import packages

```
import scanpy as sc
import pandas as pd
import squidpy as sq
import numpy as np
from scipy.spatial import *
from sklearn.preprocessing import *
from sklearn.metrics import *
from scipy.spatial.distance import *

import SDMBench.SDMBench as sdmbench
sdmbench=sdmbench.sdmbench()
```

Prepared files

First, you must download the data. You can download our processed h5ad file in the/SDMBench/Data dir, and this is one of 10x visium datasets from LIBD human dorsolateral prefrontal cortex(sample 151507).

```
adata=sc.read_h5ad('/SDMBench/Data/151507.h5ad')
adata_valid = adata[np.logical_not(adata.obs['Region'].isna())]#remove NAN
adata_valid
```

read result of your method(txt file)

The txt file has a total of one column. The first line is the name of your method, and the rest of the lines are the prediction results. You can download our test file in the /SDMBench/Tutorial/new_method.txt directory.

```
pred=pd.read_csv('new_method.txt')
```

compute ari

```
ari=sdmbench.compute_ARI(adata_valid,f'Region',f'pred')
```

compute nmi

```
nmi=sdmbench.compute_NMI(adata_valid,f'Region',f'pred')
```

compute CHAOS

```
chaos=sdmbench.compute_CHAOS(adata_valid,f'pred')
```

compute PAS

```
pas=sdmbench.compute_PAS(adata_valid,f'pred',spatial_key='spatial')
```

compute ASW

```
asw=sdmbench.compute_ASW(adata_valid,f'pred',spatial_key='spatial')
```

compute HOM

```
hom=sdmbench.compute_HOM(adata_valid,f'Region',f'pred')
```

compute COM

```
com=sdmbench.compute_COM(adata_valid,f'Region',f'pred')
```

compute marker_score

```
moranI,gearyC=sdmbench.marker_score(adata_valid,f'Region')
```

output result

```
output_df = pd.DataFrame([[nmi,hom,com,chaos,pas,asw,moranI,gearyC]],
                         index = [pred.columns[0]],#your method name

columns=[['Accuracy','Accuracy','Accuracy','Continuity','Continuity','Continuity','Marker
score','Marker score'],['NMI','HOM','COM','CHAOS','PAS','ASW','Moran\'I','Geary\'s C']])

output_df.to_excel('./output_result.xlsx')
```