```
In [1]: cd ../../
        /Users/in-divye.singh/Documents/Projects/MIC_predictor
In [2]: import json
        import numpy as np
        import pandas as pd
        import seaborn as sns
        import matplotlib.pyplot as plt
In [3]: from notebooks.utils import *
        import importlib
        import sys
        importlib.reload(sys.modules['notebooks.utils'])
        from notebooks.utils import *
In [4]: from sklearn.manifold import TSNE
In [5]: avp_ic50 = pd.read_csv("data/raw/AVP-IC50Pred_train.csv")
        ha_avp = pd.read_csv("data/raw/HA_AVP.csv")
        df = pd.concat([avp_ic50[['Sequence', 'MIC']], ha_avp], axis=0).drop_dup
        licates(['Sequence']).reset_index(drop=True)
        df = sequence filtering(df)
        # df = df.sample(frac=1).reset index(drop=True)
In [6]: results = pd.read csv("results/knn regressor all data combination.csv",
        sep=';')
```

In [7]: results

Out[7]:

	Data	Regressor	Best_parameters	MSE	
0	aa_freq	KNN	"{'metric': 'chebyshev', 'n_neighbors': 1, 'w	4238.627327	32
1	dipep_freq	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	3578.824434	27
2	tripep_freq	KNN	"{'metric': 'chebyshev', 'n_neighbors': 1, 'w	5870.207139	40
3	avg_protvec	KNN	"{'metric': 'chebyshev', 'n_neighbors': 1, 'w	5264.466418	32
4	physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4032.816185	32
5	aa_freq+dipep_freq	KNN	"{'metric': 'chebyshev', 'n_neighbors': 2, 'w	2713.243562	28
6	aa_freq+tripep_freq	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	3078.615787	27
7	aa_freq+avg_protvec	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	3872.983691	29
8	aa_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4032.815319	32
9	dipep_freq+tripep_freq	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	3957.573630	28
10	dipep_freq+avg_protvec	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	3812.866251	28
11	dipep_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4338.643744	32
12	tripep_freq+avg_protvec	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	4392.751276	30

	Data	Regressor	Best_parameters	MSE	
13	tripep_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4335.419158	32
14	avg_protvec+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4341.027995	32
15	aa_freq+dipep_freq+tripep_freq	KNN	"{'metric': 'chebyshev', 'n_neighbors': 1, 'w	5004.976604	34
16	aa_freq+dipep_freq+avg_protvec	KNN	"{'metric': 'chebyshev', 'n_neighbors': 3, 'w	2906.852170	30
17	aa_freq+dipep_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4338.552297	32
18	aa_freq+tripep_freq+avg_protvec	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	4469.164472	30
19	aa_freq+tripep_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4335.356502	32
20	aa_freq+avg_protvec+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4341.027995	32
21	dipep_freq+tripep_freq+avg_protvec	KNN	"{'metric': 'euclidean', 'n_neighbors': 1, 'w	4067.402527	28
22	dipep_freq+tripep_freq+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4335.174994	32
23	dipep_freq+avg_protvec+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4353.697911	32
24	tripep_freq+avg_protvec+physicochemical_prop	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4337.730653	32
25	aa_freq+dipep_freq+tripep_freq+avg_protvec	KNN	"{'metric': 'chebyshev', 'n_neighbors': 1, 'w	3780.234082	29
26	aa_freq+dipep_freq+tripep_freq+physicochemical	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4335.181708	32

	Data F	Regressor	Best_parameters	MSE	
	27 aa_freq+dipep_freq+avg_protvec+physicochemical	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4353.705690 32	
	28 aa_freq+tripep_freq+avg_protvec+physicochemica	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4353.634235 32	
	29 dipep_freq+tripep_freq+avg_protvec+physicochem	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4337.572838 32	
	30 aa_freq+dipep_freq+tripep_freq+avg_protvec+phy	KNN	"{'metric': 'euclidean', 'n_neighbors': 2, 'w	4337.572838 32	
In [8]:	<pre>print(f"Best MAPE: {results['MAPE'].min()}") print(f"Best performing data: {results.loc[results['MAPE'].argmin()]['Da ta']}") print(f"Best parameters: {results.loc[results['MAPE'].argmin()]['Best_pa rameters']}")</pre>				
	<pre>Best MAPE: 38427.619517675776 Best performing data: dipep_freq+avg_protvec Best parameters: "{'metric': 'euclidean', 'n_neighbors': 1, 'weights': 'uniform'}"</pre>				

Analysis

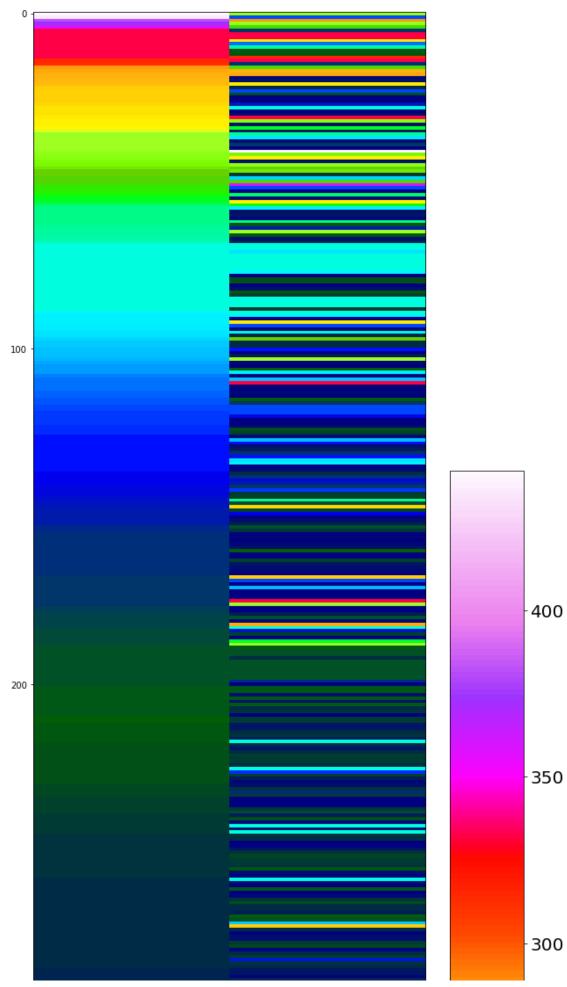
```
dipep_freq = reduce_by_kmer_frequency(df, kmer=2)
In [9]:
In [10]: uniprot embedding = biovec.models.load protvec("data/embeddings/uniprot
         kmer 3 contextWindow 10 vector 100 reduction None")
         avg_protvec = convert_sequences_to_avg_vectors(df['Sequence'], uniprot_e
         mbedding)
         avg protvec = avg protvec.reset index(drop=True)
         /Users/in-divye.singh/anaconda3/envs/life-science/lib/python3.6/site-pa
         ckages/smart_open/smart_open_lib.py:254: UserWarning: This function is
         deprecated, use smart open.open instead. See the migration notes for de
         tails: https://github.com/RaRe-Technologies/smart_open/blob/master/READ
         ME.rst#migrating-to-the-new-open-function
           'See the migration notes for details: %s' % MIGRATION NOTES URL
         Creating vectors: 100% | 712/712 [00:00<00:00, 1125.60sequenc
         e/sl
In [11]: dipep_protvec = pd.concat([avg_protvec, dipep_freq], axis=1)
         from sklearn.neighbors import NearestNeighbors
In [12]:
```

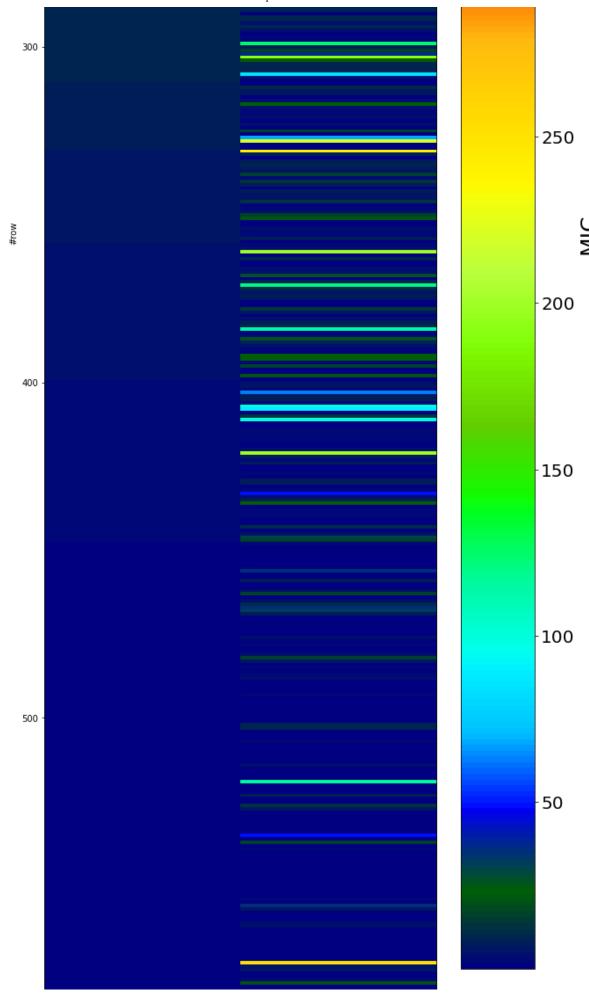
```
In [13]:
         def plot nbr mic(data, target, n neighbors=1, metric='euclidean', n jobs
         =10):
             data = data.reset index(drop=True)
             target = target.reset_index(drop=True)
             nearesr neighbors = NearestNeighbors(n neighbors=n neighbors, metric
         =metric, n jobs=n jobs)
             nearesr neighbors.fit(data)
             grph = nearesr neighbors.kneighbors graph(n neighbors=n neighbors).t
         odense()
             neighbors = np.where(grph == 1)
             neighbors = np.array([[i]+neighbors[1][np.where(neighbors[0]==i)[0]]
         .tolist() for i in range(data.shape[0])])
             mic nbrs = np.full(neighbors.shape, np.nan)
             for i in range(mic nbrs.shape[1]):
                 mic_nbrs[:,i] = target[neighbors[:,i]]
             plt.figure(figsize=(5*mic nbrs.shape[1],50))
             im = plt.imshow(mic nbrs, cmap='gist ncar', interpolation='none') #p
         lt.cm.get cmap('gist rainbow', 75)
             cbar = plt.colorbar(im)
             cbar.ax.tick params(labelsize=20)
             cbar.set_label('MIC', fontsize=25)
             plt.axis('auto')
             plt.xlabel('neighbors', fontdict={'size':5*mic_nbrs.shape[1]})
             plt.ylabel('#row', fontdict={'size':5*mic nbrs.shape[1]})
             plt.xticks(fontsize=5*mic_nbrs.shape[1])
             plt.yticks(fontsize=5*mic nbrs.shape[1])
             plt.show()
```

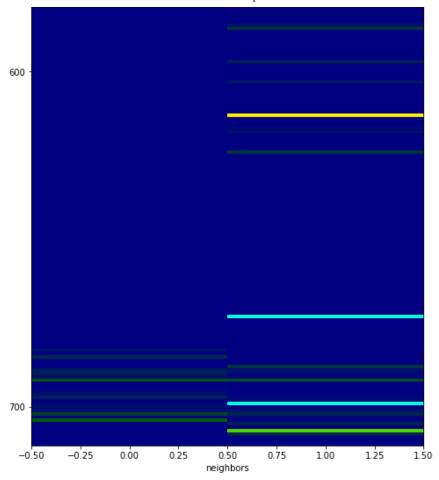
Observation

For kNN to give good results, sequences which are closer together should have MIC values closer together. But it is seen from below plot that many of the sequences with higher MIC values have low MIC value sequeces as their neighbors. However, as we look at lower MIC value sequences, they start to have low MIC value sequeces as their neighbors.

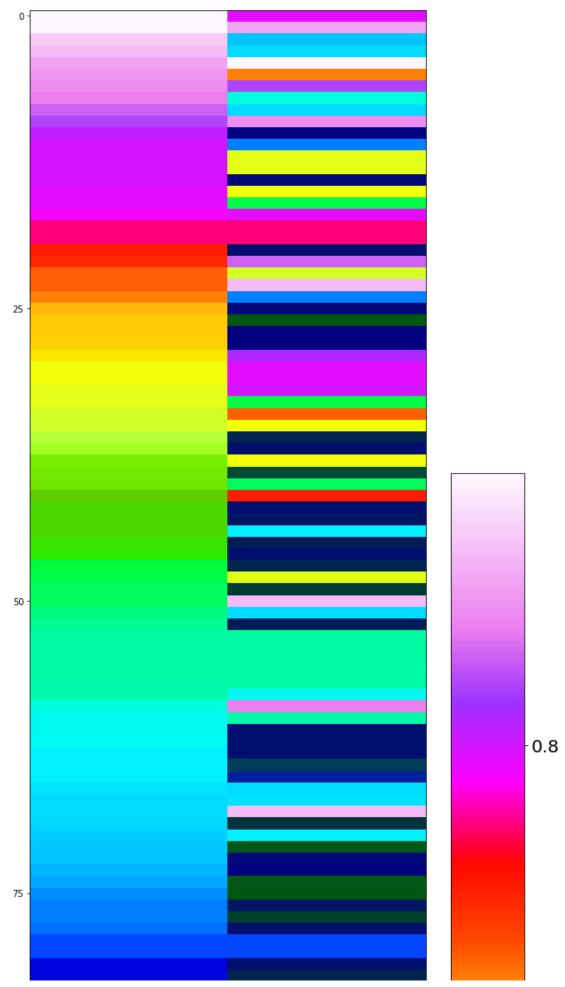
In [14]: plot_nbr_mic(dipep_protvec, df['MIC'], n_neighbors=1)

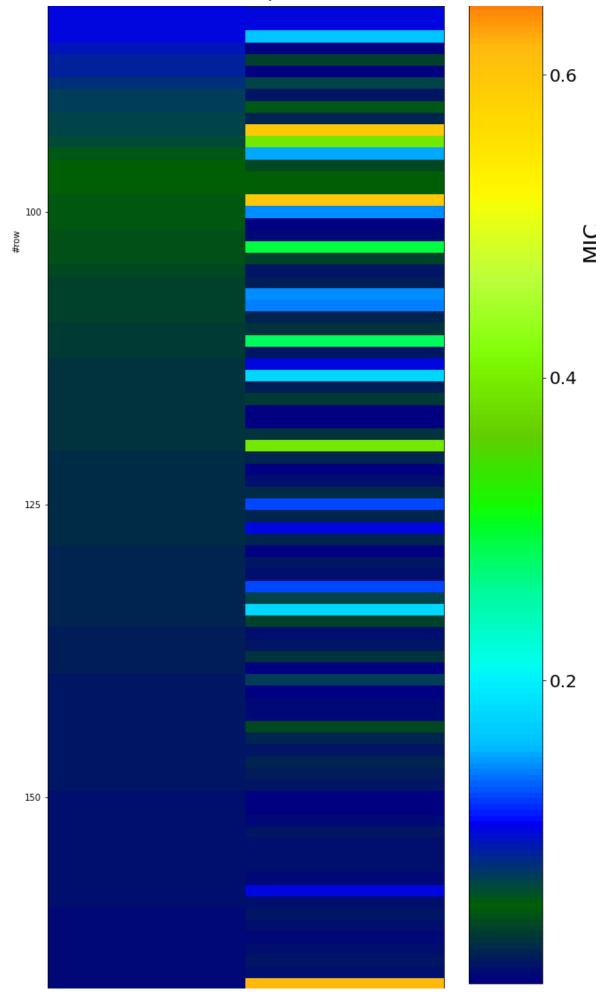


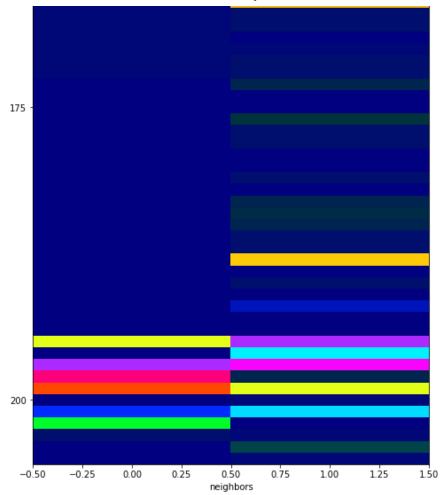




In [17]: plot_nbr_mic(dipep_protvec[mask], df['MIC'][mask], n_neighbors=1)







In []: