To Bayes or Not To Bayes: Model Averaging for Bayesian Classifiers

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Brett T. Beutell

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Irena Swanson

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I want to thank a few people.

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Abstract

The preface pretty much says it all.

Dedication

You can have a dedication here if you wish.

Introduction

If it were not for convention, this chapter could perhaps be titled, "An Irresponsibly Quick Introduction to Bayes' Theorem." It is wholly optional for the reader who has taken an undergraduate course in mathematical statistics. This chapter introduces the ideas, terminology, and some historical minutiae about Bayesian reasoning. Naturally, we provide a statement of Bayes' theorem for events and distributions.

0.1 Much Ado About Bayes

At its inception, Bayes' theorem was not particularly controversial. Pierre Simon LaPlace offered its first formalization in the early 19th century, and he believed (incorrectly, as was proven by the mid-twentieth century) that with a sufficient amount of data, the answers it provided were equivalent to those obtained from his frequency based methods [McGrayne, 2011]. As time passed, LaPlace preferred his frequentist techniques for the relative ease of their calculations, but he did not outright condemn the use of Bayes in practice. Interestingly, over a half-century after his death, LaPlace's failure to disown Bayesian reasoning caught the attention of a Scottish mathematician named George Chrystal, who remarked, "The indiscretions of great men should be quietly allowed to be forgotten" [McGrayne, 2011].

Chrystal's comment represents the attitude of early twentieth century statisticians quite well. At the time, frequentism reigned supreme, and the attitude towards Bayes' theorem and its role in statistics was surprisingly sour. For years, statisticians in the academy who employed Bayesian reasoning feared for their reputation if they explicitly made reference to Bayes' theorem in their work [McGrayne, 2011].

Fortunately, with due thanks to the computational advances of the past three decades, Bayes survived its temporary relegation to the catacombs of statistics, and it has emerged as an astoundingly useful tool for the modern statistician. The phrase "Bayesian Inference" fails to evoke the contention it once did. Furthermore, it is now far more commonplace for statisticians to use both Bayesian and frequentist techniques in their work, tailoring their methods to the problem at hand [Liu et al, 2013].

Summarily, the use of Bayesian reasoning is no longer divisive or taboo, and it is a recent phenomenon that we may begin our inquiry without several pages apologizing for our inferential philosophy. With that said, it does not hurt to quickly consider the differences between a Bayesian and a frequentist.

0.2 Bayes'd and Confused

Suppose we seek an estimate of a parameter over some set of random variables. We may call said parameter θ and our random variables (or, *data*) $\vec{X}$. We use $\vec{X}$ to talk about our data in the abstract (that is, before they are observed), and we denote a particular set of observed values as $\vec{x}$.

We represent the conditional probability of θ given a set of observed data as $P(\theta|\vec{X} = \vec{x})$. Vice versa, the conditional probability of the data given a fixed $\theta = \theta_0$ can be written $P(\vec{X}|\theta = \theta_0)$. Note that for the former conditional distribution, we are fixing our data and considering θ a random variable, whereas for the latter, we are doing the converse.

"To Bayes"

Bayesians prefer the former conditional PDF. To a Bayesian, θ is uncertain, so the best means of knowing more about θ is directly through the data. Notably, the choice of words here contains an important qualifier; Bayesians want to know "*more*" about θ. Hence, they specify what is already known about the parameter. Similar to the way mathematicians or logicians use axioms, Bayesians find it important to represent in their methods what it is that they already presume to be true.

We can think of a Bayesian model's presumed truths (often called *prior beliefs*, the *prior distribution* or, simply, the *prior*) as a starting point, from which data are used to *update* the subjective belief about the estimate. Bayesians use what are called *non-informative priors* to approximate a lack of prior knowledge about θ.

Besides the inherent subjectivity of the prior, the essential characteristic of Bayesian methods is that they treat parameters as random variables. Consequently, Bayesian estimates can return a probability distribution for θ, which is called the *posterior distribution* of θ. The posterior describes the relative likelihoods of different values of θ given the data and given the *a priori* beliefs encoded in the prior distribution.

"Not To Bayes"

For the student of frequentism, the Bayesian approach may lend itself to confusion (or, years ago, anger), since frequentists treat θ as fixed ($\theta = \theta_0$), and think of their observed data as probabilistic draws that, in the long run, converge to a particular distribution.

Frequentist techniques have two main advantages. Namely, the math involved in their calculations is generally tidy, and their calculations do not require the subjective prior of Bayes' theorem. However, frequentist methods often suffer from having rigid and unintuitive interpretations.

For instance, a frequentist p-value in a hypothesis test is a conditional probability that assumes the null hypothesis (e.g., $\theta = \theta_0$) is true. Hence, it evaluates how probable the observed data would be if $\theta = \theta_0$. On the other hand, a Bayesian p-value would provide the probability of the null hypothesis being true, conditioned on the data. To see this symbolically, consider that $P(\vec{X} = \vec{x}|\theta = \theta_0)$ is, by definition, a statement that concerns the probability of observing $\vec{x}$, given that $\theta = \theta_0$, whereas $P(\theta = \theta_0|\vec{X} = \vec{x})$ is the probability of the parameter taking a specific value. Frequentists are more apt to talk about the probability of seeing our data, given θ is a specific value.

Table 1: A Broad Comparison of Bayesian and Frequentist Methodologies

	To the Bayesian	**To the frequentist**
Parameters are	Distributions	Fixed-valued
Subjective assessment is	Essential	Disturbing

0.3 The First Rule of Bayes' Club

We introduce a formal, symbolic expression of Bayes' theorem. Given Ω, the set of all possible events, and events $A, B \in \Omega$, we write:

$$P(A|B) = \frac{P(B|A)P(A)}{P(B)},$$

where P is a function from Ω to $[0, 1]$, and $P(\Omega) = 1$. We may also call Ω the *sample space*.

The proof of Bayes' theorem for events follows quickly from the axioms of probability and the definition of conditional probability. For our purposes, we note that Bayes' theorem also extends to probability distributions. Let θ be our parameter of interest and x be an observation of a random variable X. Let $\pi(\theta)$ be the prior probability distribution on θ, and let $f(X = x|\theta)$ be a density function for X. We may then express the posterior as follows:

$$\pi(\theta|X = x) = \frac{f(x|\theta)\pi(\theta)}{\int_{\theta\in\Theta} f(x|\theta)\pi(\theta)d\theta} \propto f(x|\theta)\pi(\theta),$$

where $\propto$ denotes proportionality, Θ is the set of all possible parameter values, and clearly, the denominator is equal to $f(x)$. When the domain of θ is discrete, we replace the integral in the denominator with a summation.

The above is conventionally presented alongside the pithy, assonant phrase, "The posterior is proportional to the prior times the likelihood." The numerator of Bayes' theorem is used so frequently that it has its own name, the *marginal* of the posterior. Because the denominator, also called the *normalization constant*, can be a ghastly integral, it is often more practical to reason about the posterior in terms of its marginal. For example, the denominator of Bayes' theorem disappears from consideration when we compare two possible parameter values given the data. (Not to get ahead of ourselves, but this property of proportionality is also central to running Markov Chain Monte Carlo simulations.)

0.4 Classification and Learning

A *classification model* is a statistical model where, given some data about an observation, we seek to predict its *class*, an unknown categorical variable. We may borrow the language of machine learning and call the predictor variables in our model *features*. When we speak of *learning* the parameters of a classification model, we assume that there is a set of pre-classified data from which we can make inferences about future unclassified data.

We shall define a Bayesian classifier in the proceeding chapter, but we will not address the specifics of learning model parameters. For some insightful examples on how Bayesian classifiers learn parameters, the reader is encouraged to read David Heckerman's "A Tutorial on Learning With Bayesian Networks," which is available online [Heckerman, 1996]. A URL is provided under the references.

Chapter 1

The Bayesian Network

Bayesian Networks are a useful means of visualizing and reasoning about classification models. Put succinctly, a Bayesian Network is a directed acyclic graph (DAG) where each node represents a random variable in the model, and each edge represents a conditional dependency between two random variables.

1.1 Classification at a Glance

Suppose we have a set of random variables $V = \{C, X_1, \ldots, X_n\}$, and we seek to predict the value of C, a categorical variable, using $X_1, \ldots, X_n$. We call C the *class variable*, and we refer to the X_i as the *feature variables*. For notational convenience, we may denote the set of feature variables by $\vec{X}$, and we may denote a single set of observed values of $\vec{X}$ as the vector $\vec{x} = (X_1 = x_1, \ldots, X_n = x_n)$.

The Bayesian Approach

Let C have k possible classes. The goal in a classification setting is to find the probabilities of each class of C, given the observed values of the feature variables. Usually (but not always), we seek the value of the class that maximizes the value of $P(C|\vec{X})$. We appeal to Bayes' theorem:

$$P(C = c_i|\vec{X}) = \frac{P(\vec{X}|C = c_i)P(C = c_i)}{\displaystyle\sum_{c_j \in \text{dom}\{C\}} P(\vec{X}|C = c_j)P(C = c_j)},$$

where $P(\vec{X}|C = c_i)$ is the likelihood function and $P(C = c_i)$ is the prior probability for the class variable when it is equal to c_i. Notably, we need not compute the denominator of the posterior, since

$$\arg\max_{c_i \in \text{dom}\{C\}} \{P(C = c_i|\vec{X} = \vec{x})\} = \arg\max_{c_i \in \text{dom}\{C\}} \{P(\vec{X} = \vec{x}|C = c_i)P(C = c_i)\}.$$

To see why, compare the posterior distributions of two possible class values, c_i and c_j, given a vector of inputs $\vec{X}$. Assuming these classes have nonzero posterior probabilities, the normalization constant disappears from the following equation:

$$\frac{P(C = c_i|\vec{X} = \vec{x})}{P(C = c_j|\vec{X} = \vec{x})} = \frac{\frac{P(\vec{x}|c_i)P(c_i)}{P(\vec{x})}}{\frac{P(\vec{x}|c_j)P(c_j)}{P(\vec{x})}} = \frac{P(\vec{x}|c_i)P(c_i)}{P(\vec{x}|c_j)P(c_j)}.$$

Clearly, then, if we obtain a value greater than 1 from the above, we find the class c_i to be more likely than c_j, given the data. Since the normalization constant $P(\vec{x})$ can be unwieldy to compute, this is a very convenient property of Bayesian classifiers.

Finding the Marginal

With a few simple results from probability theory, we can refactor the numerator of the posterior. For starters, we invoke the multiplication rule:

$$P(\vec{X}|C)P(C) = P(C, X_1, \dots, X_n).$$

Then, for convenience, we define $X_0 \equiv C$ and apply the chain rule of probability to obtain

$$P(X_0, \dots, X_n) = P(\cap_{i=0}^{n} X_i) = \prod_{j=0}^{n} P(X_j| \cap_{k=0}^{j-1} X_k).$$

Thus, finding the marginal requires calculation of all of the conditional dependencies between feature variables in $\vec{X}$, and in order to accurately classify an input $\vec{x}$, we should construct a model that accounts for these conditional dependencies.

1.2 Directed Graphs

Let V be a set $\{V_0, V_1, \dots, V_n\}$, and let E be a set of ordered pairs (V_i, V_j) on $V \times V$, (for $n, i, j \in \mathbb{Z}^+$). A *directed graph* G is defined as the tuple (V, E). We call members of V *vertices* or *nodes*, and we call members of E *edges* or *arcs*. Importantly, the order of vertices that compose a particular edge $E_i = (V_j, V_k)$ encodes the *direction* of the edge. I.e., E_i is said to be an edge *from* V_j *to* V_k, (for $i, j, k \in \mathbb{Z}^+$). Figure 1.1 provides an example of how we might illustrate a directed graph. In this context, $V = \{V_0, V_1, V_2\}$ and $E = \{(V_0, V_1), (V_0, V_2), (V_2, V_1)\}$.

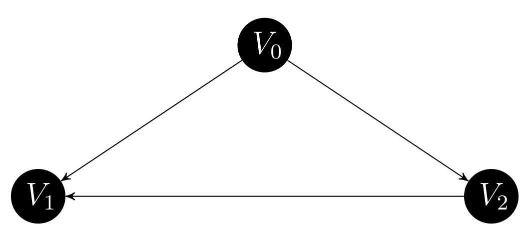

Figure 1.1: A simple directed graph with 3 nodes and 3 edges

Paths and Cycles

It is natural to consider the *paths* through G. A path P of length n is simply an ordered n-tuple of edges. We refer to the first and last nodes of P as the *starting node* V_s and *terminal node* V_t, respectively. With the exception of V_t, if the i^{th} member of P is an edge that points *to* the node V_j, then the $(i+1)^{\text{th}}$ member is an edge pointing *from* node V_j to another node V_k. Thus, a path of length n defines a sequence of $n+1$ nodes, such that each node has an edge from itself to its successor. By $\mathcal{P}(G)$, let us mean the family of all paths defined on G. For any $P \in \mathcal{P}(G)$, we call P a *cycle* if $V_s = V_t$. We say that a graph G is *cyclic* if there exists at least one cycle in $\mathcal{P}(G)$. Otherwise, we say that G is *acyclic*.

Relatives

The vocabulary used to describe the relationships amongst nodes in a graph is markedly familial. Given the nodes $V_i, V_j, V_k \in V$, we say that V_i is an *ancestor* of V_j if there exists a $P \in \mathcal{P}(G)$ such that V_i precedes V_j in the sequence of nodes defined by P. Conversely, we call V_j a *descendant* of V_i. We also give special names to a node's immediate ancestors and descendants. Formally, for V_j, we may define the set of *parents* of V_j as $\{V_i : (V_i, V_j) \in E\}$. Similarly, we define the set of *children* of V_j as $\{V_k : (V_j, V_k) \in E\}$. A node whose set of parents is empty is called the *root* of our graph.

The Adjacency Matrix

We may represent $G = (V, E)$, where $V = \{V_0, \ldots, V_{n-1}\}$ has order n, with an $n \times n$ matrix $A = (a_{ij})$, such that for each entry a_{ij},

$$a_{ij} = \begin{cases} 1, & \text{if} \quad (V_{i-1}, V_{j-1}) \in E; \\ 0, & \text{otherwise.} \end{cases}$$

We refer to A as a *binary node-node adjacency matrix* or just an *adjacency matrix*. For example, the adjacency matrix corresponding to the first figure of this section is

$$\begin{pmatrix} 0 & 1 & 1 \\ 0 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}$$

since there is an arc from V_0 to V_1, an arc from V_0 to V_2, and an arc from V_2 to V_1. We may also consider the sum of powers of A,

$$Y = A + A^2 + \cdots + A^n = \sum_{i=1}^{n} A^i.$$

The resulting matrix is (y_{ij}), where y_{ij} represents the number of unique paths from $V_s \equiv V_{i-1}$ to $V_t \equiv V_{j-1}$ in $\mathcal{P}(G)$. Thus, to formalize the notion of an acyclic graph, we say that $G = (V, E)$ is acyclic if $tr(Y) = 0$. Otherwise, G is cyclic. To continue our example from above, we calculate Y to be

$$\begin{pmatrix} 0 & 2 & 1 \\ 0 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}$$

which is consistent with our visualization of the graph. (For example, we identify two distinct paths from V_0 to V_1, so $y_{1,2} = 2$.)

1.3 Bayesian Networks

Let $\mathcal{B} \equiv (G, \Theta)$, where $G = (V, E)$ is a directed acyclic graph, $V = \{V_0, V_1, \ldots, V_n\}$ is a set of $n+1$ random variables, and Θ is a set of parameter estimates generated from some pre-classified data. Each parameter of Θ corresponds to an arc in the graph G. (That is, the parameters of our model are conditional probabilities.) We say that $\mathcal{B}$ is a Bayesian network.

Restricted Bayesian Networks

A *restricted* Bayesian network caps the number of possible conditional dependencies for a given feature variable at some nonnegative integer k. Hence, the graph that represents the network should have at most k arcs from each of its feature nodes. The Tree Augmented Network (TAN), displayed below, is an example of a restricted Bayesian Network with $k = 1$.

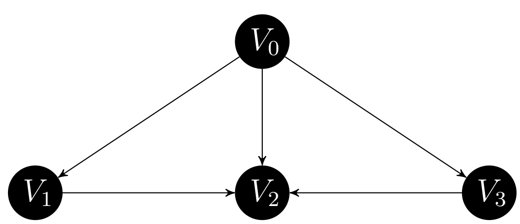

Figure 1.2: TAN with three features

Of course, a Bayesian network without restrictions on its nodes' conditional dependencies is called an *unrestricted* Bayesian network.

1.4 Bayesian Classifiers

A Bayesian classifier is simply a Bayesian network applied to a classification problem. We consider the necessary structural and decision theoretic modifications to $\mathcal{B}$ that are necessary for this application.

Networks Constraints

In a classification setting, we call V_0 the class variable, and we also place particular constraints on the graph of $\mathcal{B}$ [Liu et al, 2013]. Namely, we require that the adjacency matrix A of G satisfies the following properties:

$$\sum_{i=1}^{n} a_{i1} = 0, \quad \text{and} \quad \sum_{j=1}^{n} a_{1j} \neq 0.$$

In words, we mean there are no directed edges pointing to the class node, and the class node has an edge to at least one feature node. Obviously, the class node is the root of G.

Making a Decision

To predict the class C of an input $\vec{x}$, we use a *decision rule*. Our decision rule provides a means of selecting one proposed classification over another, given a set of pre-classified data and the unclassified input $\vec{x}$. Recall that in surveying the general problem of classification, we chose a decision rule that returned the class maximizing our posterior probability. Albeit common, this is not the only possible decision rule. For instance, there may be an unequal cost associated with certain misclassifications of $\vec{x}$. In such cases, we can modify our decision rule's *loss function* accordingly; however, this facet of decision theory is not central to our discussion.

The Naive Bayes Classifier

The NBC assumes conditional independence amongst feature variables of the model in order to yield a more wieldy computation of the posterior. In light of its reductive assumption, the NBC is a surprisingly effective means of classifying data.

Recall that the posterior distribution of the class variable $C \equiv X_0$ has the following property:

$$P(X_0|X_1, \ldots, X_n) \propto P(X_0, \ldots, X_n) = P(\cap_{i=0}^{n} X_i) = \prod_{j=0}^{n} P(X_j| \cap_{k=0}^{j-1} X_k).$$

If we assume independence amongst the feature variables $X_1, \ldots, X_n$, then the above simplifies to

$$P(X_0) \prod_{j=1}^{n} P(X_j| \cap_{k=0}^{j-1} X_k) = P(C) \prod_{j=1}^{n} P(X_j|C).$$

Note that our independence assumption makes the NBC's graph a restricted Bayesian network with $k = 0$.

Example: Spam Detection

Spam detection is an oft-cited example of a classification problem. It is suitable for our discussion, since it is an area of classification that has benefited greatly from application of Bayes' rule. For example, in a 1998 study, researchers at Microsoft found that existing methods for spam-filtering were significantly out-performed by a simple Naïve Bayes classifier [Sahami et al, 1998]. We shall use their work to contextualize the preceding sections.

Suppose we are given a set of 1,000 emails, and for each email, we record four pieces of information according to the table below:

Table 1.1: Information on a set of 1,000 emails

Information	**Description**
Spam	Whether or not the email was spam
Domain	The domain of the email's sender (e.g., @reed.edu)
Hyperlinks	A count of the number of hyperlinks in the body of the email
Timestamp	The time at which the email was sent

Note that we assume a human has pre-classified each email as either spam or not-spam, which is necessary for our classifier to learn the parameters of the model's network.

It is generally easier to learn the parameters of a Bayesian network when the feature variables are categorical. Thus, we might use the domain information to create a variable that indicates whether or not the sender's domain ended in ".edu." For the count of hyperlinks, we might define categories of Low (0 to 4 hyperlinks), Medium (5 to 10 hyperlinks), and High (more than 10 hyperlinks). Using the timestamp of the emails, we might create an indicator for whether or not an email was sent after midnight but before noon. In the end, we could assign our variables to nodes in a graph as follows:

Table 1.2: Variables from the training set of 1,000 emails

Node	**Variable**	**Description**
V_0	spam	1 if Spam; 0 otherwise
V_1	edu	1 if from .edu; 0 otherwise
V_2	link-count	Low, Medium, or High
V_3	AM	1 if sent between midnight and noon; 0 otherwise

Because of its independence assumption, our Naïve Bayes classifier $\mathcal{B} = (G, \Theta)$ has a graph with the structure depicted in Figure 1.3. To complete the classifier, we would learn our model parameters from the training set. The parameters in our example would be $P(V_0|V_1)$, $P(V_0|V_2)$, and $P(V_0|V_3)$.

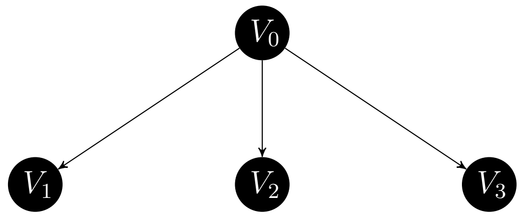

Figure 1.3: A Naive Bayes Classifier

1.5 Model Structure

We mentioned in the previous section that the Naïve Bayes classifier is a surprisingly effective model. The performance of the NBC is surprising because in practice, feature variables are rarely independent, and ignoring the dependencies between them should give us biased probability estimates for $P(C|\vec{X})$. However, even if our probability estimates are incorrect, we can still predict classifications correctly, so long as their relative probabilities conform with a correct classification of the data [Domingos and Pazzani, 1996].

That being said, the NBC is not all-powerful. It works better than we would expect, but it is not guaranteed to be optimal when the feature variables of our model are not all independent [Domingos and Pazzani, 1996]. Hence, to improve upon the NBC, we need a means of finding the structure of our Bayesian classifier's network.

The Structure Space

By $\mathcal{G}$, we denote the space of all possible graphs for a set of random variables V. Unfortunately, the order $\mathcal{G}$ is *super-exponential* on the order of V. Specifically, if n is the number of nodes in a graph, the structure space increases in size at a rate of $2^{O(n^2 \log n)}$, which makes exhaustive search through $\mathcal{G}$ impractical for unrestricted networks with even a moderate number of variables [Friedman and Koeller, 2001]. Importantly, we may choose between two modes of reasoning about model structure.

Model Selection

The first, called *model selection*, involves finding the most probable model structure given our data, which we can then use to estimate our parameters. Generally, this would involve cleverly searching through the space of possible models (or a subset thereof) and ranking structures according to a scoring function. The structure with the highest score would be our most likely model, and we then would use it to estimate our parameters.

Model Averaging

The second technique, called *model averaging* is a little more involved. In lieu of selecting one high-scoring model, model averaging would have us make estimates across a space of possible network structures, which are each weighted by their probability of being the correct model. Hence, model averaging is a useful tool when we have several model structures that are roughly equiprobable. There are a handful ways to go about model averaging, and we shall get to one of them in due time. For now, though, it suffices to know that model averaging is computationally very difficult, so we require a means to approximate it by simulation.

Chapter 2

Monte Carlo with Markov Chains

The reader may be familiar with Good Old Fashioned Monte Carlo (GOFMC) methods involving independent and identically distributed (IID) data. However, Monte Carlo simulations can also be done with a surprisingly simple stochastic process called Markov Chains. In fact, these Markov Chain Monte Carlo (MCMC) techniques are quite useful for approximating draws from posterior distributions for which we cannot easily find the normalization constant.

This chapter provides a cursory overview of GOFMC, and then defines Markov chains with the intent of introducing a class of algorithms for Markov Chain Monte Carlo simulation. We close with an application of MCMC to averaging estimates over Bayesian network structures.

2.1 GOFMC

An Intuitive Example

Imagine we seek to find the area of a peculiar two-dimensional shape called Minnesota. We are given no general formula for its area, and all of our attempts to analytically represent the curve that traces its perimeter have proven themselves fruitless. With credit to a talk on Monte Carlo Tree Search given by Peter Drake at the University of Portland, the technique suggested by GOFMC would be the following:

1. Place Minnesota inside a square with edges of known length s.
2. Randomly throw n darts such that they land inside the square.
3. Record x, the number of darts that landed inside Minnesota.
4. Multiply the proportion of darts that hit Minnesota ($\frac{x}{n}$) by the area of the square.

Symbolically, our GOFMC estimator for the area would be

$$s^2 * \sum_{j=1}^{n} \frac{\iota(x_j)}{n},$$

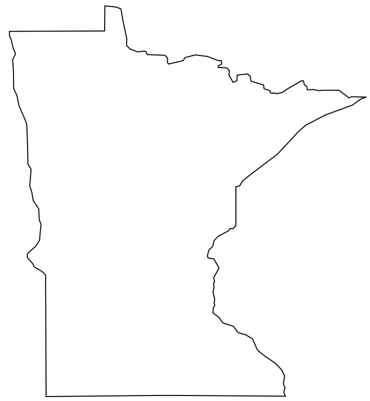

Figure 2.1: A two-dimensional shape called Minnesota

where the x_j represent dart throws, and

$$\iota(x_j) = \begin{cases} 1, & \text{if the dart hit Minnesota;} \\ 0, & \text{otherwise.} \end{cases}$$

The following illustrates our dart-throwing technique:

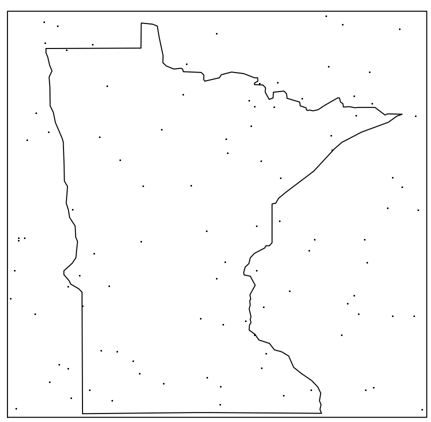

Figure 2.2: Estimating the Area of an Oddly Shaped State

Obviously, our estimate is not exact, but as $n \to \infty$, the Law of Large Numbers tells us that we get closer and closer to the true area of Minnesota. Thus is the motivation for GOFMC.

The General Case

Suppose we are given a distribution π and we seek to find the expectation of a function f over π. The central idea of GOFMC is that we may generate IID random variables

$X_1, \ldots, X_n$ from π in order to estimate $E[f(X_i)]$. A logical choice of estimator would thus be

$$\frac{1}{n}\sum_{i=1}^{n} f(X_i).$$

Of course, with an estimate comes the corresponding notion of its error. In this case, we define the GOFMC error as

$$\epsilon = E[f(X_i)] - \frac{1}{n}\sum_{i=1}^{n} f(X_i).$$

By application of the Central Limit Theorem, we know that as $n \to \infty$, the above converges to a normal distribution with a mean $\mu = 0$ and variance inversely proportional to n. Hence, with large enough n, we can produce accurate estimates from our randomly generated data.

2.2 Markov Chains

Andrey Markov used his eponymous chain only once in practice, to analyze the occurrence of vowels in a Pushkin poem [McGrayne, 2011]. According to legend, Enrico Fermi ran Markov chains in his head to combat insomnia, but we normal humans tend to reserve such calculations for computers [McGrayne, 2011]. Though they can be treacherous to compute, the basic intuition behind Markov chains is, thankfully, fairly easy to grasp.

Definition

Let s_i be a state from a set of possible states (the *state space*) $\mathcal{S}$, and let I be an index set. What we call a *Markov chain* $\theta^{(i)}$ is a collection of states from $\mathcal{S}$ indexed by $i \in I$. Markov chains can be thought of as a sequence of probabilistic transitions from state to state, where the probability of transitioning to the next state in the chain depends solely on the current state.

Thus, Markov chains have associated *transition probabilities*. When $\mathcal{S}$ is discrete and has finite order n, we may specify these probabilities in an n by n *transition matrix*, $T = (t_{jk})$, where $t_{jk} = P(\theta^{i+1} = s_k|\theta^i = s_j)$. Each row of T admits a probability distribution for a corresponding state in $\mathcal{S}$.

Using T, we may define a *transition function* $p : \mathcal{S} \times \mathcal{S} \to [0, 1]$ on our Markov chain, where $p(s_j, s_k) = t_{jk}$. Consistent with our definition above, $p(s_j, s_k)$ is a conditional probability for $\theta^{i+1} = s_k$ that depends solely on the information that $\theta^i = s_j$, and not on any past or future states of the chain. For the sake of concision, we may also refer to transitions as *steps*, and when the chain assumes a state s_j, we also say that it *hits* state s_j.

Example: Andrey the Chameleon

To illustrate our definition of a Markov chain, we introduce a charismatic chameleon named Andrey. Suppose that Andrey the chameleon can only assume four distinct colors: blue, green, yellow, or red. Hence, Andrey's state space $\mathcal{S}$ may be written as $\mathcal{S} = \{B, G, Y, R\}$.

We assume that Andrey has no control over the color to which he changes. Instead, his color changes are a probabilistic process, and each change depends only upon the color that he currently assumes. Andrey's transition matrix T is given by

$$\begin{array}{c} \\ B \\ G \\ Y \\ R \end{array} \begin{array}{c} \begin{array}{cccc} B & G & Y & R \end{array} \\ \begin{pmatrix} .25 & .25 & .25 & .25 \\ .8 & .1 & .1 & 0 \\ .5 & .3 & .02 & .18 \\ 1 & 0 & 0 & 0 \end{pmatrix} \end{array}$$

For example, t_{2j} is the probability distribution $P(\theta^{i+1}|\theta^i = G)$. That is, if Andrey is currently green, he has an 80% chance of next turning blue, a 10% chance of remaining green, a 10% chance of turning yellow, and a 0% chance of turning red.

A possible run of Andrey's associated Markov chain for $1 \leq i \leq 3$ might look like the following:

$$(\theta^1 = \mathrm{B}, \quad \theta^2 = \mathrm{G}, \quad \theta^3 = \mathrm{B}).$$

Notice, however, that it would be impossible to observe the following collection of states:

$$(\theta^1 = \mathrm{B}, \quad \theta^2 = \mathrm{R}, \quad \theta^3 = \mathrm{Y}),$$

since $p(\mathrm{R}, \mathrm{Y}) = 0$.

Basic Properties

We say a state $s_j \in \mathcal{S}$ is *irreducible* if it is possible to (eventually) get to any other $s_k \in \mathcal{S}$, starting from s_j. If all $s_j \in \mathcal{S}$ are irreducible, the Markov chain $\theta^{(i)}$ over $\mathcal{S}$ is also said to be irreducible.

By Z_j we denote the number of steps before a chain hits state s_j for the first time. We refer to this quantity as the *recurrence* or *hitting time* for state s_j. We denote the number of steps before a chain hits s_j an arbitrary number of times as Z_j^q, where q is a positive integer. Clearly, Z_j^q is always an integer, and Z_j is simply shorthand for Z_j^1. We also define $Z_j^0 = 0$.

Since Markov chains are stochastic processes, Z_j^q is a random variable. Hence, we may consider its expectation $E[Z_j^q]$. If for all $s_j \in \mathcal{S}$, the expected hitting time is finite ($E[Z_j^1] < \infty$), then we say our Markov chain is *positive recurrent*.

A state s_j is *periodic* if $\theta^(i)$ can only return to s_j after a number of steps equal to a multiple of some positive integer $k > 1$. Markov chains that contain no periodic states are called *aperiodic*. We say a Markov chain is *ergodic* if it is both aperiodic and positive recurrent.

Lastly, the *stationary distribution* π of a Markov chain is a PDF such that the transition matrix T of $\theta^{(i)}$ maintains π. Symbolically, this looks like the following:

$$\sum_{s_j \in \mathcal{S}} \pi(s_j) * p(s_j, s_k) = \sum_{s_j \in \mathcal{S}} \pi(s_j) * P(s_k|s_j) = \pi(s_k).$$

The stationary distribution is not guaranteed to exist, but once the run of a Markov chain admits a stationary distribution π, it stays in π.

Non-trivial Properties

A Markov chain that is irreducible and aperiodic must be positive recurrent.

For a stationary distribution π, we find that $\pi(s_j) * E[Z_j] = 1$.

2.3 The Ergodic Theorem

The Ergodic Theorem for Markov chains is an analog of the Law of Large Numbers for IID data. It ties together the concepts of aperiodicity, positive recurrence, and the stationary distribution. Importantly, it is through a basic corollary to the Ergodic theorem that we are able to justify use of MCMC in order to estimate draws from intractable distributions.

Preliminary Results

Proof of the Ergodic Theorem for Markov chains requires some preliminary results. Rigorous treatment of the following two results can be found in Chapter 1 of James Norris' *Markov Chains* [Norris, 1998].

First, the proportion of times we hit s_j in an ergodic Markov chain $\theta^{(i)}$ is the same regardless of the initial state θ^0 of the chain as n goes to ∞.

Second, we define $U_j^q = Z_j^q - Z_j^{q-1}$. Intuitively, this is the number of steps from the $(q-1)^{\text{th}}$ hit of s_j to the q^{th} hit of s_j in a Markov chain. Clearly, then,

$$\sum_{k=1}^{r} U_j^k = (Z_j^1 - Z_j^0) + \cdots + (Z_j^{r-1} - Z_j^{r-2}) + (Z_j^r - Z_j^{r-1}) = Z_j^r.$$

Moreover, if we consider the expectation of these quantities, we see that for all $q > 0$,

$$E[U_j^q] = E[Z_j^q - Z_j^{q-1}] = q * E[Z_j] - (q-1) * E[Z_j] = E[Z_j],$$

This follows from the linearity of expectation.

Lastly, we note that for a stationary distribution π, we have $\pi(s_j) * E[Z_j] = 1$.

Statement and Proof

Let $\theta^{(i)}$ be an ergodic Markov Chain. Let $V_j(n)$ be defined as follows:

$$V_j(n) = \sum_{i=0}^{n-1} \iota_j(\theta^i),$$

where

$$\iota_j(\theta^i) = \begin{cases} 1, & \text{if} \quad \theta^i = s_j; \\ 0, & \text{otherwise.} \end{cases}$$

We interpret $V_j(n)$ as the number of visits to state s_j before θ^n in our Markov chain. Let $E[Z_j] = m_j$ be the expected hitting time of state s_j. Then,

$$P\left(\frac{V_j(n)}{n} \longrightarrow \frac{1}{m_j}, \text{ as } n \to \infty\right) = 1.$$

That is, the proportion of times we hit s_j converges in probability to the inverse of the expected recurrence time.

Proof. We begin our proof by recalling that the proportion of times we hit s_j in our ergodic Markov chain is the same regardless of θ^0 as $n \to \infty$. Hence, without loss of generality, we assume s_j is the initial state of the chain ($\theta^0 = s_j$).

Now, recall from our preliminary results that

$$\sum_{k=1}^{q} U_j^k = Z_j^q,$$

and for all positive integers q,

$$E[U_j^q] = E[Z_j] = m_j.$$

Hence, we treat $\frac{1}{n}\sum_{k=1}^{n} U_j^k$ as an estimator for m_j, and by the Strong Law of Large Numbers, we obtain the following as $n \to \infty$:

$$P\left(\frac{\sum_{k=1}^{n} U_j^k}{n} \to m_j\right) = 1$$

Now, we write

$$\sum_{k=1}^{V_j(n)} U_j^k \leq n - 1,$$

where our sum gives us the number of steps until the last hit of s_i before θ^n in the chain. Obviously, then, the sum could not exceed $n-1$, since we are only considering the number of steps to a state that must occur before the n^{th} step. We may also consider

$$\sum_{k=1}^{V_j(n)+1} U_j^k \geq n,$$

which is the number of steps until the first hit of s_j after step θ^{n-1}. Thus, we may squeeze n and divide the resulting inequality by $V_j(n)$.

$$\frac{\sum_{k=1}^{V_j(n)} U_j^k}{V_j(n)} \leq \frac{n}{V_j(n)} \leq \frac{\sum_{k=1}^{V_j(n)+1} U_j^k}{V_j(n)}$$

.

Using the convergence of the U_j^k to m_j, our sums become

$$\frac{V_j(n) * m_j}{V_j(n)} \leq \frac{n}{V_j(n)} \leq \frac{(V_j(n)+1) * m_j}{V_j(n)}$$

,

and we see $\lim_{n\to\infty} \frac{V_j(n)+1}{V_j(n)}$ is 1, giving us

$$m_j \leq \frac{n}{V_j(n)} \leq m_j.$$

Hence, as $n \to \infty$,

$$P\left(\frac{n}{V_j(n)} \longrightarrow m_j\right) = 1,$$

and we have our result. □

Corollary

Suppose we run an ergodic Markov chain $\theta^{(i)}$ with stationary distribution π for n steps, where n is large. The consequence of the Ergodic theorem for Markov chains is that π is the unique stationary distribution of the chain, and $\frac{V_j(n)}{n}$ yields an estimate of $\frac{1}{m_j}$, which is equal to $\pi(s_j)$, since $\pi(s_j) * m_j = 1$.

2.4 Metropolis-Hastings for MCMC

Recall that in the case of GOFMC, we have a distribution π from which we can easily simulate random draws, and we then estimate the expectation of a function over π through random draws from π. Thus, to perform GOFMC, we must be able to specify the distribution of π. Sometimes, however, we are not so lucky as to be able to fully compute the PDF of our distribution of interest. This occurs frequently in high-dimensional Bayesian analyses, where the denominator of our posterior calculation can be a function integrated over hundreds of dimensions, if not more. Thus, we seek an alternative way to simulate draws from π when we only know how to calculate the marginal of π. For this, we use a Markov chain.

Detailed Balance

To construct a Markov chain with a stationary distribution equal to our posterior π, we need to ensure that the stationary distribution of our chain exists. To that end, given a transition function p, we introduce the *detailed balance* condition. That is, for all $s_j, s_k \in \mathcal{S}$,

$$\pi(s_j)p(s_j, s_k) = \pi(s_k)p(s_k, s_j),$$

which we rearrange as

$$\frac{\pi(s_j)}{\pi(s_k)} = \frac{p(s_k, s_j)}{p(s_j, s_k)}.$$

This condition is not necessary for the convergence of our chain to the posterior, but it suffices [Gamerman and Lopes, 2006].

Proposal and Acceptance

Next, we consider the specifics of the transition function p, which must guarantee that π is the unique stationary distribution of our Markov chain. To that end, we split p into a *proposal function*, q, which randomly proposes a new state in $\mathcal{S}$, and an *acceptance rule*, α, which returns the probability that we accept the proposed transition:

$$p(s_j, s_k) = q(s_j, s_k)\alpha(s_j, s_k).$$

We may assume the proposal function is a random walk with symmetric error, so that $q(s_j, s_k)$ is the probability $P(s_k|s_j)$ for our random walk. It is not wholly necessary to require q have symmetric error, but it suffices for our purposes [Gamerman and Lopes, 2006].

Construction of the acceptance rule is slightly more involved. Suppose we are in state s_j, and q proposes a move to state s_k. We accept the transition to state s_j with probability equal to

$$\alpha(s_j, s_k) = \begin{cases} \min\{1, \frac{\pi(s_k)q(s_j|s_k)}{\pi(s_j)q(s_k|s_j)}\}, & \textbf{if} \quad s_j \neq s_k; \\ 1 - \int q(s_j, s_k)\alpha(s_j, s_k)ds_k, & \textbf{otherwise}. \end{cases}$$

When the state space $\mathcal{S}$ is finite, the integral above is a summation. By any means, the result is a Markov chain that converges to π, our posterior distribution.

Methodological Issues

We face two issues with running Markov chains to approximate the posterior. First, if we sample from the chain directly, each sample depends upon the previous sample. Hence, taking all of the values from our simulation would not be an IID sample from the posterior. Secondly, the Markov chain may be guaranteed to converge to the posterior, but in its early iterations, the samples that it produces may not approximate the posterior distribution. Our solutions to these issues are heuristic, but they help to reduce the error of our estimates. To deal with the latter issue, we can run a *burn-in* period for the chain, which gives it time to *mix* to the posterior. To resolve the former issue, we sample every n^{th} state of the chain.

2.5 Bayesian Model Averaging for Bayesian Networks

One application of MCMC is to the realm of Bayesian model averaging. In this scenario, we consider $\mathcal{G}$, the space of all possible graph structures for a Bayesian network $\mathcal{B}$.

Being Bayesian About Structure

Let $G \in \mathcal{G}$ be a possible structure for $\mathcal{B}$. Let D be the set of all observed data used to train the parameters Θ of $\mathcal{B}$. As Bayesians, we treat G as a random variable, and we express its posterior as

$$P(G|D) = \frac{P(D|G)P(G)}{P(D)},$$

where

$$P(D) = \sum_{G \in \mathcal{G}} P(D|G)P(G).$$

Regarding the above summation, recall that $\mathcal{G}$ has dimension that grows super-exponentially with respect to the order of V, the number of variables in the model. Thus, computation of the normalizing constant of the posterior is undesirable. However, the likelihood function for the data D given a network structure G has a manageable closed form expression when we the data are composed of categorical random variables [Baesans et al, 2002]. Hence, we can use Markov Chain Monte Carlo to sample from the posterior $P(G|D)$.

The Proposal

For the sake of illustration, we suppose the current state of the chain is $G = (V, E)$. The proposal function q for our Metropolis-Hastings algorithm randomly chooses an ordered pair of vertices (V_i, V_j) for $V_i, V_j \in V,\ i \neq j$. Then, if $(V_i, V_j) \in E$, q proposes the structure $G' = (V, E - \{(V_i, V_j)\})$, which is the removal of the given arc from E. Otherwise, q proposes addition of the arc (V_i, V_j) to E, so long as such an addition preserves the acyclic property of the graph structure. We denote the count of all directed acyclic graphs with one fewer or one greater arc than G as $\mathcal{N}(G)$. Hence, the probability that q proposes a graph $G' \in \mathcal{G}$ (given the current graph is G) is $\frac{1}{\mathcal{N}(G)}$.

The Acceptance

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