

- Hidden Markov Model (HMM)

- model of time series data

Markov property: what happens next only depends on what happens now.

Often a bit restrictive if we don't observe everything

- HMM: hidden state $h_t \in \{1, 2, \dots, r\}$

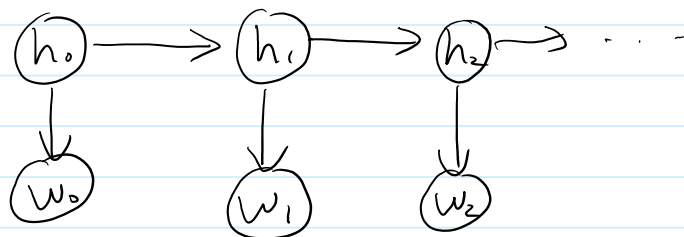
$t = 1, 2, \dots$ denotes time
"transition" matrix P

$$\Pr[h_{t+1} = i \mid h_t = j] = P_{ij}$$

observations $w_t \in \{1, 2, \dots, n\}$

observation matrix Q

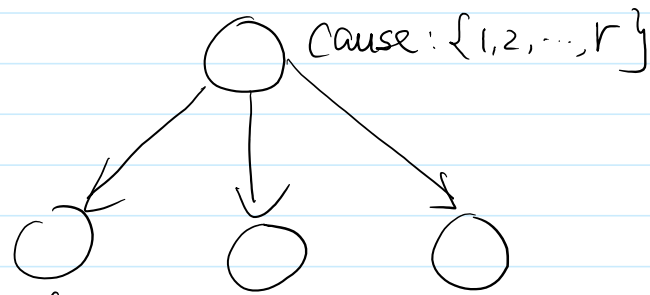
$$\Pr[w_t = i \mid h_t = j] = Q_{ij}$$



- multi-view interpretation

- rank 1 tensor \iff 3 independent variables

- rank r tensor \iff 3 variables that are independent conditioned on 1 of r "causes"



try to find this structure in the model!

- for HMM: w_0, w_1, w_2 are independent conditioned on h_1

$$\Pr[w_0, w_1, w_2] = \sum_{i=1}^r \Pr[w_0|h_i] \Pr[w_1|h_i] \Pr[w_2|h_i] \Pr[h_i]$$

low rank tensor!

$\Pr[w_1|h_i] = Q$ $\Pr[w_2|h_i] = QP$
 using these information, can recover Q, P if both have rank r

- Extension: Phylogenetic tree reconstruction

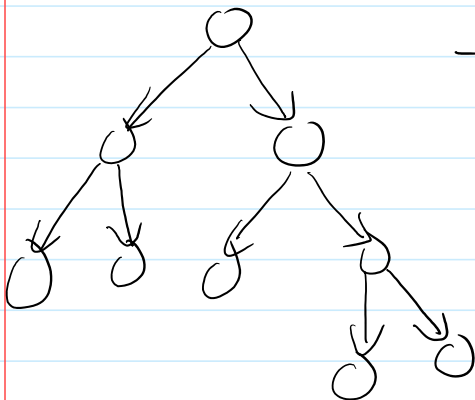
- model for evolution of species

- for each species, n locations in DNA sequence

- assumption: these locations are "useless" and independent (probably not true)

they evolve according to a random transition matrix

$$(\Pr[A \rightarrow C] \dots 4 \times 4)$$



- phylogenetic tree

- nodes = species

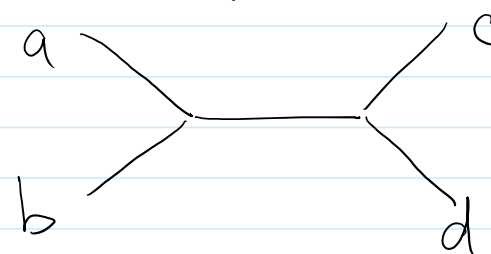
- branches: one species separates into two species

- only leaves are observed

internal nodes correspond to extinct species.

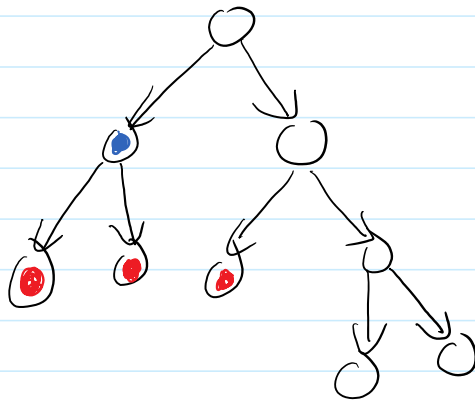
- Goal: ① Find the tree structure

② Learn the transition matrix

- ① : use "Quartet test": measure "distance" between nodes in this case
- 
- $d(a,b) + d(c,d) < d(a,c) + d(b,d)$
 $d(a,b) + d(c,d) < d(a,d) + d(b,c)$

For every 4 leaves, can find out which pair "met" first in the tree. Possible to construct the tree based on these information.

- ②



Notice: the three red leaves are independent conditioned on blue node.

Can use tensor decomposition to learn the transition from blue to any red leaf.