2

Background

This chapter lays the foundation for probabilistic modeling of neural spike trains. We start by introducing the language of generative models, which allow us to formalize, in probabilistic terms, our hypotheses about dynamics and low-dimensional structure. The key ingredients are latent variables that reflect the underlying state of the system and conditional distributions that relate these variables to the observed data. Once we understand the basics of this language, we can begin to articulate hypotheses about dynamical data in the form of generative time series models. Section 2.2 enumerates a few common motifs of time series modeling that will be used throughout this thesis. Finally, given a model and an observed spike train, we can invert the model and reason about the posterior distribution over latent variables using Bayesian inference algorithms such as Markov Chain Monte Carlo and mean field variational inference, which are introduced in Section 2.3. At the end of this chapter, we will have the basic foundation necessary to start looking for structure in neural data. The rest of the thesis will build upon this foundation by developing more sophisticated models and increasingly efficient inference algorithms, and by putting them to use on real neural recordings.

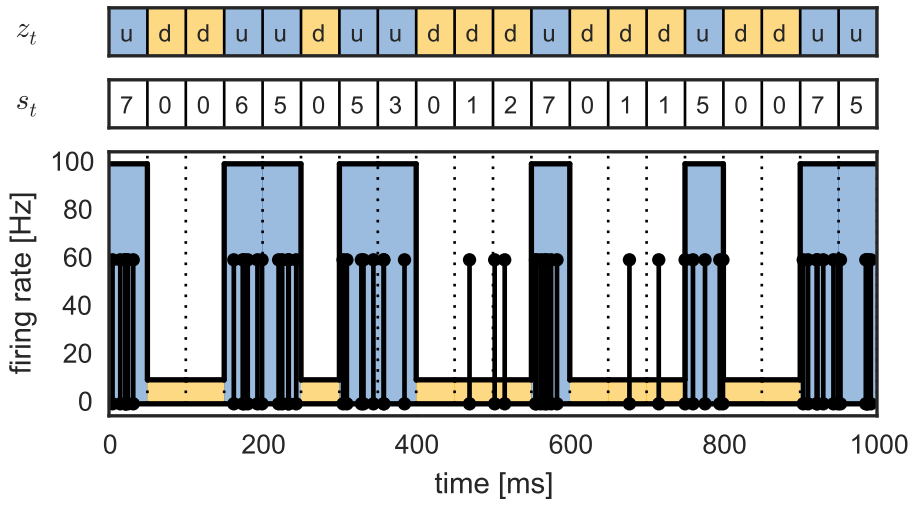

Figure 2.1: A simple neuron that randomly switches between an *up* and a *down* state every 50ms. Here, time bins are colored blue and yellow depending on the latent state, z_t. Each state has an associated firing rate from which a Poisson number of spikes, s_t, is drawn. Precise spike times are uniformly distributed over the 50ms interval.

Generative Probabilistic Models

Generative probabilistic models tell a story of how data comes to be. While this story never captures every physical detail, it serves as an idealized version, capturing the essence of the system. For example, when modeling a neural spike train, we will ignore the states of individual ion channels and the nonlinear dynamics of membrane potential and instead characterize the instantaneous *firing rate* of a neuron — the probability that a neuron spikes at any moment in time.

As a simple illustration, consider the following generative process. Suppose a neuron has two states, an *up* state and a *down* state. In the *up* state, it spikes at a high rate, say 100Hz, and in the *down* state it fires less frequently, say at 10Hz. Assume that every 50ms the neuron flips a coin to decide its new state and then fires a random number of spikes according to the firing rate associated with that state. For the sake of simplicity, assume the precise spike times are uniformly distributed over the 50ms interval. Once the interval has elapsed, the neuron flips another coin and its rate immediately changes to reflect its new state. Our goal is to infer the latent state of the neuron given the observed spikes.

Clearly, this generative story contains many simplifying assumptions and omits a great

amount of detail. In addition to assuming that spiking is adequately captured by firing rates, the notion that a neuron has only two firing rates and that it randomly switches between them is a gross simplification. Nevertheless, this very simple model captures patterns of spiking that have been observed in actual experiments (Cowan and Wilson, 1994; Shu et al., 2003).

We can formalize this generative story with a probabilistic model that specifies a distribution over latent states and observed spike counts. Let $s_t \in \mathbb{N}$ denote the number of spikes counted in the t-th time bin, and $z_t \in \{\textit{up}, \textit{down}\}$ denote the corresponding state of the neuron. The assumption that states are drawn from a coin flip corresponds to the prior distribution, $z_t \sim \text{Discrete}(\boldsymbol{\pi})$, where $\boldsymbol{\pi} = [\pi_{\textit{up}}, \pi_{\textit{down}}]$ is a nonnegative vector that sums to one and specifies the probability of *up* and *down* states.* Implicitly, we have assumed that $\boldsymbol{\pi} = \left[\frac{1}{2}, \frac{1}{2}\right]$, though this need not be the case. We previously said that the neurons fire a random number of spikes according to their state-dependent firing rate; now we will formalize this by assuming, $s_t \sim \text{Poisson}(\lambda_{z_t} \cdot \Delta t)$, where $\Delta t = 0.05$s, $\lambda_{\textit{up}} = 100$ spikes/s, and $\lambda_{\textit{down}} = 10$ spike/s.

Figure 2.1 shows a neural spike train sampled from this generative model. The time bins are colored blue or yellow depending on whether the neuron is in the *up* or *down* state, respectively. The precise spike times are denoted by black vertical lines with circular endpoints. Above, the vector of observed spike counts, $\boldsymbol{s} = \left[s_1, \ldots, s_T\right]$, and the vector of latent states, $\boldsymbol{z} = \left[z_1, \ldots, z_T\right]$, are shown. We will use this notation throughout the thesis: bold symbols like $\boldsymbol{s}$ will denote arrays of variables; lowercase bold symbols will typically denote vectors.

The generative procedure defines the *likelihood* of any given set of observed spike counts and corresponding latent states. This can be written as a conditional distribution where the

*The notation $z \sim \mathrm{P}(\theta)$ means that the random variable z is sampled from (or distributed according to) the distribution P, which is parameterized by θ. When we write $\mathrm{P}(z \mid \theta)$ we refer to the density (assuming it exists) of P evaluated at z. A list of commonly used distributions and their densities is given in Appendix A.

state probabilities and firing rates are given. We have,

$$p(\boldsymbol{s}, \boldsymbol{z} \mid \boldsymbol{\pi}, \boldsymbol{\lambda}) = p(\boldsymbol{z} \mid \boldsymbol{\pi})\, p(\boldsymbol{s} \mid \boldsymbol{z}, \boldsymbol{\lambda}) \tag{2.1}$$

$$= \prod_{t=1}^{T} p(z_t \mid \boldsymbol{\pi})\, p(s_t \mid \lambda_{z_t}) \tag{2.2}$$

$$= \prod_{t=1}^{T} \mathrm{Discrete}(z_t \mid \boldsymbol{\pi})\, \mathrm{Poisson}(s_t \mid \lambda_{z_t} \cdot \Delta t). \tag{2.3}$$

Since Δt is a constant, we do not include it as a random variable in the joint distribution or explicitly condition on it.

The probabilistic model specifies the particular factorization of the likelihood implied by the generative story. Eq. 2.1 applies the product rule of probability, and reflects the assumptions that $\boldsymbol{z}$ depends only on $\boldsymbol{\pi}$ and $\boldsymbol{s}$ depends only on $\boldsymbol{z}$ and $\boldsymbol{\lambda}$. In going from (2.1) to (2.2), we have asserted that the latent states z_t and $z_{t'}$ are conditionally independent given $\boldsymbol{\pi}$, and that the spike counts s_t and $s_{t'}$ are conditionally independent given their corresponding latent states and firing rates. This conditional independence assumption, which was implicit in the generative story, becomes explicit when we factor the likelihood into a product over time bins. Eq. 2.3 specifies the functional form of the conditional distributions. When we hypothesize relationships between different variables, we are making assertions about the factorization and the form of the likelihood. In Section 2.2, we explore different patterns of conditional dependence that provide the building blocks of models for dynamic data.

So far, we have assumed that the firing rates and state probabilities are known, but in practice this is a bit unreasonable. To complete the probabilistic model, we need to combine the likelihood function with a *prior distribution* that captures our uncertainty about these parameters. For example, a more reasonable hypothesis is that neurons have two firing rates, and while we do not know their exact values, we can specify a distribution over them, $p(\boldsymbol{\lambda})$. Similarly, we may not know the exact probability of each state, $\boldsymbol{\pi}$, but perhaps we can specify a prior, $p(\boldsymbol{\pi})$, that captures our intuition that the states should be equally likely *a priori*. Putting this all together, we can now write down the *joint distribution* of our

probabilistic model — the product of the likelihood and the prior distributions:

$$p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\pi}, \boldsymbol{\lambda}) = p(\boldsymbol{s}, \boldsymbol{z} \mid \boldsymbol{\pi}, \boldsymbol{\lambda})\, p(\boldsymbol{\pi})\, p(\boldsymbol{\lambda}). \tag{2.4}$$

When constructing a probabilistic model, we express these prior intuitions and simultaneously make inference easier by using *conjugate* prior distributions.

Conjugate Prior Distributions

A conjugate prior ensures that the conditional distribution of a parameter, given the data, will have a tractable form. Specifically, the conditional distribution will have the same form as the prior. For example, take the parameter, λ_{up}. If we look at the likelihood as a function of λ_{up} and ignore terms that do not depend on this parameter, we have,

$$\begin{aligned} p(\boldsymbol{s}, \boldsymbol{z} \mid \boldsymbol{\pi}, \boldsymbol{\lambda}) &\propto \prod_{t=1}^{T} \left[\text{Poisson}(s_t \mid \lambda_{up} \cdot \Delta t)\right]^{\mathbb{I}[z_t = up]} \\ &\propto \prod_{t=1}^{T} \left[\lambda_{up}^{s_t}\, e^{-\lambda_{up} \cdot \Delta t}\right]^{\mathbb{I}[z_t = up]} \\ &= \lambda_{up}^{s_{up}}\, e^{-\lambda_{up} \cdot t_{up}}, \end{aligned}$$

where

$$\begin{aligned} s_{up} &= \sum_{t=1}^{T} s_t \cdot \mathbb{I}[z_t = up], \\ t_{up} &= \sum_{t=1}^{T} \Delta t \cdot \mathbb{I}[z_t = up], \end{aligned}$$

and $\mathbb{I}[x]$ is an indicator function that equals one if x evaluates to true and equals zero otherwise.

Now consider a gamma prior distribution,

$$\begin{aligned} p(\lambda_{up} \mid \alpha, \beta) &= \mathrm{Gamma}(\lambda_{up} \mid \alpha, \beta) \\ &\propto \lambda_{up}^{\alpha-1}\, e^{-\lambda_{up} \cdot \beta}. \end{aligned}$$

The conditional distribution over λ_{up} given the observed spike counts, the latent states, and the prior is proportional to the likelihood times the prior. This simplifies to,

$$\begin{aligned} p(\lambda_{up} \mid \boldsymbol{s}, \boldsymbol{z}, \alpha, \beta) &\propto p(\boldsymbol{s}, \boldsymbol{z} \mid \boldsymbol{\pi}, \boldsymbol{\lambda})\, p(\lambda_{up} \mid \alpha, \beta) \\ &\propto \lambda_{up}^{s_{up}+\alpha-1}\, e^{-\lambda_{up}(t_{up}+\beta)} \\ &\propto \mathrm{Gamma}(\lambda_{up} \mid s_{up} + \alpha,\ t_{up} + \beta). \end{aligned}$$

Since both the prior and the the conditional distribution over λ_{up} are in the gamma family, we say gamma prior is conjugate with this product-of-Poissons likelihood. Moreover, the parameters of conditional distribution only depend on $\boldsymbol{s}$ and $\boldsymbol{z}$ through simple *sufficient statistics*, s_{up} and t_{up}. A Dirichlet prior distribution on the state probability, $\mathrm{Dir}(\boldsymbol{\pi} \mid \gamma)$, is similarly conjugate with the product of discrete densities in the likelihood that links $\boldsymbol{\pi}$ and $\boldsymbol{z}$. In fact, conjugate priors exist for all likelihoods in the *exponential family*. These ideas are thoroughly discussed in standard Bayesian statistics and machine learning textbooks like Gelman et al. (2013); Murphy (2012).

Latent Variables, Parameters, and Hyperparameters As our models become increasingly complicated, we will often distinguish between the different types of random variables. The states, $\boldsymbol{z}$, are called *local latent variables* because there is one for each data point. The unknown latent state probability and the firing rates, $\{\boldsymbol{\pi}, \boldsymbol{\lambda}\}$, are either called *parameters* or *global latent variables* because their dimension is fixed. The remaining values, $\{\alpha, \beta, \gamma\}$, are called *hyperparameters*. These are constants that we set prior to performing inference. Typically, these can be tuned by cross-validation, or simply set based on intuition and physical constraints. For conciseness, we will refer to the set of all parameters as $\boldsymbol{\theta}$ and the set of hyperparameters as $\boldsymbol{\eta}$.

Representations of Spike Trains

One of the first decisions we must make is how to represent our data. In this thesis we will focus on modeling spike trains, which are sequences of discrete events in time. These spike trains typically come from spike sorting algorithms applied to extracellular recordings from multi-electrode arrays (Lewicki, 1998) or from deconvolution algorithms applied to optically recorded calcium fluorescence traces (Pnevmatikakis et al., 2016; Vogelstein et al., 2010). Reducing the data to a set of spike times often results in enormous compression. Rather than considering electrode potentials, which may be sampled at upwards of 10kHz, or calcium fluorescence traces, which are highly autocorrelated due to the relatively slow dynamics of calcium concentration in cells, we only consider the times of action potentials.

The most general representation of a spike train is a set of real-valued times for each neuron. In Figure 2.1, this corresponds to the temporal locations of each black spike. When there is more than one neuron, we have a set of *marked* spike times, which we call,

$$\mathcal{S} = \{(s_m, c_m)\}_{m=1}^{M} \subset [0, T] \times \{1, \ldots, N\}.$$

Each member of this set consists of a real-valued spike time s_m in the interval $[0, T]$, and an integer, $c_m \in \{1, \ldots, N\}$, that specifies the index of the cell that generated this spike. M is the total number of spikes on all neurons.

This continuous-time representation is warranted when the temporal resolution of the data is considerably higher than the timescale of typical action potentials. For example, multi-elecrode arrays typically have sampling intervals of 0.1ms or smaller, whereas the width of action potentials is on the order of 1ms. This allows us to specify the spike time as an effectively real-valued number.

Sets of discrete events like these are typically modeled as realizations of a *marked point process* (Daley and Vere-Jones, 2003). Such a process is defined by its nonnegative firing rates[†], $\{\lambda_n(t \mid \mathcal{H}_t)\}_{n=1}^{N}$, where $\mathcal{H}_t$ captures the history of the process through time t. For example, the history may include the previous spikes, $\mathcal{H}_t = \{(s_m, c_m) : s_m < t\}$, as well as some external covariates. If we consider a small time window, $[t, t + \Delta t)$, and take the limit as Δt approaches zero, $\lambda_n(t \mid \mathcal{H}_t) \cdot \Delta t$ is the expected number of spikes fired by neuron n

[†]In the point process literature, these firing rates are called *conditional intensity functions*.

in the window $[t, t + \Delta t)$.

The limiting perspective on the conditional intensity functions suggests an alternative, discrete-time representation. Rather than modeling a set of continuous spike times and conditional firing rates, we may instead represent a spike count matrix, $\boldsymbol{S}$, and the corresponding rate matrix, $\boldsymbol{\Lambda}$, where,

$$\boldsymbol{S} = \begin{bmatrix} s_{1,1} & \cdots & s_{1,N} \\ \vdots & & \vdots \\ s_{T,1} & \cdots & s_{T,N} \end{bmatrix}, \qquad \boldsymbol{\Lambda} = \begin{bmatrix} \lambda_{1,1} & \cdots & \lambda_{1,N} \\ \vdots & & \vdots \\ \lambda_{T,1} & \cdots & \lambda_{T,N} \end{bmatrix}.$$

Here, $s_{t,n} \in \mathbb{N}$ denotes the number of spikes fired in the t-th time bin by the n-th neuron, and $\lambda_{t,n} \in \mathbb{R}_+$ denotes the corresponding firing rate. Sometimes, the effects we are interested in studying occur at relatively slow time scales, so discretizing may provide valuable compression while retaining most of the relevant information. For example, if we are studying neural dynamics on the order of minutes, then simply knowing how many spikes occurred each second may provide most of the relevant information, while precise, millisecond-resolution spike timing may be superfluous.

However, the primary reason to discretize spike times into a matrix of counts is that the statistics and machine learning community has developed a much broader set of models for matrices than for sets of continuous time events. In the next section, we will explore a number of common modeling motifs that can be applied to time series data represented as matrices, and many of the chapters of this thesis will focus on extending these motifs in novel ways.

Motifs of Time Series Models

The art of probabilistic modeling lies in balancing two conflicting concerns: our model should capture as much of the relevant structure in the data as possible, drawing on our intuition and our existing knowledge of the system, yet at the same time we wish to limit the complexity of the model so that we may perform inference efficiently. One way to balance

these goals is to compose our model out of common, well-studied motifs.

Motifs correspond to factorizations of probabilistic models. To visualize these motifs, we represent the probabilistic model in the form of a directed acylcic graph. Each node in the graph corresponds to a random variable, and shaded nodes indicate which variables are observed. The edges represent conditional dependencies. For example, in the mixture model shown in Figure 2.2, the spike count s_2 has incoming edges from the corresponding latent state z_2 and the firing rates, $\boldsymbol{\lambda}$. Thus, the joint probability distribution contains the factor, $p(s_2 \mid z_2, \boldsymbol{\lambda})$. Since the graph is directed and acyclic, we read off the factors starting with the root nodes, $p(\boldsymbol{\pi})$ and $p(\boldsymbol{\lambda})$, and ending with the leaf nodes, $p(s_t \mid z_t, \boldsymbol{\lambda})$. In this way, the graph captures the factorization of the joint probability distribution and specifies a particular subset of all possible joint distributions over this set of variables.

The edges of the graph do not, however, specify the type of the random variable or functional form of the factors. For example, a node may indicate either a discrete or a continuous random variable, and an edge may indicate an arbitrary form of dependence, like a linear relationship. In this way, two models may share the same graph but have fundamentally different interpretations. This is true of mixture models and factor analysis models shown in Figure 2.2. Some patterns of factorization, types, and dependencies are used over and over again and form the building blocks for more complex models. Next, we discuss a few of the common motifs shown in Figure 2.2.

Mixture Models Our working example from Section 2.1 is an instance of a simple mixture model. The firing rate assumes only two values, and the observed spike counts are a mixture of counts drawn from the *up* state and counts from the *down* state. We can easily extend this to populations of neurons and mixtures of more than two states. Suppose there are now K states, such that $z_t \in \{1, \ldots, K\}$. Furthermore, we generalize the rates $\lambda_{\textit{up}}$ and $\lambda_{\textit{down}}$, to vectors of rates, one for each neuron and state. In a slight abuse of notation, let $\boldsymbol{\lambda}_k = [\lambda_{k,1}, \ldots, \lambda_{k,N}]$ denote a vector of rates in which $\lambda_{k,n}$ is the firing rate of the n-th neuron in state k.

In a mixture model, the latent states are discrete, the time bins are conditionally independent, and the dependence of s_t on z_t and $\boldsymbol{\lambda}$ is linear. To see the latter claim, note that that the instantaneous firing rate of neuron n can be written, $\sum_{k=1}^{K} \mathbb{I}[z_t = k] \cdot \lambda_{k,n}$. These

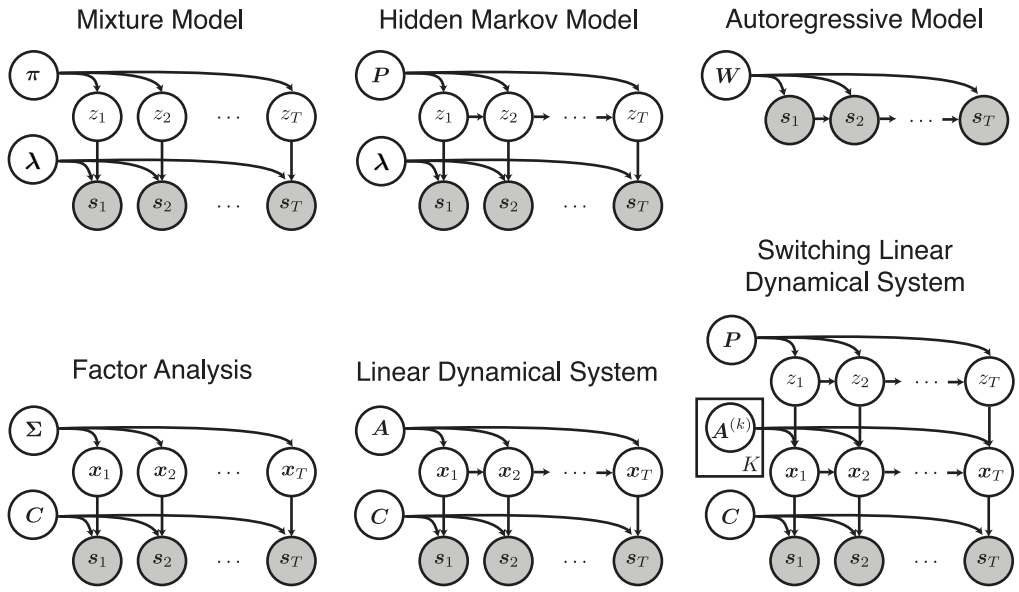

Figure 2.2: Motifs of time series models. By introducing conditional dependencies and layers of random variables, we construct models that reflect sophisticated hypotheses about the structure underlying the data. See Section 2.2 for detailed description.

three properties suggest multiple dimensions along which the mixture model may be generalized.

HIDDEN MARKOV MODELS First, let's address the conditional independence of time bins in the mixture model. According to this model, the distribution over latent states factors into a product, $p(\boldsymbol{z} \mid \boldsymbol{\pi}) = \prod_t p(z_t \mid \boldsymbol{\pi})$. This clearly ignores the temporal dynamics of neural data. Instead, we may hypothesis that latent states obey Markovian dynamics,

$$\begin{aligned} p(\boldsymbol{z} \mid \boldsymbol{\pi}^{(0)}, \boldsymbol{P}) &= p(z_1 \mid \boldsymbol{\pi}^{(0)}) \prod_{t=2}^{T} p(z_t \mid z_{t-1}, \boldsymbol{P}) \\ &= \text{Discrete}(z_1 \mid \boldsymbol{\pi}^{(0)}) \prod_{t=2}^{T} \text{Discrete}(z_t \mid \boldsymbol{\pi}^{(z_{t-1})}), \end{aligned}$$

where $\boldsymbol{\pi}^{(0)} \in [0,1]^K$ is a discrete probability distribution over initial states, and

$$\boldsymbol{P} = \begin{bmatrix} — & \boldsymbol{\pi}^{(1)} & — \\ & \vdots & \\ — & \boldsymbol{\pi}^{(K)} & — \end{bmatrix},$$

is a $K \times K$ transition matrix where the row, $\boldsymbol{\pi}^{(k)} \in [0,1]^K$, specifies a discrete conditional distribution over z_t given $z_{t-1} = k$. This is known as a hidden Markov model (HMM) (Baum and Petrie, 1966; Rabiner, 1989), and the corresponding graphical model is shown in Figure 2.2. Chapter 7 studies some of the challenges involved in selecting the number of states, K, in a nonparametric way.

Autoregressive Models In an HMM, correlations in spike counts from one bin to the next arise from correlations in the underlying latent states. Alternatively, we may directly model the rate as a function of previous spike counts. For example, consider an autoregressive model with linear dynamics,

$$\lambda_{t,n} = \sum_{n'=1}^{N} \sum_{d=1}^{D} w_{n' \to n}^{(d)} \cdot s_{t-d,n'}. \tag{2.5}$$

The weight, $w_{n' \to n}^{(d)}$, specifies the influence that spikes on neuron n' have on the rate of neuron n at an offset of d time bins in the future. Unlike the HMM, which has an autoregressive model for latent states, here the autoregression governs the rates directly. Moreover, this autoregressive model sums over the spike counts of all neurons over the past D time bins, allowing delayed interactions. Figure 2.2 shows the graph structure of an autoregressive model in the special case that $D = 1$.

In continuous time, autoregressive interactions like these are the basis of the Hawkes process (Hawkes, 1971), a mutually-excitatory point process. Chapter 3 will study these models in great detail, and Chapter 4 will extend the Hawkes process inference algorithms to their discrete time counterparts.

One complication of this formulation is that negative weights could lead to negative fir-

ing rates, which would invalidate the assumptions of the model. The easiest way to address this issue is to require nonnegative weights, $w^{(d)}_{n' \to n} \in \mathbb{R}_+$. This implicitly instantiates the hypothesis that interactions between spikes on one neuron and the rate of another is always excitatory — a spike can never decrease the future firing rate. While this is not the most biologically realistic model given our knowledge of excitatory and inhibitory synapses, it is important to remember that this is simply a descriptive model of firing rate dynamics, and it does not necessarily map onto physical synaptic connections. As we will show, the weights inferred by this type of excitatory autoregressive model can still provide useful insight into the structure of neural activity.

Nonlinear Autoregressive Models In order to capture both excitatory and inhibitory autoregressive weights, we need to introduce a nonlinear function that ensures a nonnegative firing rate. Specifically, assume that,

$$\begin{aligned} \psi_{t,n} &= \sum_{n'=1}^{N} \sum_{d=1}^{D} w^{(d)}_{n' \to n} \cdot s_{t-d,n'}, \\ \lambda_{t,n} &= g\left(\psi_{t,n}\right). \end{aligned}$$

The nonlinear function $g(\cdot) : \mathbb{R} \to \mathbb{R}_+$ maps a real valued "activation," $\psi_{t,n}$, into a nonnegative firing rate, $\lambda_{t,n}$. In this formulation, the weights may be either positive or negative to reflect either excitatory or inhibitory interactions, respectively. In computational neuroscience, this is often called a generalized linear model (GLM) (Paninski, 2004; Truccolo et al., 2005; Pillow et al., 2008), since the linear-nonlinear cascade that links spike history to firing rate is an instance of the GLM commonly used in statistics (Nelder and Baker, 1972). Chapter 5 combines these nonlinear autoregressive models with prior distributions on the underlying network and derives efficient Bayesian inference algorithms to fit them to data.

Factor Models HMM's introduced dynamics to the mixture model and nonlinear autoregressive models generalized the linear functional dependence. Factor models generalize the discrete nature of the random variables with a continuous analogue. For example, consider a model in which the discrete variable $z_t \in \{1, \ldots, K\}$ is replaced by a discrete

probability distribution $\boldsymbol{\pi}_t \in [0,1]^K$. The rate is then a nonnegative combination,

$$\lambda_{t,n} = \sum_{k=1}^{K} \pi_{t,k} \cdot \lambda_{k,n}.$$

This is naturally interpreted as a *mixed membership model* in which the rates at each time bin derive from a mixture of discrete latent states with mixing weights $\boldsymbol{\pi}_t$. In text modeling, this motif is the basis of the latent Dirichlet allocation (LDA) model (Blei et al., 2003).

Alternatively, we may replace the discrete latent state with a continuous one, $\boldsymbol{x}_t \in \mathbb{R}^K$. As in the nonlinear autoregressive model, we can retain the linear form and introduce an elementwise nonlinearity to ensure nonnegative firing rates:

$$\begin{aligned} p(\boldsymbol{x}) &= \prod_{t=1}^{T} \mathcal{N}(\boldsymbol{x}_t \mid \mathbf{0}, \boldsymbol{\Sigma}), \\ \psi_{t,n} &= \sum_{k=1}^{K} x_{t,k} \cdot c_{k,n}, \\ \lambda_{t,n} &= g(\psi_{t,n}). \end{aligned}$$

Here, $c_{k,n}$ is an entry in the real valued matrix $\boldsymbol{C} \in \mathbb{R}^{K \times N}$, and $\boldsymbol{\Sigma} = \operatorname{diag}([\sigma_1^2, \ldots, \sigma_K^2])$. This corresponds to a factor analysis model. Unlike standard factor analysis, however, here the observations are discrete spike counts rather than Gaussian observations.

Linear Dynamical Systems In the same way that HMM's extend mixture models with temporal dynamics, linear dynamical systems (LDSs) extend factor models with linear autoregressive dynamics in the latent state. We simply replace the prior on $\boldsymbol{x}$ with a model of the form,

$$p(\boldsymbol{x}) = \mathcal{N}(\boldsymbol{x}_1 \mid \mathbf{0}, \boldsymbol{\Sigma}) \prod_{t=2}^{T} \mathcal{N}(\boldsymbol{x}_t \mid \boldsymbol{A}\boldsymbol{x}_{t-1}, \boldsymbol{\Sigma}),$$

where $\boldsymbol{A} \in \mathbb{R}^{K \times K}$ specifies the linear dynamics of the latent state. The elementwise nonlinear mapping from latent states to firing rates is the same as in the factor model, but now

the linear autoregressive nature of the dynamics induces correlations in spike counts from one time bin to the next.

Hierarchical Extensions These motifs — continuous and discrete latent states, linear autoregressive dynamics, and nonlinear link functions — provide a foundation for constructing probabilistic models for spike trains. Atop this foundation, we may layer additional random variables reflecting hypotheses about shared structure. For example, a switching linear dynamical system, shown in Figure 2.2 and studied in Chapter 8, combines discrete *and* continuous latent states (Murphy, 2012; Fox, 2009). Likewise, Chapters 3, 4, and 5 consider structured prior distributions on the weights of autoregressive models, and Chapter 7 considers nonparametric Bayesian priors on the number of states in an HMM. Once the dynamics model has been specified, it is easy to test a variety of hypotheses about hierarchical structure. In order to fit these models, however, we need efficient inference algorithms that capitalize on the compositional structure of the model.

Bayesian Inference

Given an observed spike train, our goal is to compute the posterior distribution over latent variables, $\boldsymbol{z}$, and parameters, $\boldsymbol{\theta}$, of the model. For example, in an HMM the latent variables are the dynamic latent states and the parameters are $\boldsymbol{\theta} = \{\boldsymbol{P}, \boldsymbol{\lambda}\}$, the transition matrix and the firing rates for each latent state. Bayes' rule relates the posterior distribution to the joint distribution of our probabilistic model,

$$p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s}) = \frac{p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})}{p(\boldsymbol{s})} = \frac{p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})}{\int p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta}) \, \mathrm{d}\boldsymbol{z} \, \mathrm{d}\boldsymbol{\theta}}. \tag{2.6}$$

Unfortunately, the denominator in Eq. 2.6 involves an integral that is intractable for all but the simplest models. Instead, we must resort to approximate algorithms like Markov chain Monte Carlo (MCMC) and mean field variational inference. We will briefly describe each of these in turn.

Markov Chain Monte Carlo

Markov chain Monte Carlo (MCMC) algorithms are a central component of modern machine learning, and many texts are devoted to the subject (e.g. Geyer, 1992; Gilks, 2005; Robert and Casella, 2013). The fundamental idea is to generate a collection of samples from the posterior distribution and use them to estimate expectations. Specifically, given a set of samples,

$$\left\{ \left(\boldsymbol{z}^{(1)}, \boldsymbol{\theta}^{(1)}\right), \ldots, \left(\boldsymbol{z}^{(L)}, \boldsymbol{\theta}^{(L)}\right) \right\},$$

where

$$\boldsymbol{z}^{(\ell)}, \boldsymbol{\theta}^{(\ell)} \sim p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s}),$$

we can form a Monte Carlo estimate of the expectation of a function $f(\boldsymbol{z}, \boldsymbol{\theta})$ with respect to the posterior,

$$\mathbb{E}_{p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s})}\left[f(\boldsymbol{z}, \boldsymbol{\theta})\right] \approx \frac{1}{L} \sum_{\ell=1}^{L} f\left(\boldsymbol{z}^{(\ell)}, \boldsymbol{\theta}^{(\ell)}\right).$$

When the samples are independently drawn from the posterior, the strong law of large numbers states that the Monte Carlo estimate converges to the true expectation almost surely, implying that these Monte Carlo estimates are unbiased. Moreover, if the function f is real-valued, the variance of the Monte Carlo estimator scales as $\mathcal{O}(L^{-1})$ regardless of the dimension of $\boldsymbol{z}$ and $\boldsymbol{\theta}$.

To collect these samples, we design a Markov chain to stochastically explore the space of latent variables and parameters. The chain iteratively samples a new state according to its transition operator, $\mathcal{T}\left((\boldsymbol{z}, \boldsymbol{\theta}) \to (\boldsymbol{z}', \boldsymbol{\theta}')\right)$, which specifies the probability of transitioning from state $(\boldsymbol{z}, \boldsymbol{\theta})$ to state $(\boldsymbol{z}', \boldsymbol{\theta}')$. Each state the Markov chain visits is taken as a sample. If we design the Markov chain appropriately, we guarantee that the transition operator will asymptotically visit states according to their posterior probability.

When states are sampled with a Markov chain, it is no longer true that the samples are independent. In fact, the transition operator often leads to relatively local updates, which

in turn lead to autocorrelation in the sequence of samples. This does not affect the bias of the Monte Carlo estimate, but it does affect the constant in the asymptotic $\mathcal{O}(L^{-1})$ convergence rate. However, in addition to the increased variance, MCMC algorithms also suffer from a transient bias due to the fact that the initial state is not drawn from the posterior distribution (we would not be using MCMC if we could sample from the posterior directly). Fortunately, the transient bias of the Monte Carlo estimator also decays as $\mathcal{O}(L^{-1})$. Since the mean squared error of an estimator is equal to its variance plus its bias squared, and since both variance and bias scale inversely with L, the asymptotic effect of the transient bias is insignificant compared to that of the variance.

The critical property of our Markov chain is that, asymptotically, it visits states with probability equal to the true posterior probability. For this asymptotic guarantee to hold, the posterior distribution must be invariant with respect to the transition operator, which is defined by the following equivalence,

$$p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s}) = \int p\big(\boldsymbol{z}', \boldsymbol{\theta}' \mid \boldsymbol{s}\big)\, \mathcal{T}\big((\boldsymbol{z}', \boldsymbol{\theta}') \to (\boldsymbol{z}, \boldsymbol{\theta})\big)\, \mathrm{d}\boldsymbol{z}'\, \mathrm{d}\boldsymbol{\theta}'. \tag{2.7}$$

Intuitively, an invariant, or "stationary" distribution with respect to $\mathcal{T}$ has the property that if we randomly sample a state from the stationary distribution and apply the transition operator, the resulting state will be drawn from the stationary distribution as well. When $\boldsymbol{z}$ and $\boldsymbol{\theta}$ are discrete, the stationary distribution is an eigenvector of a transition matrix with an eigenvalue of one.

In addition to leaving the posterior distribution invariant, the Markov chain must also converge to this stationary distribution regardless of where it starts. If this property holds, the Markov chain is *ergodic*, and the posterior distribution is the unique stationary distribution of the chain. One simple sufficient condition that ensures ergodicity is that the transition probability be strictly positive for all states.

Designing an MCMC algorithm thus boils down to designing a valid transition operator. This is typically done by composing a sequence of operators, $\mathcal{T} = \mathcal{T}_1 \circ \ldots \circ \mathcal{T}_K$, each of which leaves the stationary distribution intact. While there are many ways of developing these transition operators, one of the most common is to sample from the conditional distribution of one variable while holding the rest fixed. This leads to an algorithm called

Gibbs sampling (Geman and Geman, 1984).

Gibbs Sampling

Consider a transition operator, $\mathcal{T}_{\boldsymbol{z}}$, that only updates $\boldsymbol{z}$, holding $\boldsymbol{\theta}$ constant. In order to update $\boldsymbol{z}$, it samples from the conditional distribution, $p(\boldsymbol{z} \mid \boldsymbol{\theta}, \boldsymbol{s})$. To see that this transition operator leaves the posterior distribution invariant, we plug it into (2.7):

$$\begin{aligned}
\int \mathcal{T}_{\boldsymbol{z}}\big((\boldsymbol{z}', \boldsymbol{\theta}') \to (\boldsymbol{z}, \boldsymbol{\theta})\big)\, p\big(\boldsymbol{z}', \boldsymbol{\theta}' \mid \boldsymbol{s}\big)\, \mathrm{d}\boldsymbol{z}'\, \mathrm{d}\boldsymbol{\theta}' & \\
&= \int p(\boldsymbol{z} \mid \boldsymbol{\theta}', \boldsymbol{s})\, \delta_{\boldsymbol{\theta}'}(\boldsymbol{\theta})\, p\big(\boldsymbol{z}', \boldsymbol{\theta}' \mid \boldsymbol{s}\big)\, \mathrm{d}\boldsymbol{z}'\, \mathrm{d}\boldsymbol{\theta}' \\
&= \int p(\boldsymbol{z} \mid \boldsymbol{\theta}', \boldsymbol{s})\, \delta_{\boldsymbol{\theta}'}(\boldsymbol{\theta})\, p\big(\boldsymbol{\theta}' \mid \boldsymbol{s}\big) \underbrace{\int p\big(\boldsymbol{z}' \mid \boldsymbol{\theta}', \boldsymbol{s}\big)\, \mathrm{d}\boldsymbol{z}'}_{=1}\, \mathrm{d}\boldsymbol{\theta}' \\
&= p(\boldsymbol{z} \mid \boldsymbol{\theta}, \boldsymbol{s})\, p(\boldsymbol{\theta} \mid \boldsymbol{s}) \\
&= p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s}).
\end{aligned}$$

The same holds for a transition operator that samples $p(\boldsymbol{\theta} \mid \boldsymbol{z}, \boldsymbol{s})$, or even a single element of these sets, $p(\theta_j \mid \boldsymbol{\theta}_{\neg j}, \boldsymbol{z}, \boldsymbol{s})$. Here, θ_j is one parameter, like the transition matrix in an HMM, and $\boldsymbol{\theta}_{\neg j}$ is the set of all other parameters except for the j-th.

Many compositional models are designed such that these conditional distributions are easy to sample from. For example, if the model is defined with conjugate prior distributions, as described above, the conditional distributions have closed forms that can often be sampled exactly. Moreover, some model motifs enable more efficient types of Gibbs updates outlined below:

- Block Gibbs Sampling: In some cases, entire subsets or "blocks" of random variables can be updated by a single transition operator. Consider the conditional distribution over a single latent state in an HMM, z_t, given all other variables,

  $$p(z_t \mid \boldsymbol{s}, \boldsymbol{z}_{\neg t}, \boldsymbol{\theta}) \propto p(z_t \mid z_{t-1}, \boldsymbol{\theta})\, p(z_{t+1} \mid z_t, \boldsymbol{\theta})\, p(\boldsymbol{s}_t \mid z_t, \boldsymbol{\theta}).$$

  A naïve Gibbs sampling algorithm would enumerate the K possible values of z_t,

compute their posterior probability, and sample accordingly. However, this would be horribly inefficient when the states are highly correlated. Given z_{t-1} and z_{t+1}, the state z_t may essentially be deterministic. Thus, even if there is genuine uncertainty over the state sequence as a whole, this simple transition operator may get stuck in a single state sequence assignment. This would be an example of "poor mixing." To be precise, let $\widetilde{p}_\ell$ be the distribution over states of the chain after running ℓ iterations (starting from a given initial state). A Markov chain is said to mix poorly if it takes exponentially many steps before the total variation distance between the ℓ-step distribution, $\widetilde{p}_\ell$, and the true posterior distribution, p, shrinks to less than ϵ. One way to improve mixing, at least empirically, is to perform joint updates of many variables simultaneously, leveraging model-specific structure.

Consider a Gibbs step that simulatneously updates the entire state sequence of an HMM. The conditional distribution of $\boldsymbol{z}$ is proportional to the joint distribution,

$$p(\boldsymbol{z} \mid \boldsymbol{s}, \boldsymbol{\theta}) \propto p(z_1 \mid \boldsymbol{\theta})\, p(\boldsymbol{s}_1 \mid z_1, \boldsymbol{\theta}) \prod_{t=2}^{T} p(z_t \mid z_{t-1}, \boldsymbol{\theta})\, p(\boldsymbol{s}_t \mid z_t, \boldsymbol{\theta}).$$

While there are K^T possible assignments of $\boldsymbol{z}$, since the conditional distribution is chain structured (each state depends only on the previous state and the current spike counts), we can actually sample this distribution using dynamic programming without enumerating all possible assignments (e.g. Bishop, 2006).

- Block Parallel Gibbs Sampling: A special case of block Gibbs sampling occurs when an entire block of variables is conditionally independent given the rest. For example, consider the conditional distribution of $\boldsymbol{z}$ in a mixture model,

$$p(\boldsymbol{z} \mid \boldsymbol{\theta}, \boldsymbol{s}) \propto \prod_{t=1}^{T} p(z_t \mid \boldsymbol{\theta})\, p(\boldsymbol{s}_t \mid z_t, \boldsymbol{\theta}).$$

Since the conditional distribution factors into a product, the individual latent variables are conditionally independent of one another. That is, the update to z_t does not depend on the updated value of $z_{t'}$. This allows us to sample new latent states in

parallel using as many processors or threads as we have at our disposal.

- Collapsed Gibbs Sampling: Another special case of block Gibbs sampling occurs when the conditional distribution can be factored using the product rule. For example, consider a model with two highly correlated latent variables, z_1 and z_2. Naïvely alternating between sampling $p(z_1 \mid z_2, \boldsymbol{\theta}, \boldsymbol{s})$ and $p(z_2 \mid z_1, \boldsymbol{\theta}, \boldsymbol{s})$ will lead to poor mixing, so we would like to update them jointly. Suppose, however, that it is challenging to directly sample the full conditional distribution $p(z_1, z_2 \mid \boldsymbol{\theta}, \boldsymbol{s})$. By the sum and product rules of probability,

$$\begin{aligned} p(z_1, z_2 \mid \boldsymbol{\theta}, \boldsymbol{s}) &= p(z_2 \mid z_1, \boldsymbol{\theta}, \boldsymbol{s})\, p(z_1 \mid \boldsymbol{\theta}, \boldsymbol{s}) \\ &= p(z_2 \mid z_1, \boldsymbol{\theta}, \boldsymbol{s}) \int p(z_1, z_2 \mid \boldsymbol{\theta}, \boldsymbol{s})\, \mathrm{d}z_2. \end{aligned}$$

  If it is possible "collapse" the second variable and obtain a tractable closed form solution for $p(z_1 \mid \boldsymbol{\theta}, \boldsymbol{s})$, then we can sample the pair of variables jointly in a two step procedure. First, sample z_1 from its marginal conditional distribution, $p(z_1 \mid \boldsymbol{\theta}, \boldsymbol{s})$, and then sample $p(z_2 \mid z_1, \boldsymbol{\theta}, \boldsymbol{s})$. We use this technique in the spike-and-slab models of Chapter 5.

- Augmented Gibbs Sampling: Just as it is possible to collapse some variables during block updates, in other cases it is possible to introduce *auxiliary* variables that make the model conditionally conjugate and thus easier to work with. For example, in some cases $p(\boldsymbol{z} \mid \boldsymbol{\theta}, \boldsymbol{s})$ is challenging to sample from, but by introducing an auxiliary variable, $\boldsymbol{\omega}$, it becomes easier to sample from the conditional distributions of the full model, $p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\omega}, \boldsymbol{\theta})$. It is as if we "un-collapse" $\boldsymbol{\omega}$ and then perform augmented Gibbs sampling in two steps,

$$\begin{aligned} \boldsymbol{z}' &\sim p(\boldsymbol{z} \mid \boldsymbol{\omega}, \boldsymbol{\theta}, \boldsymbol{s}), \\ \boldsymbol{\omega}' &\sim p(\boldsymbol{\omega} \mid \boldsymbol{z}', \boldsymbol{\theta}, \boldsymbol{s}). \end{aligned}$$

  As long as the original joint distribution, $p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})$, is equal to the marginal distribution, $\int p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\omega}, \boldsymbol{\theta})\, \mathrm{d}\boldsymbol{\omega}$, the samples $\{\boldsymbol{z}^{(\ell)}, \boldsymbol{\theta}^{(\ell)}\}$ will be distributed accord-

ing to $p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s})$. Thus, simply discarding the samples of $\boldsymbol{\omega}$ leaves a set of samples drawn from the desired posterior. This technique of *data augmentation* is a powerful tool that we use throughout this thesis.

Mean Field Variational Inference

Variational inference methods (Jordan et al., 1999; Wainwright and Jordan, 2008) take a fundamentally different approach to approximating the posterior distribution. Rather than collecting a set of samples, variational methods attempt to find the distribution within a tractable family of distributions that most closely matches the true posterior. Thus, inference becomes an optimization problem.

Let's assume the variational posterior is parameterized by $\boldsymbol{\vartheta}$, and call the variational distribution, $q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})$. [‡] To find the optimal $q(\cdot)$, we optimize a functional, $\mathcal{L}[q]$, called the *variational lower bound*, which provides a lower bound on the log marginal likelihood, $\log p(\boldsymbol{s})$. Specifically, we can write the log marginal likelihood as an expectation with respect to q,

$$\begin{aligned}
\log p(\boldsymbol{s}) &= \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log \frac{p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})}{p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s})}\right] \\
&= \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log \frac{p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})}{q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})}\right] + \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log \frac{q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})}{p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s})}\right] \\
&= \mathcal{L}[q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})] + \mathrm{KL}(q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta}) \,||\, p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s}) \\
&\geq \mathcal{L}[q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})].
\end{aligned}$$

where $\mathrm{KL}(q \,||\, p)$ is the KL-divergence between distributions q and p. The last line follows from the fact that the KL-divergence is nonnegative and equal to zero if and only if the distributions are identical. Thus, optimizing this functional is equivalent to minimizing the KL-divergence between the variational distribution and the true posterior.

Our goal is to maximize the variational lower bound over a parameterized family of tractable distributions, $\mathcal{Q}$. In *mean field variational inference*, we take $\mathcal{Q}$ to be the family

[‡] We use a semicolon to indicate that $q(\boldsymbol{z}, \boldsymbol{\theta})$ is parameterized by $\boldsymbol{\vartheta}$. Since $\boldsymbol{\vartheta}$ is not a random variable, q is not strictly a conditional distribution and the vertical bar notation is inappropriate.

of fully factorized distributions,

$$\mathcal{Q} = \left\{ q : q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta}) \propto \prod_{t=1}^{T} q_t(z_t; \vartheta_t) \prod_{j=1}^{J} q_j(\theta_j; \vartheta_j) \right\}.$$

We will set these parameters, $\boldsymbol{\vartheta}$, in order to maximize the variational lower bound over the set of distributions in $\mathcal{Q}$.

In general, this objective function is not concave, so we should not expect to find a global optimum. However, we can still use local optimization and multiple random restarts with the hope of finding a global optimum. For mean field variational inference, a simple approach is to perform coordinate ascent on the parameters of one variational factor at a time, holding the rest fixed. Given the equivalence between maximizing the variational lower bound and minimizing the KL-divergence, we can derive the general form of a mean field update. Consider updating the variational factor for θ_j. We have,

$$\begin{aligned}
\mathrm{KL}(q \,||\, p) &= \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log q(\boldsymbol{z}, \boldsymbol{\theta})\right] - \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log p(\boldsymbol{z}, \boldsymbol{\theta} \mid \boldsymbol{s})\right] \\
&\simeq \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta})}\left[\log q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})\right] - \mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta};\boldsymbol{\vartheta}_)}\left[\log p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})\right] \\
&\simeq \mathbb{E}_{q_j(\theta_j;\vartheta_j)}\left[\log q_j(\theta_j; \vartheta_j)\right] - \mathbb{E}_{q(\theta_j;\vartheta_j)}\left[\mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta}_{\neg j};\boldsymbol{\vartheta}_{\neg j})}\big[\log p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})\big]\right] \\
&\simeq \mathrm{KL}\big(q_j(\theta_j; \vartheta_j) \,||\, \widetilde{p}_j(\theta_j)\big), \qquad (2.8)
\end{aligned}$$

where $\simeq$ denotes equality up to an additive term that is constant with respect to θ_j, and

$$\widetilde{p}_j(\theta_j) \propto \exp\left\{\mathbb{E}_{q(\boldsymbol{z},\boldsymbol{\theta}_{\neg j};\boldsymbol{\vartheta}_{\neg j})}\big[\log p(\boldsymbol{s}, \boldsymbol{z}, \boldsymbol{\theta})\big]\right\}. \qquad (2.9)$$

We are able to separate the expectations in the third line of (2.8) due to the factorized form of $q(\boldsymbol{z}, \boldsymbol{\theta}; \boldsymbol{\vartheta})$. Since KL-divergence is minimized when the two distributions are equal, the optimal $q_j(\theta_j; \vartheta_j)$, given the variational factors for the remaining variables, is equal to $\widetilde{p}_j(\theta_j)$. As in the Gibbs sampling algorithms developed before, the expectation in (2.9) is often greatly simplified by the factorization of the joint distribution in our probabilistic model. Moreover, when the model is constructed out of conjugate distributions, these mean field updates can be computed in closed form.

Structured Mean Field Just as block Gibbs sampling enables more efficient updates for sets of correlated random variables, structured mean field algorithms allow groups of random variables to share a variational factor. For example, in an HMM, we can group the latent states $\boldsymbol{z}$ together in a shared factor, $q(\boldsymbol{z})$, that does not necessarily factor into a product over time bins. If the optimal shared factor given by (2.9) has a tractable form, we can perform coordinate ascent on the variational lower bound by updating the parameters of the shared factor, rather than sequentially updating individual factors for each time bin. As a result, our coordinate ascent algorithm will converge much more rapidly. The only other requirement is that it must be possible to compute the expectations with respect to the shared factor. In the case of HMMs, the same type of dynamic programming algorithm that enables efficient block sampling also enables efficient calculation of expectations.

Model Comparison

Now that we have developed the tools to formulate models and perform Bayesian inference, we need a way to compare and criticize our models. The easiest way, and the primary way used throughout this thesis, is to compare the models based on how well they predict held-out data. Suppose that at the beginning of the experiment, we reserve a set of spike counts, $\boldsymbol{s}_{\text{test}}$, to be used for model comparison. Once we have used Bayesian inference to compute a posterior distribution over the model's parameters and latent variables, we can then compute the predictive likelihood,

$$p(\boldsymbol{s}_{\text{test}} \mid \boldsymbol{s}_{\text{train}}) = \int p(\boldsymbol{s}_{\text{test}} \mid \boldsymbol{z}_{\text{test}}, \boldsymbol{\theta})\, p(\boldsymbol{z}_{\text{test}} \mid \boldsymbol{\theta})\, p(\boldsymbol{\theta} \mid \boldsymbol{s}_{\text{train}})\, \mathrm{d}\boldsymbol{z}_{\text{test}}\, \mathrm{d}\boldsymbol{\theta}. \tag{2.10}$$

Notice that this is an expectation with respect to the *posterior* distribution of $\boldsymbol{\theta}$ given the training data, and a *marginal* distribution in that it involves an integration over the latent variables associated with the test data. This integral is typically intractable, but we can construct a Monte Carlo estimate given samples from the approximate posterior,

$$p(\boldsymbol{s}_{\text{test}} \mid \boldsymbol{s}_{\text{train}}) \approx \frac{1}{L} \sum_{\ell=1}^{L} p(\boldsymbol{s}_{\text{test}} \mid \boldsymbol{z}_{\text{test}}^{(\ell)}, \boldsymbol{\theta}^{(\ell)})$$

where

$$\begin{aligned}\boldsymbol{\theta}^{(\ell)} &\sim p(\boldsymbol{\theta} \mid \boldsymbol{s}_{\text{train}}),\\ \boldsymbol{z}_{\text{test}}^{(\ell)} &\sim p(\boldsymbol{z}_{\text{test}} \mid \boldsymbol{\theta}^{(\ell)}).\end{aligned}$$

When Bayesian inference is performed with MCMC, the samples $\{\boldsymbol{\theta}^{(\ell)}\}$ are simply the states visited by the Markov chain. When variational methods are used, we assume they are drawn from the variational posterior, $q(\boldsymbol{\theta})$.

This is by no means the only method of comparing models. In "fully Bayesian" analyses, it is common to compare models on the basis of their *marginal likelihood*, $p(\boldsymbol{s})$ (Kass and Raftery, 1995). Recall that this is the quantity that variational methods attempt to lower bound. Unfortunately, we cannot evaluate the tightness of variational lower bounds because they depend on the KL-divergence, which is intractable.

Instead, we may resort to other methods of approximating the marginal likelihood. Notice that,

$$p(\boldsymbol{s}) = \int p(\boldsymbol{s} \mid \boldsymbol{z}, \boldsymbol{\theta})\, p(\boldsymbol{z} \mid \boldsymbol{\theta})\, p(\boldsymbol{\theta})\, \mathrm{d}\boldsymbol{z}\, \mathrm{d}\boldsymbol{\theta} \tag{2.11}$$

is equal to the predictive likelihood in the absence of training data. Unfortunately, training data plays the crucial role of winnowing the posterior distribution over parameters. Without this constraint, simple Monte Carlo estimates like those used to approximate the predictive likelihood will suffer from extremely high variance. Instead, more sophisticated methods, like annealed importance sampling (Neal, 2001) are typically employed.

Finally, another means of evaluating and criticizing models is via *posterior predictive checks* (PPCs) (Box, 1980; Gelman et al., 2013; Blei, 2014). Though we do not make use of them in this thesis, we note that they provide a slightly different view on model performance. Rather than assessing how well the model predicts held-out data, they assess how well statistics of data simulated from the posterior distribution match statistics calculated from samples of the real data. Rather than evaluating how well one model performs relative to another, PPCs assess how well the model explains relevant aspects of the data.

Conclusion

With this background, we have the basic tools necessary to formulate models, perform Bayesian inference, and evaluate model performance. However, as we incorporate more structure into our model and scale up to larger datasets, inference quickly becomes computationally intractable. This thesis is about extending the frontier of models and motifs at our disposal by leveraging model structure to develop efficient inference algorithms. One of the major techniques we use is the introduction of auxiliary variables that render the model conjugate and enable block parallel Gibbs samplers or structured mean field algorithms. Essentially, these methods provide nice "axes" for inference. While this increases the dimensionality of the posterior, it is sometimes easier to make two simple updates rather than one hard update. These insights enable us to push the frontier of modeling and inference for complex discrete datasets like neural spike trains, and extend the set of motifs in our modeling toolkit.

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