubplot:xlabel='decision: Inflammation of urinary bladder', ylabel='Density'>



In [16]:
```
sns.distplot(df['decision: Nephritis of renal pelvis origin'])
```

```
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

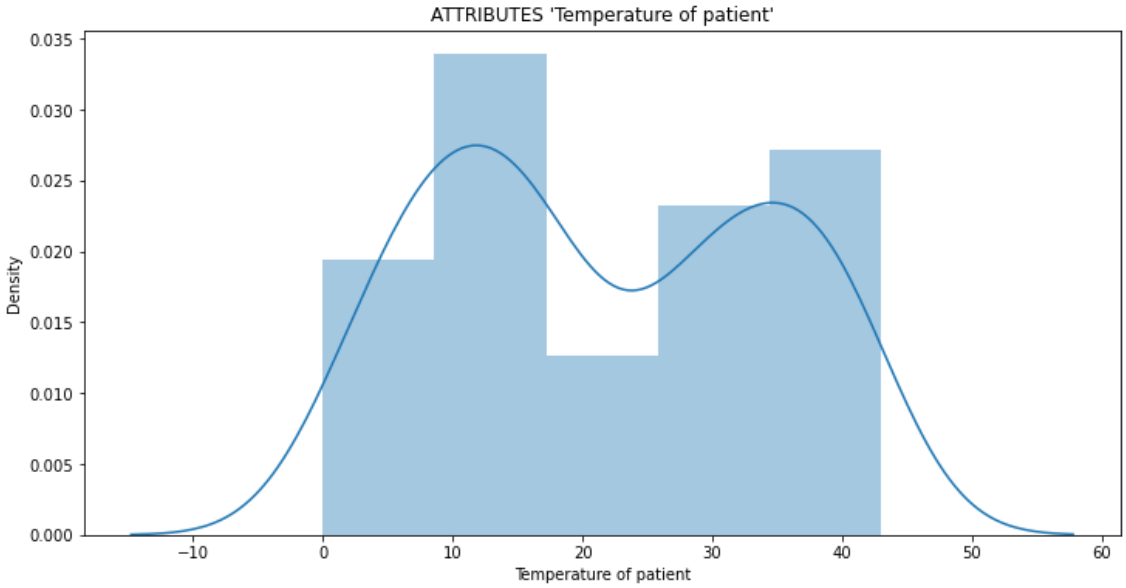
Out [16]: <AxesSubplot:xlabel='decision: Nephritis of renal pelvis origin', ylabel='Density'>

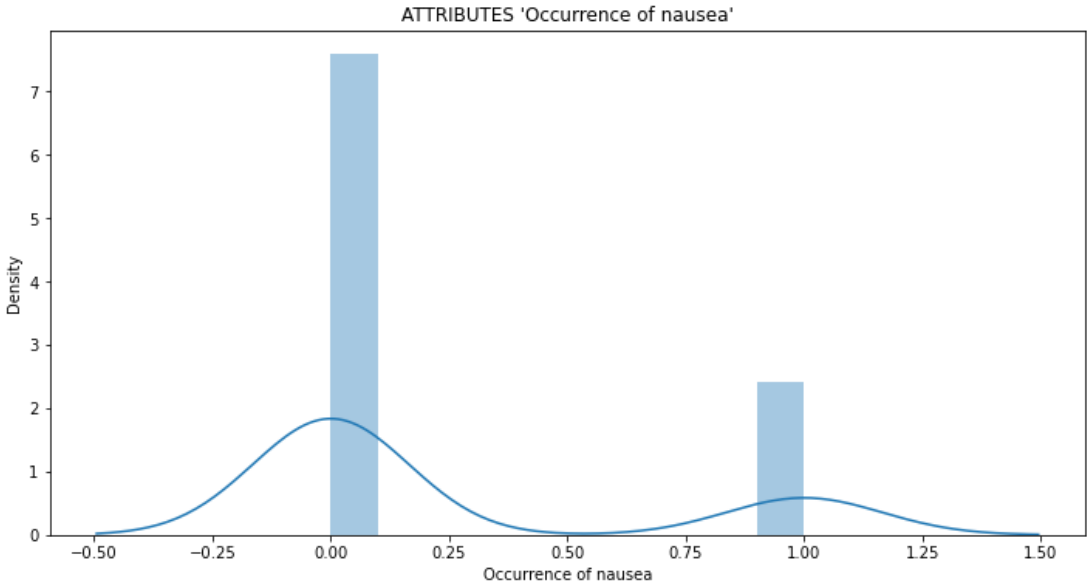


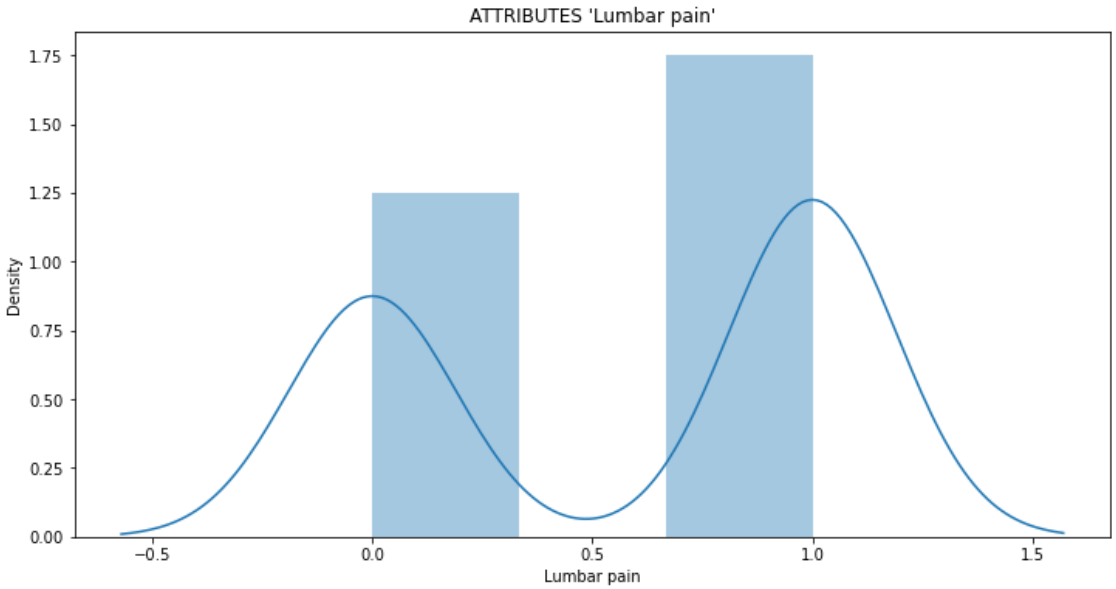
In [17]:
```
for i in df.columns[:-1]:
    plt.figure(figsize=(12,6))
    plt.title("ATTRIBUTES '%s'"%i)
    sns.distplot(df[i])
```

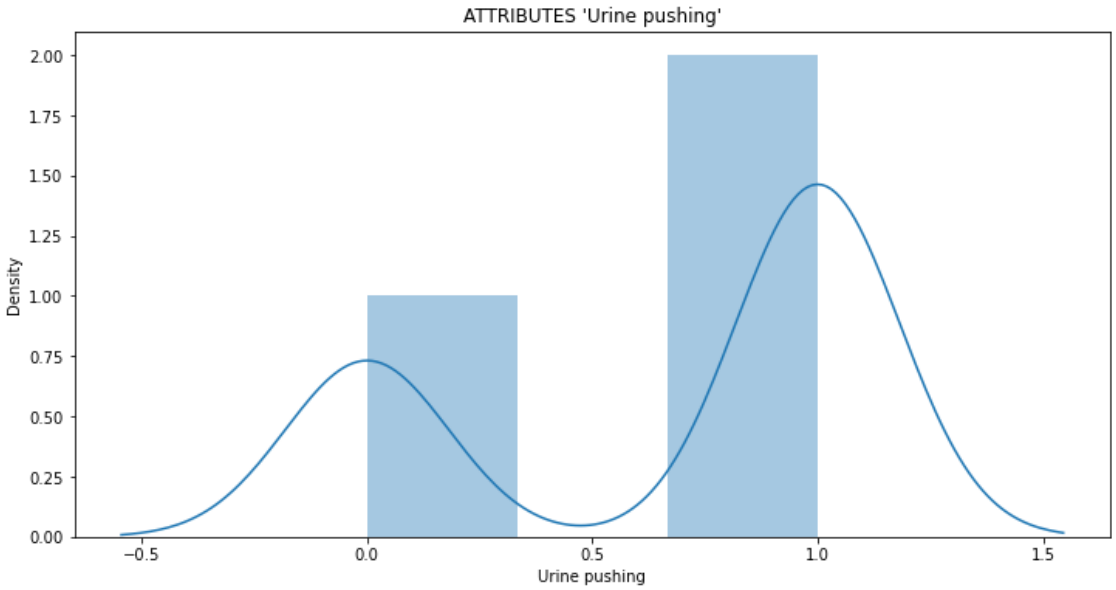
```
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

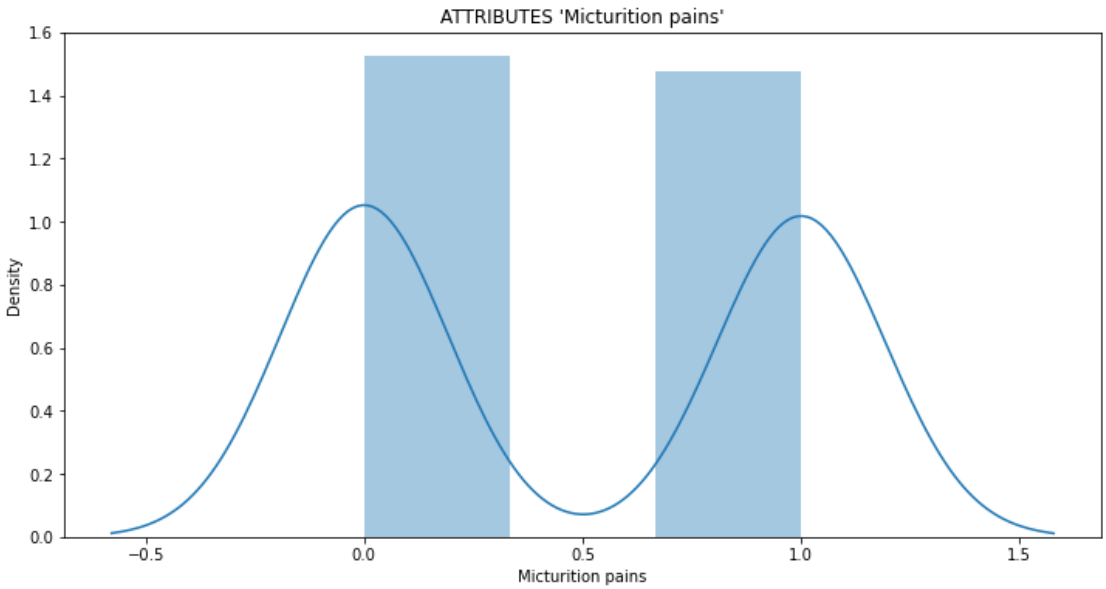
```
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
/opt/conda/lib/python3.7/site-packages/seaborn/distributions.py:2557: FutureWarning:
`distplot` is a deprecated function and will be removed in a future version. Please
adapt your code to use either `displot` (a figure-level function with similar
flexibility) or `histplot` (an axes-level function for histograms).
  warnings.warn(msg, FutureWarning)
```

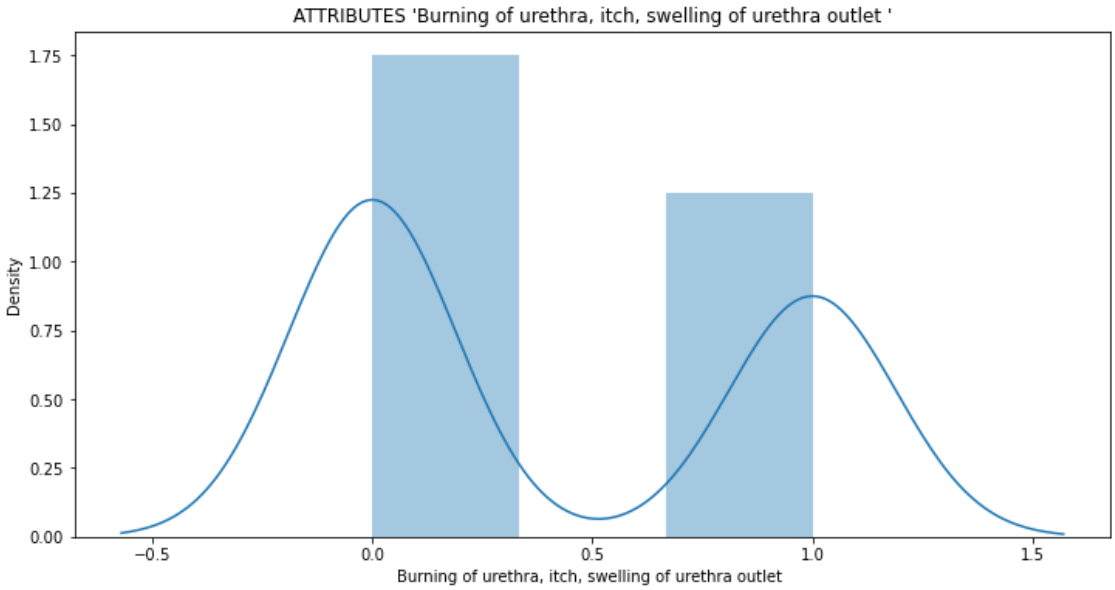


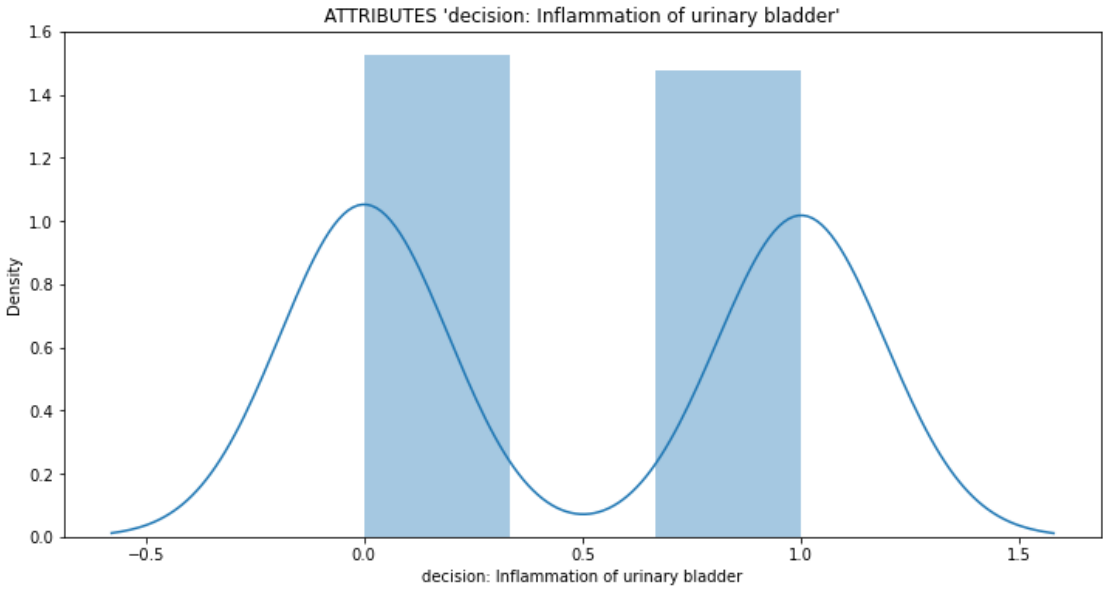



ATTRIBUTES 'Lumbar pain'
Density
Lumbar pain


ATTRIBUTES 'Urine pushing'
Density
Urine pushing

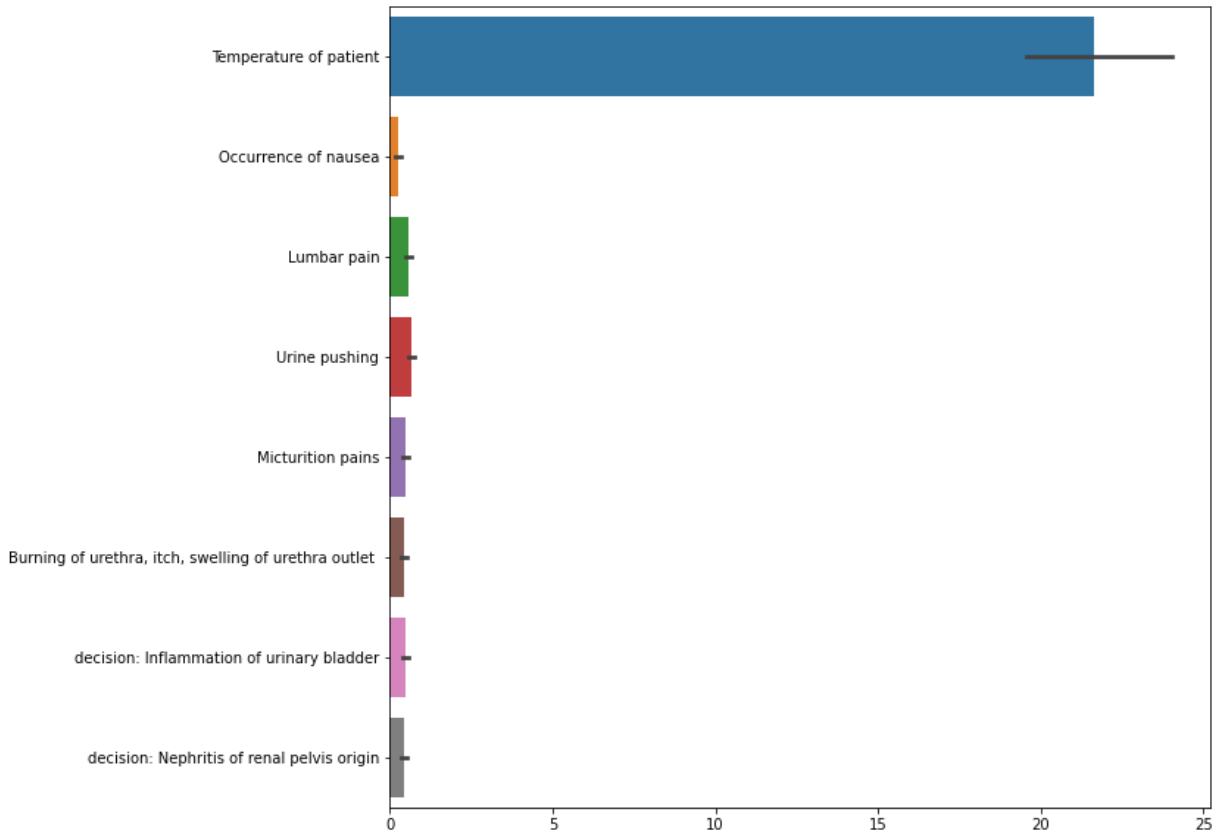

ATTRIBUTES 'Micturition pains'
Density
Micturition pains





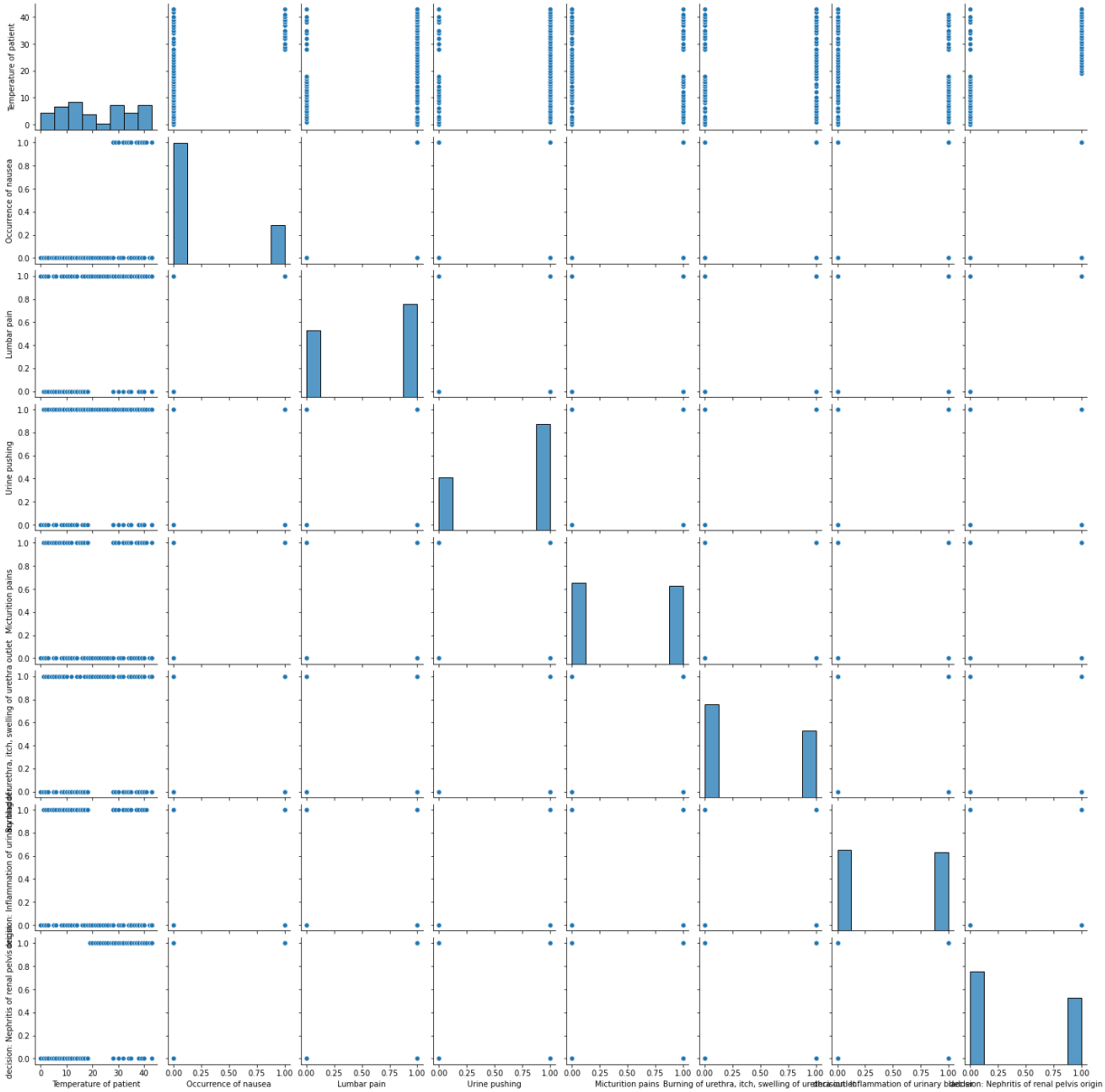
In [18]:
```
plt.figure(figsize=(10, 10))
sns.barplot(data = df, orient='h')
```

Out [18]: <AxesSubplot:>



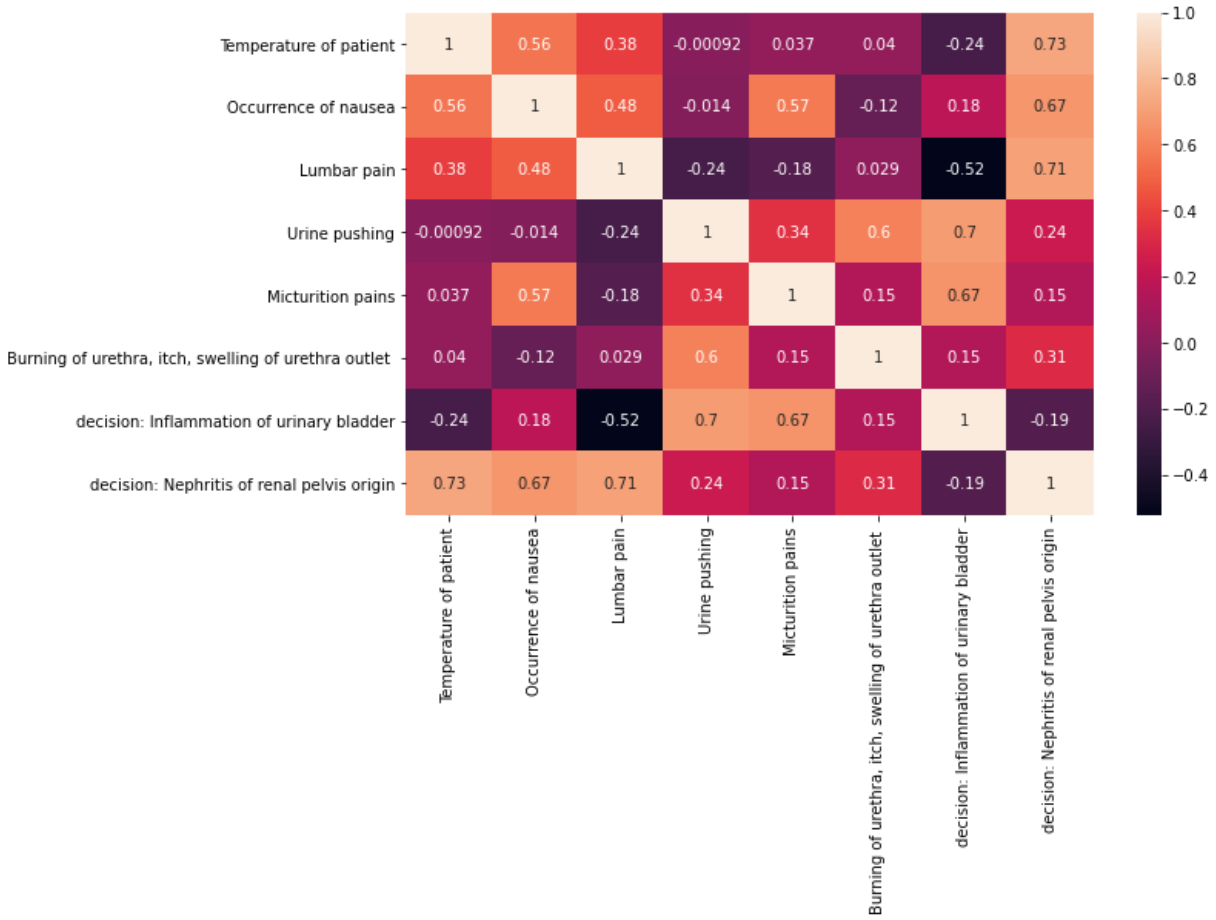
In [19]:
```
sns.pairplot(data=df)
```

Out [19]: <seaborn.axisgrid.PairGrid at 0x7f3680c8bd90>



In [20]:
```
fig = plt.figure(figsize=(10,6))
sns.heatmap(df.corr(), annot=True)
```

Out [20]: <AxesSubplot:>



In [21]:
```
M = df
M.head()
```

Out [21]:

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet	decision: Inflammation of urinary bladder	decision: Nephritis of renal pelvis origin
0	0	0	1	0	0	0	0	0
1	1	0	0	1	1	1	1	0
2	1	0	1	0	0	0	0	0
3	2	0	0	1	1	1	1	0
4	2	0	1	0	0	0	0	0

In [22]:
```
X = M.drop(['decision: Inflammation of urinary bladder', 'decision: Nephr
           axis="columns")
X.head()
```

Out [22]:

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet
0	0	0	1	0	0	0
1	1	0	0	1	1	1
2	1	0	1	0	0	0

	Temperature of patient	Occurrence of nausea	Lumbar pain	Urine pushing	Micturition pains	Burning of urethra, itch, swelling of urethra outlet
3	2	0	0	1	1	1
4	2	0	1	0	0	0

In [23]:
```
y = M['decision: Inflammation of urinary bladder']
y.head()
```

Out [23]:
```
0    0
1    1
2    0
3    1
4    0
Name: decision: Inflammation of urinary bladder, dtype: int64
```

In [24]:
```
z = M['decision: Nephritis of renal pelvis origin']
z.head()
```

Out [24]:
```
0    0
1    0
2    0
3    0
4    0
Name: decision: Nephritis of renal pelvis origin, dtype: int64
```

In [25]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
```

In [26]:
```
from sklearn.naive_bayes import GaussianNB

model = GaussianNB()

model.fit(X_train, y_train)
```

Out [26]:
```
GaussianNB()
```

In [27]:
```
model.score(X_test, y_test)
```

Out [27]:
```
0.9166666666666666
```

In [ ]:
```

```

In [28]:
```
from sklearn.tree import DecisionTreeClassifier

dtc = DecisionTreeClassifier()

dtc.fit(X_train, y_train)
```

Out [28]:
```
DecisionTreeClassifier()
```

In [29]:
```
dtc.score(X_test, y_test)
```

Out [29]:
```
1.0
```

In [ ]:
```

```

In [30]:
```
from sklearn.model_selection import train_test_split
X_train, X_test, z_train, z_test = train_test_split(X, z, test_size=0.2)
```

In [31]:
```
from sklearn.naive_bayes import GaussianNB

clf = GaussianNB()

clf.fit(X_train, z_train)
```

Out [31]: GaussianNB()

In [32]:
```
clf.score(X_test, z_test)
```

Out [32]: 1.0

In [ ]:
```

```

In [33]:
```
from sklearn.ensemble import RandomForestClassifier

rfc = RandomForestClassifier()

rfc.fit(X_train, z_train)
```

Out [33]: RandomForestClassifier()

In [34]:
```
rfc.score(X_test, z_test)
```

Out [34]: 1.0

In [ ]:
```

```