## BME-230B Spring 2019 HW 2 Question 4

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## 4.a. [10 pts]

Turn in code that can compute a bb-l-k-NNG from a given bb-k-NNG. In addition to the input bb-k-NNG, the method should take in a parameter specifying the number of subsampled graphs that should be returned. Each of the returned subsampled graphs should represent a distinct subsampled bb-l-k-NNG from the given input graph. Fill in the l\_k\_bbknn method in euclid\_bknn.py. You can set the I parameter accordingly. NOTE: in order to run this function successfully you will have to run the bbknn() method first, and then run the l\_k\_bbknn method. Consult example usage within euclid\_bbknn.py.

Question 4.a see bblknn.py (bblknn.py)

```
In [1]: from euclid bbknn import bbknn graph
        from bblknn import bblknn graph
        import matplotlib.pyplot as plt
        import scanpy as sc
        import numpy as np
        print("scanpy.__version__:{}".format(sc.__version__))
        scanpy.__version__:1.4
In [2]: | %%time
        anndata = sc.read("PBMC.merged.h5ad")
        CPU times: user 4.2 s, sys: 128 ms, total: 4.32 s
        Wall time: 1.52 s
In [3]: %%time
        # run our implementation of batch-balanced nearest neighbors and update ann
        bbknn graph(anndata, neighbors within batch=6, runPCA=True, pcs=50)
        CPU times: user 5min 5s, sys: 9.08 s, total: 5min 14s
        Wall time: 4min 50s
Out[3]: <euclid bbknn.bbknn graph at 0x7f0f33ba5390>
In [4]: | # run louvain clustering on bb6nn
        sc.tl.louvain(anndata, flavor='igraph', directed=False, use weights=True)
In [5]: # save louvain assignments for bb6nn so we can use them in part b
        bb6nn_louvain = anndata.obs['louvain']
```

```
In [6]: %%time
# run our implementation of subsampled batch-balanced nearest neighbors
bblknn_graph(anndata, k_per_batch=6, 1=3, n_components=50)

CPU times: user 6min 20s, sys: 16.4 s, total: 6min 37s
Wall time: 5min 17s

Out[6]: <bblknn.bblknn_graph at 0x7f0e50a3eeb8>
```

## 4.b. [10 pts]

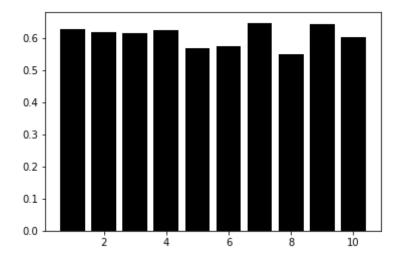
Turn in a bar plot of the Adjusted Rand Index (ARI) for Louvain clusters obtained from 10 independently subsampled bb-3-6-NNGs compared to the Louvain clusters obtained on the original bb-6-NNGs. Also report the average and standard deviations of the ARI. Based on these results, would you conclude these clusters are robust? Justify your answer. Hint: check if your ARI is significantly better than chance.

```
In [9]: from sklearn.metrics.cluster import adjusted_rand_score
        # number of samples to run
        samples = 10
        # list of ARIs obtained from each sample
        results = []
        for sample in range(samples):
            # subsample batch-balanced nearest neighbors
            bblknn graph(anndata, k per batch=6, 1=3, n components=50)
            # run louvain clustering on subsampled graph
            sc.tl.louvain(anndata)
            bb3 6nn louvain = anndata.obs['louvain']
            # calculate and store ARI
            ars = adjusted rand score(bb6nn louvain, bb3 6nn louvain)
            results.append(ars)
            # print iteration progress
            print(sample+1, end=' ')
```

1 2 3 4 5 6 7 8 9 10

```
In [11]: # plot ARIs and print statistics
    plt.bar(range(1, len(results)+1), results, color='black')
    print('Average:', np.mean(results), 'SD:', np.std(results))
```

Average: 0.6062524085875942 SD: 0.031101843378884712



```
In [2]: # calculate t-statistic to determine significance of the mean as compared t
#t = (sample-mean - population-mean) / (sample-std-dev / sqrt(n))
sampleMean = 0.6062524085875942
populationMean = 0
sampleStdDev = 0.031101843378884712
n = 10
t = (sampleMean - populationMean ) / (sampleStdDev / 10 ** 1/2)
print("t = {}".format(t))
```

t = 389.84982414205314

```
In [3]: # now convert t-statistic to p-value
    from scipy import stats
    import numpy as np
    p = stats.t.sf(np.abs(t), n-1)*2
    print("p = {}".format(p))
```

p = 2.447313138582953e-20

Based on our results, we conclude that the clustering is robust. The mean of 0.60 with a p-value of 2.4\*e-20 (nearly 0) suggests that our ARI is significantly better than chance.