# Small Project 2

605.451 Principles of Computational Biology

1. Given the following HMM, and a observed sequence of walked -> shopped -> cleaned

   a. Manually or write code to calculate the most likely state path that generates the observed sequence using Viterbi algorithm. (25 points)
   b. Manually or write code to calculate the overall probability of the observation using Forward algorithm. (25 points)
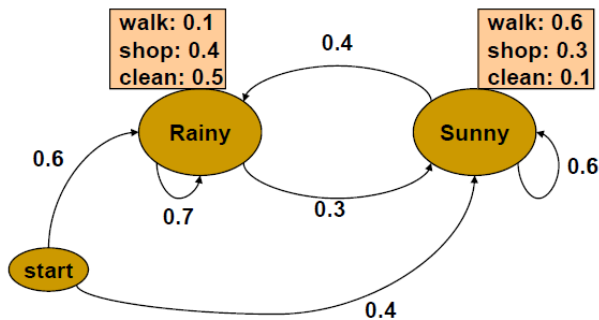
What to turn in

- Turn in your DP table and answers for task a, b.
- Turn in your source code if you solve the problems by programming.

2. Given the following multiple sequence alignments, please build a HMM and estimate all the parameters for the protein family profile (50 points).

   ACATT - - - - C

   ACCAT - - - - C

   ACAAT - - - - C

   ACAATGCGCA

What to turn in

- Turn in the HMM diagram with all the parameters