

```
In [ ]: import matplotlib.pyplot as plt
import numpy as np
import scanpy as sc

In [ ]: def read_scn_single_file_no_ss(path, CT="0", ST="0"):
    adata = sc.read_csv(path, first_column_names=True).T
    adata.var_names_make_unique()
    adata.obs_names_make_unique()
    adata.obs["CT"] = CT
    adata.obs["ST"] = ST
    return adata

def get_ct_from_path(path):
    ct_string = path.split("_")[1].split(".")[0]
    ct_number = int(ct_string[2:])
    ct_number %= 24
    return str(ct_number).zfill(2)

def read_all_scn():
    paths = [
        "SCN/GSM3290582_CT14.csv",
        "SCN/GSM3290583_CT18.csv",
        "SCN/GSM3290584_CT22.csv",
        "SCN/GSM3290585_CT26.csv",
        "SCN/GSM3290586_CT30.csv",
        "SCN/GSM3290587_CT34.csv",
        "SCN/GSM3290588_CT38.csv",
        "SCN/GSM3290589_CT42.csv",
        "SCN/GSM3290590_CT46.csv",
        "SCN/GSM3290591_CT50.csv",
        "SCN/GSM3290592_CT54.csv",
        "SCN/GSM3290593_CT58.csv",
    ]
    adatas = [
        read_scn_single_file_no_ss(path, get_ct_from_path(path)) for path
    ]
    adata = adatas[0].concatenate(adatas[1:])
    return adata
```

Initializing adata object

```
In [ ]: adata = read_all_scn()

/var/folders/c4/wctb_gj70v0_v8tlv9zqdnr0000gn/T/ipykernel_56601/271857776
7.py:35: FutureWarning: Use anndata.concat instead of AnnData.concatenate,
AnnData.concatenate is deprecated and will be removed in the future. See t
he tutorial for concat at: https://anndata.readthedocs.io/en/latest/concat
enation.html
    adata = adatas[0].concatenate(adatas[1:])

In [ ]: sc.pp.filter_genes(adata, min_cells=3)
sc.pp.filter_cells(adata, min_genes=500)
sc.pp.normalize_per_cell(adata, counts_per_cell_after=1e4)
sc.pp.log1p(adata)
```

```
sc.tl.pca(adata, svd_solver='arpack')
sc.pp.neighbors(adata, n_neighbors=10, n_pcs=40)
```

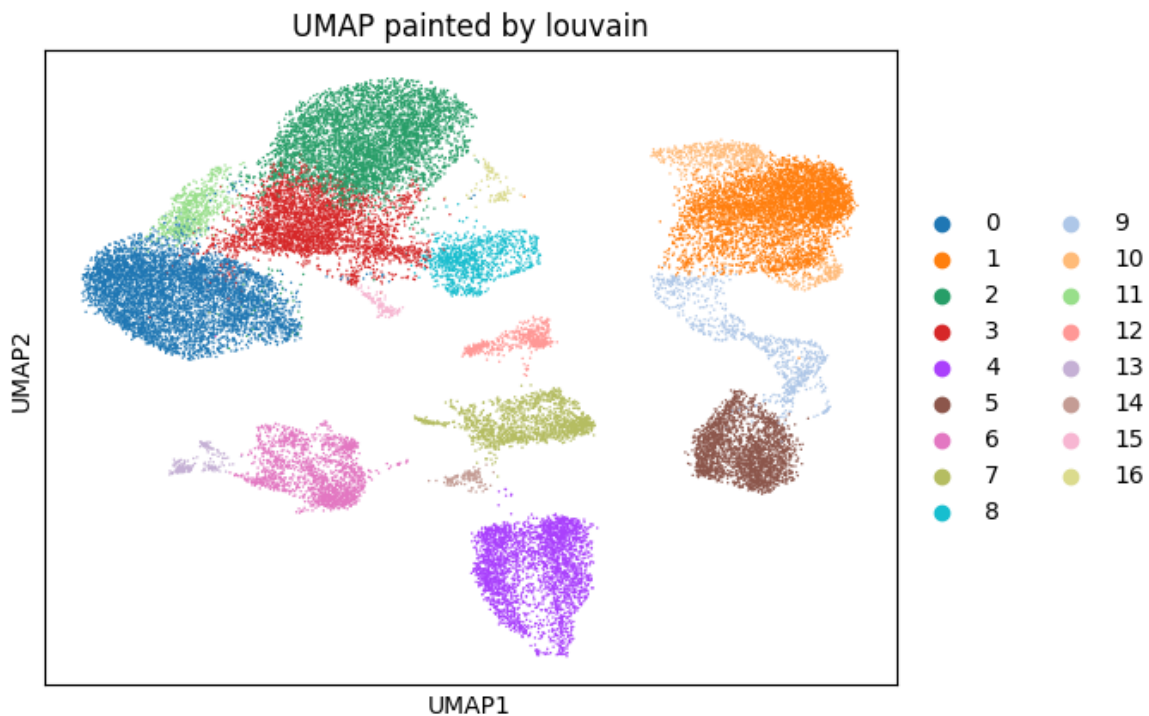
```
In [ ]: sc.tl.louvain(adata, resolution=0.7)
sc.tl.umap(adata)
sc.pl.umap(adata, color='louvain', title=("UMAP painted by louvain"))
marker_genes = ['Agt', 'Itm2a', 'Tmem212', 'Hexb', 'Celf4', 'Pdgfra', 'Top2a',
sc.pl.umap(adata, color=['louvain']+marker_genes)
sc.pl.dotplot(adata, marker_genes, groupby='louvain')
```

/Users/shahareliyah/Deskto/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_tools/scatterplots.py:1251: FutureWarning: The default value of 'ignore' for the 'na_action' parameter in pandas.Categorical.map is deprecated and will be changed to 'None' in a future version. Please set na_action to the desired value to avoid seeing this warning

```
color_vector = pd.Categorical(values.map(color_map))
```

/Users/shahareliyah/Deskto/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_tools/scatterplots.py:394: UserWarning: No data for colormapping provided via 'c'. Parameters 'cmap' will be ignored

```
cax = scatter(
```

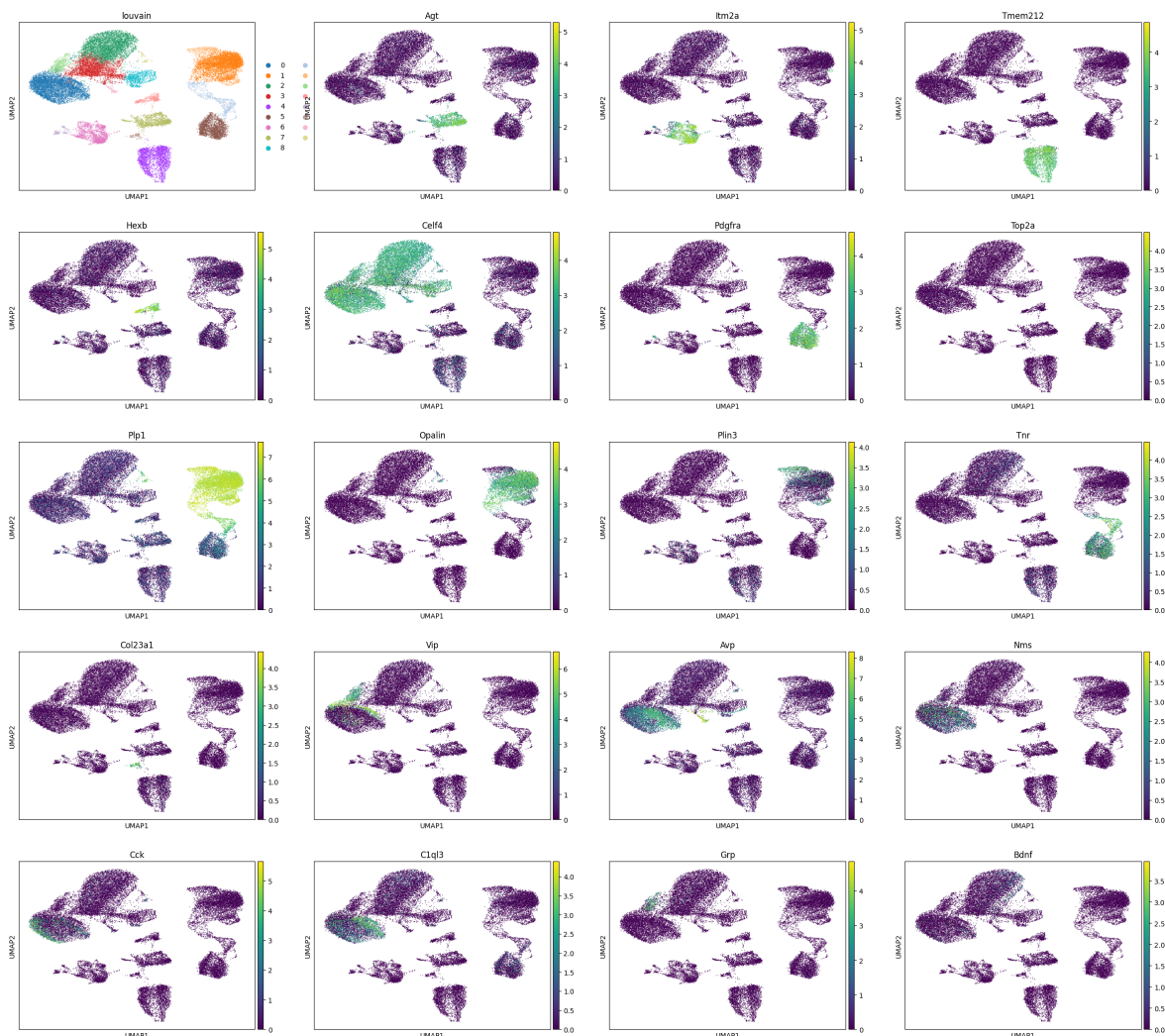


/Users/shahareliyah/Deskto/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_tools/scatterplots.py:1251: FutureWarning: The default value of 'ignore' for the 'na_action' parameter in pandas.Categorical.map is deprecated and will be changed to 'None' in a future version. Please set na_action to the desired value to avoid seeing this warning

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/Users/shahareliyah/Desktop/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_dotplot.py:168: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future version of pandas. Pass observed=False to retain current behavior or observed=True to adopt the future default and silence this warning.

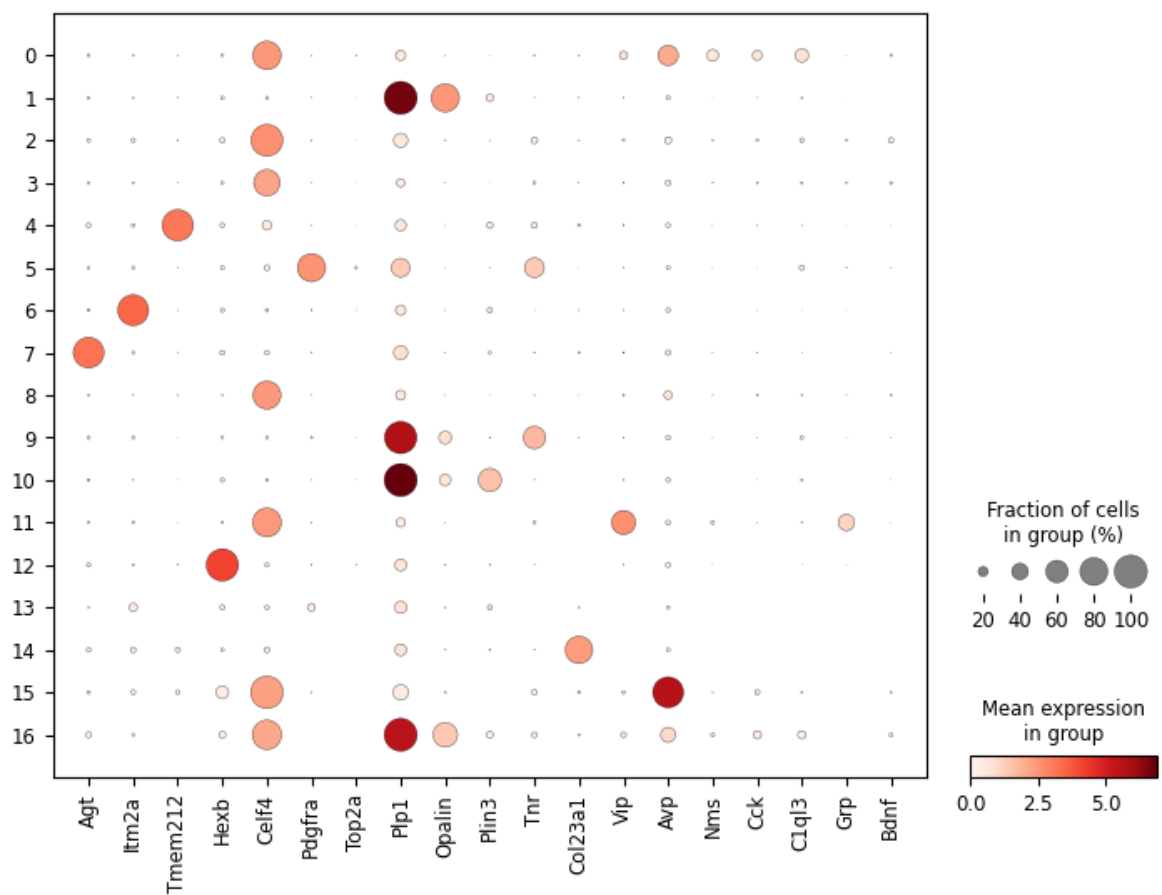
```
obs_bool.groupby(level=0).sum() / obs_bool.groupby(level=0).count()
```

/Users/shahareliyah/Desktop/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_dotplot.py:178: FutureWarning: The default of observed=False is deprecated and will be changed to True in a future version of pandas. Pass observed=False to retain current behavior or observed=True to adopt the future default and silence this warning.

```
dot_color_df = self.obs_tidy.groupby(level=0).mean()
```

/Users/shahareliyah/Desktop/lab/scanpy-tutorials-master/env/lib/python3.9/site-packages/scanpy/plotting/_dotplot.py:747: UserWarning: No data for colormapping provided via 'c'. Parameters 'cmap', 'norm' will be ignored

```
dot_ax.scatter(x, y, **kwargs)
```



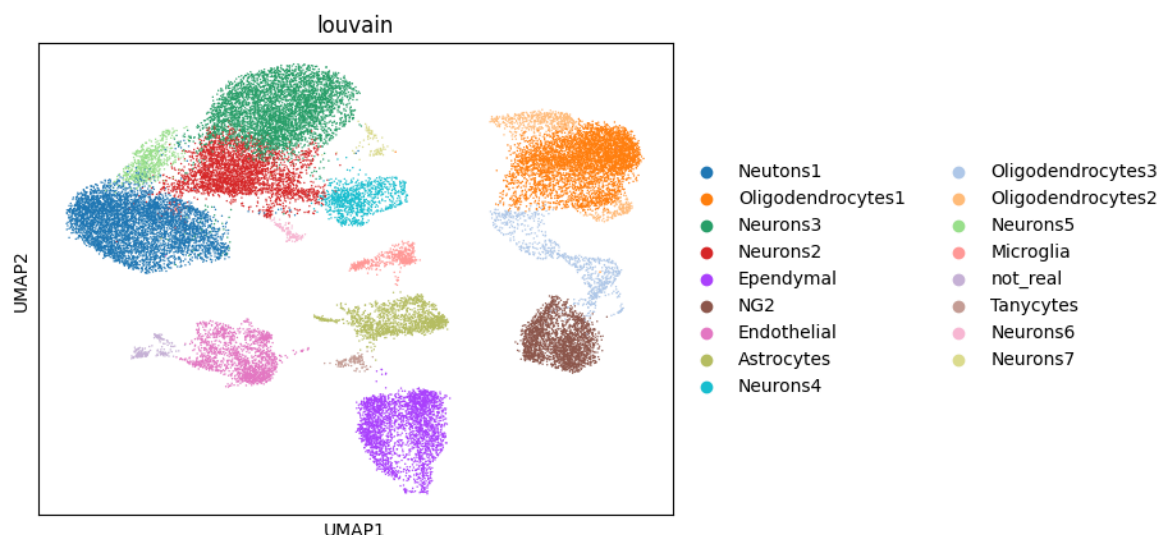
```
In [ ]: sc.pl.umap(adata, color=['louvain'])
```

```
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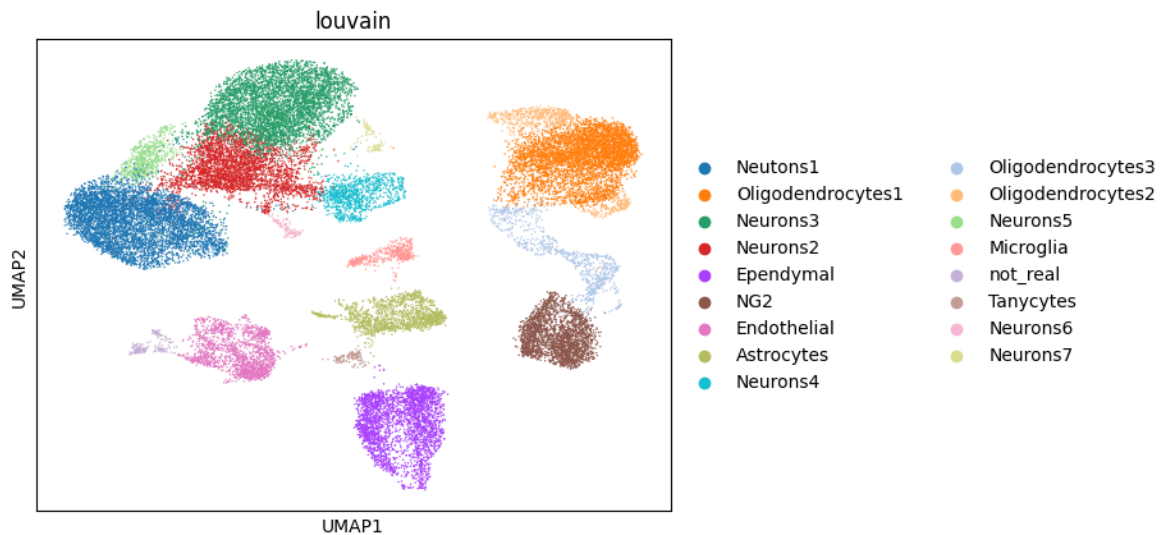


```
In [ ]: new_cluster_names = [
    "Neutons1",
    "Oligodendrocytes1",
    "Neurons3",
    "Neurons2",
    "Ependymal",
    "NG2",
    "Endothelial",
    "Astrocytes",
    "Neurons4",
    "Oligodendrocytes3",
    "Oligodendrocytes2",
    "Neurons5",
    "Microglia",
    "not_real",
    "Tanycytes",
    "Neurons6",
    "Neurons7",
]
adata.rename_categories("louvain", new_cluster_names)
```

```
In [ ]: sc.pl.umap(adata, color=['louvain'])
orig_adata = adata.copy()
```

```
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```



```
In [ ]: clusters = adata.obs['louvain'].unique()
cts = adata.obs['CT'].unique()
```

```
In [ ]: from numpy import linalg as LA
```

```
def von_ne(M):
    e, _ = LA.eig(M)
    e=e[e>0.0000001]
    e = e/np.sum(e)
    t = e * np.log(e)
    return -np.sum(t)
```

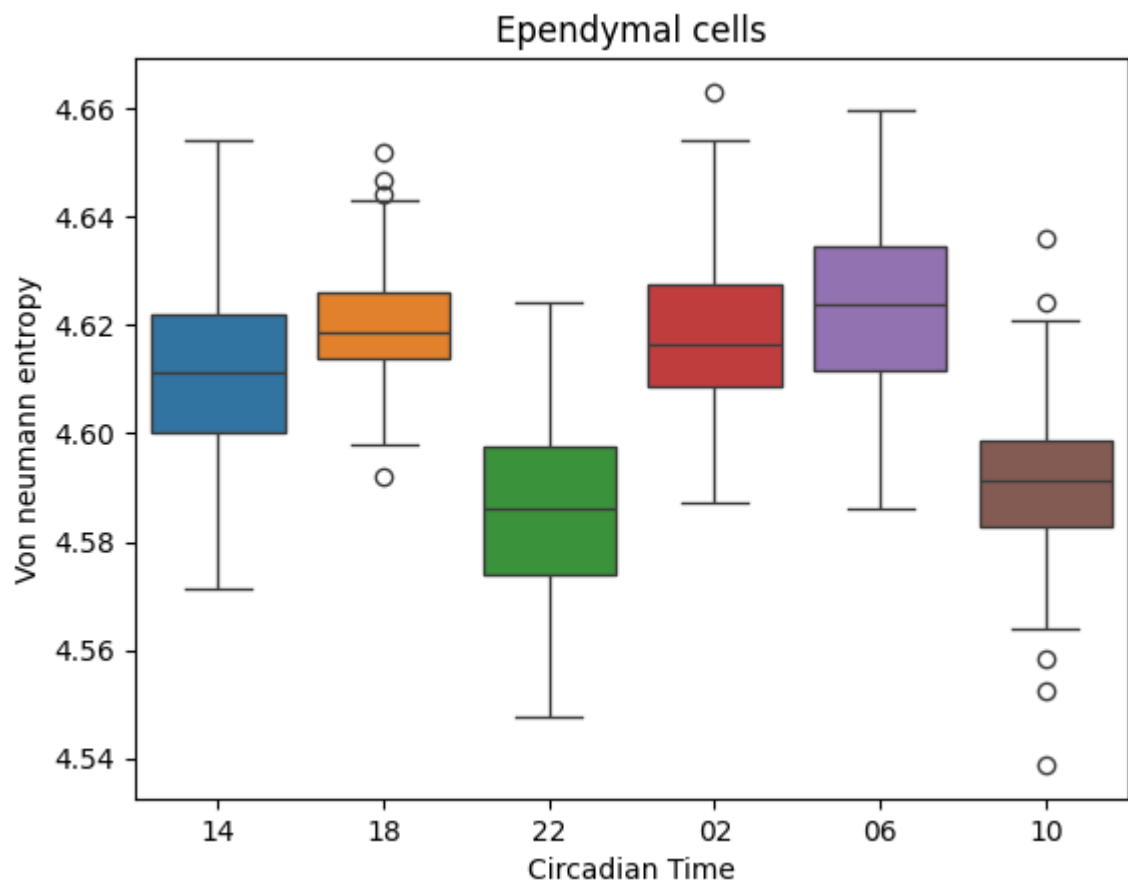
```
In [ ]: result_dict = {}
k = 100
clusters_to_check = ['Ependymal', 'Endothelial']
n_samples = [ 300, 150]
for cluster_num, cluster in enumerate(clusters_to_check) :
    sample_size = n_samples[cluster_num]
    result_dict[cluster] = []
    for ct in cts:
        entropies=np.zeros(k)
        for i in range(k):
            subset = adata[(adata.obs['louvain'] == cluster) & (adata.obs
sc.pp.subsample(subset, n_obs=sample_size, random_state=i)
            expression_matrix = subset.X
            cov = (expression_matrix @ expression_matrix.T)
            vn_entropy = von_ne(cov)
            entropies[i] = vn_entropy
        result_dict[cluster].append(entropies)
```

```
In [ ]: import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt

# Now we can create the box plots
for cluster in clusters_to_check:
    ax = sns.boxplot(data=result_dict[cluster])
    ax.set_xticklabels(cts)
    ax.set_xlabel('Circadian Time')
    ax.set_ylabel('Von neumann entropy')
```

```
plt.title(f'{cluster} cells')  
plt.show()
```

```
/var/folders/c4/wctb_gj70v0_v8tlv9zqdnr0000gn/T/ipykernel_56601/397327580  
9.py:9: UserWarning: set_ticklabels() should only be used with a fixed num  
ber of ticks, i.e. after set_ticks() or using a FixedLocator.  
ax.set_xticklabels(cts)
```



```
/var/folders/c4/wctb_gj70v0_v8tlv9zqdnr0000gn/T/ipykernel_56601/397327580  
9.py:9: UserWarning: set_ticklabels() should only be used with a fixed num  
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