Question 4

a. p0: [0.88 0. 0. 0. 0.04 0. 0.09 0.]

b. First 5*5 values

Tr: [[6.02e-01 3.41e-02 1.21e-01 3.68e-02 1.03e-01]
[4.61e-01 2.19e-02 4.18e-02 2.53e-02 4.52e-02]
[8.54e-02 3.56e-03 8.15e-01 4.90e-03 5.42e-03]
[1.61e-01 7.77e-03 2.13e-02 7.03e-01 3.13e-02]
[5.62e-02 5.89e-04 7.56e-04 3.39e-03 9.18e-01]]

Stationary Distribution: [1.78e-01 1.17e-02 2.24e-01 3.89e-02
3.36e-01 9.79e-05 2.10e-01 3.17e-04]

c. Ob: [[0.06 0.01 0.07 0.05 0.03]
[0.05 0.02 0.05 0.04 0.05]
[0.06 0.02 0.03 0.05 0.06]
[0.09 0.01 0.08 0.09 0.04]
[0.12 0.01 0.05 0.09 0.04]]

d. We can take one more random variable for size. Also another approach could to create a random variable which has the probability of any character being a delimiter.

e. I used a small a model, the one used in the class to check the code, and manually confirmed the output

File:1l9g.txt P(x6|o(0)) = [7.39e-02 4.83e-03 1.59e-01 3.39e-02
6.79e-01 1.62e-05 4.85e-02 1.47e-04]

File:1h6h.txt P(x9|o(2)) = [1.26e-01 5.39e-03 2.71e-02 5.85e-02
6.77e-01 1.93e-05 1.05e-01 1.01e-04]

File:1rdr.txt logp(o(4)) = -929.182828473

Code:

```
import numpy as np
from os import walk
mypath = 'proteins/'  # use path to data files
_, _, filenames = next(walk(mypath), (None, None, []))

np.set_printoptions(precision=2)

mSeq = len(filenames)        # read in each sequence
# mSeq = 10
o,x = [],[]
for i in range(mSeq):
    f = open('proteins/' +  filenames[i] , 'r')
```

```
    o.append( f.readline()[:-1] )  # strip trailing '\n'
    x.append( f.readline()[:-1] )
    f.close()

xvals, ovals = set(),set()  # extract the symbols used in x and o
for i in range(mSeq):
    xvals |= set(x[i])
    ovals |= set(o[i])
xvals = list( np.sort( list(xvals) ) )
ovals = list( np.sort( list(ovals) ) )
dx,do = len(xvals),len(ovals)

for i in range(mSeq):       # and convert to numeric indices
    x[i] = np.array([xvals.index(s) for s in x[i]])
    o[i] = np.array([ovals.index(s) for s in o[i]])

p0 = np.zeros(dx)
for i in range(mSeq):
    p0[x[i][0]] += 1

p0 = p0/sum(p0)
print 'p0:', p0

Tr = np.zeros((dx,dx))
for seq in range(mSeq):
    for s in range(len(x[seq])-1):
        Tr[x[seq][s]][x[seq][s+1]] += 1
Tr = Tr/Tr.sum(axis=1)[:,None]
print 'Tr:', Tr[:5,:5]

print np.matmul(p0,np.linalg.matrix_power(Tr,100))


Ob = np.zeros((dx,do))

for seq in range(mSeq):
    for s in range(len(x[seq])):
        Ob[x[seq][s]][o[seq][s]]+=1
Ob = np.asarray(Ob/Ob.sum(axis=1)[:,None])

print 'Ob:', Ob[:5,:5]

# o = [1,2,3]

def markovMarginals(o,p0,Tr,Ob):
    '''Compute p(o) and the marginal probabilities p(x_t|o) for a Markov model
       defined by P[xt=j|xt-1=i] = Tr(i,j) and P[ot=k|xt=i] = Ob(i,k) as numpy matrices'''
    dx,do = Ob.shape   # if a numpy matrix
    L = len(o)
```

```
    f = np.zeros((L,dx))
    r = np.zeros((L,dx))
    p = np.zeros((L,dx))
    f[0,:] = p0*Ob[:,o[0]]    # compute initial forward message
    log_pO =  np.log(f[0,:].sum())  # update probability of sequence so far
    f[0,:] /= f[0,:].sum()  # normalize (to match definition of f)

    for t in range(1,L):    #       compute forward messages
            f[t,:] = np.matmul(f[t-1,:],Tr)*Ob[:,o[t]]
        log_pO += np.log(f[t,:].sum())
        f[t,:] /= f[t,:].sum()

    r[L-1,:] = np.ones(dx)  # initialize reverse messages
    p[L-1,:] = r[L-1,:]*f[L-1,:]  # and marginals


    for t in range(L-2,-1,-1):
        r[t,:] =  np.matmul(Tr,r[t+1,:]*Ob[:,o[t+1]])
        r[t,:] /= r[t,:].sum()
        p[t,:] = r[t,:]*f[t,:]
        p[t,:] /= p[t,:].sum()

    return log_pO, p

def testMarkovMarginals():
            Tr = np.asarray([[0, 0, 1],[.33, .66, 0], [.5, .5, 0]])
            Ob = np.asarray([[1,0],[.5,.5],[0,1]])
            p0 = np.asarray([.33, .33, .33])
            O = [0,1]
            log_pO, p = markovMarginals(O,p0, Tr,Ob)
            print p

testMarkovMarginals()
_, p = markovMarginals(o[0],p0,Tr,Ob)
print p[6]

_, p = markovMarginals(o[2],p0,Tr,Ob)
print p[6]

log_pO, _ = markovMarginals(o[4],p0,Tr,Ob)
print log_pO
```