In [1]:

```
from scgenome.tantalus import get_data
from scgenome.qc import qc_cn
from IPython.display import display

hmmcopy_tickets = [
#     'SC-1935',
    'SC-1936',
#     'SC-1937',
]

sample_ids = [
#     'SA922',
    'SA921',
#     'SA1090',
]

data = get_data(hmmcopy_tickets, sample_ids, cached=True)
cn_data = data[0]
segs_data = data[1]
metrics_data = data[2]
align_metrics_data = data[3]

print("cn_data.head()")
display(cn_data.head())

#cn = qc_cn(metrics_data, cn_data)
#print("cn.head()")
#display(cn.head())
```

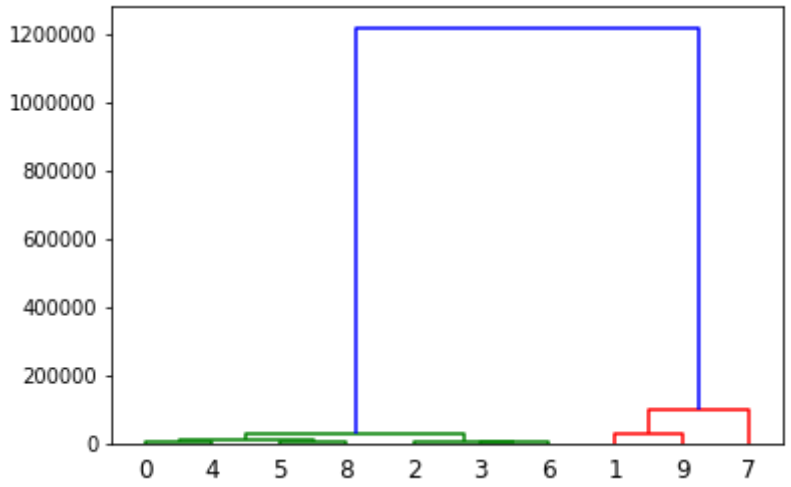
```
/Users/massoudmaher/Documents/Code/scgenome/scgenome/utils.py:56: SettingWithCopyWarning:
A value is trying to be set on a copy of a slice from a DataFrame.
Try using .loc[row_indexer,col_indexer] = value instead

See the caveats in the documentation: http://pandas.pydata.org/pandas-docs/stable/indexing.html#inde
xing-view-versus-copy
  df[col] = df[col].astype('category')
/Users/massoudmaher/Documents/Code/scgenome/scgenome/utils.py:57: SettingWithCopyWarning:
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-docs/stable/indexing.html#inde
xing-view-versus-copy
  df[col] = df[col].cat.set_categories(col_categories[col])
2019-09-07 14:27:28,713 - INFO - cdfa9ee0-a8b7-4060-aeb8-f02e0bf6aabe - TokenRequest:Getting token w
ith client credentials.
2019-09-07 14:27:29,053 - INFO - cdfa9ee0-a8b7-4060-aeb8-f02e0bf6aabe - OAuth2Client:Get Token Serve
r returned this correlation_id: cdfa9ee0-a8b7-4060-aeb8-f02e0bf6aabe

cn_data.head()
```

	chr	start	end	reads	gc	copy	state	cell_id	sample_id	library_id
0	1	1	500000	0	-1.000000	NaN	2	SA921-A90554A-R12-C09	SA921	A90554A
1	1	500001	1000000	41	-1.000000	NaN	2	SA921-A90554A-R12-C09	SA921	A90554A
2	1	1000001	1500000	6	0.598332	1.754408	2	SA921-A90554A-R12-C09	SA921	A90554A
3	1	1500001	2000000	10	0.539498	1.873090	2	SA921-A90554A-R12-C09	SA921	A90554A
4	1	2000001	2500000	9	0.594508	2.515035	2	SA921-A90554A-R12-C09	SA921	A90554A

In [2]:
```
# Subset small amount of cells
n_cell = 10

keep_cells = cn_data["cell_id"].value_counts().index[0:n_cell]
sub_cn_data = cn_data[cn_data["cell_id"].isin(keep_cells)]
```

In [3]:
```
# BHC them!
from scgenome.cncluster import bayesian_cluster

linkage, clusters, cell_ids = bayesian_cluster(sub_cn_data, n_states = sub_cn_data["state"].max())
```

In [4]:
```
from scipy.cluster.hierarchy import dendrogram
from scgenome.simulation import get_plot_data

plinkage, plot_data = get_plot_data(linkage)
f = dendrogram(plot_data)
```



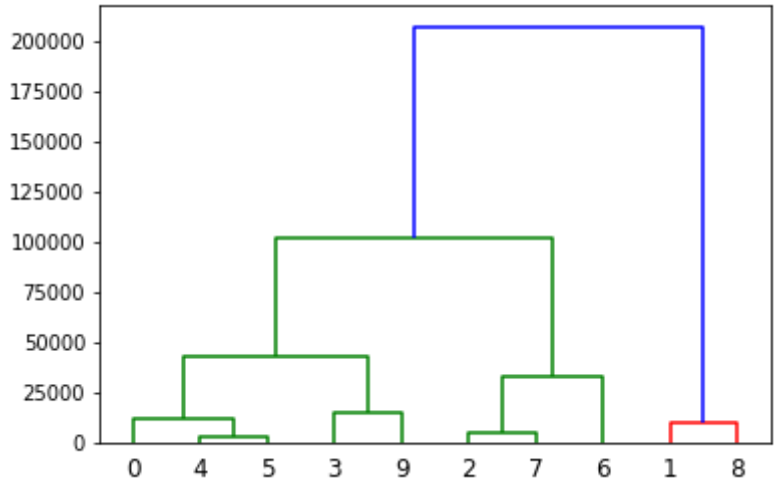
In [5]:
```
hmmcopy_tickets = ['SC-1937']
sample_ids = ['SA1090']

xdata = get_data(hmmcopy_tickets, sample_ids, cached=True)
xcn_data = xdata[0]
xsegs_data = xdata[1]
xmetrics_data = xdata[2]
xalign_metrics_data = xdata[3]

print("cn_data.head()")
display(xcn_data.head())
```

```
/Users/massoudmaher/Documents/Code/scgenome/scgenome/utils.py:56: SettingWithCopyWarning:
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-docs/stable/indexing.html#inde
xing-view-versus-copy
  df[col] = df[col].astype('category')
/Users/massoudmaher/Documents/Code/scgenome/scgenome/utils.py:57: SettingWithCopyWarning:
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-docs/stable/indexing.html#inde
xing-view-versus-copy
  df[col] = df[col].cat.set_categories(col_categories[col])
2019-09-07 14:28:39,389 - INFO - 2acd6420-8b86-47f7-a868-186119d6de86 - TokenRequest:Getting token w
ith client credentials.
2019-09-07 14:28:39,547 - INFO - 2acd6420-8b86-47f7-a868-186119d6de86 - OAuth2Client:Get Token Serve
r returned this correlation_id: 2acd6420-8b86-47f7-a868-186119d6de86

cn_data.head()
```

	chr	start	end	reads	gc	copy	state	cell_id	sample_id	library_id
0	1	1	500000	2	-1.000000	NaN	2	SA1090-A96213A-R34-C64	SA1090	A96213A
1	1	500001	1000000	42	-1.000000	NaN	2	SA1090-A96213A-R34-C64	SA1090	A96213A
2	1	1000001	1500000	43	0.598332	3.017390	2	SA1090-A96213A-R34-C64	SA1090	A96213A
3	1	1500001	2000000	42	0.539498	1.936414	2	SA1090-A96213A-R34-C64	SA1090	A96213A
4	1	2000001	2500000	36	0.594508	2.439622	2	SA1090-A96213A-R34-C64	SA1090	A96213A

In [6]:
```
# Subset small amount of cells
xkeep_cells = xcn_data["cell_id"].value_counts().index[0:n_cell]
xsub_cn_data = xcn_data[xcn_data["cell_id"].isin(xkeep_cells)]
```

In [7]:
```
# BHC them!
xlinkage, xclusters, xcell_ids = bayesian_cluster(xsub_cn_data, n_states = xsub_cn_data["state"].max
())

xplinkage, xplot_data = get_plot_data(xlinkage)
f = dendrogram(xplot_data)
```



In [8]:
```
# Combine two datasets and see if we can seperate
sub_cn_data["cell_id"] = "cl1_" + sub_cn_data["cell_id"].astype("str")
xsub_cn_data["cell_id"] = "cl2_" + xsub_cn_data["cell_id"].astype("str")

bi_cn_data = sub_cn_data.append(xsub_cn_data)
bilinkage, biclusters, bicell_ids = bayesian_cluster(bi_cn_data, n_states = bi_cn_data["state"].max
())

biplinkage, biplot_data = get_plot_data(bilinkage)
#f = dendrogram(biplot_data, labels = bicell_ids.str[2])
```

```
/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-packages/ipykernel_launcher.py:2:
SettingWithCopyWarning:
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-docs/stable/indexing.html#inde
xing-view-versus-copy

/Users/massoudmaher/Documents/Code/scgenome/scg/lib/python3.7/site-packages/ipykernel_launcher.py:3:
SettingWithCopyWarning:
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-docs/stable/indexing.html#inde
xing-view-versus-copy
  This is separate from the ipykernel package so we can avoid doing imports until
```

In [9]:
```
from scgenome import utils
```

In [20]:
```
bi_cn_mat, bi_cn_meas, bi_cn_ids = utils.cn_data_to_mat_data_ids(bi_cn_data, data_id="state")
#def cn_data_to_mat_data_ids(cn_data, data_id=CN_DATA_ID, cell_id=CELL_ID,
#                            index_ids=INDEX_IDS, value_ids=VALUE_IDS):
y_labels = bi_cn_ids.str[2].astype(int) - 1
```

In [24]:
```
nbiplot_data = biplot_data.copy()
nbiplot_data[:,2] = np.log(nbiplot_data[:,2])
```

In [28]:
```
g = sns.clustermap(bi_cn_meas, col_cluster=False, row_linkage=nbiplot_data, yticklabels = y_labels, cmap="YlGnBu")
```