Efficient Data Augmentation in Dynamic Models for Binary and Count Data

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Abstract

Dynamic linear models with Gaussian observations and Gaussian states lead to closed-form formulas for posterior simulation. However, these closed-form formulas break down when the response or state evolution ceases to be Gaussian. Dynamic, generalized linear models exemplify a class of models for which this is the case, and include, amongst other models, dynamic binomial logistic regression and dynamic negative binomial regression. Finding and appraising posterior simulation techniques for these models is important since modeling temporally correlated categories or counts is useful in a variety of disciplines, including ecology, economics, epidemiology, medicine, and neuroscience. In this paper, we present one such technique, Pólya-Gamma data augmentation, and compare it against two competing methods. We find that the Pólya-Gamma approach works well for dynamic logistic regression and for dynamic negative binomial regression when the count sizes are small. Supplementary files are provided for replicating the benchmarks.

Keywords: Bayesian, Binomial, Logistic, Regression, Simulation

1 Introduction

1.1 Bayesian inference for complex discrete data

Bayesian inference for discrete-data models has long been recognized as a challenging problem, due to the analytically inconvenient form of the likelihood functions that arise. This
makes it much more difficult to fit discrete models with rich stochastic structure. This is
in stark contrast to the case of real-valued data, for which the Bayesian literature contains
a tremendous variety of highly structured models. These tools allow us to handle data sets
that are not merely large, but also dense: varying in time or space, rich with covariates,
or layered with multi-level structure. This level of sophistication is made possible by the
mathematical and computational simplicity of the Gaussian likelihood, and the flexibility of
the mixture-of-Gaussians class.

Given the widespread need for rich discrete-data models, much work has been done on
making them amenable to Bayesian inference. The traditional approach is to work directly
with the discrete-data likelihood, whether via numerical integration [Skene and Wakefield,
1990], analytic approximations [Carlin, 1992, Bradlow et al., 2002, Gelman et al., 2008,
Forster, 2010], or the Metropolis-Hastings algorithm [Dellaportas and Forster, 1999, Dobra
et al., 2006]. These methods are used in popular R packages that implement MCMC for
non-Gaussian models [Martin et al., 2011]. Unfortunately, none lead to a fully automatic
approach to posterior inference, as they require either approximations (whose quality must
be validated) or the choice of a tuning constant (as in the Metropolis–Hastings sampler) that
strongly affects performance. In practice, these difficulties limit users to simple models and
small data sets, especially in the case of non-i.i.d. data.

This paper considers the particular situation of integer-valued outcomes collected over
time. This kind of data may be found in, for example, ecology or epidemiology when modeling
populations of species or outbreaks of infections, and in neuroscience when modeling brain
activity as manifest in neural spike trains. Such data sets are archetypal of the wider pattern
of computational difficulty associated with discrete data sets: in addition to the non-Gaussian
likelihood, one must also account for the temporal correlation. Autoregressive-like models
are helpful in this regard, at the cost of making posterior inference more difficult.

We directly address this problem, proposing an elegant and efficient data augmentation technique for dynamic models with binomial likelihoods. This includes the logistic regression model and its variants (for binary and categorical data), along with the negative-binomial model (for count data). Our approach involves a data-augmentation scheme based on the family of Polya-Gamma distributions. As we will show, this is the crucial step in allowing a wide class of models to be handled using simple variations on established techniques for Bayesian inference in linear Gaussian state-space models.

1.2 Background

The origin of dynamic logit and negative-binomial models can be traced to their static ancestors, which, in turn, are successors to the linear model. We provide a brief overview of this evolution and the inferential challenges that arise along the way.

Generalized linear models (GLMs) parameterize the expectation and variance of the response in terms of a linear combination of the predictors, \( \psi_t = x_t' \beta \), and lead to tractable models for counts, categories, and other non-real valued data [Wedderburn, 1974, McCullagh and Nelder, 1989]. Strictly speaking, one need not specify the distribution of the response, just its first two moments, but since we are interested in Bayesian inference we will restrict our attention to situations in which the likelihood \( f(y_t | \psi_t) \) is specified. When the likelihood comes from the exponential family of distributions, one may easily calculate the posterior mode and associated error estimates; however, the corresponding posterior distribution is usually difficult to sample, requiring Metropolis-Hastings sampling, Gibbs sampling via data augmentation, or some other MCMC method.

Dynamic generalized linear models (DGLMs) permit an evolving relationship between
the response and the covariates via time-varying regression coefficients, \( \{\beta_t\}_{t=1}^T \), so that \( \psi_t = x'_t \beta_t \) for \( t = 1, \ldots, T \). One must specify a prior for \( \{\beta_t\}_{t=1}^T \), which controls how quickly \( \{\beta_t\}_{t=1}^T \) may change, to complete the model. It is common to let \( \{\beta_t\}_{t=1}^T \) be a Gaussian AR(1) process or a Gaussian random walk. In either case, one recovers a state-space model characterized by the observation distribution \( f(y_t|\psi_t) \) for the response and the Markovian evolution distribution \( g(\beta_t|\beta_{t-1}) \) for the hidden states. Transitioning from the static to the dynamic model is a small step conceptually but a big step practically; in particular, it becomes even more difficult to generate posterior samples.

To clarify the challenge of simulating \( \{\beta_t\}_{t=1}^T \{y_t\}_{t=1}^T \) for dynamic generalized linear models, it is helpful to consider more and less tractable state-space models. State-space models with non-Gaussian, non-linear responses and non-linear evolution equations are less tractable. One may efficiently approximate the filtered distributions of such models, \( p(\beta_t|\{y_s\}_{s=1}^t) \), using sequential methods, but the lack of structure makes sampling from the posterior of \( \{\beta_t\}_{t=1}^T \) difficult. In contrast, dynamic linear models (DLMs) with Gaussian states and Gaussian observations are more tractable: one may sample the posterior distribution of the states using the forward filter backward sample (FFBS) algorithm [Carter and Kohn, 1994; Frühwirth-Schnatter, 1994], a procedure that is linear in the number of observations and thus quite efficient. However, the FFBS algorithm breaks down outside of these vary narrow assumptions. Dynamic generalized linear models that have Gaussian, linear evolution equations, but non-Gaussian, non-linear response distributions sit between these extremes. Within this class, the FFBS algorithm is not immediately applicable, but the linear evolution equations give one hope of finding a clever way to reintroduce it. Many approaches follow this path, combining techniques used for generalized linear models with the FFBS algorithm. However, these amalgamations are not always as effective as their
constituent parts. In particular, Metropolis-Hastings based techniques for GLMs do not translate well to the dynamic setting, as \( \{\beta_t\}_{t=1}^T \) is of much higher dimension than \( \beta \). Data augmentation techniques for GLMs that lead to a Gaussian complete conditional for \( \beta \) provide a preferable approach since the corresponding complete conditional for \( \{\beta_t\}_{t=1}^T \) will coincide with the likelihood of a DLM and hence the FFBS algorithm. (See Section 2 for details.) But such data augmentation tricks are difficult to find. Recently, Polson et al. [2013b] introduced a data augmentation trick for GLMs with binomial likelihoods and that is what we exploit here.

### 1.3 Previous efforts

Approaches to posterior simulation date back to at least West et al. [1985], who employ a conjugate updating, backward sampling (CUBS) strategy to generate approximate posterior draws. Their strategy is to use an approximation of the filtered distributions \( \beta_t | \{y_s\}_{s=1}^T \) when backwards sampling. The CUBS method is also \( O(T) \) as \( T \) varies, but requires solving \( T \) non-linear equations, which is time consuming.

Metropolis-Hastings based approaches can take approximate draws and make them exact by introducing an accept/reject step. The challenge is to devise a good approximation so that the probability of accepting a proposal is reasonable. As the dimension of the quantity one wants to sample increases, this becomes more difficult. A potential solution is to break the high-dimensional quantity into pieces and sample the complete conditional of these pieces sequentially, that is to do Metropolis-Hastings within Gibbs sampling. However, sampling the high-dimensional quantity in blocks tends to increase the correlation between the successive samples within the Markov chain. Thus, one must try to strike a balance between blocks that are too large, leading to poor acceptance rates, and blocks that are
too small, leading to excessive autocorrelation. One finds an extreme form of the blocking approach in Carlin et al. [1992], prior to the advent of the FFBS.

Given this general strategy, one must still figure out how to pick a good proposal distribution. Since \( f \) comes from the exponential family, it is natural to use the Laplace approximation to arrive at a Gaussian proposal, as this coincides with the iteratively reweighted least squares procedure for generalized linear models [Gamerman, 1997]. One may follow a similar strategy by first doing a change of coordinates to sample the disturbances instead of the hidden states and then use a Laplace approximation [Shephard and Pitt, 1997; Gamerman, 1998]. Advocates of this strategy suggest that the subsequent blocking possesses less intrinsic autocorrelation. Migon et al. [2013] show that the CUBS approximation of West et al. [1985] is a good proposal, and based upon our own computational experiments we find that, indeed, the approach of Migon et al. [2013] is better than sampling blocks of disturbances. However, none of these Metropolis-Hastings proposals are completely satisfactory. In particular, Migon et al. [2013] is still time consuming, requiring \( T \) non-linear solves for each MCMC iteration.

Data augmentation provides a preferable approach. If one finds a data augmentation scheme for the static problem, that is when \( \psi_t = x'_t \beta \), so that the complete conditional of \( \beta \) is Gaussian, then the corresponding complete conditional of \( \{ \beta_t \}_{t=1}^T \) for the dynamic analog will coincide with a DLM and one may use the FFBS algorithm. But finding such a scheme is difficult since it requires auxiliary variables that (1) yield a Gaussian complete conditional for \( \beta \) and (2) can be sampled efficiently. Examples that almost meet both criterions include McFadden [1974], where (1) is not met, and Holmes and Held [2006], where (2) can be significantly improved.

Frühwirth-Schnatter and Frühwirth and their colleagues Fussl, Held, Rue, and Wagner
have developed fixes for these shortcomings that rely upon approximating distributions using discrete mixtures of Gaussians. Their work has lead to data augmentation schemes that satisfy (1) and (2), in an approximate though accurate sense, for binomial and multinomial logistic regression [Frühwirth-Schnatter and Frühwirth, 2007, 2010, Fussl et al., 2013], Poisson regression [Frühwirth-Schnatter and Wagner, 2006, Frühwirth-Schnatter et al., 2009], and negative binomial regression [Frühwirth-Schnatter et al., 2009]. (In the sequel, for dynamic binomial logistic regression, we will limit our comparison to Fussl et al. [2013] since it appears to be the best choice within Frühwirth-Schnatter et al.’s discrete mixture cornucopia.) While their methods work well, several rely upon precomputing large tables of weights, means, and variances for the components of a collection of mixtures that approximate an entire family of distributions. Further all of the discrete mixture of normal techniques make use of at least two layers of auxiliary variables. One would prefer to avoid many layers of latents since this may inhibit traversing the posterior landscape and enlarges the memory footprint when storing the latent states.

The situation is significantly harder once one abandons the structure we have assumed to this point. Geweke and Tanizaki [2001] have reviewed a plethora of approaches within the more general setting of state-space models, none of which work that well. Godsill et al. [2004] show how to sample smoothed states, \( \{\beta_t\}_{t=1}^{T} | \{y_t\}_{t=1}^{T} \), using particle methods; however, this is relatively expensive in comparison to filtering states. Recently, Geweke et al. [2013] leveraged the power of GPUs as a way to significantly speed up sequential Monte Carlo, an interesting avenue not considered herein.
2 Pólya-Gamma data augmentation

We consider DGLMs with binomial likelihoods: $f(y_t|q_t) = c(y_t)q_t^{a_t}(1 - q_t)^{d_t}$, where $a_t$ and $d_t$ may depend on $y_t$ but do not depend upon $q_t$. Logistic regression and negative binomial regression are two common models that fit within this regime. It is preferable to express the likelihood $f$ in terms of the log odds, $\psi_t = \log \frac{q_t}{1-q_t}$, since this is the scale on which we linearly model the covariates:

$$f(y_t|\psi_t) = c(y_t) \frac{\exp(\psi_t)^{a_t}}{(1 + \exp(\psi_t))^{b_t}},$$

where $b_t = a_t + d_t$. Given a collection of observations $y = \{y_t\}_{t=1}^T$, the posterior distribution of the hidden states $B = \{\beta_t\}_{t=1}^T$ is

$$p(B|y) = c(y) \left[ \prod_{t=1}^T \frac{\exp(\psi_t)^{a_t}}{(1 + \exp(\psi_t))^{b_t}} \right] p(B),$$

where $\psi_t = x_t'\beta_t$. (We will use the generic function $p$ to denote a probability density.) Following [Polson et al.] [2013b], one may introduce a collection of independent Pólya-Gamma random variates $\omega = \{\omega_t\}_{t=1}^T$, $\omega_t \sim \text{PG}(b_t, \psi_t)$ for $t = 1, \ldots, T$, to construct the joint distribution

$$p(B, \omega|y) = c(y) \left[ \prod_{t=1}^T \frac{\exp(\psi_t)^{a_t}}{(1 + \exp(\psi_t))^{b_t}} p(\omega_t | b_t, \psi_t) \right] p(B),$$

via the conditional structure $p(B, \omega|y) = p(\omega|B, y)p(B|y)$. The PG($b_t, \psi_t$) density possesses the special form

$$p(\omega_t | b_t, \psi_t) = \cosh^{b_t}(\psi_t/2) \exp(-\omega_t \psi_t^2/2)p(\omega_t),$$
which is useful since the ratio

$$\cosh^{b_t}(\psi_t/2)/(1 + \exp(\psi_t))^{b_t} \propto \exp(-\psi_t b_t/2)$$

so that, upon completing the square, the complete conditional of \( B \) is

$$p(B|\omega, y) \propto \left[ \prod_{t=1}^T \exp \left( -\frac{\omega_t}{2} \left( \frac{\kappa_t}{\omega_t} - \psi_t \right)^2 \right) \right] p(B), \quad \psi_t = x'_t \beta_t,$$

where \( \kappa_t = a_t - b_t/2 \). A single term from the product above is identical to the likelihood of a pseudo-data point \( z_t = \kappa_t/\omega_t \) drawn from \( z_t \sim N(\psi_t, 1/\omega_t) \). Thus, if \( p(B) \) specifies that \( B \) is a Gaussian AR(1) process, then sampling the complete conditional for \( B \) is equivalent to sampling \( (B|\{z_t\}_{t=1}^T) \) from the DLM

$$\begin{cases} 
  z_t = \psi_t + \nu_t, \quad \nu_t \sim N(0, 1/\omega_t) \\
  \psi_t = x'_t \beta_t \\
  \beta_t = \mu + \Phi(\beta_{t-1} - \mu) + \epsilon_t, \quad \epsilon_t \sim N(0, W). 
\end{cases}$$

Collecting the complete conditional for \( B \) and for \( \omega \) leads to posterior simulation by Gibbs sampling: draw \( (B|\omega, y) \) using the FFBS algorithm and draw \( (\omega|B, y) \) by taking independent samples of \( \omega_t \sim \text{PG}(b_t, \psi_t) \) for \( t = 1, \ldots, T \). Polson et al. [2013b] describe how to sample from PG distributions and implement this sampler in the R package BayesLogit [Polson et al., 2013a]. Sampling any hyperparameters, like the autocorrelation coefficient of the AR(1) process or the innovation variance, follows using standard conjugate or MCMC techniques.

**Example 1.** Suppose that one observes binomial outcomes \( y_t \sim \text{Binom}(n_t, q_t) \) for \( t =
1, \ldots, T. Letting \( \psi_t \) be the log-odds, the data generating distribution is

\[
p(y_t|\psi_t) = c(y_t) \frac{\exp(\psi_t y_t)}{\left(1 + \exp(\psi_t)\right)^{n_t}}.
\]

Thus the complete conditional \((B|y, \omega)\) may be simulated by using forward filter backward sampling with pseudo-data \( z_t = \kappa_t/\omega_t \) where \( \kappa_t = y_t - n_t/2 \).

**Example 2.** Suppose that one observes counts according to \( y_t \sim \text{NB}(d, q_t) \) for \( t = 1, \ldots, T \), where \( d \) is the number of failures before observing \( y_t \) successes, also interpreted as a positive real-valued dispersion coefficient, and \( q_t \) is the probability of observing a success. Letting \( \psi_t \) be the log-odds, the data generating distribution is

\[
p(y_t|\psi_t) = c(y_t, d) \frac{\exp(\psi_t y_t)}{\left(1 + \exp(\psi_t)\right)^{y_t + d}}.
\]

In negative binomial regression, it is common to model the log-mean, \( \lambda_t = \psi_t + \log(d) = x_t'\beta_t \), instead of the log-odds. This requires only a slight modification. Following the work above, the complete conditional \((\omega_t|\beta_t, d)\) is \( \text{PG}(b_t, \psi_t) \) where \( b_t = y_t + d \). However, the DLM used to estimate \( B \) is now

\[
\begin{align*}
z_t &= \lambda_t + \nu_t, & \nu_t \sim N(0, 1/\omega_t) \\
\lambda_t &= x_t'\beta_t \\
\beta_t &= \mu + \Phi(\beta_{t-1} - \mu) + \varepsilon_t, & \varepsilon_t \sim N(0, W)
\end{align*}
\]

where \( z_t = \kappa_t/\omega_t + \log(d) \) and \( \kappa_t = (y_t - d)/2 \).

As an initial illustration, we fit a negative-binomial AR(1) model to four years (2008–11) of weekly data on flu incidence in Texas, collected from the Texas Department of State Health
Figure 1: Incidence of influenza-like illness in Texas, 2008–11, together with the estimated mean from the negative-binomial AR(1) model. The blanks in weeks 21-41 correspond to missing data. The grey lines depict the upper and lower bounds of a 95% predictive interval.

Services. Let $y_t$ denote the number of reported cases of influenza-like illness in week $t$. We assume that these counts follow a negative-binomial model, which will allow over-dispersion relative to the Poisson. Figure 1 shows the results of the fit. For simplicity, we assumed an improper uniform prior on the dispersion parameter $d$, and fixed $\phi$ and $\sigma^2$ to 0.98 and 1, respectively, but it is straightforward to place hyper-priors upon each parameter, and to sample them in a hierarchical fashion. It is also straightforward to incorporate fixed effects in the form of regressors.

3 Comparison

3.1 Ease of implementation

The new data-augmentation approach outlined here may be evaluated along two axes: ease of use (measured in the fixed cost of time-to-implementation by the design of a bespoke statistical model), and pure efficiency (measured by runtime of the algorithm). Our numerical
comparisons show that for all the Pólya-Gamma technique has excellent effective sampling rates with its strongest competition coming from the data augmentation approaches of Fussl et al. [2013] and Frühwirth-Schnatter et al. [2009].

But pure efficiency is not the only consideration, and we will preface these results with a few brief comments about the structure of the various algorithms, especially regarding their ease of use. Both Fussl et al. [2013] and Frühwirth-Schnatter et al. [2009] rely on mixture representations of the data-generating process that are reminiscent of Albert and Chib [1993]. The difference from the probit model is that, in the logit and negative-binomial cases, directly mimicking the Albert/Chib missing-data mechanism does not lead to a conditionally Gaussian representation. Rather, it leads to an exotic distribution that must be approximated by a discrete mixture of normal random variables. Crucially, the parameters of this exotic distribution depend on the data. Therefore, one cannot simply consider a single troublesome distribution, but rather an entire family of such distributions, and therefore a corresponding family of approximations.

This family, moreover, is uncountably large, and cannot be captured by a finite collection of approximations. One must therefore find a way to interpolate between approximations to cover the entire parametric space. That is, in order for the overall scheme to be practical, one must resort to approximations of approximations.

The papers by Fussl et al. [2013] and Frühwirth-Schnatter et al. [2009] show how to stitch these two approximations together to yield an approximate sampling method for any model in the class. In both cases, the set of discrete mixture-of-normals approximations, along with the needed interpolation scheme, may be precomputed; and it is these extensive prior computations that account for the method’s success on the pure-efficiency axis. We have not included the time required by such computations in our comparisons, but this upfront cost,
and the inexactness of the method, must be borne in mind by practitioners.

The Pólya-Gamma approach, meanwhile, is both exact and simple. It depends only upon Equation (1), which directly turns an intractable likelihood into a familiar Gaussian form. This holds not just for the AR(1) prior presented previously, but for any linear evolution equation, such as a dynamic factor model. Since the requisite Gaussian machinery is well established, the only challenge is sampling the conditional distribution of the latent variables. This, too, requires working with a distribution that will seem exotic to most Bayesian practitioners, at least initially. But this cost has already been borne: the only step here is to simulate Pólya-Gamma random variates, which can be done using the BayesLogit R Package. (The C code used by the BayesLogit package is freely available, so this applies equally to any scripting language that can make calls to external C routines.) Thus, the only novel aspect of implementing the Pólya-Gamma data augmentation approach is to insert one extra module—effectively, one extra line of code—into an existing sampling scheme.

It is also worth considering that the Polya-Gamma class is a relatively new distributional family. Further research will likely bring a more efficient sampler that will diminish any gaps in performance. These gains will be realized simply by plugging in the new sampling module into existing code. We would argue that this blend of simplicity, modularity, and efficiency is ideal for practitioners.

3.2 Efficiency

As reflected in Section 1.3, there are many alternative techniques for sampling posterior distributions that arise from modeling discrete or countable time-varying data. Here we compare our data augmentation approach to the best alternatives: Fussl et al. [2013] and Frühwirth-Schnatter et al. [2009] for binomial logistic regression and negative binomial regression using
data augmentation and Migon et al. [2013] for the same models using a Metropolis-Hastings based approach.

Since Markov Chains generate correlated samples we compare methods by measuring how fast each procedure produces nearly independent samples, that is we measure the effective sampling rate (ESR). To that end, we employ the effective sample size (ESS), which approximates the number of “independent” draws produced by a sample of \( M \) correlated draws. One may view the ESS as an estimate of the number of samples produced after having thinned the \( M \) correlated samples so that remaining draws appear independent. From Holmes and Held [2006], the effective sample size is

\[
ESS_{it} = M \left( 1 + 2 \sum_{k=1}^{\ell} \rho_k(\beta_{it}) \right)
\]

where \( \rho_k(\beta_{it}) \) is the \( k \)th lagged autocorrelation of the chain corresponding to the \( i \)th component of \( \beta_t \). The effective sampling rate is the ratio of the effective sample size to the time taken to generate the post-burn-in samples; thus, it measures the rate at which the Markov Chain produces independent draws after initialization and burn-in.

To mitigate MCMC sample variation, 10 batches of 12,000 samples are taken and the last 10,000 draws are recorded. For batch \( m \), we compute the component-wise effective sample size \( ESS_{it}^m \) corresponding to the univariate chain for \( \beta_{it} \). Taking the mean over batches produces the average, component-wise effective sample size \( \overline{ESS}_{it} \) and, after normalizing each batch by time, the average, component-wise effective sampling rate \( \overline{ESR}_{it} \). Following, Frühwirth-Schnatter and Frühwirth [2010], the primary metric of comparison is the median
effective sampling rate,

\[ \text{med} \left\{ ESR_{it} : i = 1, \ldots, P; \ t = 1, \ldots, T \right\}. \]

We consider synthetic data sets with a variety of characteristics. For dynamic binomial logistic regression, we consider log odds of the form \( \alpha + \mathbf{x}_t' \mathbf{\beta} \) where \( \alpha \) is a scalar and \( \{ \mathbf{\beta}_t \}_{t=1}^{T} \) is a 2-dimensional AR(1) process with autocorrelation coefficient \( \Phi = 0.95 I_2 \). Four different synthetic data sets are constructed, allowing the covariates \( \{ \mathbf{x}_t \}_{t=1}^{T} \) to have lots or little of correlation and letting the responses \( y_t \) arise from Binom\( (n, q_t) \), \( t = 1, \ldots, T \) with either \( n = 1 \) or \( n = 20 \) trials. The setup is almost identical for dynamic negative binomial regression except that we model the log-mean as \( \alpha + \mathbf{x}_t' \mathbf{\beta} \) and consider responses with \( \alpha = \log(10) \) or \( \alpha = \log(100) \) corresponding to average count sizes of roughly 10 or 100. Further details may be found in the supplementary material.

Some caution is warranted when comparing methods as the effective sampling rate is sensitive to a procedure’s implementation and the hardware on which it is run. (Supplementary files have been provided so that users may examine the performance of these methods on their own.) The routines are written primarily in R. We use code from Fussl [2012] and Frühwirth-Schnatter [2007] for the discrete mixture of normals methods. All benchmarks are carried out on an Ubuntu machine with Intel Core i5-3570 3.4GHz processor and 8GB of RAM. Some computations were burdensome in R, and hence we wrote wrappers to C to speed up the MCMC simulations. In particular, both data augmentation methods implement forward filtering and backward sampling using a C wrapper. The Pólya-Gamma technique calls C code to sample random variates using version 0.2-4 of the BayesLogit package [Polson et al., 2013a]. The conjugate updating and backwards sampling of Migon et al. [2013]
is done in C. Having a C wrapper to forward filter and backwards sample is particularly important, as our C implementation is much faster than the corresponding R code. Were we to use the slower R version, our results would favor the Pólya-Gamma method, as it has better effective sample sizes and would spend less time, proportionally, sampling the latent random variables.

Polson et al. [2013b] outline the expected performance of the Pólya-Gamma data augmentation technique, which depends heavily on how quickly one can generate Pólya-Gamma random variates. In their original algorithm, sampling Pólya-Gamma random variates from $PG(b, \psi)$ is fast when $b$ is a small integer, but slow when $b$ is large. Windle [2013] provides an improved method for sampling $PG(b, \psi)$; however sampling large $b$ is still slower than sampling small $b$. These differences in computational cost are important, as one must sample $\omega_t \sim PG(b_t, \psi_t), t = 1, \ldots, T$, for each MCMC iteration under Pólya-Gamma data augmentation. In binomial logistic regression, $b_t = n_t$ where $n_t$ is the number of trials at each response $y_t$. Hence, when there are few trials, as is usually the case, the PG method will do well. For negative binomial regression $b_t = y_t + d_t$ where $y_t$ is the response and $d_t$ is the dispersion. Thus, larger average counts sizes will lead to longer MCMC simulations.

In general, we find these principles to hold. The Pólya-Gamma data augmentation technique performs well for dynamic binomial logistic regression when the number of trials of the response is small, showing a roughly 25% better ESR for binary logistic regression than Fussl et al. [2013]; however, Fussl et al. [2013] does slightly better when the number of trials is large. Similarly, the Pólya-Gamma technique outpaces Frühwirth-Schnatter et al. [2009] in negative binomial regression when the average number of counts is small, but loses when the average number of counts is large. The Metropolis-Hastings approach of Migon et al. [2013] does the worst in all of the tests. Part of its poor performance is due to a non-linear
solve that must be made $T$ times when forward filtering. We did not attempt to optimize the performance of this non-linear solver, and hence some improvement may be possible, though the disparity in ESRs suggests that any improvement would not be enough to compete with either data augmentation approach. As a check upon Migon et al. [2013], we also implemented a Metropolis-Hastings sampler that draws blocks of disturbances using Laplace approximations. This fared worse still.

Of note, the Pólya-Gamma method almost always has superior effective sample sizes. Hence faster Pólya-Gamma samplers could push the Pólya-Gamma data augmentation technique to the top for all of the models considered. Table [1] provides a summary of the benchmarks; details may be found in the supplementary material.

### Table 1: A summary of the benchmarking results.

ESR PG/dRUM and ESR PG/FS report the ratio of the median effective sampling rate for the PG method compared to the best alternative, which in both cases is the discrete mixture of normal approaches [Fussl et al., 2013, Frühwirth-Schnatter et al., 2009]. A higher ratio corresponds to the PG method doing better. $n$ corresponds to the number of trials for the binomial response while $\mu$ corresponds to the approximate mean for the negative binomial response. $f$ determines whether there is a low or high amount of correlation between the covariates. Est. AR indicates whether the parameters of the AR process were estimated or not.

|                  | Dynamic Binom. Logistic Reg. | Dynamic Neg. Binomial Reg. |
|------------------|-----------------------------|-----------------------------|
|                  | Est. | ESR | PG/dRUM | Est. | ESR | PG/FS |
| n f AR PG/dRUM   |      |     |         |      |     |       |
| 1 low no         | 1.26 |     |         | 10 low no | 1.03 |
| 1 low yes        | 1.30 |     |         | 10 low yes | 1.86 |
| 1 high no        | 1.23 |     |         | 10 high no | 1.15 |
| 1 high yes       | 1.23 |     |         | 10 high yes | 1.06 |
| 20 low no        | 0.91 |     |         | 100 low no | 0.76 |
| 20 low yes       | 0.98 |     |         | 100 low yes | 0.82 |
| 20 high no       | 0.83 |     |         | 100 high no | 0.76 |
| 20 high yes      | 0.98 |     |         | 100 high yes | 0.78 |
4 Conclusion

The Pólya-Gamma data augmentation approach to dynamic models of counts or categories is elegant, efficient, and leads to familiar complete conditionals in the quantity of interest, making it easy to implement and customize. Thus, it is an excellent choice for almost any modeling scenario. For those concerned most with computational efficiency, there is one caveat to this conclusion: the approach of Frühwirth-Schnatter et al. [2009] can lead to faster raw computations, at the cost of the implementational challenges already described.

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