In [23]:
```python
import pandas as pd
```

In [24]:
```python
import numpy as np
```

In [25]:
```python
import seaborn as sns
```

In [26]:
```python
from matplotlib import pyplot as plt
```

In [43]:
```python
gwdata = pd.read_csv(r'C:\Users\hp\Downloads\data visulaization\gwdata.csv')
```

In [44]:
```python
gwdata
```

Out[44]:

	S.No	STATE	pH	Conductivity	BOD	Nitrate N	Faecal Coliform	Total Coliform	Total Dissolved Solids	Fluoride
0	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1	1.0	AP	7.0	776.0	2.0	9.0	3.0	70.0	782.0	1.0
2	2.0	AP	8.0	620.0	2.0	4.0	4.0	70.0	623.0	1.0
3	3.0	AP	8.0	759.0	2.0	2.0	5.0	84.0	764.0	0.0
4	4.0	AP	7.0	2536.0	3.0	23.0	6.0	93.0	2576.0	1.0
...	...	...	...	...	...	...	...	...	...	...
377	530.0	WB	8.0	472.0	1.0	0.0	2.0	2.0	447.0	0.0
378	531.0	WB	8.0	339.0	1.0	0.0	2.0	6.0	486.0	1.0
379	532.0	WB	7.0	1057.0	1.0	0.0	6.0	19.0	1429.0	0.0
380	533.0	WB	7.0	1211.0	1.0	0.0	18.0	53.0	1198.0	0.0
381	534.0	WB	8.0	669.0	1.0	1.0	2.0	2.0	478.0	0.0

382 rows × 10 columns

In [30]:
```python
gwdata.dtypes
```

Out[30]:
```
S.No                      float64
STATE                      object
pH                        float64
Conductivity              float64
BOD                       float64
Nitrate N                 float64
Faecal Coliform           float64
Total Coliform             object
Total Dissolved Solids    float64
Fluoride                   object
dtype: object
```

In [31]: `gwdata.columns`

Out[31]: Index(['S.No', 'STATE', 'pH', 'Conductivity', 'BOD', 'Nitrate N',
                'Faecal Coliform', 'Total Coliform', 'Total Dissolved Solids',
                'Fluoride'],
               dtype='object')

In [32]:
```python
def convert_to_nan(gwdata):
    n_col = gwdata.shape[1]
    for index in range(n_col):
        gwdata.iloc[:, index] = gwdata.iloc[:, index].replace("NAN", np.nan)
    return gwdata

gwdata = convert_to_nan(gwdata)
```
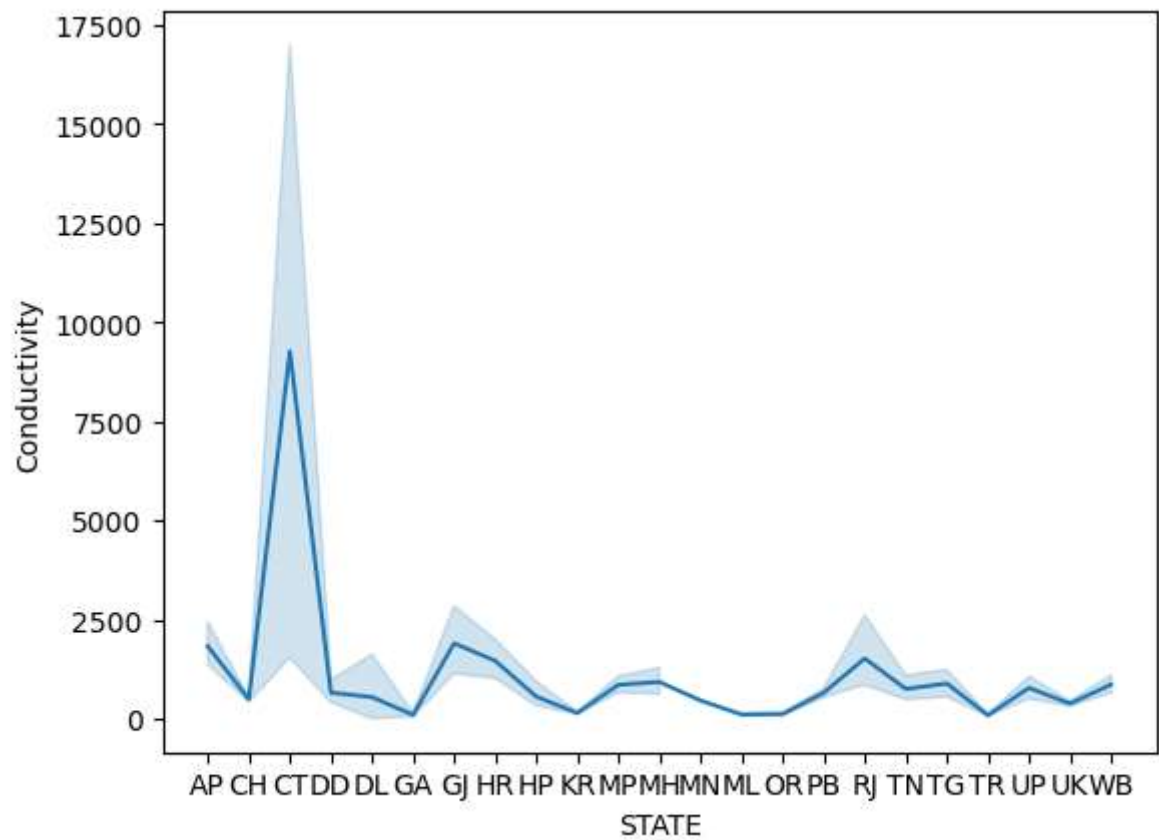
In [33]: `sns.barplot(x='STATE', y='pH', data=gwdata)`

Out[33]: <Axes: xlabel='STATE', ylabel='pH'>
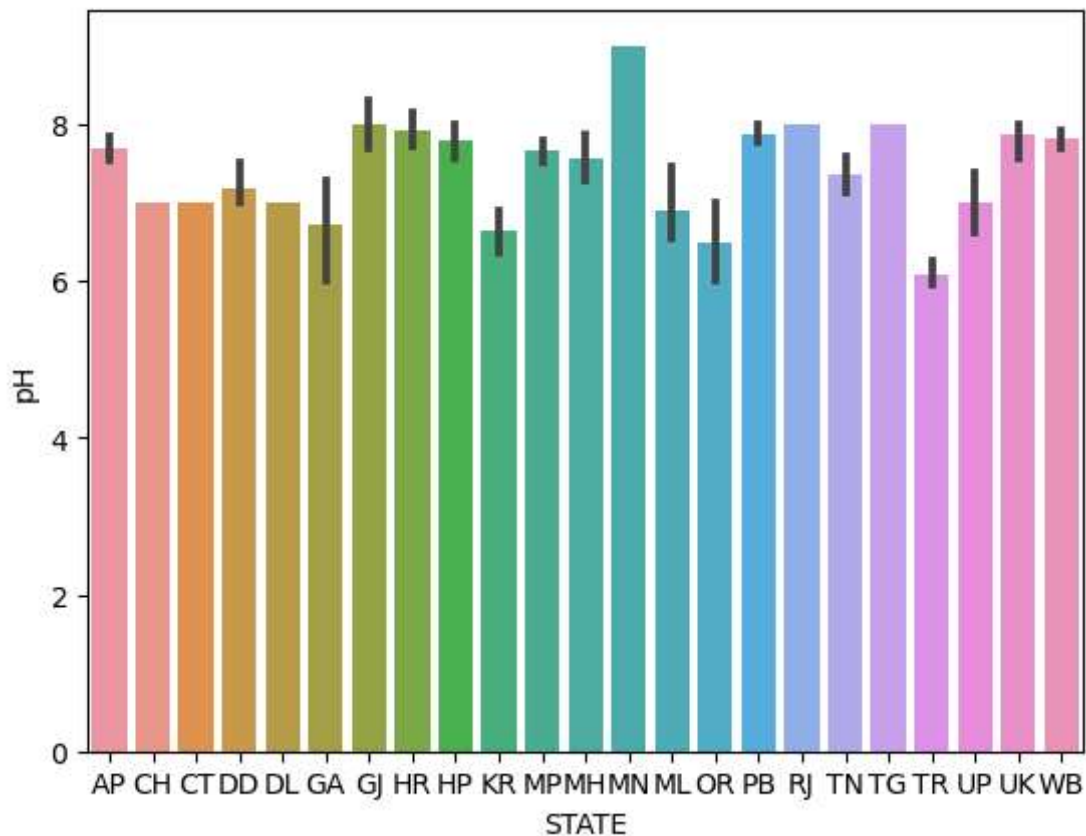
```
In [34]: sns.lineplot(x='STATE', y='Conductivity', data=gwdata)
```
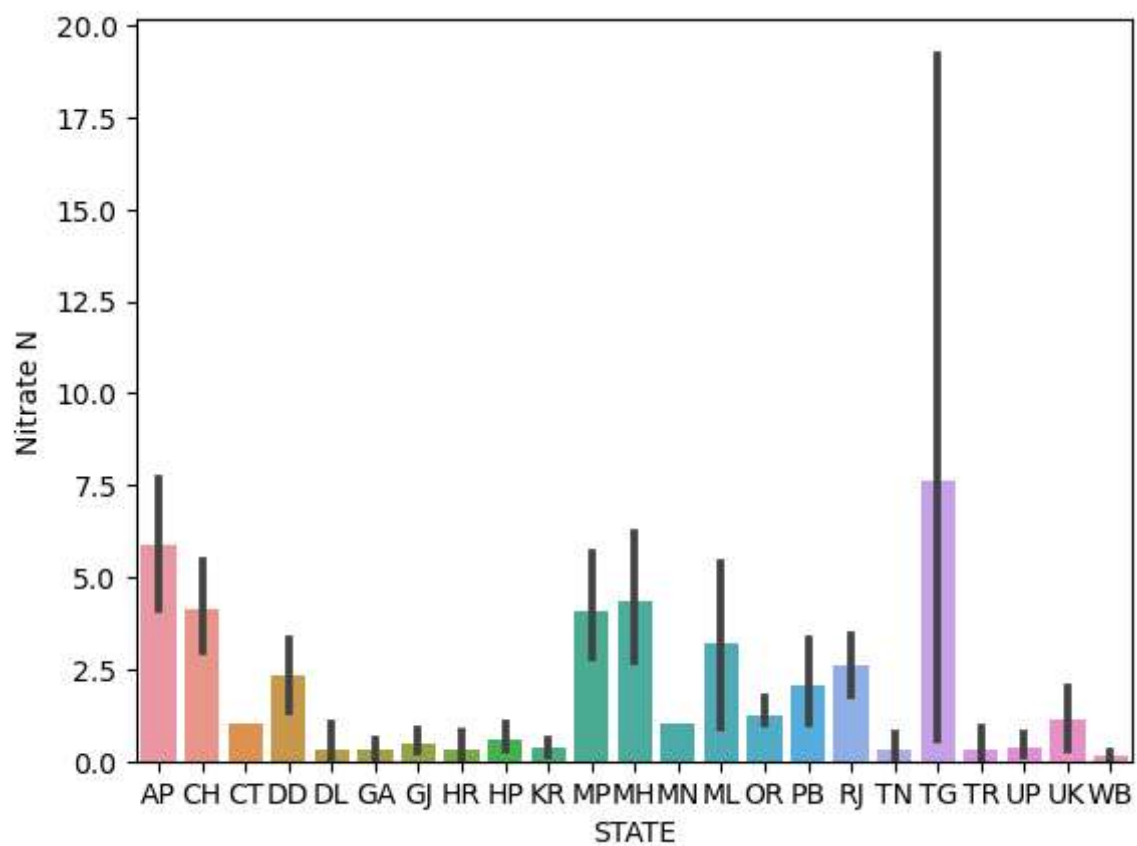
Out[34]: <Axes: xlabel='STATE', ylabel='Conductivity'>

In [35]: `sns.barplot(x='STATE', y='BOD', data=gwdata)`

Out[35]: `<Axes: xlabel='STATE', ylabel='BOD'>`
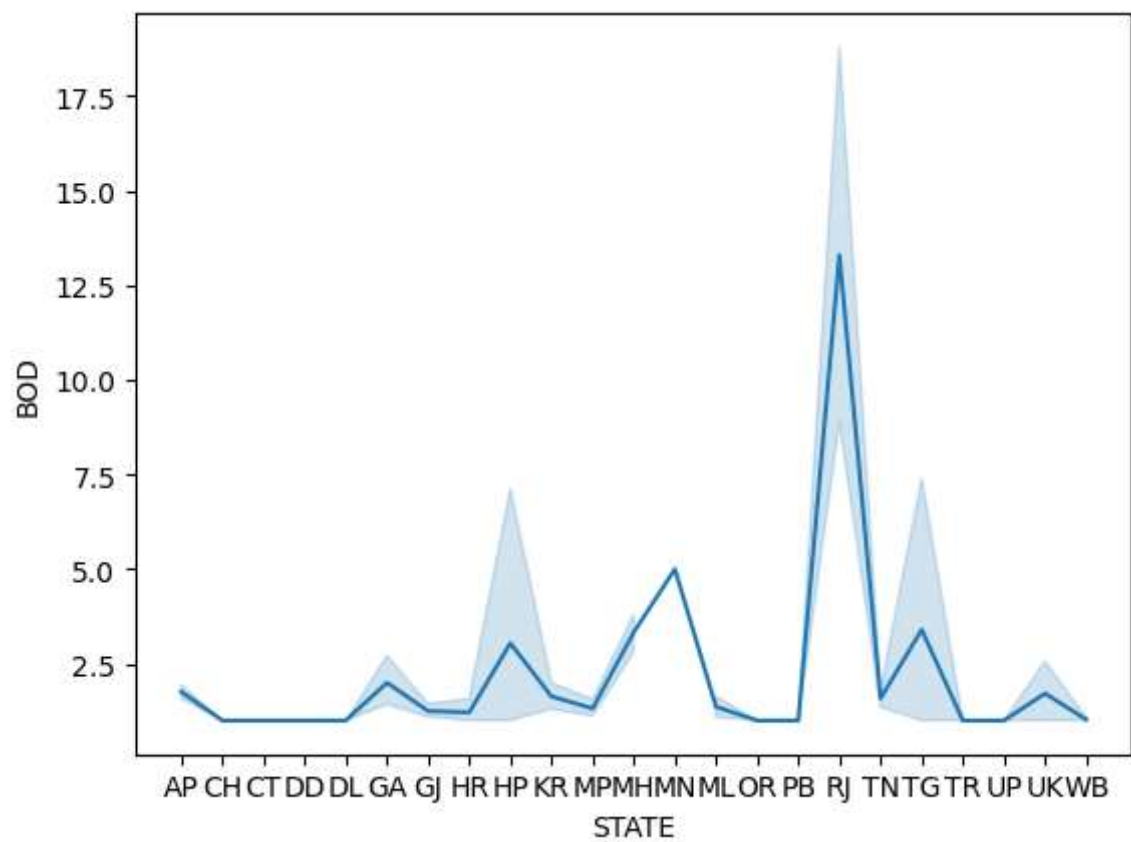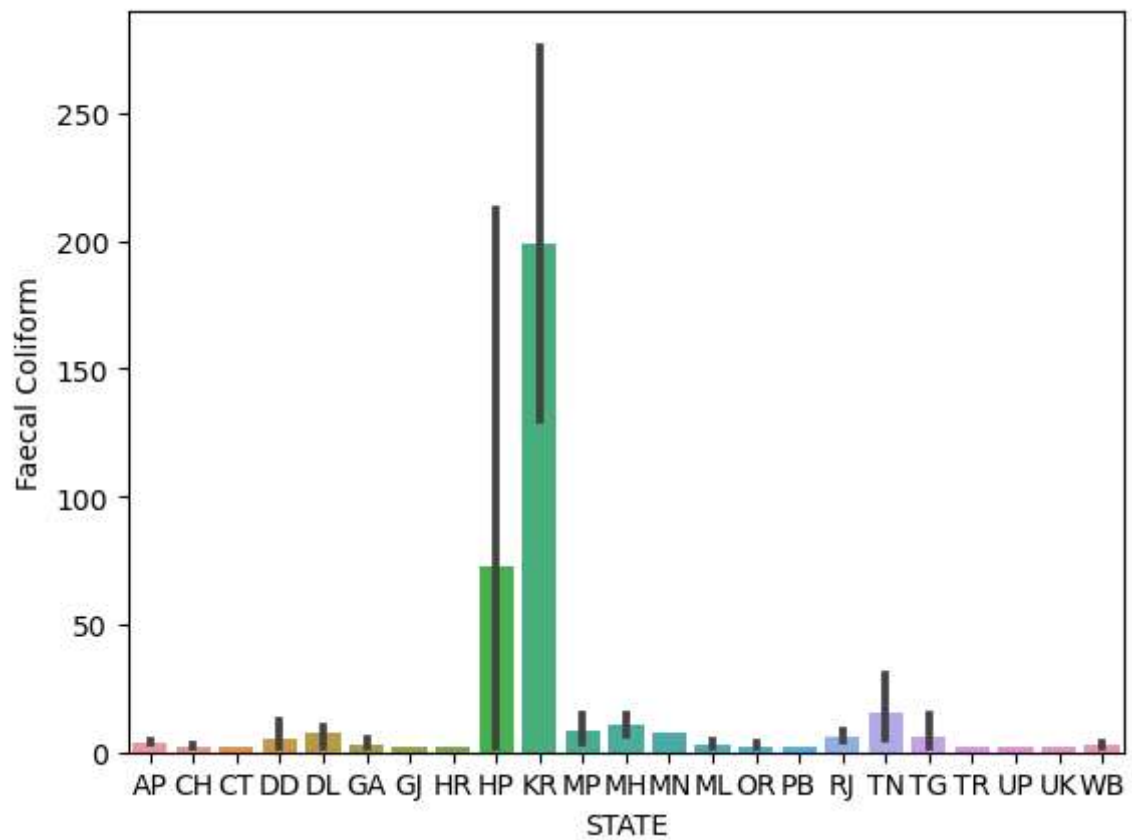
In [39]:
```python
sns.barplot(x='STATE', y='Nitrate N', data=gwdata)
```

Out[39]: `<Axes: xlabel='STATE', ylabel='Nitrate N'>`
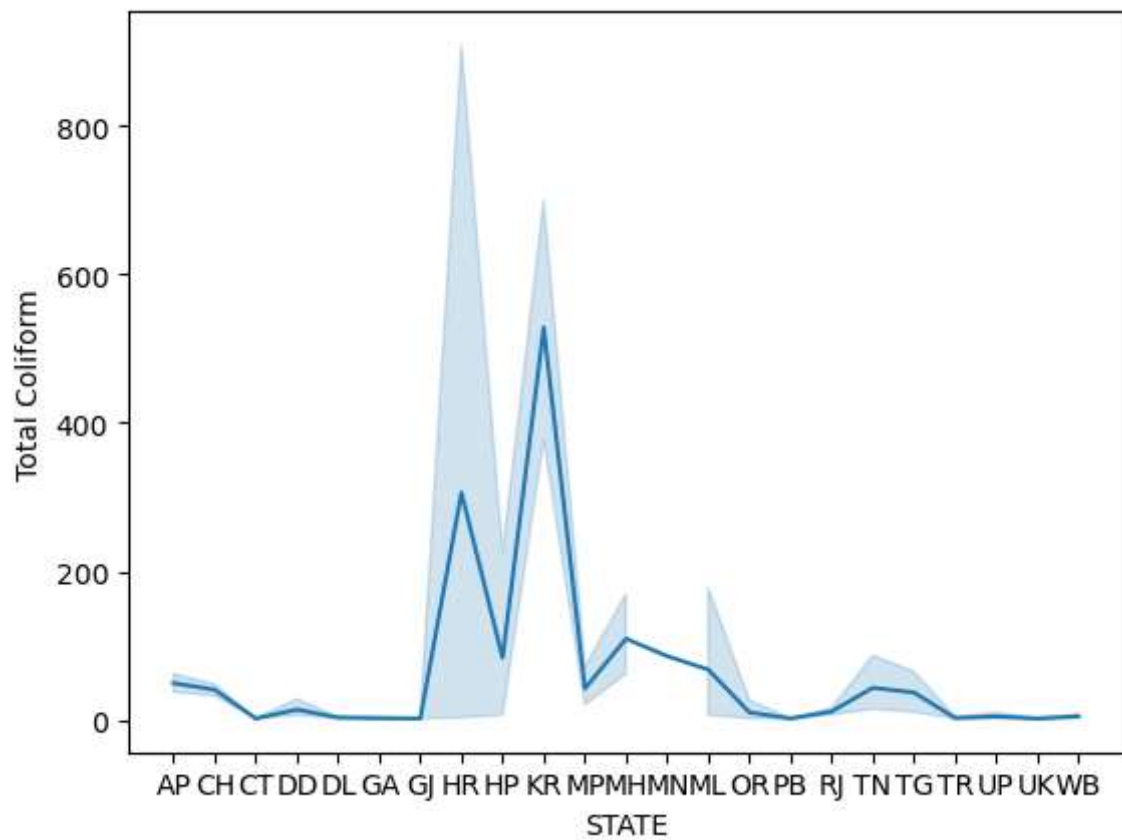
In [40]: `sns.barplot(x='STATE', y='Faecal Coliform', data=gwdata)`

Out[40]: `<Axes: xlabel='STATE', ylabel='Faecal Coliform'>`
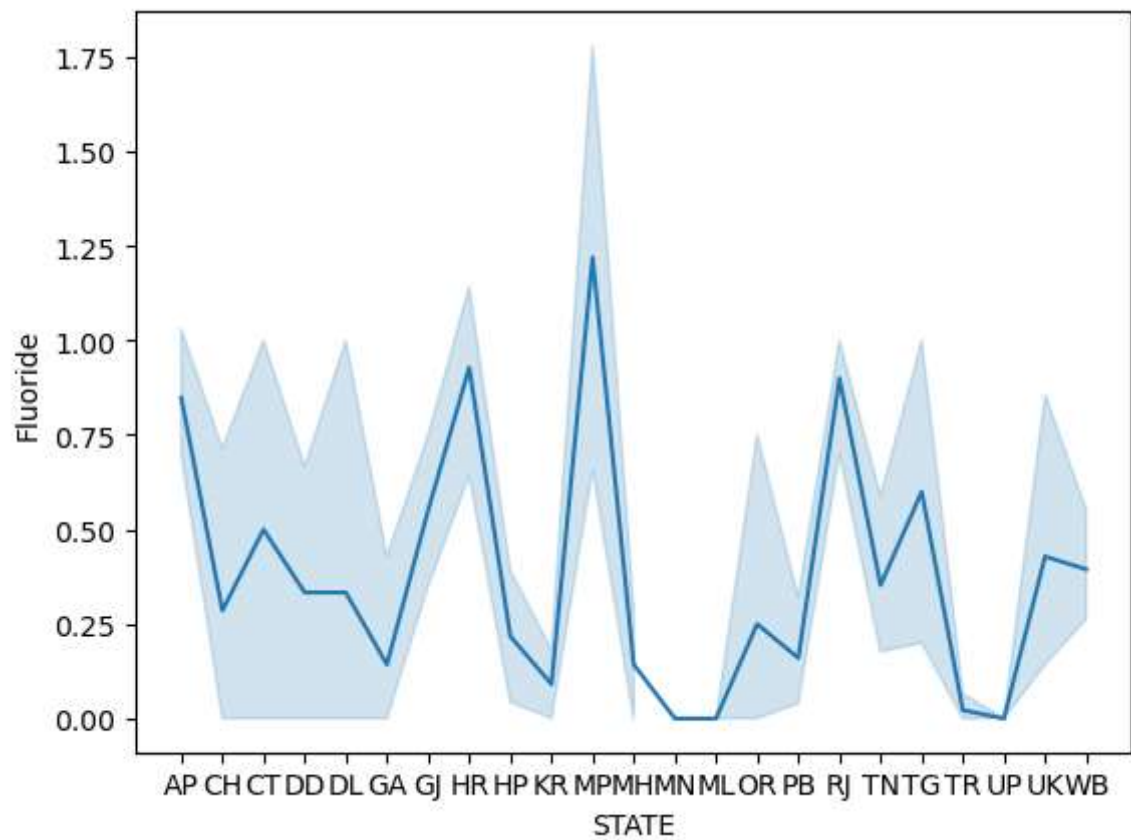
In [45]: `sns.lineplot(x='STATE', y='Total Coliform', data=gwdata)`

Out[45]: `<Axes: xlabel='STATE', ylabel='Total Coliform'>`
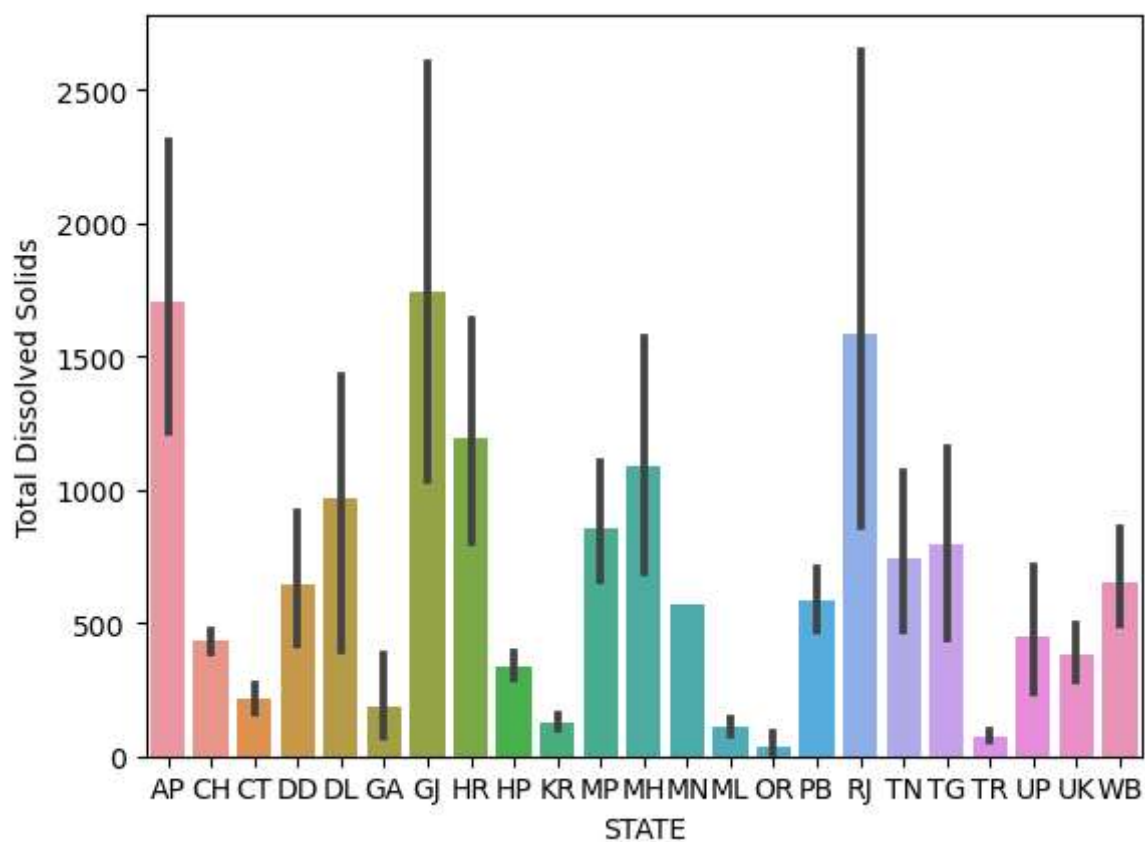
In [50]: `sns.lineplot(x='STATE', y='Fluoride', data=gwdata)`

Out[50]: `<Axes: xlabel='STATE', ylabel='Fluoride'>`

In [49]: `sns.barplot(x='STATE', y='Total Dissolved Solids', data=gwdata)`

Out[49]: `<Axes: xlabel='STATE', ylabel='Total Dissolved Solids'>`

In [ ]: