Q1

1. In the four connected undirected graphical model, the maximal cliques were pairs between each connected node. However in the 8 connected graphical model, the maximal cliques are now 4 nodes in sizes. So, instead of using the potential between pairs of connected nodes, we now need to consider the potential between the 4-node maximal cliques.

Our parameters will be the potentials of the 4-cliques. Using similar notation to the one seen in class, we have potentials ψpqrs where p,q,r and s are nodes in a 4-clique.

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1. When pixels are only connected to its four neighbors, the energy of the graphical model can be described by the difference between pairs of pixels. However, in the 8 –connected model, the model is described by the differences within each 4-clique.

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2. Set the evidence along the left most nodes of the image ( since the there is evidence along all left most edges)
3. Now, set the initial values of all the other variables in the graph G randomly.
4. Loop
5. Pick a non-evidence variable xn with uniform probability, keep all other variables the same
6. Sample xn by p(xn|\*\*\*\*\*\*\*\*
7. Set the graph to G’ with the sampled value of xn, keeping all the other variables the same. Save the current values as one gibbs sample

Q2 \*\*\*\*\*\*\*\*\*\*\*

Q3.a) We should have two parameters for the coupled hidden markov model for every parameter that we have in the standard hidden markov model, there are some slight modifications for some parameters.

Using the notation from the assignment, and from the class notes:

* We have the probability of the first state s(0), written as π(s)
* We have the probability of the first state u(0), written as π(u)
* We have the probability of s’ ( the next s state) given s AND u, p(s’|s,p), written as a(s)
* We have the probability of u’ ( the next u state) given s AND u, p(u’|s,p), written as a(u)
* Wehave the probability of observation y given current state p(y|s), written as b(s)
* Wehave the probability of observation z given current state p(z|u), written as b(u)

b) This will be similar to the forward algorithm in standard HMMs.

We create two tables, one for the s chain and one for the u chain. Say that s has N possible states and u has M possible states.

In the s table we calculate:

α(s)j(t) = p( **y**1:t , st = j | θ) = , where j is a possible state of s.

In the u table we calculate:

α(u)j(t) = p( **z**1:t , ut = j | θ) = , where j is a possible state of u.

For the first states:

α(s)j(1) = π(s)jb(s)j(y1),

α(u)j(1) = π(u)jb(u)j(z1).

Going from t= 1 to T, the subsequent states:

Once we’ve calculated the α values up to T, we can get the probability of the sequence of observations in our chain (in bold means the sequence of observations):

We multiply together the probability of each sequence of observations to get the probability for both sets of observations occurring together:

c)

This would be similar to forward backward algorithm in standard HMMs. The forward algorithm was stated above.

In the backward algorithm, we create two tables to calculate β values (β(s) and β(u)). These values are the probabilities for the set of observations from time t to the end of the HMM

First set β(s)j(T) and β(u)j­(T) to 1.

Then loop backwards from t = T to t =1

The values at time t = 1 are:

As in standard forward backward, we can get the probability of the entire sequence of observations and we are in state i at time step t.

Again, to calculate the probability that we are in states st =I and ut=j at time t, we can multiply the two probabilities together.

d)