MVE550 2020 Lecture 5.1
Compendium chapter 2
Introduction to Hidden Markov Models

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Example: Not quite a Markov chain

Exercise 2.20 from Dobrow:

- Let $X_0, X_1, \ldots$ be a Markov chain with transition matrix

$$P = \begin{bmatrix} 0 & 1 & 0 \\ 0 & 0 & 1 \\ p & 1-p & 0 \end{bmatrix}$$

for some $0 < p < 1$. Let g be the function defined by

$$g(x) = \begin{cases} 0, & \text{if } x = 1 \\ 1, & \text{if } x = 2, 3 \end{cases}$$

If we let $Y_n = g(X_n)$ for $n \geq 0$ is $Y_0, Y_1, \ldots$ a Markov chain?

- Common phenomenon: The underlying process may reasonably be a Markov chain, but what we observe is not!

Hidden Markov Models

- A Hidden Markov Model (HMM) consists of
  - a Markov chain $X_0, \ldots, X_n, \ldots,$, and
  - another sequence $Y_0, \ldots, Y_n, \ldots,$ so that

$$\Pr(Y_k \mid Y_0, \ldots, Y_{k-1}, X_0, \ldots, X_k) = \Pr(Y_k \mid X_k)$$

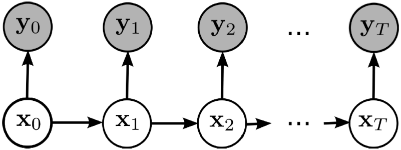
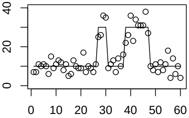


Figure: A hidden Markov model.

- In some models we instead have $\Pr(Y_k \mid Y_0, \ldots, Y_{k-1}, X_0, \ldots, X_k) = \Pr(Y_k \mid Y_{k-1}, X_k)$. There are then extra arrows from y_{k-1} to y_k in the figure above.
- Generally, $Y_0, \ldots, Y_k \ldots,$ are *observed*, while $X_0, \ldots, X_k \ldots,$ are *hidden*.
- In our applications, the X_k have a finite state space and the Y_k are discrete.

Example 1: Cough medicine

- Each day i a pharmacy sells Y_i bottles of cough medicine. We assume $Y_i \sim \text{Poisson}(X_i)$ where X_i is the "underlying demand", X_i has possible values 10 and 30, and is modelled by a Markov chain with transition matrix $P = \begin{bmatrix} 0.95 & 0.05 \\ 0.2 & 0.8 \end{bmatrix}$.
- A simulation from the flu model. The full line represents the underlying expected demand for cough-medicine, based on whether there is a flu-infection in the area or not. The dots represent the observed actual sales of the medicine.



- Can we learn about the presence of flu-infection from sales of cough-medicine?

Example 2: CpG islands

- DNA sequences may be modelled as Markov chains, with possible values A, C, G, T and the positions along the sequence as the steps in the chain.
- So-called "CpG islands" are sequences where the transition matrix (P_+) appears to be slightly different from the transition matrix (P_-) of of non-CpG islands:

$$P_+ = \begin{bmatrix} 0.180 & 0.274 & 0.426 & 0.120 \\ 0.171 & 0.368 & 0.274 & 0.188 \\ 0.161 & 0.339 & 0.375 & 0.125 \\ 0.079 & 0.355 & 0.384 & 0.182 \end{bmatrix}, \ P_- = \begin{bmatrix} 0.300 & 0.205 & 0.285 & 0.210 \\ 0.322 & 0.298 & 0.078 & 0.302 \\ 0.248 & 0.246 & 0.298 & 0.208 \\ 0.177 & 0.239 & 0.292 & 0.292 \end{bmatrix}.$$

- To detect CpG islands in a new DNA string, we set up a HMM where the underlying variable X_i has the two states: "CpG island" and "non-CpG island".

What questions do we want to ask?

- When the parameters of the HMM are known, we want to know about the values of the hidden variables X_i. For example:
  - What is the most likely sequence $X_0, \dots, X_n$ given the data?
  - What is the probability distribution for a single X_i given the data?
- When the parameters of the HMM are not known, we need to infer these from some data.
  - If data with all X_i and Y_i known is available, inference for parameters is based on counts of transitions.
  - One may also make inference from data where more things are unknown.

MVE550 2020 Lecture 5.2
Chapter 3 of Compendium
Some inference for Markov chains and HMMs

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Overview

- The Multinomial Dirichlet conjugacy.
- Inference for finte state space Markov chains.
- (Some) inference for HMMs.

The Multinomial Dirchlet conjugacy

- A vector $x = (x_1, \dots, x_k)$ of non-negative integers has a Multinomial distribution with parameters n and p, where $n > 0$ is an integer and p is a probability vector of length k, if $\sum_{i=1}^k x_i = n$ and the probability mass function is given by

$$\pi(x \mid n, p) = \frac{n!}{x_1!x_2! \dots x_k!} p_1^{x_1} p_2^{x_2} \dots p_k^{x_k}.$$

- A vector $\theta = (\theta_1, \dots, \theta_k)$ of non-negative real numbers satisfying $\sum_{i=1}^k \theta_i = 1$ has a Dirichlet distribution with parameter vector $\alpha = (\alpha_1, \dots, \alpha_k)$, if it has probability density function

$$\pi(\theta \mid \alpha) = \frac{\Gamma(\alpha_1 + \alpha_2 + \dots + \alpha_k)}{\Gamma(\alpha_1)\Gamma(\alpha_2) \cdot \Gamma(\alpha_k)} \theta_1^{\alpha_1 - 1} \theta_2^{\alpha_2 - 1} \cdots \theta_k^{\alpha_k - 1}.$$

- We have conjugacy in this case: $\theta \mid x \sim \text{Dirichlet}(\alpha + x)$.
- The predictive distribution is given by

$$\pi(x) = \frac{n!}{x_1! \dots x_k!} \cdot \frac{\Gamma(\alpha_1 + x_1)}{\Gamma(\alpha_1)} \cdots \frac{\Gamma(\alpha_k + x_k)}{\Gamma(\alpha_k)} \cdot \frac{\Gamma(\sum_{i=1}^k \alpha_i)}{\Gamma(\sum_{i=1}^k \alpha_i + x_i)}.$$

Inference for finite state space Markov chains

- Example: You have observed 0, 1, 1, 0, 0, 0, 1, 0, 0, 1, 0 from a Markov chain with possible values 0 and 1. What is the transition matrix?
- First, make table with counts of transitions: .

	0	1
0	3	3
1	3	1

- A reasonable guess for a transition matrix is then

$$P = \begin{bmatrix} 3/6 & 3/6 \\ 3/4 & 1/4 \end{bmatrix}.$$

- What should happen if we have never observed a transition $i \to j$ for two states i and j?
- What should happen if we have never observed any transition from a state i?

One solution: pseudo-counts

- Idea: If the count is zero, add some small positive number, a *pseudo-count*, so that the frequency becomes non-zero.
- The pseudo-count does not need to be an integer.
- To be "fair", we may add the same pseudo-count to all counts. We often use pseudo-counts equal to 1.
- In the example above, with pseudo-counts 1, the count table becomes

	0	1
0	4	4
1	4	2

and the transition matrix becomes

$$P = \begin{bmatrix} 4/8 & 4/8 \\ 4/6 & 2/6 \end{bmatrix}.$$

- Note how the influence of pseudo-counts approaches zero when the actual counts increase.
- What should happen if the state space is infinite?
- Generally, is there a theoretic framework to put this into?

Bayesian inference for Markov chains

- Write $P_1, \dots, P_k$ for the k rows of P, and view each P_i as an independent random variable.
- Note that observed data (counts of transitions from each state i) is Multinomially distributed given P_i.
- If we assume $P_i \sim \text{Dirichlet}(\alpha)$ for some vector $\alpha_i = (\alpha_{i1}, \dots, \alpha_{ik})$, and the counts for transitions out of i are given in the vector $c_i = (c_{i1}, \dots, c_{ik})$, then the posterior for P_i becomes $\text{Dirichlet}(\alpha_i + c_i)$.
- Note that the expectected posterior becomes the vector

$$\mathrm{E}\left(P_i \mid \text{data}\right) = \frac{\alpha_i + c_i}{\alpha_{i1} + \cdots + \alpha ik + c_{i1} + \cdots + c_{ik}}$$

  So the α_{ij} correspond exactly to pseudo-counts!
- The prior $\text{Dirichlet}(1, 1, \dots, 1)$, with all pseudo-counts equal to 1 corresponds to a uniform distribution on the set of all probability vectors P_i that sum to 1.

More conclusions from the Bayesian framework

- We can show that, if the sequence $X_0, X_1, \ldots, X_n$ is observed as data, then the posterior probabilities for X_{n+1} are $\mathrm{E}\left(P_{x_n}\right)$.
- We can extend this to compute the probability of any sequence $X_{n+1}, \ldots, X_{n+r}$ given data $X_0, \ldots, X_n$.
- If we know *a priori* that certain transitions are impossible, we can incorporate this into the prior: For example, using the prior $P_i \sim \text{Dirichlet}(1, 1, 0)$,means that transitions from state i to state 3 have probability zero.
- It is also possible to construct priors for the transition matrix P that represent other types of prior information, for example that the Markov chain must be time reversible.

Inference for the parameters of HMMs

Assume an HMM model where $X_i \in \{0,1\}$, $Y_i \in \{1,2,3\}$, and we have observed both states in some stretch of data:

X	0	0	0	0	1	1	1	1	1	0
Y	1	2	1	1	2	3	2	3	3	1

- Counting transitions, we get

	0	1
0	3	1
1	1	4

and

	1	2	3
0	4	1	0
1	0	2	3

.

- In practice, we can use pseudocounts just as in the Markov chain case. In the example above, using all pseudocounts equal to 1, we get

$$P = \begin{bmatrix} 4/6 & 2/6 \\ 2/7 & 5/7 \end{bmatrix}, Q = \begin{bmatrix} 5/8 & 2/8 & 1/8 \\ 1/8 & 3/8 & 4/8 \end{bmatrix}$$

  where P is the transition matrix of the Markov chain, and Q is the stochastic matrix of transition probabilities from X_i to Y_i.
- As for Markov chains, these results can be obtained by using priors for P and Q that are product of Dirichlet distributions.

More on inference of parameters for HMMs

- The Bayesian paradigm may be used to make predictions for later observations: In the example above, with $X_0, \dots X_9$, $Y_0, \dots Y_9$ observed, the probability vector with the three possible values of Y_{10} can be computed with the matrix product $\mathrm{E}\left(P_{x_9}\right)\mathrm{E}\left(Q\right)$.
- The priors can be adapted to incorporate actual prior information.
- For example, prior knowledge about the transitions from states of X_i to states of Y_i might lead you to model $Y_i \sim \text{Poisson}(\lambda_{X_i})$, so for each value of X_i the Y_i are Poisson distributed with parameter λ_{X_i}. Fixing a prior also on the λ_{X_i} parameters, we may then find the posteriors for these in similar ways as we have done before.

More inference questions for HMMs

- We focused above on the case where (some) parameters of the HMM are not fully known.
- If the HMM parameters are given and the Y_i are observed, the goal may instead be to learn about the values of the X_i (these methods are not part of the course):
  - Find the sequence $X_0, \ldots, X_k$ with the maximum probability given the observed $Y_0, \ldots, Y_k$ and the given model: The *Viterbi algorithm*.
  - Find the marginal distribution for each X_i given the observed $Y_0, \ldots, Y_k$ and the model: The Forward-Backward algorithm.
  - Find the *joint distribution* of $X_0, \ldots, X_k$ given the observed $Y_0, \ldots, Y_k$ and the model. In practice: Find a sequence $X_0, \ldots, X_k$ that is a *sample* from this joint distribution. This may also be done with a Forward-Backward algorithm.