Computational Systems Biology: Biology X

Bud Mishra

Room 1002, 715 Broadway, Courant Institute, NYU, New York, USA

L#4:(Feb-23-2010) Genome Wide Association Studies





・ロ・・ (日・・ (日・・ 日・)

E.

The law of causality ... is a relic of a bygone age, surviving, like the monarchy, only because it is erroneously supposed to do no harm ...

-Bertrand Russell, *On the Notion of Cause*. Proceedings of the Aristotelian Society 13: 1-26, 1913.





B Mishra Computational Systems Biology: Biology X

・ロ・・ (日・・ (日・・ 日・)

E.

Random Variables

- A (discrete) random variable is a numerical quantity that in some experiment (involving randomness) takes a value from some (discrete) set of possible values.
- More formally, these are measurable maps

 $X(\omega), \omega \in \Omega,$

from a basic probability space (Ω, F, P) (\equiv outcomes, a sigma field of subsets of Ω and probability measure *P* on *F*).

Events

$$\ldots \{\omega \in \Omega | X(\omega) = \mathbf{x}_i \} \ldots$$

same as $\{X = x_i\}$ [X assumes the value x_i].

・ロ・・ (日・・ ほ・・ (日・)

臣

Few Examples

- Example 1: Rolling of two six-sided dice. Random Variable might be the sum of the two numbers showing on the dice. The possible values of the random variable are 2, 3, ..., 12.
- Example 2: Occurrence of a specific word *GAATTC* in a genome. Random Variable might be the number of occurrence of this word in a random genome of length 3 × 10⁹. The possible values of the random variable are 0, 1, 2, ..., 3 × 10⁹.

• (1) • (

The Probability Distribution

- The probability distribution of a discrete random variable Y is the set of values that this random variable can take, together with the set of associated probabilities.
- Probabilities are numbers in the range between zero and one (inclusive) that always add up to one when summed over all possible values of the random variable.

Bernoulli Trial

• A *Bernoulli trial* is a single trial with two possible outcomes: "success" & "failure."

 $P(\text{success}) = p \text{ and } P(\text{failure}) = 1 - p \equiv q.$

 Random variable S takes the value -1 if the trial results in failure and +1 if it results in success.

$$P_{\mathrm{S}}(s) = p^{(1+s)/2}q^{(1-s)/2}, \quad s = -1, +1.$$

The Binomial Distribution

- A Binomial random variable is the number of successes in a fixed number n of independent Bernoulli trials (with success probability = p).
- Random variable *Y* denotes the total number of successes in the *n* trials.

$$P_Y(y) = \binom{n}{y} p^y q^{n-y}, \quad y = 0, 1, \dots, n.$$

・ロット (雪) ・ ヨ) ・ ・ ー)

크

The Uniform Distribution

A random variable Y has the uniform distribution if the possible values of Y are a, a + 1, ..., a + b - 1 for two integer constants a and b, and the probability that Y takes any specified one of these b possible values is b⁻¹.

$${\sf P}_{\sf Y}({\sf y})={\sf b}^{-1}, \quad {\sf y}={\sf a}, {\sf a}+1,\ldots,{\sf a}+{\sf b}-1,$$

• (1) • (

The Geometric Distribution

 Suppose that a sequence of independent Bernoulli trials is conducted, each trial having probability *p* of success. The random variable of interest is the number *Y* of trials before but not including the first failure. The possible values of *Y* are 0, 1, 2,

$$P_{Y}(y) = p^{y}q, \quad y = 0, 1, \ldots$$

A (1) > A (2) > A (2) > (1)

The Poisson Distribution

 A random variable Y has a Poisson distribution (with parameter λ > 0) if

$$P_{Y}(y) = \frac{e^{-\lambda}\lambda^{y}}{y!}, \quad y = 0, 1, \ldots.$$

 The Poisson distribution often arises as a limiting form of the binomial distribution.

크

Continuous Random Variables

- We denote a continuous random variable by *X* and observed value of the random variable by *x*.
- Each random variable X with range I has an associated density function f_X(x) which is defined, positive for all x and integrates to one over the range I.

$$\mathsf{Prob}(a < X < b) = \int_a^b f_X(x) dx.$$

・ロン ・四 ・ ・ ヨン ・ ヨン

The Normal Distribution

 A random variable X has a normal or Gaussian distribution if it has range (−∞,∞) and density function

$$f_X(\mathbf{x}) = \frac{1}{\sqrt{2\pi\sigma}} e^{-\frac{(\mathbf{x}-\mu)^2}{2\sigma^2}},$$

where μ and $\sigma > 0$ are parameters of the distribution.

・ロット (雪) ・ ヨ) ・ ・ ー)

Expectation

• For a random variable Y, and any function g(Y) of Y, the expected value of g(Y) is

$$E(g(Y)) = \sum_{y} g(y) P_{Y}(y),$$

when Y is discrete; and

$$E(g(Y)) = \int_{Y} g(y) f_{Y}(y) \, dy,$$

when Y is continuous.

• Thus,

mean(Y) =
$$E(Y) = \mu(Y)$$
,
variance(Y) = $E(Y^2) - E(Y)^2 = \sigma^2(Y)$.

Conditional Probabilities

• Suppose that A_1 and A_2 are two events such that $P(A_2) \neq 0$. Then the conditional probability that the event A_1 occurs, given that event A_2 occurs, denoted by $P(A_1|A_2)$ is given by the formula

$$P(A_1|A_2) = rac{P(A_1\&A_2)}{P(A_2)}.$$

・ロン ・四 ・ ・ ヨン ・ ヨン



• Suppose that A_1 and A_2 are two events such that $P(A_1) \neq 0$ and $P(A_2) \neq 0$. Then

$$P(A_2|A_1) = \frac{P(A_2)P(A_1|A_2)}{P(A_1)}.$$

Markov Models

Suppose there are *n* states S₁, S₂, ..., S_n. And the probability of moving to a state S_j from a state S_i depends only on S_i, but not the previous history. That is:

$$P(s(t+1) = S_j | s(t) = S_i, s(t-1) = S_{i_1}, ...) = P(s(t+1) = S_j | s(t) = S_i).$$

Then by Bayes rule:

$$P(s(0) = S_{i_0}, s(1) = S_{i_1}, \dots, s(t-1) = S_{i_{t-1}}, s(t) = S_{i_t})$$

= $P(s(0) = S_{i_0})P(S_{i_1}|S_{i_0}) \cdots P(S_{i_t}|S_{i_{t-1}}).$

HMM: Hidden Markov Models

Defined with respect to an **alphabet** Σ

- A set of (hidden) states Q,
- A $|Q| \times |Q|$ matrix of state transition probabilities $A = (a_{kl})$, and
- A $|Q| \times |\Sigma|$ matrix of emission probabilities $E = (e_k(\sigma))$.

States

Q is a set of states that emit symbols from the alphabet Σ . Dynamics is determined by a state-space trajectory determined by the state-transition probabilities.

◆□ → ◆□ → ◆ □ → ◆ □ → ◆ ○ ◆

A Path in the HMM

- Path Π = π₁π₂···π_n = a sequence of states ∈ Q* in the hidden markov model, *M*.
- x ∈ Σ* = sequence generated by the path Π determined by the model M:

$$P(\boldsymbol{x}|\boldsymbol{\Pi}) = P(\pi_1) \left[\prod_{i=1}^n P(\boldsymbol{x}_i|\pi_i) \cdot P(\pi_i|\pi_{i+1}) \right]$$

A Path in the HMM

Ρ

Note that

$$P(\mathbf{x}|\Pi) = P(\pi_1) \left[\prod_{i=1}^{n} P(\mathbf{x}_i | \pi_i) \cdot P(\pi_i | \pi_{i+1}) \right]$$
$$P(\mathbf{x}_i | \pi_i) = \mathbf{e}_{\pi_i}(\mathbf{x}_i)$$
$$P(\pi_i | \pi_{i+1}) = \mathbf{a}_{\pi_i, \pi_{i+1}}$$

 Let π₀ and π_{n+1} be the initial ("begin") and final ("end") states, respectively

$$P(x|\Pi) = a_{\pi_0,\pi_1} e_{\pi_1}(x_1) a_{\pi_1,\pi_2} e_{\pi_2}(x_2) \cdots e_{\pi_n}(x_n) a_{\pi_n,\pi_{n+1}}$$

i.e.

$$P(x|\Pi) = a_{\pi_0,\pi_1} \prod_{i=1}^{n} e_{\pi_i}(x_i) a_{\pi_i,\pi_{i+1}}.$$

n

프 > 프

Decoding Problem

- For a given sequence x, and a given path π, the model (Markovian) defines the probability P(x|Π)
- In a casino scenario: the dealer knows Π and x, the player knows x but not Π.
- "The path of x is hidden."
- Decoding Problem: Find an optimal path π* for x such that P(x|π) is maximized.

$$\pi^* = \arg \max_{\pi} P(x|\pi).$$

Hidden Markov Models

Dynamic Programming Approach

Principle of Optimality

Optimal path for the (i + 1)-prefix of x

 $x_1 x_2 \cdots x_{i+1}$

uses a path for an *i*-prefix of *x* that is optimal among the paths ending in an unknown state $\pi_i = k \in Q$.

(日) (四) (三) (三) (三) (三)

Hidden Markov Models

Dynamic Programming Approach

Recurrence: $s_k(i)$ = the probability of the most probable path for the *i*-prefix ending in state *k*

$$\forall_{k\in Q} \forall_{1\leq i\leq n} \qquad s_k(i) = e_k(x_i) \cdot \max_{l\in Q} s_l(i-1)a_{lk}.$$

(日)

Dynamic Programming

• i = 0, Base case

$$s_{begin}(0) = 1, s_k(0) = 0, \forall_{k \neq begin}.$$

• $0 < i \le n$, Inductive case

$$s_l(i+1) = e_l(x_{i+1}) \cdot \max_{k \in Q} [s_k(i) \cdot a_{kl}]$$

● *i* = *n* + 1

$$P(\pmb{x}|\pi^*) = \max_{k\in \mathsf{Q}} \pmb{s}_k(\pmb{n})\pmb{a}_{k,\mathsf{end}}$$

(日) (四) (三) (三) (三) (三)

Viterbi Algorithm

Dynamic Programing with "log-score" function

 $S_l(i) = \log s_l(i).$

- Space Complexity = O(n|Q|).
- Time Complexity = O(n|Q|).
- Additive formula:

$$S_l(i+1) = \log e_l(x_{i+1}) + \max_{k \in Q} [S_k(i) + \log a_{kl}].$$

◆□ → ◆□ → ◆ □ → ◆ □ → ◆ ○ ◆ ●

Hidden Markov Models

[End of Lecture #4]

B Mishra Computational Systems Biology: Biology X

◆□ > ◆□ > ◆豆 > ◆豆 > ̄豆 _ 釣へで