Ch.5 notes

1. Alignment score:
   1. Match: +1, mismatch : -u, insertion/deletion: -r
   2. Alignment score = #matches – u\*#mismatches-r\*indel
2. Largest common subsequence: max the length of common sequence corresponding to the max alignment score
3. Total # of symbols in 2 strings = 2 \* Alignment score(u=0,r=-1/2) + 2\*edit distance
4. Therefore, to min edit distance is same as max alignment score
5. To reconstruct the sequence:
   1. If (i,j) -> (i+1,j): deletion: newA[i+1] <- A[i+1],newB[j+1]=’ ‘
   2. If (I,j)->(I,j+1): insertion: newA[i+1]=’ ‘, newB[j+1]=B[j+1]
   3. If (I,j)->(i+1,j+1):match/mismatch: newA[i+1]=A[i+1],newB[j+1]=B[j+1]