```python
import pandas as pd
import numpy as np
import seaborn as sb
import time


train = pd.read_csv("training_data.csv")
test = pd.read_csv('test_data.csv')

train['created_at'] = pd.to_datetime(train['created_at'], errors='coerce')
test['created_at'] = pd.to_datetime(test['created_at'], errors='coerce')
test = test.loc[:, ~test.columns.str.contains('^Unnamed')]
```

```python
train.sample(9)
```

	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
6329	6329	Chloride	104.90	mmol/l	2019-09-13 06:43:54.507890+00:00	107.00	98.00	child	male
6504	6504	Sodium	142.30	mmol/l	2019-06-13 12:08:54.068000	145.00	136.00	adult	male
2871	2871	WBC	6.93	x 10³ / µl	2019-01-26 12:31:05.757000	10.00	4.00	adult	male
1776	1776	Chloride	98.00	mmol/l	2019-11-24 20:30:54.288000	107.00	98.00	adult	male
6992	6992	T4	6.00	µg/dl	2019-09-03 12:33:25.260000	12.00	4.50	old	male
2560	2560	Sodium	140.00	mmol/l	2019-11-29 08:38:20.811713+00:00	145.00	135.00	old	male
2496	2496	T4	9.70	µg/dl	2019-11-25 05:59:30.922351+00:00	11.72	4.87	child	male
8609	8609	SGPT	52.00	u/l	2019-04-14 13:22:57.407000	45.00	0.00	adult	male
7418	7418	SGPT	36.00	u/l	2019-09-01 14:17:17.519000	55.00	0.00	adult	male

Info about dataset

```python
train.describe().T
```

	count	mean	std	min	25%	50%	75%	max
patient_id	10000.0	4999.500000	2886.895680	0.00	2499.75	4999.50	7499.25	9999.0
parameter_value	10000.0	356.897325	9289.389443	-71.00	6.70	8.83	101.00	920000.0
reference_high	10000.0	372.848728	1800.575300	1.12	10.00	12.00	107.00	15000.0
reference_low	10000.0	162.951938	712.506331	0.00	4.00	4.50	98.00	5000.0

```python
test.describe().T
```

	count	mean	std	min	25%	50%	75%	max
patient_id	10000.0	4999.500000	2886.895680	0.00	2499.75	4999.500	7499.25	9999.0
parameter_value	10000.0	198.373268	1382.265136	0.05	7.10	9.575	100.00	40250.0
reference_high	10000.0	250.165145	1429.726809	1.12	10.00	12.000	107.00	11000.0
reference_low	10000.0	112.542141	562.232336	0.00	4.00	4.500	98.00	4300.0

```python
train.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 10000 entries, 0 to 9999
Data columns (total 9 columns):
 #   Column                       Non-Null Count  Dtype
---  ------                       --------------  -----
 0   patient_id                   10000 non-null  int64
 1   standard_lab_parameter_name  10000 non-null  object
 2   parameter_value              10000 non-null  float64
 3   unit                         10000 non-null  object
 4   created_at                   7057 non-null   object
 5   reference_high               10000 non-null  float64
 6   reference_low                10000 non-null  float64
 7   age_group                    10000 non-null  object
 8   gender                       10000 non-null  object
dtypes: float64(3), int64(1), object(5)
memory usage: 703.2+ KB
```

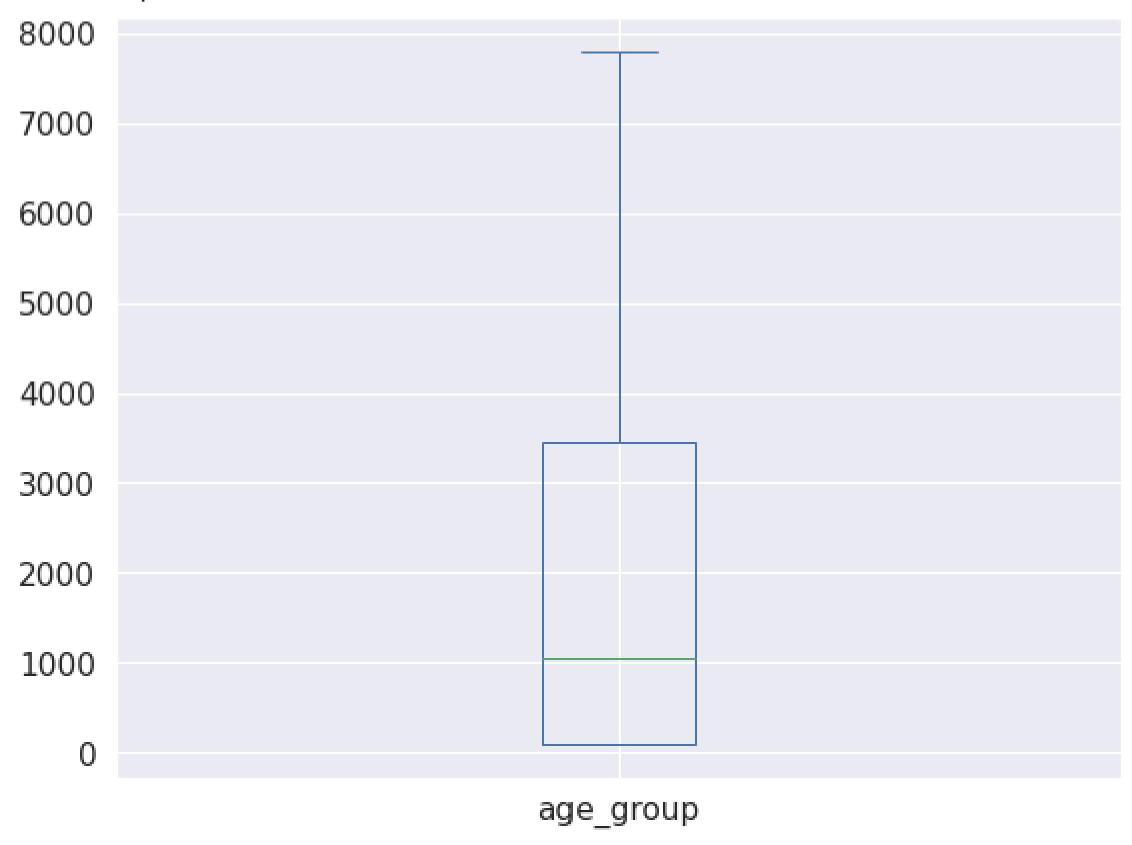
Visualize Age Group

```python
train['age_group'].value_counts().plot(kind='pie',figsize=(9,7))
```

```
<AxesSubplot:ylabel='age_group'>
```

```
train['age_group'].value_counts().plot(kind='box',figsize=(9,7))
```

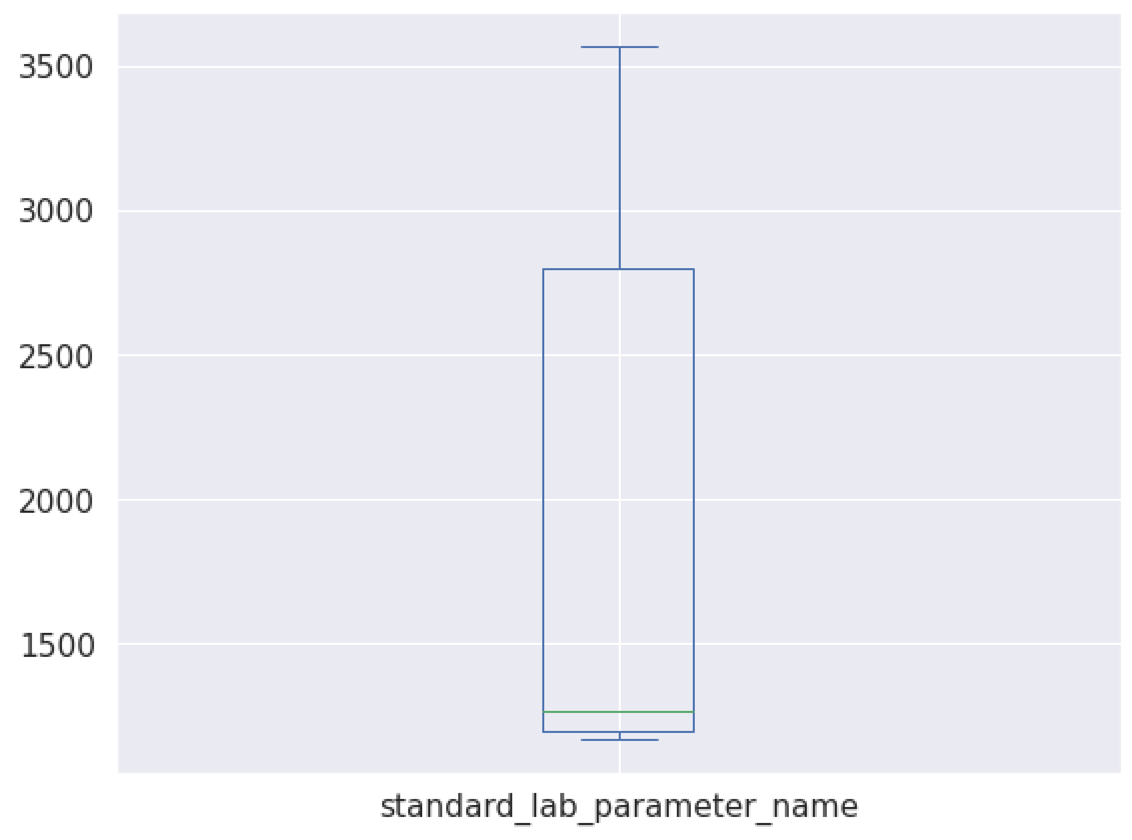
```
<AxesSubplot:>
```



Visualize Lab Parameter

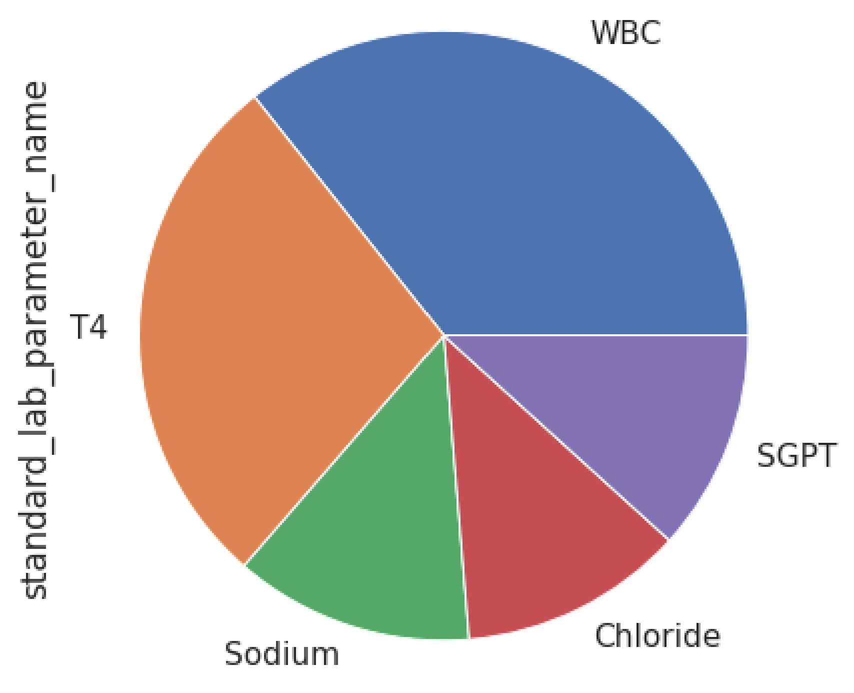
```
train['standard_lab_parameter_name'].value_counts().plot(kind='box',figsize=(9,7))
```

```
<AxesSubplot:>
```



```
train['standard_lab_parameter_name'].value_counts().plot(kind='pie',figsize=(9,7))
```

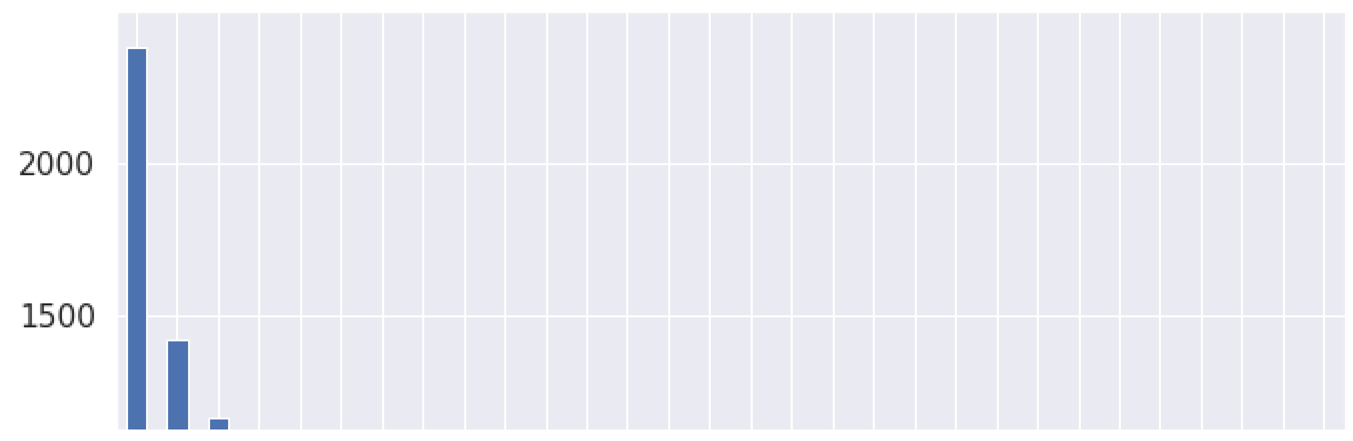
```
<AxesSubplot:ylabel='standard_lab_parameter_name'>
```



Visualize Units in dataset

```
train.unit.value_counts().plot(kind='bar',figsize=(11,7))
```

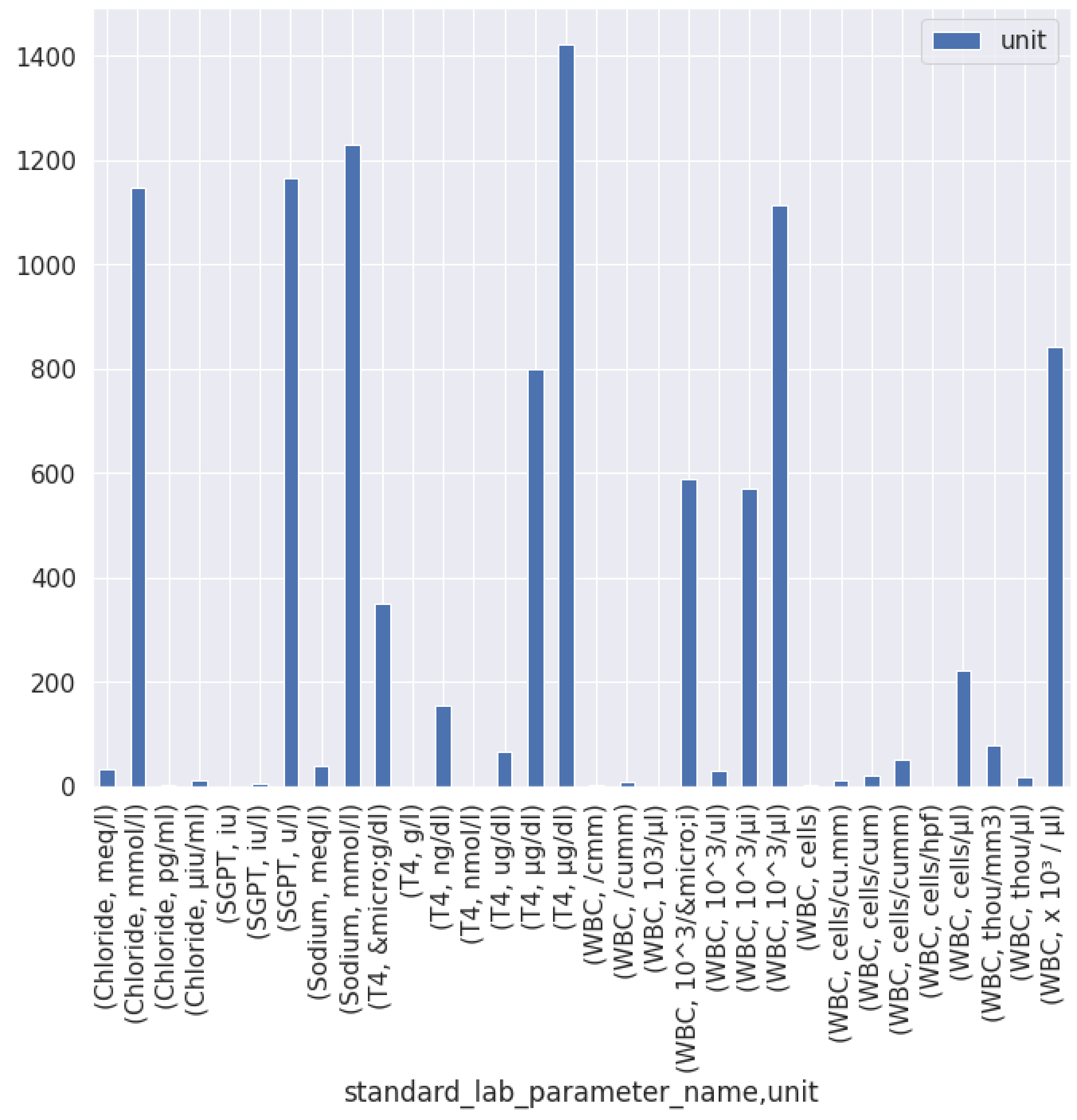
```
<AxesSubplot:>
```



Visualize unit and lab parameters

```
train.groupby(['standard_lab_parameter_name',"unit"]).agg({"unit":"count"}).plot(kind='bar',figsize=(11,9))
```

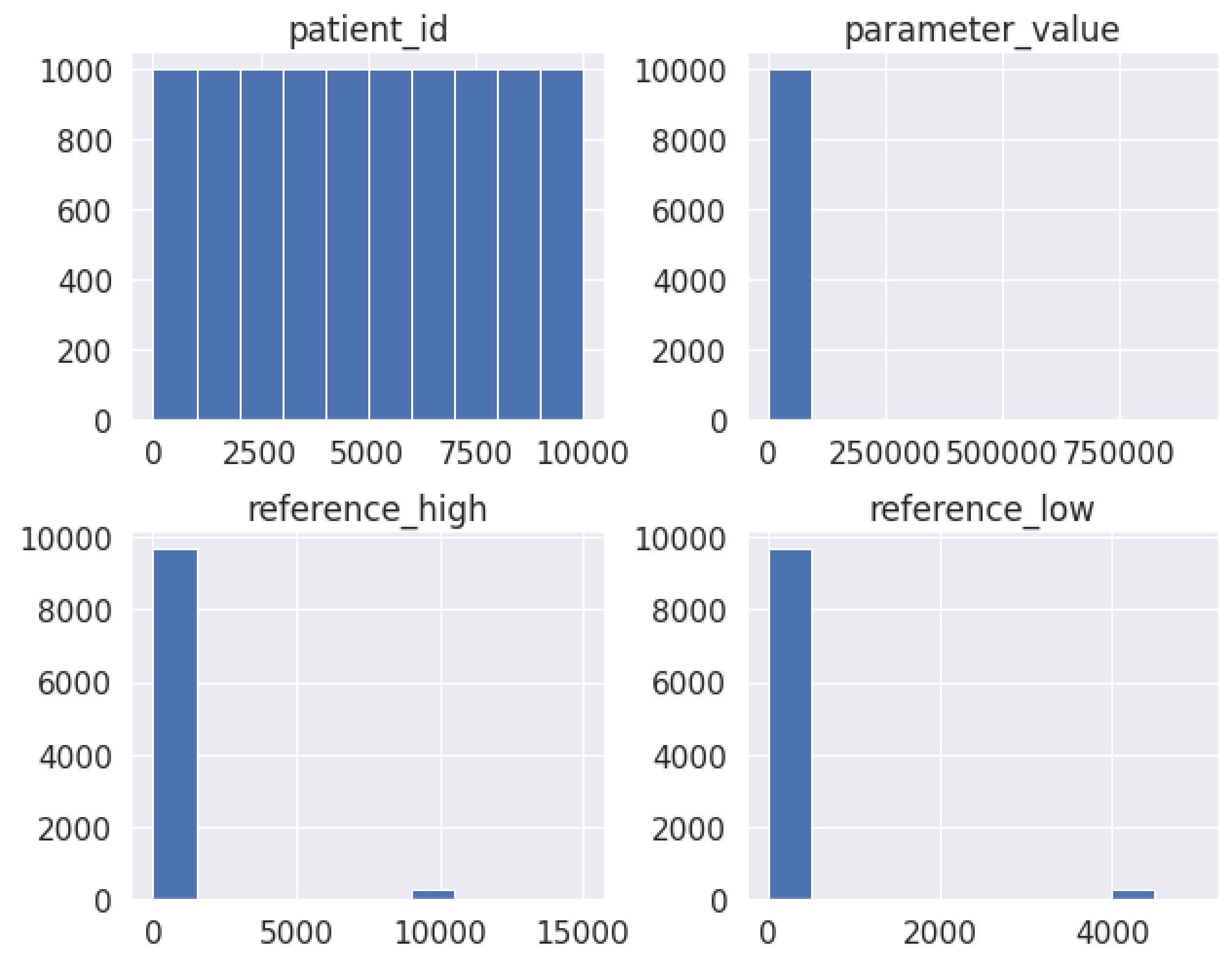
```
<AxesSubplot:xlabel='standard_lab_parameter_name,unit'>
```



```
# train.drop(['patient_id'],axis=1,inplace=True)
# test.drop(['patient_id'],axis=1,inplace=True)
```

```
train.hist(figsize=(10,8))
```

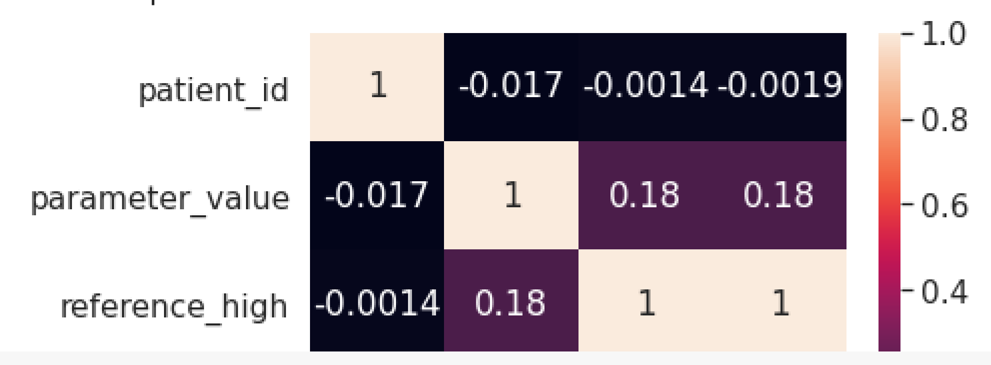
```
array([[<AxesSubplot:title={'center':'patient_id'}>,
        <AxesSubplot:title={'center':'parameter_value'}>],
       [<AxesSubplot:title={'center':'reference_high'}>,
        <AxesSubplot:title={'center':'reference_low'}>]], dtype=object)
```



Plotting Correlation

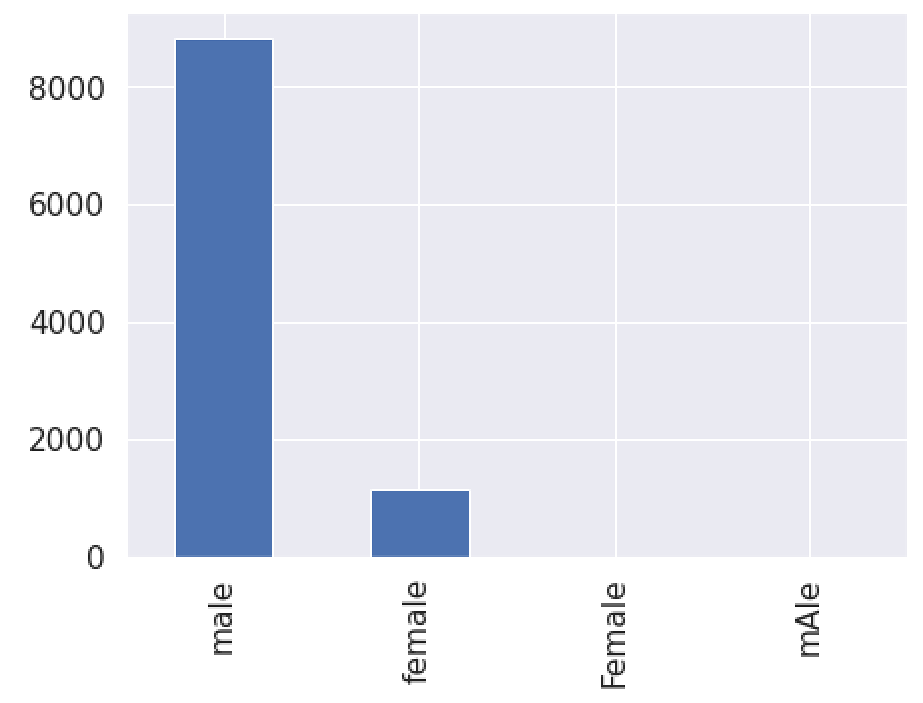
```
sb.heatmap(train.corr(), annot = True)
```

```
<AxesSubplot:>
```



```
train['gender'].value_counts().plot(kind='bar',figsize=(7,5))
```

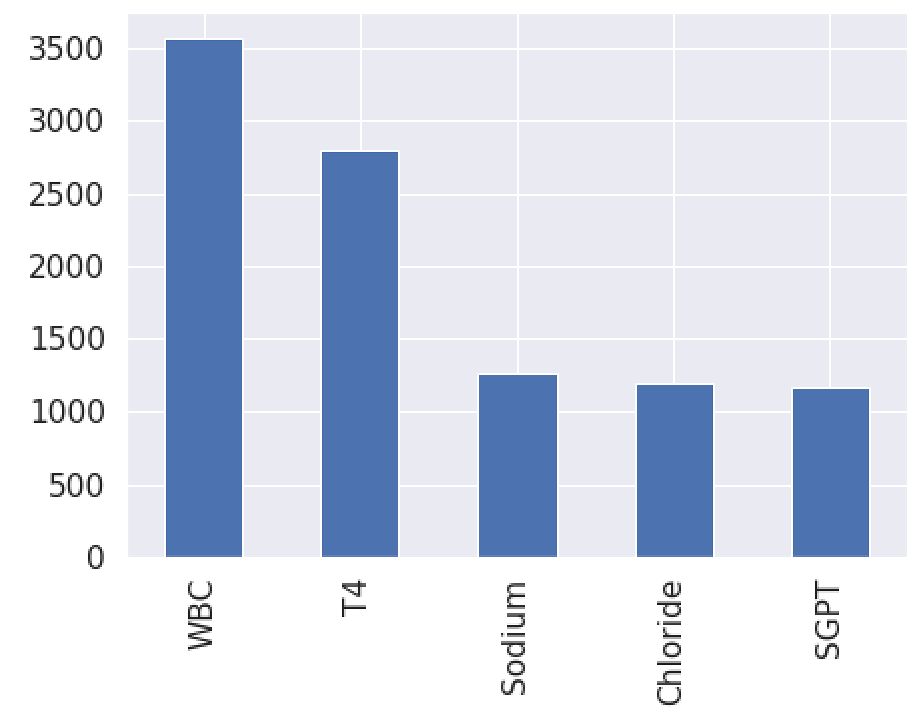
```
<AxesSubplot:>
```



```
#Chlorine

train.standard_lab_parameter_name.value_counts().plot(kind='bar',figsize=(7,5))
```

```
<AxesSubplot:>
```



Organizing data in model training format

```
train.drop(['created_at','patient_id'],axis=1,inplace=True)

gender_encode = {'male': 1,'female': 0}
train['gender'] = train['gender'].str.lower()

train['gender'] = train['gender'].replace(gender_encode)

x = train.drop(['gender'],axis=1)
x = pd.get_dummies(x)
y = train['gender']

from sklearn.model_selection import train_test_split
x_train,x_test, y_train, y_test = train_test_split(x,y,test_size=0.20,random_state=2)
```

```
# train['Year'] = train['created_at'].dt.year
# train['Month'] = train['created_at'].dt.month
# train['Day'] = train['created_at'].dt.day
```

```
x_train.shape,  y_train.shape
```

```
((8000, 42), (8000,))
```

Using RandomForest to train model

```
from sklearn.ensemble import RandomForestClassifier
clf=RandomForestClassifier(n_estimators=100)
clf.fit(x_train,y_train)

y_pred=clf.predict(x_test)
```

```
#Import scikit-learn metrics module for accuracy calculation
from sklearn import metrics
# Model Accuracy, how often is the classifier correct?
print("Accuracy:",metrics.accuracy_score(y_test, y_pred))
```

```
Accuracy: 0.8635
```

```
from sklearn.model_selection import learning_curve
```

```
sizes, training_scores, testing_scores = learning_curve(clf, x, y, cv=10, scoring='accuracy', train_sizes=np.linspac
```

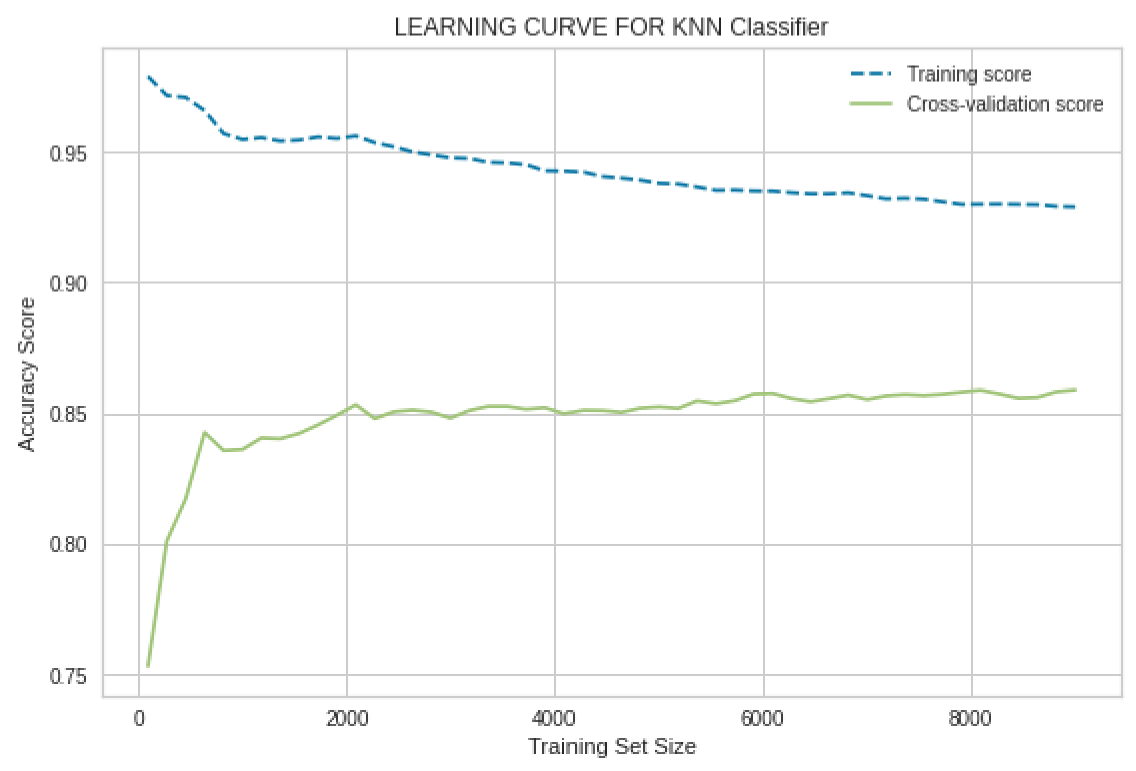
```
import matplotlib.pyplot as plt

# Mean and Standard Deviation of training scores
mean_training = np.mean(training_scores, axis=1)
Standard_Deviation_training = np.std(training_scores, axis=1)

# Mean and Standard Deviation of testing scores
mean_testing = np.mean(testing_scores, axis=1)
Standard_Deviation_testing = np.std(testing_scores, axis=1)

# dotted blue line is for training scores and green line is for cross-validation score
plt.plot(sizes, mean_training, '--', color="b",  label="Training score")
plt.plot(sizes, mean_testing, color="g", label="Cross-validation score")

# Drawing plot
plt.title("LEARNING CURVE FOR KNN Classifier")
plt.xlabel("Training Set Size"), plt.ylabel("Accuracy Score"), plt.legend(loc="best")
plt.tight_layout()
plt.show()
```



Chloride Analysis

```
train = pd.read_csv("training_data.csv")
test = pd.read_csv('test_data.csv')

test = test.loc[:, ~test.columns.str.contains('^Unnamed')]


data = pd.concat([train,test],axis=0)
data.sample(5)
```

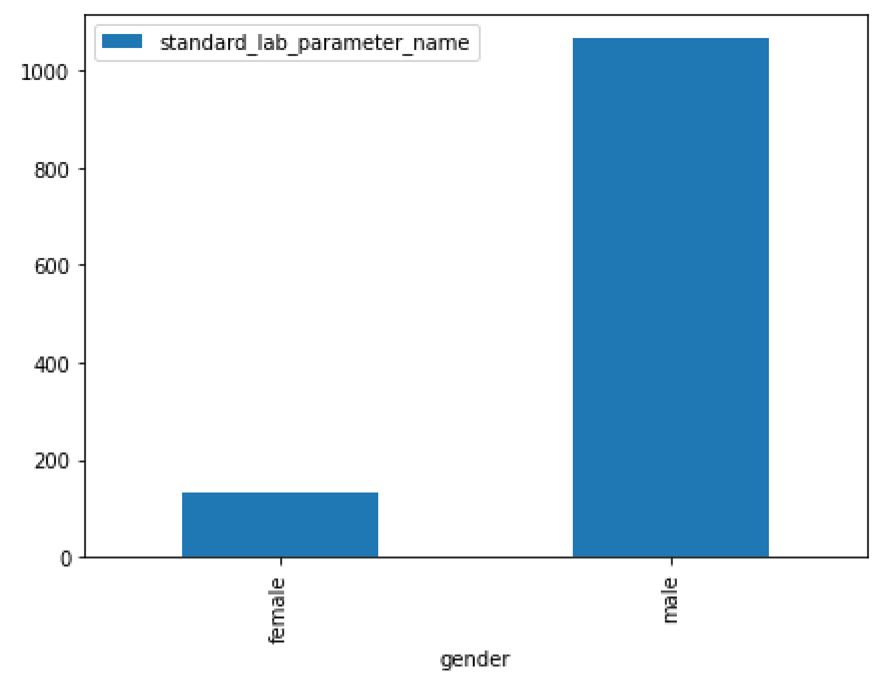
	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
5483	5483	Chloride	103.00	mmol/l	2019-05-05 12:11:58.097	107.0	98.0	adult	female
9882	9882	Sodium	141.00	mmol/l	2020-11-12 11:31:12.132213+00:00	145.0	136.0	old	NaN
4339	4339	T4	9.20	μg/dl	2019-12-22 19:50:31.002325+00:00	11.0	5.5	adult	male
7213	7213	WBC	11.20	10^3/μi	2020-11-02 18:31:41.394109+00:00	10.0	4.0	adult	NaN
6396	6396	WBC	4.74	10^3/μl	2019-09-07 05:22:10.486355+00:00	9.9	5.7	child	male

```
data = data.loc[data['standard_lab_parameter_name']=='Chloride']
data.sample(5)
```

	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
1523	1523	Chloride	106.0	mmol/l	2020-11-07 00:47:42.315256+00:00	107.0	98.0	adult	NaN
2531	2531	Chloride	104.0	mmol/l	2020-10-26 16:08:58.443424+00:00	109.0	101.0	adult	NaN
8262	8262	Chloride	106.0	mmol/l	2020-11-06 04:05:58.956922+00:00	107.0	98.0	old	NaN
6045	6045	Chloride	96.0	mmol/l	2020-11-12 08:47:24.821478+00:00	107.0	98.0	old	NaN
7736	7736	Chloride	104.6	mmol/l	2019-05-27 06:31:19.390174+00:00	108.0	98.0	adult	male

```
data.groupby(['gender']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f2531215b90>
```



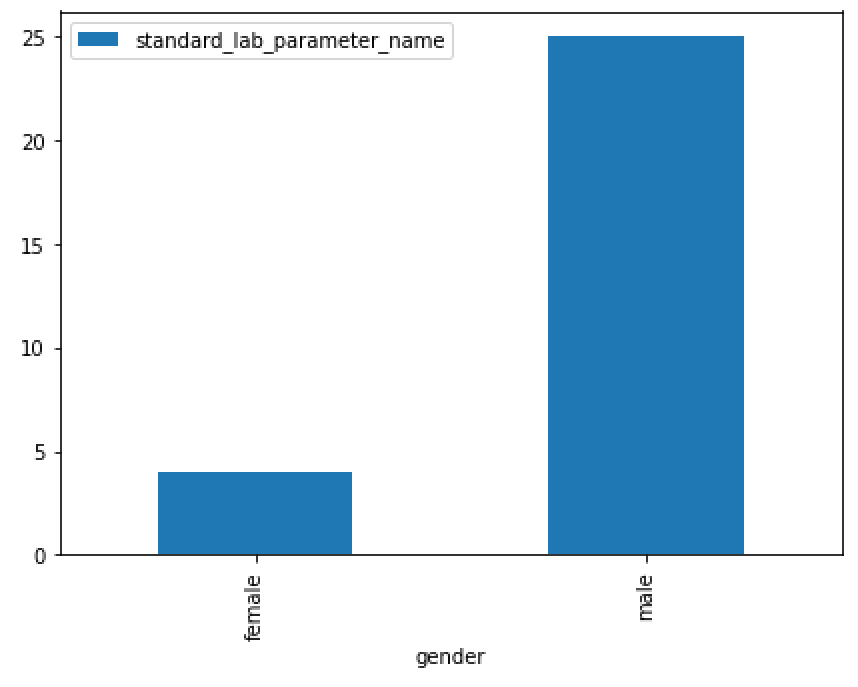
```
data_chloride_108_value = data.loc[data['parameter_value'] > 108]
```

```
data_chloride_108_value.groupby(['gender']).agg({'standard_lab_parameter_name':'count'})
```

gender	standard_lab_parameter_name
female	4
male	25

```
:hloride_108_value.groupby(['gender']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f2530b6b350>
```

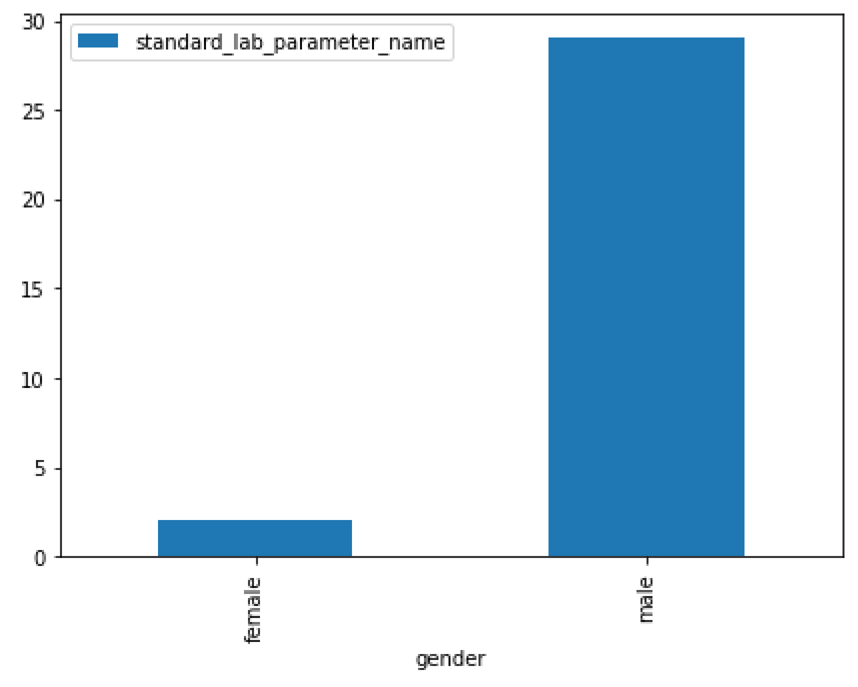


```
data_chloride_95_value = data.loc[data['parameter_value'] < 95]
data_chloride_95_value.groupby(['gender']).agg({'standard_lab_parameter_name':'count'})
```

gender	standard_lab_parameter_name
female	2
male	29

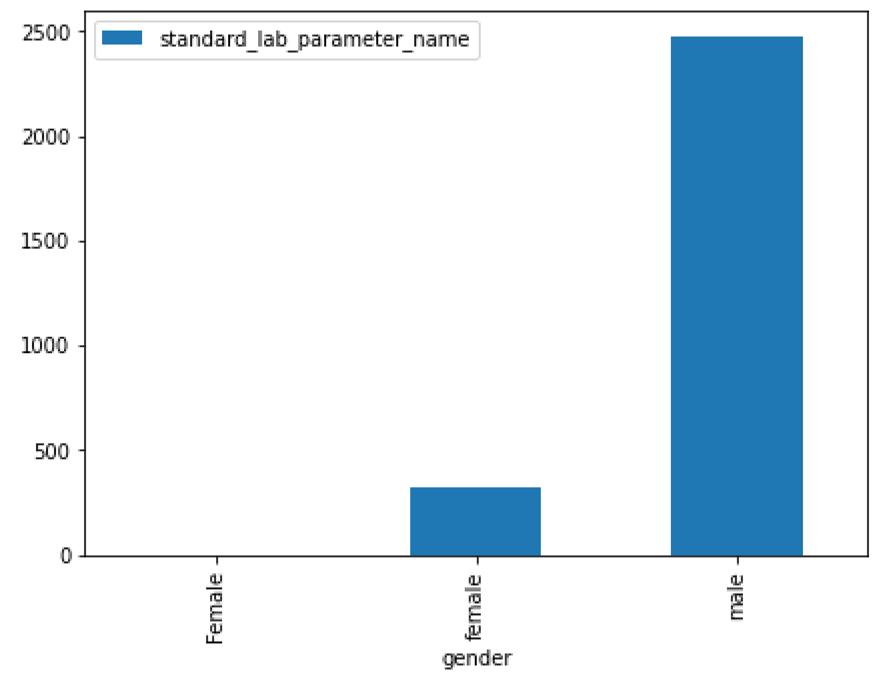
```
:hloride_95_value.groupby(['gender']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f2530b07f50>
```



```
data.groupby(['gender']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f253aa63690>
```



```
data.groupby(['age_group']).agg({'standard_lab_parameter_name':'count'})
```

age_group	standard_lab_parameter_name
adult	1808
child	23
old	573
teen	23

WBC Analysis

```
train = pd.read_csv("training_data.csv")
test = pd.read_csv('test_data.csv')

test = test.loc[:, ~test.columns.str.contains('^Unnamed')]
```

```
data = pd.concat([train,test],axis=0)
data.sample(5)
```

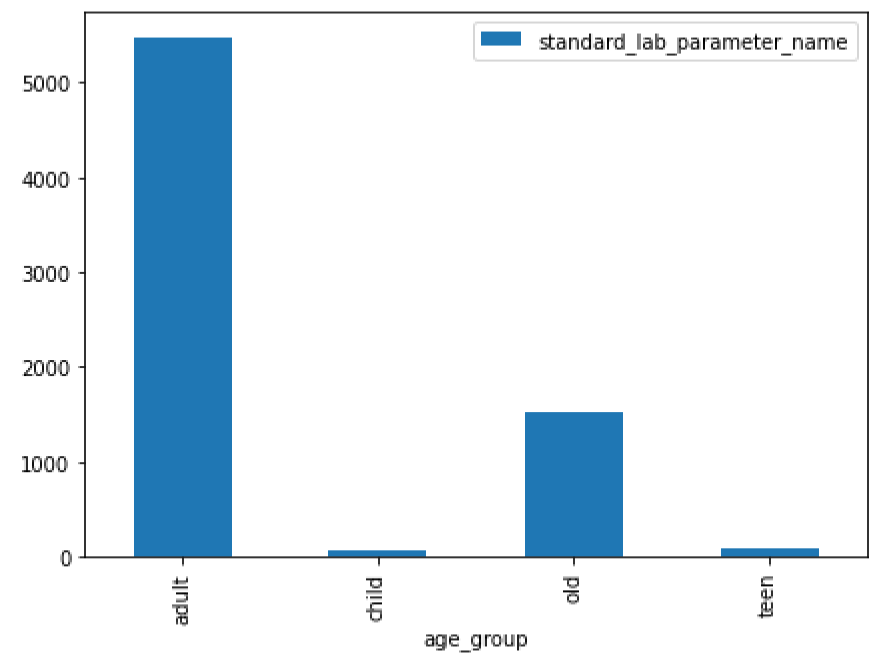
	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
5003	5003	WBC	7.2	10^3/µi	2019-11-28 02:28:01.746787+00:00	10.0	4.0	adult	male
8110	8110	WBC	9.3	10^3/µi	2020-11-18 13:49:56.770378+00:00	10.0	4.0	adult	NaN
5492	5492	WBC	6.6	10^3/µl	2020-11-11 15:28:41.958324+00:00	10.0	4.0	adult	NaN
2895	2895	Sodium	140.0	mmol/l	2020-11-18 14:52:38.659789+00:00	145.0	136.0	adult	NaN
2255	2255	T4	9.4	µg/dl	2019-11-19 08:53:09.846000+00:00	12.0	4.5	adult	male

```
data = data.loc[data['standard_lab_parameter_name']=='WBC']
data.sample(5)
```

	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
3992	3992	WBC	5.90	x 10³ / µl	2019-11-23 13:38:41.224	10.0	4.0	adult	male
3245	3245	WBC	6.02	10^3/µl	2020-11-15 12:23:40.893840+00:00	9.7	5.4	child	NaN
2314	2314	WBC	7.80	10^3/µl	2020-11-03 16:07:31.543883+00:00	10.0	4.0	adult	NaN
7293	7293	WBC	9.84	10^3/µl	2019-10-02 13:31:24.878144+00:00	10.0	4.0	adult	male
1280	1280	WBC	8.90	10^3/µi	2020-11-20 13:54:23.580817+00:00	10.0	4.0	adult	NaN

```
data.groupby(['age_group']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f253f9c4fd0>
```



T4 Analysis

```
train = pd.read_csv("training_data.csv")
test = pd.read_csv('test_data.csv')

test = test.loc[:, ~test.columns.str.contains('^Unnamed')]


data = pd.concat([train,test],axis=0)
data.sample(5)
```

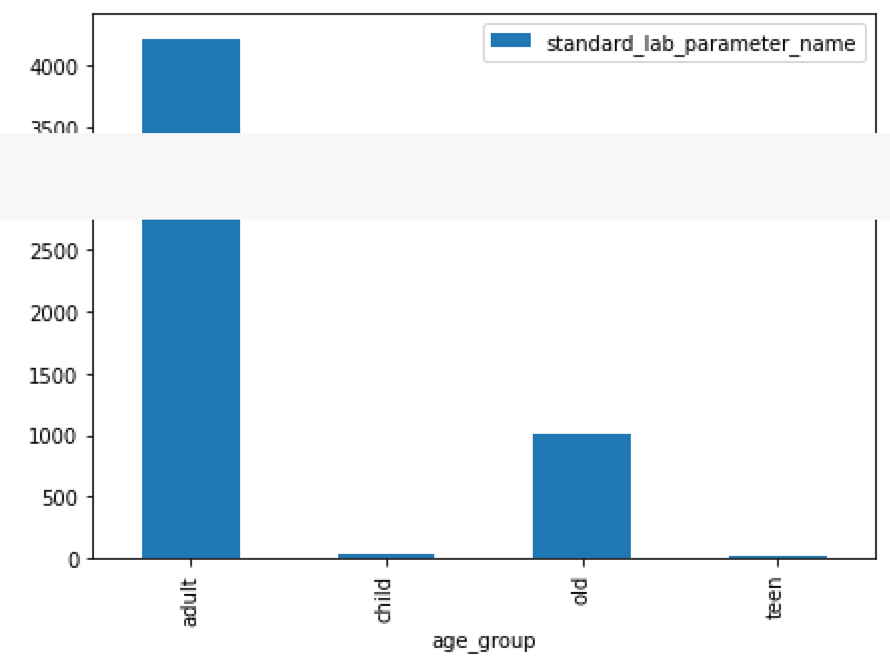
	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
4708	4708	WBC	10.80	10^3/&micro;i	2019-12-24 15:27:59.396	10.0	4.0	adult	male
9363	9363	WBC	6.60	10^3/µi	2020-10-31 13:31:52.009944+00:00	10.0	4.0	adult	NaN
9316	9316	WBC	7.02	10^3/µl	2019-12-17 14:17:48.585883+00:00	10.0	4.0	adult	male
6892	6892	Chloride	104.90	mmol/l	2019-10-15 12:54:19.588516+00:00	107.0	98.0	adult	male
2690	2690	T4	5.90	µg/dl	2019-06-26 22:37:08.787	12.0	4.5	adult	male

```
data = data.loc[data['standard_lab_parameter_name']=='T4']
data.sample(5)
```

	patient_id	standard_lab_parameter_name	parameter_value	unit	created_at	reference_high	reference_low	age_group	gender
3297	3297	T4	8.9	µg/dl	2019-11-19 01:07:38.038613+00:00	12.00	4.50	adult	female
9682	9682	T4	6.8	µg/dl	2019-11-26 14:07:55.901892+00:00	12.00	4.50	old	male
1760	1760	T4	7.9	µg/dl	2020-11-12 07:33:44.645007+00:00	12.00	4.50	adult	NaN
6385	6385	T4	9.6	µg/dl	2019-09-14 07:33:40.414533+00:00	12.00	4.50	adult	male
7286	7286	T4	5.8	µg/dl	2020-11-16 16:08:32.290193+00:00	11.72	4.87	adult	NaN

```
data.groupby(['age_group']).agg({'standard_lab_parameter_name':'count'}).plot(kind='bar',figsize=(7,5))
```

```
<matplotlib.axes._subplots.AxesSubplot at 0x7f253b04c410>
```



✓ 0s completed at 19:18