Problem 5(e)

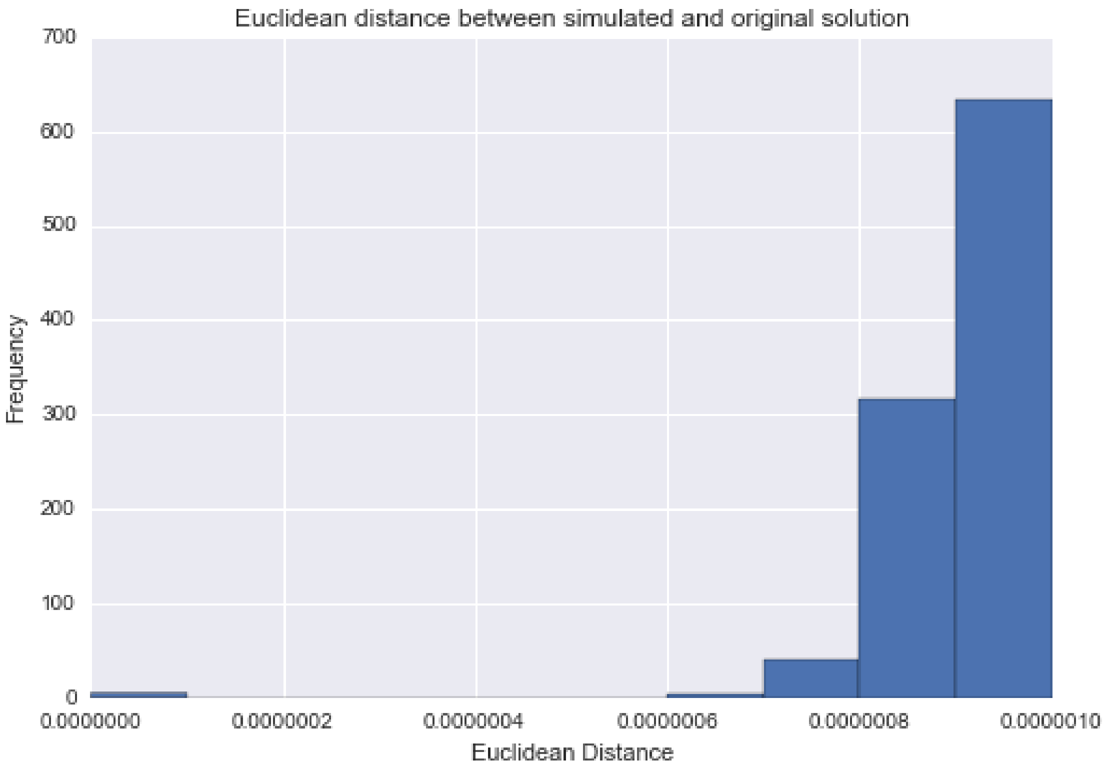
November 5, 2015

```
In [2]: %matplotlib inline
        from __future__ import division
        import numpy as np
        from numpy import linalg as LA
        import matplotlib.pyplot as plt
        import seaborn as sns
        p = np.array([1/6,1/3,1/3,1/6])
        n_indiv = 200
        n_haplotypes = 2*n_indiv
        haplotype_config = [[0,0],[0,1],[1,0],[1,1]]
        haplotype_count_dict = {'[0,0]':0,'[0,1]':0, '[1,0]':0, '[1,1]':0}
        max_iter = 1000
        def count_g(genotype,i,j,ph):
            n0000 = genotype[0,0,0,0];
            n0001 = genotype[0,0,1,0]+genotype[0,0,1,0]
            n0100 = genotype[1,0,0,0]+genotype[0,1,0,0]
            n0101 = genotype[1,0,1,0]+genotype[0,1,0,1] + genotype[0,1,1,0] + genotype[1,0,0,1]
            n0111 = genotype[1,0,1,1]+genotype[0,1,1,1]
            n1101 = genotype[1,1,1,0]+genotype[1,1,0,1]
            n0011 = genotype[0,0,1,1]
            n1111 = genotype[1,1,1,1]
            n1100 = genotype[1,1,0,0]
            d = ph[0,0]*ph[1,1]+ph[0,1]*ph[1,0]
            if(i==0 and j==0):
                return 2*n0000+n0001+n0100+n0101*(ph[0,0]*ph[1,1]/d)
            elif(i==0 and j==1):
                return 2*n0011+n0001+n0111+n0101*(ph[0,1]*ph[1,0]/d)
            elif(i==1 and j==0):
                return 2*n1100+n1101+n0100+n0101*(ph[0,1]*ph[1,0]/d)
            else:
                return 2*n1111+n1101+n0111+n0101*(ph[0,0]*ph[1,1]/d)
        norms = []
        for i in range(1,max_iter):
            assign_hap = np.random.choice(4, n_haplotypes ,p=p)
            config = []
            for ah in assign_hap:
                config.append(haplotype_config[ah])

            genotype = np.zeros((2,2,2,2))
            for j in range(0,n_haplotypes-1):
                genotype[config[j][0], config[j][1], config[j+1][0], config[j+1][1]]+=1

            n0 = np.ones((2,2))*n_indiv/2
```

```
    ph = np.zeros((2,2))
    pnew = n0/n_haplotypes
    while (LA.norm(ph.flatten()-pnew.flatten(),2)>1e-6):
        n0[0,0] = count_g(genotype,0,0,pnew)
        n0[0,1] = count_g(genotype,0,1,pnew)
        n0[1,0] = count_g(genotype,1,0,pnew)
        n0[1,1] = count_g(genotype,1,1,pnew)
        ph = pnew
        pnew = n0/n_haplotypes
    norms.append(LA.norm(ph.flatten()-pnew.flatten(),2))
```

```
In [5]: plt.hist(norms)
        plt.xlabel('Euclidean Distance')
        plt.ylabel('Frequency')
        plt.title('Euclidean distance between simulated and original solution')
```

```
Out[5]: <matplotlib.text.Text at 0x108594810>
```



```
In [ ]:
```