Лабораторная работа №2. Обработка признаков, ч.1

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Импорт библиотек

In [1]:

```
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import scipy.stats as stats
from sklearn.impute import KNNImputer
from sklearn.preprocessing import OneHotEncoder
%matplotlib inline
```

Загрузка и просмотр датасета

Датасет содержит данные о качестве питьевой воды в 3276 водоемах мира. Для анализа качества используются 9 числовых показателей, таких как pH, жесткость и концентрация различных вредных веществ.

In [2]:

```
data = pd.read_csv('/content/drive/MyDrive/MMO/water_potability.csv')
```

In [3]:

```
data.shape
```

Out[3]:

```
(3276, 10)
```

In [4]:

```
data.head()
```

Out[4]:

	ph	Hardness	Solids	Chloramines	Sulfate	Conductivity	Organic_carbon	Trihalomethanes	Turbidity	Potability
0	NaN	204.890455	20791.318981	7.300212	368.516441	564.308654	10.379783	86.990970	2.963135	0
1	3.716080	129.422921	18630.057858	6.635246	NaN	592.885359	15.180013	56.329076	4.500656	0
2	8.099124	224.236259	19909.541732	9.275884	NaN	418.606213	16.868637	66.420093	3.055934	0
3	8.316766	214.373394	22018.417441	8.059332	356.886136	363.266516	18.436524	100.341674	4.628771	0
4	9.092223	181.101509	17978.986339	6.546600	310.135738	398.410813	11.558279	31.997993	4.075075	0

In [5]:

```
data = data.iloc[:,:-1]
```

1. Заполнение пропусков

Заполним пропуски с применением `KNNImputer`

In [6]:

```
# Количество пропусков
missing_values = [(i, data[i].isnull().sum()) for i in data.columns if data[i].isnull().sum() != 0]
missing_values
```

Out[6]:

```
[('ph', 491), ('Sulfate', 781), ('Trihalomethanes', 162)]
```

In [7]:

```
cols_to_impute = [i[0] for i in missing_values]
cols_to_impute
```

Out[7]:

```
['ph', 'Sulfate', 'Trihalomethanes']
```

In [8]:

```
data_to_impute = data[cols_to_impute]
data_to_impute
```

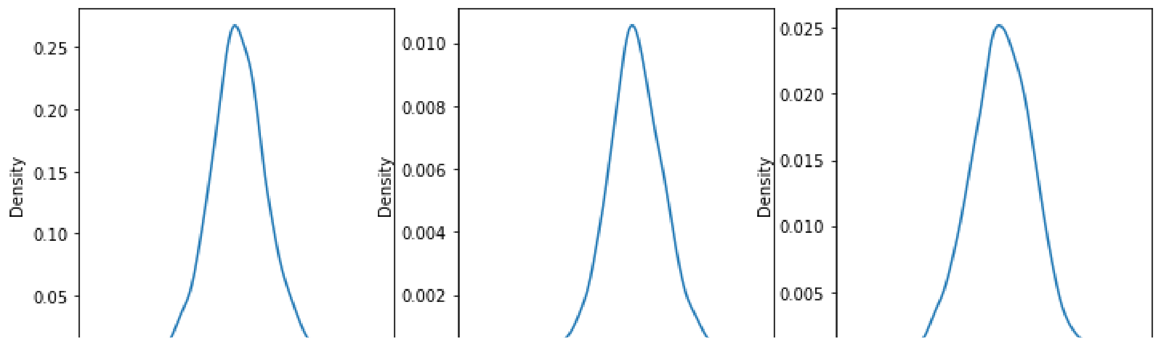
Out[8]:

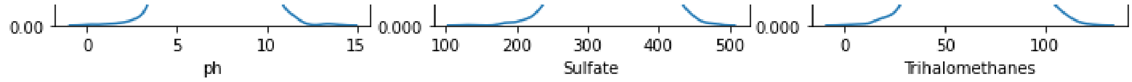
	ph	Sulfate	Trihalomethanes
0	NaN	368.516441	86.990970
1	3.716080	NaN	56.329076
2	8.099124	NaN	66.420093
3	8.316766	356.886136	100.341674
4	9.092223	310.135738	31.997993
...	...	...	...
3271	4.668102	359.948574	66.687695
3272	7.808856	NaN	NaN
3273	9.419510	NaN	69.845400
3274	5.126763	NaN	77.488213
3275	7.874671	NaN	78.698446

3276 rows × 3 columns

In [9]:

```
n_cols = 3
n_rows = 1
fig, axes = plt.subplots(nrows=n_rows, ncols=n_cols, figsize=(12, 4))
for i, column in enumerate(data_to_impute):
  sns.kdeplot(data_to_impute[column], ax=axes[i%n_cols])
```





In [10]:

```
imputer = KNNImputer(n_neighbors=3)
temp_data = pd.DataFrame(imputer.fit_transform(data))
temp_data.columns = data.columns
imputed_data = temp_data[cols_to_impute]
imputed_data.columns = ["KKN_3_{}".format(i) for i in imputed_data.columns]
imputed_data
```

Out[10]:

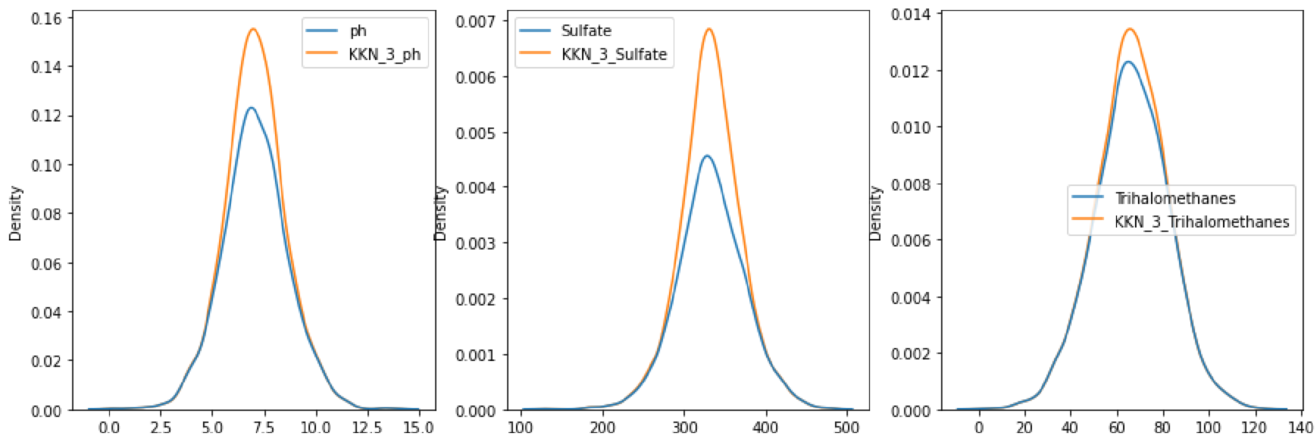
	KKN_3_ph	KKN_3_Sulfate	KKN_3_Trihalomethanes
0	6.655223	368.516441	86.990970
1	3.716080	351.285226	56.329076
2	8.099124	347.323743	66.420093
3	8.316766	356.886136	100.341674
4	9.092223	310.135738	31.997993
...	...	...	...
3271	4.668102	359.948574	66.687695
3272	7.808856	368.086095	56.689055
3273	9.419510	316.571962	69.845400
3274	5.126763	334.293598	77.488213
3275	7.874671	333.330087	78.698446

3276 rows × 3 columns

In [11]:

```
new_data = data_to_impute.join(imputed_data)

n_rows = 1
n_cols = 3
fig, axes = plt.subplots(nrows=n_rows, ncols=n_cols, figsize=(15, 5))
for i in range(len(data_to_impute.columns)):
  sns.kdeplot(data=new_data.iloc[:, [i, i+3]], ax=axes[i])
```



In [12]:

```
data = data.join(imputed_data)

data = data.drop(['ph', 'Sulfate', 'Trihalomethanes'], axis=1)
```

2. Нормализация числовых признаков

Проанализируем схожесть распределений числовых признаков с нормальным распределением

In [13]:

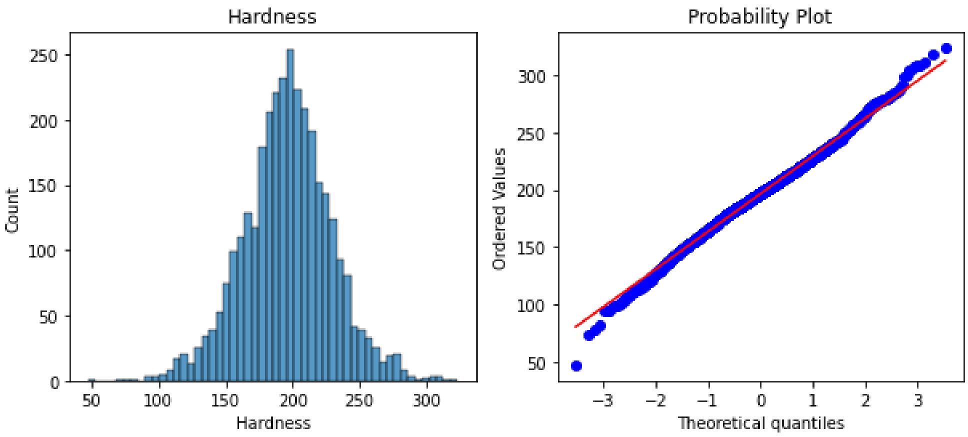
```
def diagnostic_plots(column):
  fig, axes = plt.subplots(nrows=1, ncols=2, figsize=(10, 4))
  plt.axes(axes[0])
  plt.title(column)
  sns.histplot(data[column], ax=axes[0])
  stats.probplot(data[column], dist='norm', plot=axes[1])
```

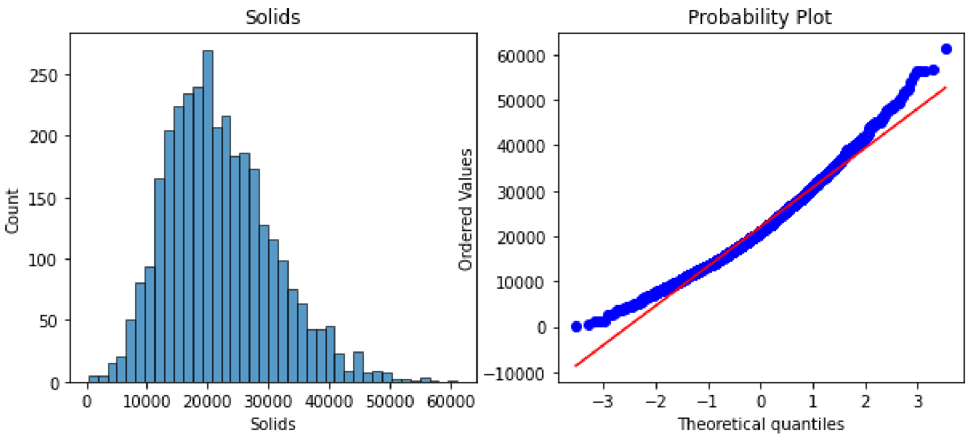
In [14]:

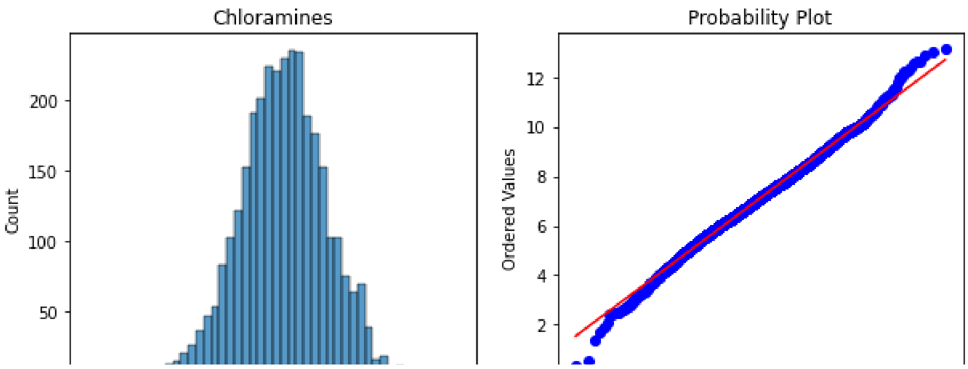
```
[diagnostic_plots(column) for column in data]
```

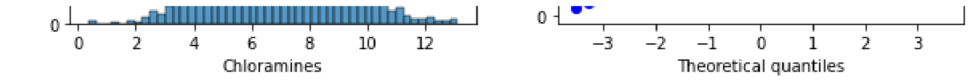
Out[14]:

```
[None, None, None, None, None, None, None, None, None]
```

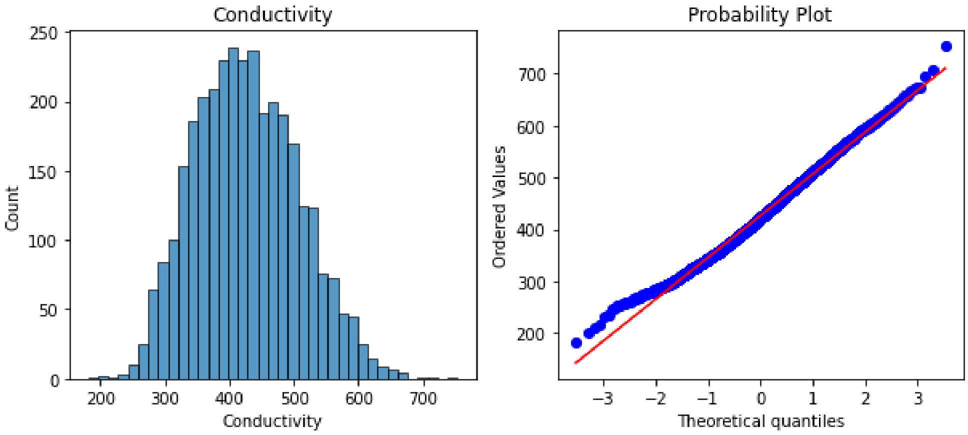




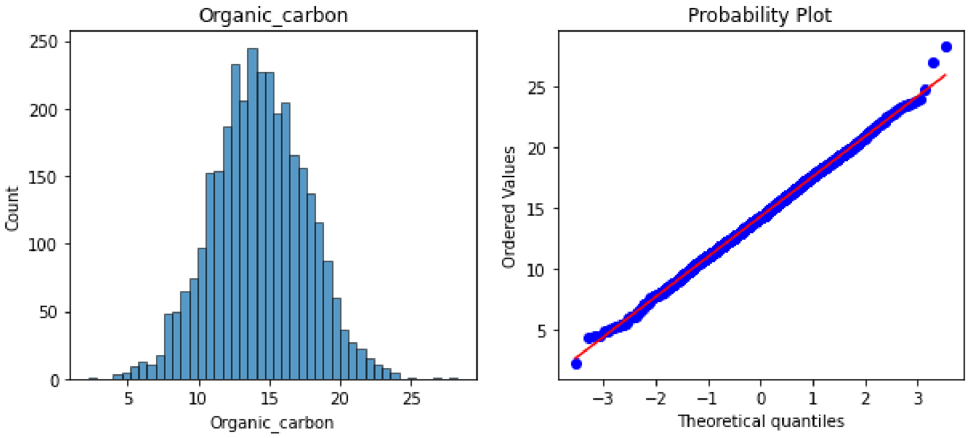




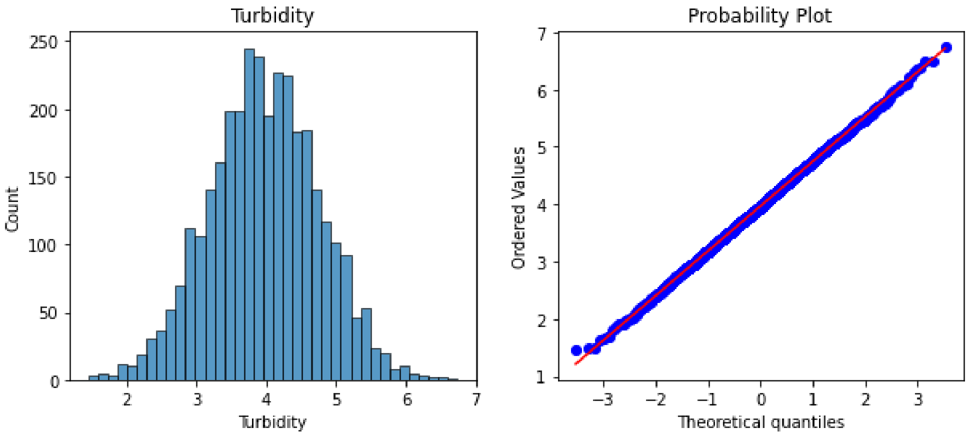
Chloramines
Theoretical quantiles



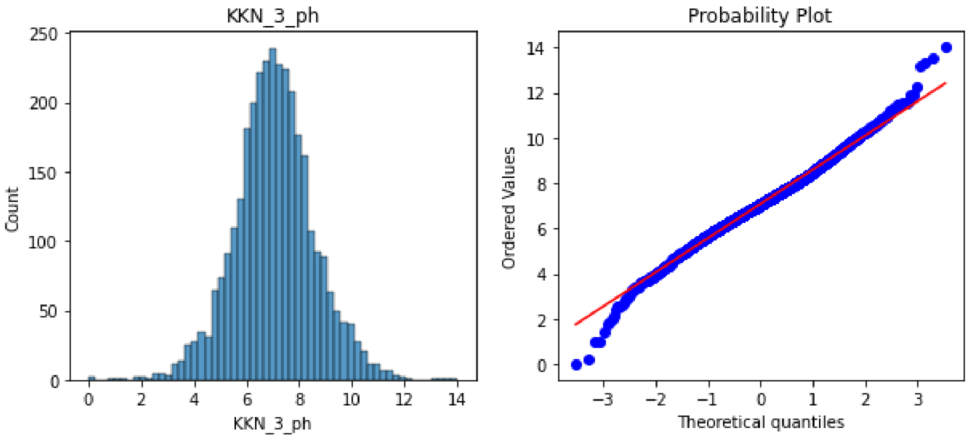
Conductivity
Count
Probability Plot
Ordered Values
Theoretical quantiles



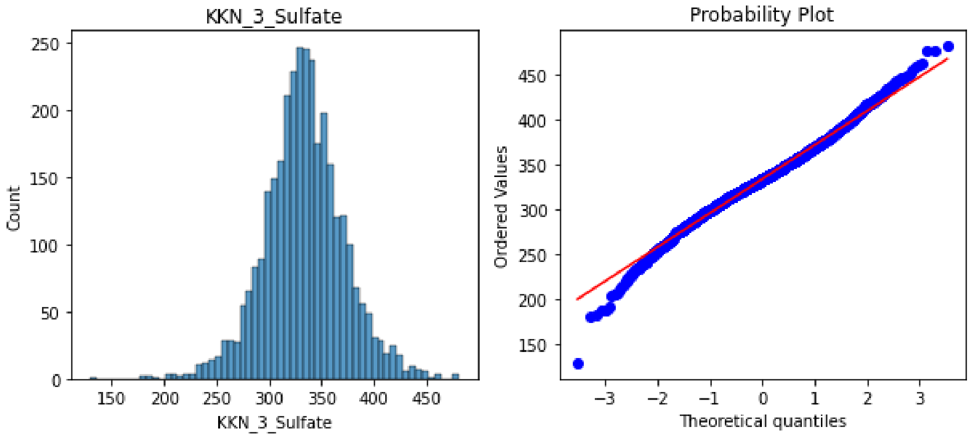
Organic_carbon
Count
Probability Plot
Ordered Values
Theoretical quantiles

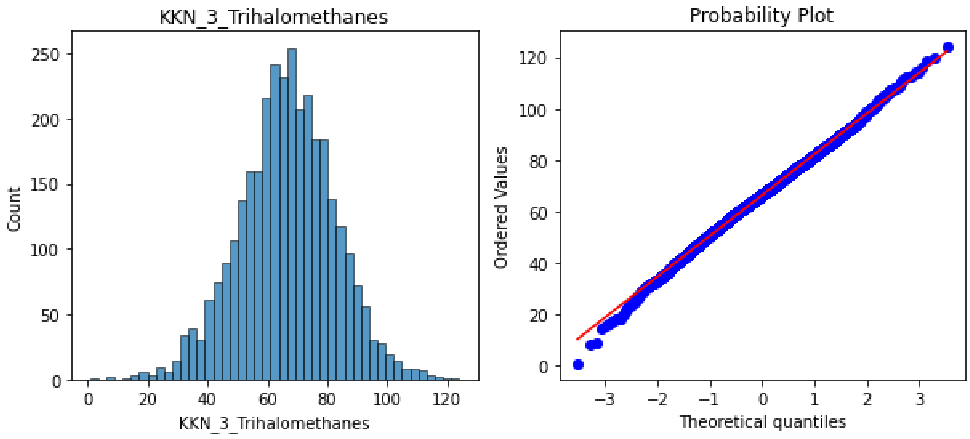


Turbidity
Count
Probability Plot
Ordered Values
Theoretical quantiles



KKN_3_ph
Count
Probability Plot
Ordered Values
Theoretical quantiles



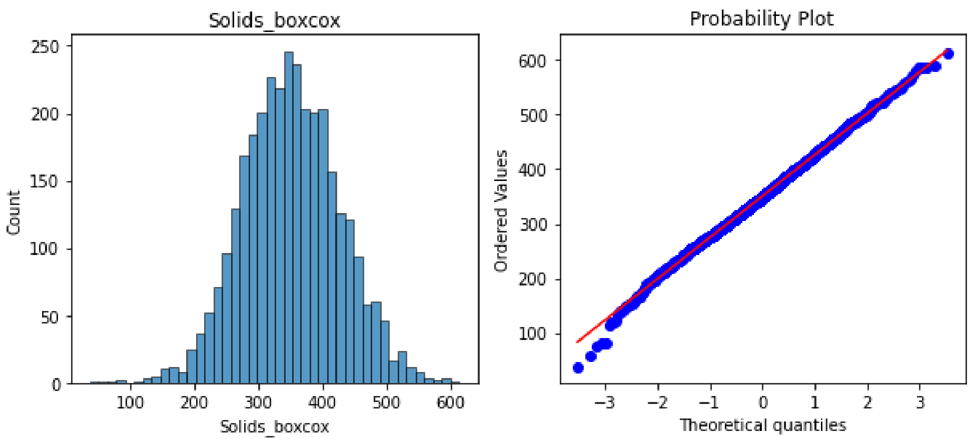


Признак `Solids` обладает распределением, наиболее отличным от нормального. Именно его и следует нормализовать.

In [15]:

```
data['Solids_boxcox'], param = stats.boxcox(data['Solids'])
print('Оптимальное значение λ = {}'.format(param))
diagnostic_plots('Solids_boxcox')
```

```
Оптимальное значение λ = 0.5239560378014094
```



3. Кодирование категориальных признаков

In [16]:

```
data = pd.read_csv('/content/drive/MyDrive/MMO/games.csv')
```

In [17]:

```
data['winner'].value_counts()
```

Out[17]:

```
white    10001
black     9107
draw       950
Name: winner, dtype: int64
```

In [18]:

```
ohe = OneHotEncoder()
ohe_matrix = ohe.fit_transform(data[['winner']])
ohe_matrix
```

Out[18]:

```
<20058x3 sparse matrix of type '<class 'numpy.float64'>'
 with 20058 stored elements in Compressed Sparse Row format>
```

In [19]:

```
data['winner'][:10]
```

Out[19]:

```
0    white
1    black
2    white
3    white
4    white
5     draw
6    white
7    black
8    black
9    white
Name: winner, dtype: object
```

In [20]:

```
ohe_matrix.todense()[:10]
```

Out[20]:

```
matrix([[0., 0., 1.],
        [1., 0., 0.],
        [0., 0., 1.],
        [0., 0., 1.],
        [0., 0., 1.],
        [0., 1., 0.],
        [0., 0., 1.],
        [1., 0., 0.],
        [1., 0., 0.],
        [0., 0., 1.]])
```

In [21]:

```
pd.get_dummies(data[['winner']])[:10]
```

Out[21]:

	winner_black	winner_draw	winner_white
0	0	0	1
1	1	0	0

	winner_black	winner_draw	winner_white
2	0	0	1
3	0	0	1
4	0	0	1
5	0	1	0
6	0	0	1
7	1	0	0
8	1	0	0
9	0	0	1