In [1]:
```
from scgenome import tantalus
import pandas as pd
from IPython.display import display
from scgenome import utils, cncluster, simulation, cnplot
import scipy.cluster.hierarchy as sch
import matplotlib.pyplot as plt
import numpy as np
import seaborn as sns
import time
```

In [2]:
```
all_cn_data_fp = "/Users/massoudmaher/data/sc_1935_1936_1937_cn_data_qc.
csv"
all_cn_data = pd.read_csv(all_cn_data_fp)
all_cn_data = all_cn_data.iloc[:,1:]
```

In [3]:
```
hmmcopy_tickets = ['SC-1935', 'SC-1936', 'SC-1937']
sample_ids = [["SA922"], ['SA921'], ['SA1090']]

# spike in params
total_ncells = 100
proportions = [0.3, 0.3, 0.4]

# bhc params
n_states = 12
alpha = 0.3
prob_cn_change = 0.8
bhc_incon = 2 # inconsistent score used for making clusters from bhc
bhc_depth = 2

# naive clusering params
naive_method = "complete"
naive_metric = "cityblock"
naive_incon = 1.1
naive_depth = 2

# Params for testing threshold values
params = simulation.expand_grid({"transform":["log","none"], "criterion"
: ["inconsistent"], "threshold": np.arange(0.025, 2, step=0.05)})
params = pd.concat([params, simulation.expand_grid({"transform":["log",
"none"], "criterion": ["distance"], "threshold": np.arange(3, 20, step=1
)})])
```

In [4]:
```
subsample = utils.get_cn_data_submixture(all_cn_data, total_ncells, hmmc
opy_tickets, sample_ids, proportions=proportions)

mixed_cn_data = subsample["mixed_cn_data"]
mixed_cn_data["origin_id_int"] = mixed_cn_data["origin_id"].factorize()[
0]
cell_counts = subsample["cell_counts"]
```

```
/Users/massoudmaher/Documents/Code/scgenome/scgenome/utils.py:169: Sett
ingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-d
ocs/stable/indexing.html#indexing-view-versus-copy
  jira_cn_data[origin_field_name] = hmmcopy_tickets[i]
```

In [5]:
```
start = time.time()
bhc_linkage, bhc_root, bhc_cell_ids, matrix_data, measurement, variances
= (
    cncluster.bayesian_cluster(mixed_cn_data, n_states=n_states, alpha=a
lpha, prob_cn_change=prob_cn_change)
)
print(f"{time.time()-start}s for BHC on {total_ncells} cells")
```

```
155.69063305854797s for BHC on 100 cells
```

In [17]:
```
bhc_linkage, bhc_plot_data = simulation.get_plot_data(bhc_linkage)
lbhc_plot_data = bhc_plot_data.copy()
lbhc_plot_data[:,2] = np.log(lbhc_plot_data[:,2]) # Log because the high
est link is way higher

naive_linkage = sch.linkage(measurement, method=naive_method, metric=nai
ve_metric)
lnaive_linkage = naive_linkage.copy()
lnaive_linkage[:,2] = np.log(lnaive_linkage[:,2])
```

In [18]:
```
def apply_fn(row):
    if row["transform"] == "log":
        df = lbhc_plot_data
    else:
        df = bhc_plot_data
    return sch.fcluster(df, row["threshold"], criterion=row["criterion"
])
params["bhc_fcluster"] = params.apply(apply_fn, axis=1)
params["bhc_num_clusters"] = params["bhc_fcluster"].apply(lambda x: len(
set(x)))

def apply_fn(row):
    if row["transform"] == "log":
        df = lnaive_linkage
    else:
        df = naive_linkage
    return sch.fcluster(df, row["threshold"], criterion=row["criterion"
])
params["naive_fcluster"] = params.apply(apply_fn, axis=1)
params["naive_num_clusters"] = params["naive_fcluster"].apply(lambda x:
len(set(x)))

params.head()
```

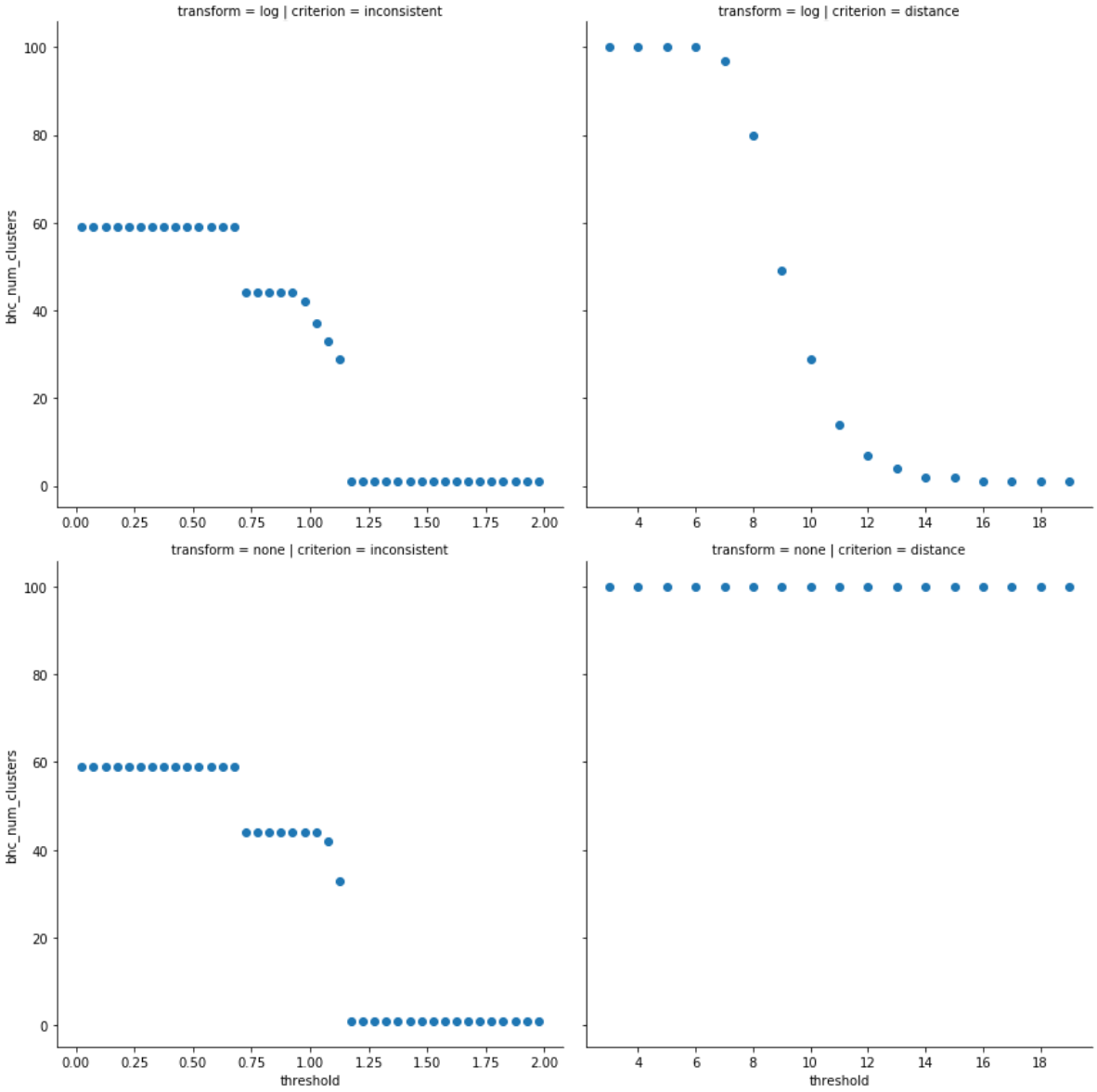
Out[18]:

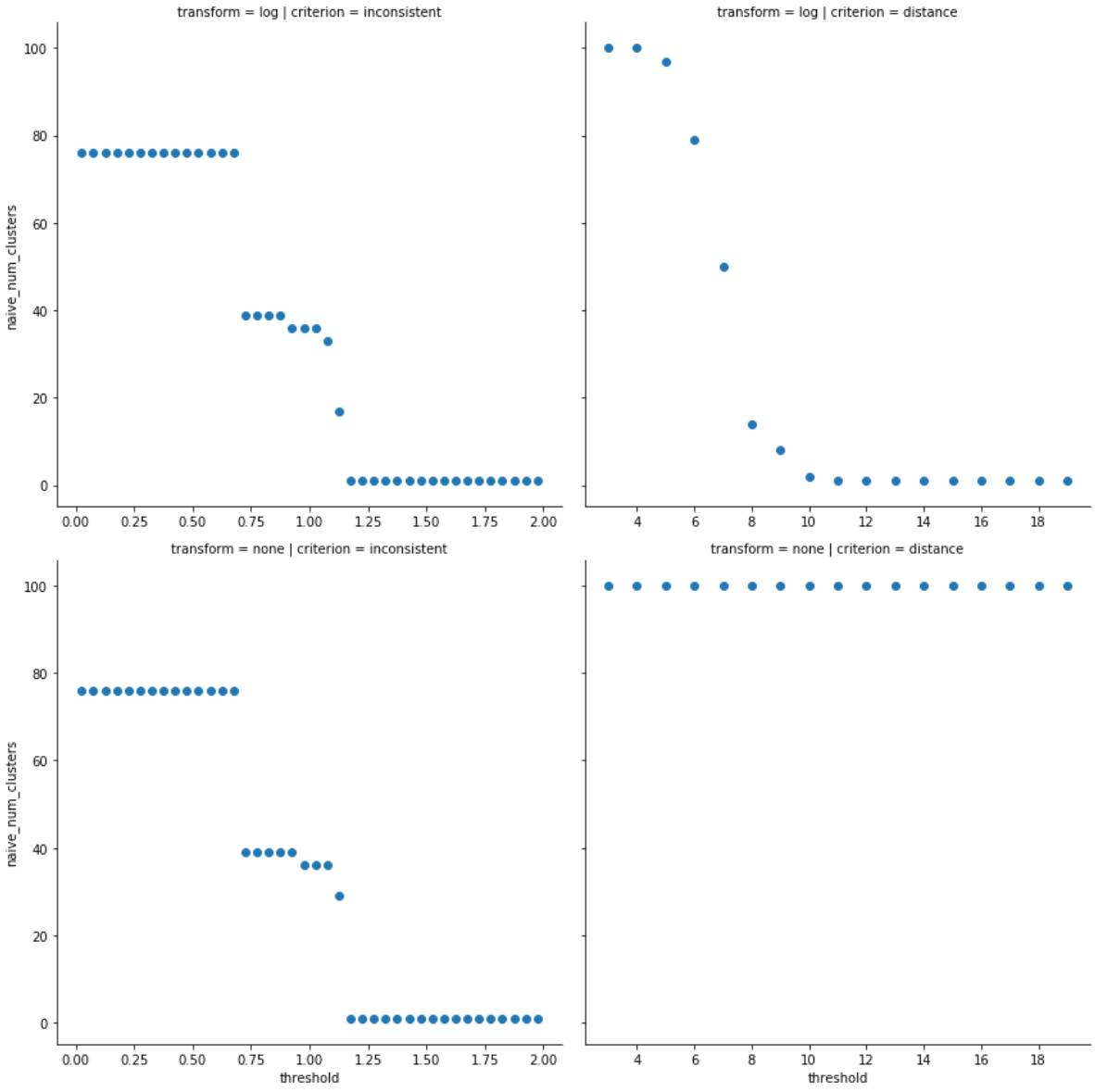
	transform	criterion	threshold	fcluster	num_clusters	bhc_fcluster	bhc_num_clusters	naiv
0	log	inconsistent	0.025	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[13, 5,
1	log	inconsistent	0.075	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[13, 5,
2	log	inconsistent	0.125	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[13, 5,
3	log	inconsistent	0.175	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[13, 5,
4	log	inconsistent	0.225	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[1, 9, 3, 14, 15, 23, 7, 26, 11, 3, 26, 11, 10...	59	[13, 5,

In [19]:

```
g = sns.FacetGrid(data=params, col="criterion", row="transform", size=6,
sharey=True, sharex=False).add_legend()
g = g.map(plt.scatter, "threshold", "bhc_num_clusters")

g = sns.FacetGrid(data=params, col="criterion", row="transform", size=6,
sharey=True, sharex=False).add_legend()
g = g.map(plt.scatter, "threshold", "naive_num_clusters")
```

```
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-packages/seaborn/axisgrid.py:230: UserWarning: The `size` paramter has been renamed to `height`; please update your code.
  warnings.warn(msg, UserWarning)
```

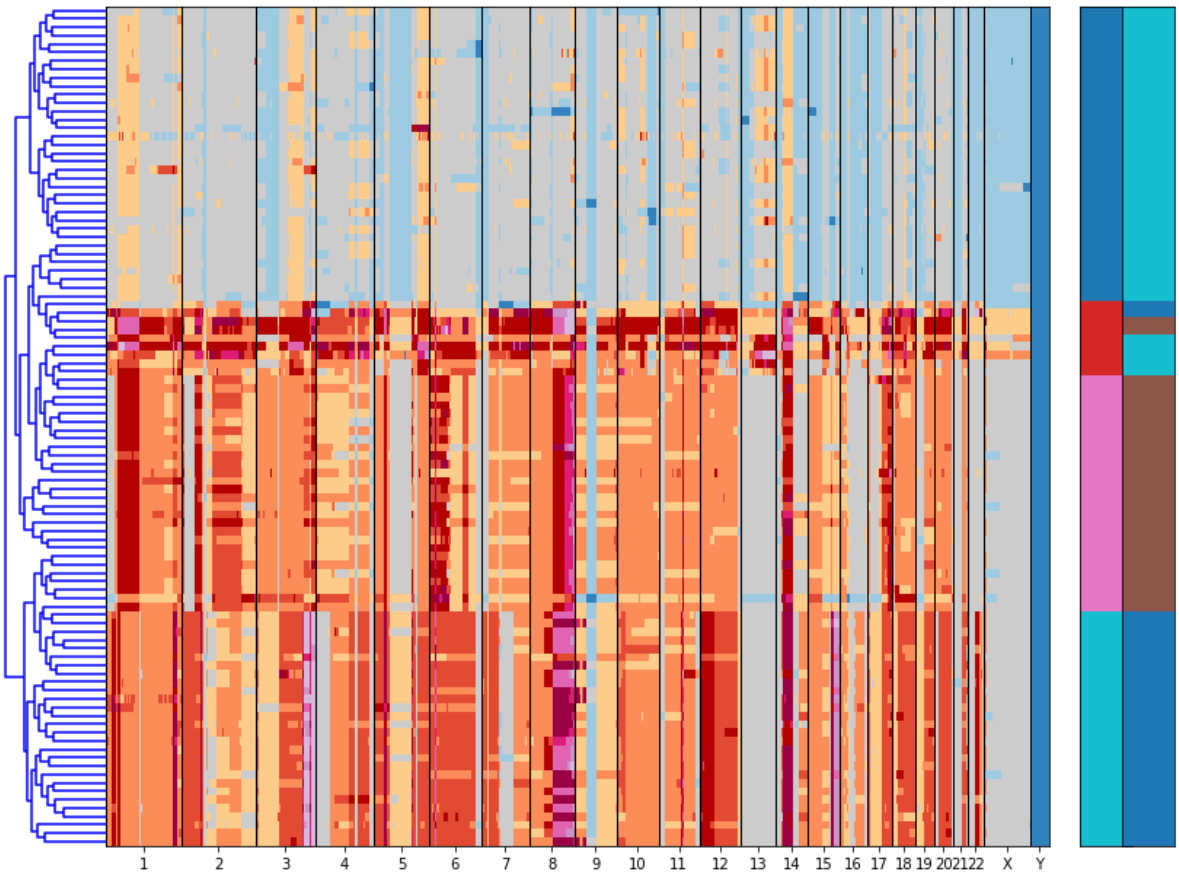




Rightmost bar represents where sample originally came frome

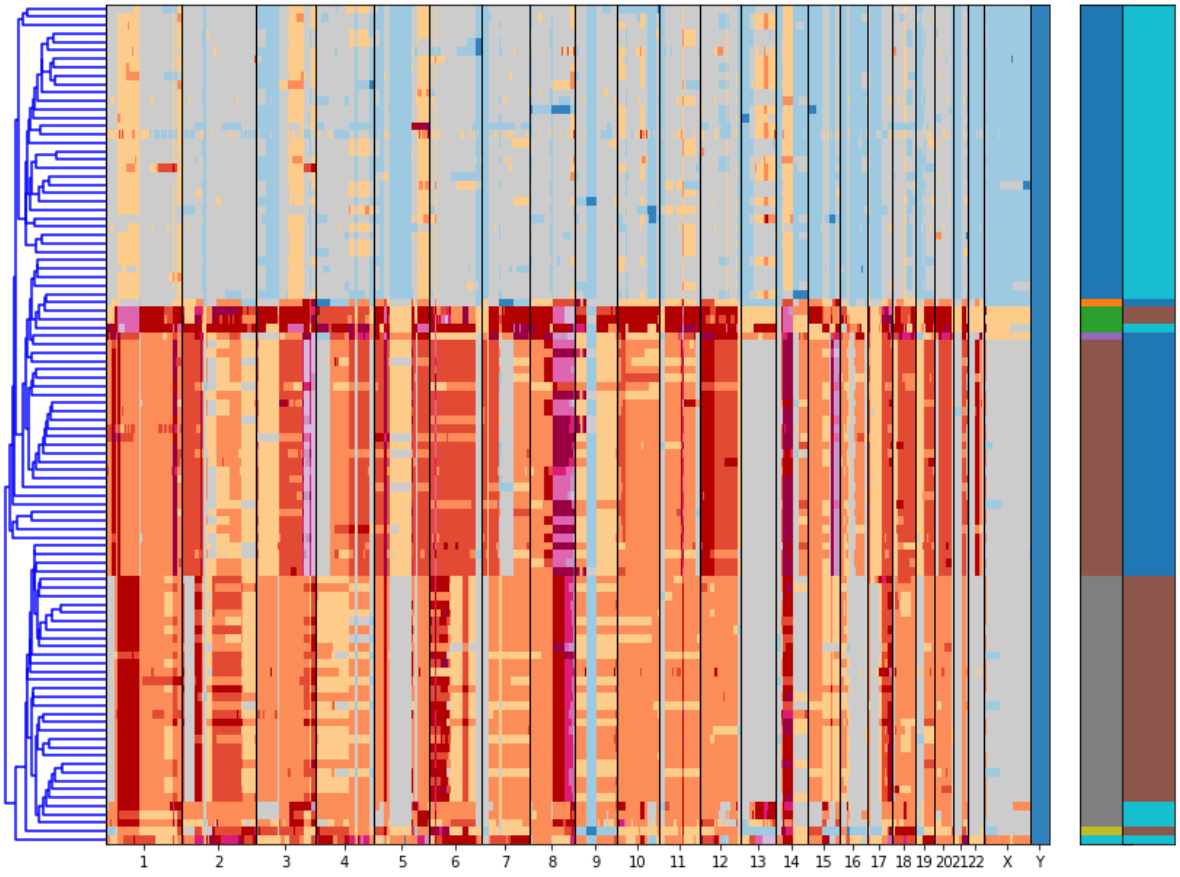
In [20]:
```
cmixed_cn_data = mixed_cn_data.copy()
clustering = sch.fcluster(lbhc_plot_data, 13, criterion="distance")
cmixed_cn_data = cncluster.prune_cluster(clustering, bhc_cell_ids, mixed
_cn_data)

fig = plt.figure(figsize=(10, 8))
bimatrix_data = cnplot.plot_clustered_cell_cn_matrix_figure(
    fig, cmixed_cn_data, "state", cluster_field_name="bhc_cluster_id",
    linkage=lbhc_plot_data, origin_field_name="origin_id_int")
```

```
/Users/massoudmaher/Documents/Code/scgenome/scgenome/cnplot.py:50: Clus
terWarning: scipy.cluster: The symmetric non-negative hollow observatio
n matrix looks suspiciously like an uncondensed distance matrix
  Y = sch.linkage(D, method='complete')
```



In [22]:
```
naive_clusters = sch.fcluster(lnaive_linkage, 9, criterion="distance")
assert len(set(naive_clusters)) > 1
nmixed_cn_data = cncluster.prune_cluster(naive_clusters, bhc_cell_ids, m
ixed_cn_data,
                                         cluster_field_name="naive_clust
er_id")
fig = plt.figure(figsize=(10, 8))
bimatrix_data = cnplot.plot_clustered_cell_cn_matrix_figure(
    fig, nmixed_cn_data, "state", cluster_field_name="naive_cluster_id",
    linkage=lnaive_linkage, origin_field_name="origin_id_int")
```

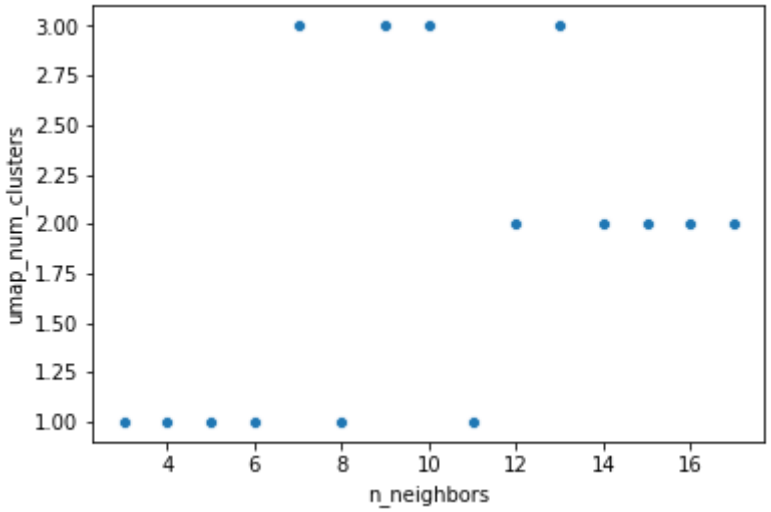
```
/Users/massoudmaher/Documents/Code/scgenome/scgenome/cnplot.py:50: Clus
terWarning: scipy.cluster: The symmetric non-negative hollow observatio
n matrix looks suspiciously like an uncondensed distance matrix
  Y = sch.linkage(D, method='complete')
```

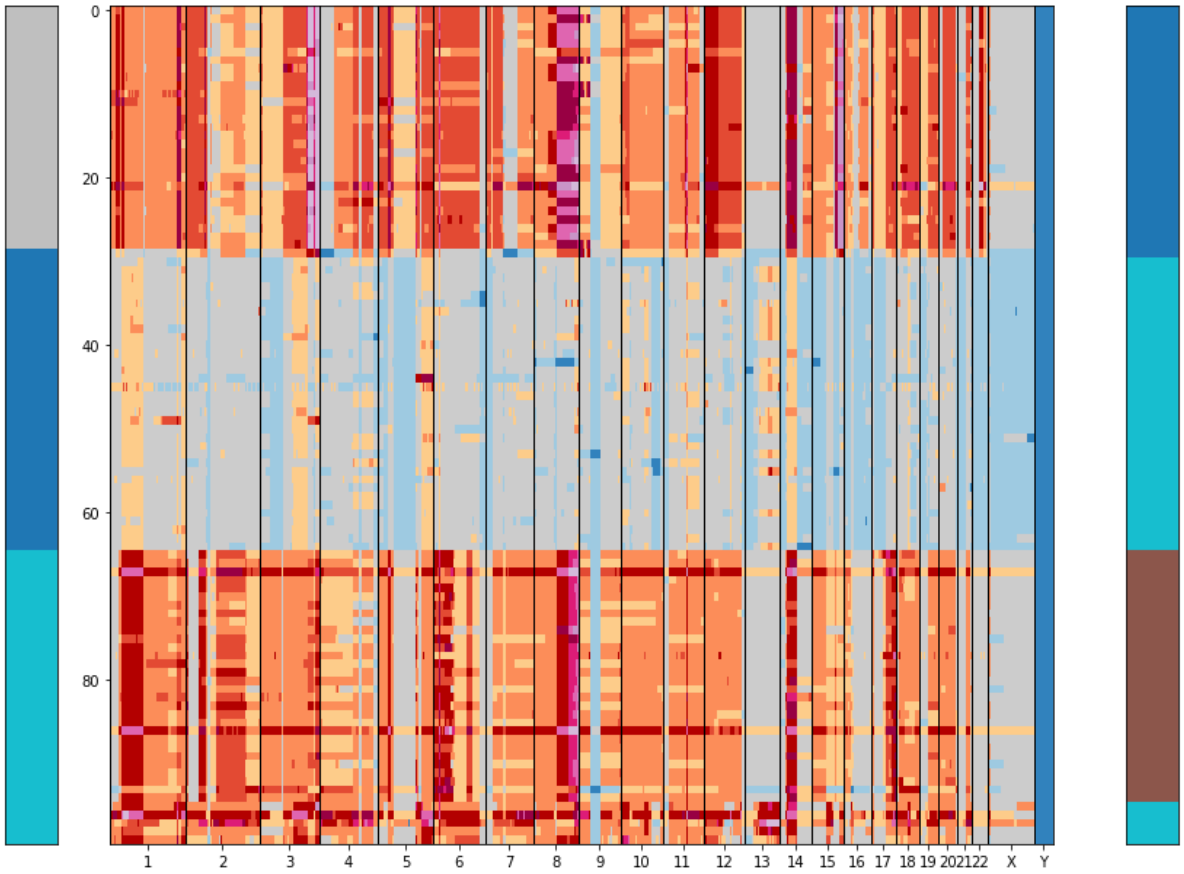


In [34]:

```
umap_params = utils.expand_grid({"n_neighbors": np.arange(3,18,step=1)})
def apply_fn(row):
    return cncluster.umap_hdbscan_cluster(matrix_data["state"], n_neighb
ors=row["n_neighbors"])

umap_params["umap_clusters"] = umap_params.apply(apply_fn, axis=1)
umap_params["umap_num_clusters"] = umap_params["umap_clusters"].apply(la
mbda x: len(set(x["cluster_id"])))

sns.scatterplot(data=umap_params, x="n_neighbors", y="umap_num_clusters"
)

umap_df = cncluster.umap_hdbscan_cluster(matrix_data["state"], n_neighbo
rs=10)
umixed_cn_data = mixed_cn_data.merge(umap_df, how="inner")

fig = plt.figure(figsize=(10, 8))
bimatrix_data = cnplot.plot_clustered_cell_cn_matrix_figure(
    fig, umixed_cn_data, "state", cluster_field_name="cluster_id",
    linkage=None, origin_field_name="origin_id_int")
#def umap_hdbscan_cluster(
#        cn,
#        n_components=2,
#        n_neighbors=15,
#        min_dist=0.1,
#):
```

```
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-pack
ages/umap/spectral.py:229: UserWarning: Embedding a total of 8 separate
connected components using meta-embedding (experimental)
  n_components
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-pack
ages/sklearn/manifold/spectral_embedding_.py:237: UserWarning: Graph is
not fully connected, spectral embedding may not work as expected.
  warnings.warn("Graph is not fully connected, spectral embedding"
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-pack
ages/umap/spectral.py:229: UserWarning: Embedding a total of 8 separate
connected components using meta-embedding (experimental)
  n_components
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-pack
ages/sklearn/manifold/spectral_embedding_.py:237: UserWarning: Graph is
not fully connected, spectral embedding may not work as expected.
  warnings.warn("Graph is not fully connected, spectral embedding"
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-pack
ages/umap/spectral.py:229: UserWarning: Embedding a total of 4 separate
connected components using meta-embedding (experimental)
  n_components
/Users/massoudmaher/Documents/Code/scgenome/scgenome/cnplot.py:50: Clus
terWarning: scipy.cluster: The symmetric non-negative hollow observatio
n matrix looks suspiciously like an uncondensed distance matrix
  Y = sch.linkage(D, method='complete')
```





Umap does better-- especially considering that it runs way faster

In [ ]: