Compressing Parameters in Bayesian Logistic Sequence Prediction Models

Longhai Li

Joint work with Radford M. Neal

longhai@utstat.toronto.edu

Department of Statistics
University of Toronto
Toronto, Ontario, CANADA

The 3rd Monte Carlo Workshop

Harvard University, 13 May 2007

Difficulty When Using High-Order Interactions

In many situations, the response depends on the high-order interactions of predictors. However, it is difficult to consider such high-order interactions due to the many parameters needed, e.g. there are 3^k interactions for k binary features:

- Computationally intensive
- May overfit the data

Bayesian methods will not overfit the data, but still have computational difficulty. With more parameters, a Markov chain sampler

- Takes longer to update one iteration
- May need more iterations to converge
- May get trapped more easily in a local mode
- Requires more memory

Our Solution: Compressing Parameters

Groups of predictors have the same value for all training cases. The number of groups, G, is much smaller than the number of parameters when considering high-order interactions. The likelihood function therefore depends only on the group sums:

$$L^{\beta}(\beta_{11}, \dots, \beta_{1,n_1}, \dots, \beta_{G1}, \dots, \beta_{G,n_G}) = L\left(\sum_{k=1}^{n_1} \beta_{1k}, \dots, \sum_{k=1}^{n_G} \beta_{Gk}\right)$$
$$= L(s_1, \dots, s_G)$$

We use priors as $\beta_{gk} \sim N(0, \sigma_{gk}^2)$ or $\beta_{gk} \sim \text{Cauchy}(0, \sigma_{gk})$, because the priors of s_g 's can be found easily:

$$s_g \sim N\left(0, \; \sum_{k=1}^{n_g} \sigma_{gk}^2
ight) \quad ext{or} \quad s_g \sim ext{Cauchy}\left(0, \; \sum_{k=1}^{n_g} \sigma_{gk}
ight)$$

The posterior of the s_q 's given the training data \mathcal{D} :

$$P(\boldsymbol{s} \mid \mathcal{D}) = \frac{1}{c(\mathcal{D})} L(s_1, \ldots, s_G) P_1^s(s_1) \cdots P_g^s(s_G)$$

Splitting the Compressed Parameters

After obtaining the samples of s_g 's using MCMC, we can recover the original parameters, using the splitting distribution. The following shows for group g:

$$P(\beta_{g1}, \dots, \beta_{g,n_g-1} \mid s_g) = \prod_{k=1}^{n_g-1} P_{gk}(\beta_{gk}) P_{g,n_g} \left(s_g - \sum_{k=1}^{n_g-1} \beta_{gk} \right) / P_g^s(s_g)$$

The above distribution is unrelated to \mathcal{D} . To justify this, map original β_{gk} 's to a set of new parameters in light of training data:

$$(\beta_{g1},\ldots,\beta_{g,n_g-1},\beta_{g,n_g}) \Longrightarrow (\beta_{g1},\ldots,\beta_{g,n_g-1},s_g = \sum_{k=1}^{n_g} \beta_{gk})$$

The posterior of the new parameters is:

$$P(\mathbf{s}, \boldsymbol{\beta} \mid \mathcal{D}) = \frac{1}{c(\mathcal{D})} L(s_1, \dots, s_G) \prod_{g=1}^{G} \prod_{k=1}^{n_g-1} P_{gk}(\beta_{gk}) P_{g,n_g} \left(s_g - \sum_{k=1}^{n_g-1} \beta_{gk} \right)$$

Predicting for a Test Case

Storing all β_{gk} 's requires a huge amount of space. If we split s_g 's temporarily only for one test case, we need only split s_g into two parts.

After re-indexing β 's, the function for making prediction for a test case can be written as:

$$a\left(\sum_{k=1}^{t_1}\beta_{1k}, \ldots, \sum_{k=1}^{t_G}\beta_{Gk}, \sum_{k=1}^{t_*}\beta_{*k}\right) = a(s_1^t, \ldots, s_G^t, s_*^t) = a(s^t, s_*^t)$$

Only need to sample from $P(s_q^t \mid s_g)$:

$$P(s_g^t \mid s_g) = P_g^{(1)}(s_g^t) P_g^{(2)}(s_g - s_g^t) / P_g^s(s_g)$$

where $P_g^{(1)}$ and $P_g^{(2)}$ are the priors of $\sum_{k=1}^{t_g} \beta_{gk}$ and $\sum_{k=t_g+1}^{n_g} \beta_{gk}$.

In case of Gaussian priors used,

$$s_g^t \mid s_g \sim N \left(s_g \frac{(\sigma_g^{(1)})^2}{(\sigma_g^{(1)})^2 + (\sigma_g^{(2)})^2}, (\sigma_g^{(1)})^2 \left(1 - \frac{(\sigma_g^{(1)})^2}{(\sigma_g^{(1)})^2 + (\sigma_g^{(2)})^2} \right) \right)$$

Splitting a Cauchy Variable

The density of the splitting distribution when using Cauchy priors:

$$P(s_g^t \mid s_g) = \frac{1}{C} \frac{1}{\left(\sigma_g^{(1)}\right)^2 + (s_g^t)^2} \frac{1}{\left(\sigma_g^{(2)}\right)^2 + (s_g^t - s_g)^2}$$

When $s_q \neq 0$ or $\sigma_g^{(1)} \neq \sigma_g^{(2)}$, the CDF is:

$$F(s_g^t; s_g, \sigma_g^{(1)}, \sigma_g^{(2)}) = \frac{1}{C} \left[r \log \left(\frac{(s_g^t)^2 + (\sigma_g^{(1)})^2}{(s_g^t - s_g)^2 + (\sigma_g^{(2)})^2} \right) + \frac{1}{C} \left(\frac{s_g^t}{s_g^{(1)}} + \frac{1}{C} \right) \right] + \frac{1}{C} \left[r \log \left(\frac{s_g^t}{s_g^{(1)}} + \frac{1}{C} \right) + \frac{1}{C} \right] + \frac{1}{C} \left[r \log \left(\frac{s_g^t}{s_g^{(1)}} + \frac{1}{C} \right) + \frac{1}{C} \right] \right]$$

We use inverse method to sample from above distribution, with inverse CDF found by some numerical method, such as Illinois method.

Logistic Sequence Prediction Models (LSPM)

We want to model $P(x_{O+1} \mid x_1, \dots, x_O)$, where x_1, \dots, x_O, x_{O+1} is a discrete sequence.

We use the linear logistic models with indicators for all interaction patterns:

$$P(x_{O+1} = k \mid \boldsymbol{x}_{1:O}, \boldsymbol{\beta}^{(1)}, \dots, \boldsymbol{\beta}^{(K)}) = \frac{\exp(l(\boldsymbol{x}_{1:O}, \boldsymbol{\beta}^{(K)}))}{\sum_{j=1}^{K} \exp(l(\boldsymbol{x}_{1:O}, \boldsymbol{\beta}^{(j)}))}$$

where

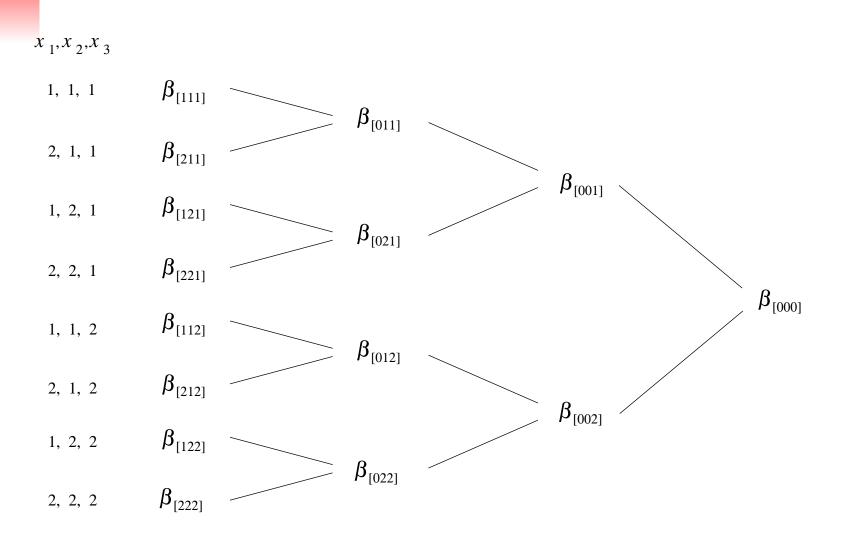
$$l\left(\boldsymbol{x}_{1:O}, \boldsymbol{\beta}^{(k)}\right) = \sum_{\mathcal{P} \in \boldsymbol{\mathcal{S}}} \beta_{\mathcal{P}}^{(k)} \ I(\boldsymbol{x}_{1:O} \in \mathcal{P}) = \beta_{[0 \cdots 0]}^{(k)} + \sum_{t=1}^{O} \beta_{[0 \cdots x_t \cdots x_O]}^{(k)}$$

where S is the set of all patterns with all zero's at the start.

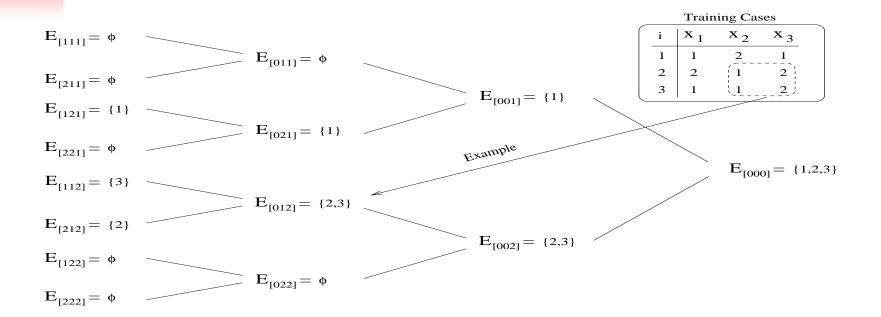
We use the following priors:

$$\begin{split} \sigma_t &\sim & \mathsf{Inverse\text{-}\mathsf{Gamma}}(\alpha_t\,, (\alpha_t+1)\,w_t), \; \mathsf{for} \; t=0,\dots, O \\ \beta_{\mathcal{P}}^{(k)} \mid \sigma_{o(\mathcal{P})} &\sim & N(0,\sigma_{o(\mathcal{P})}^2) \; \mathsf{or} \; \mathsf{Cauchy}(0,\sigma_{o(\mathcal{P})}), \; \mathsf{for} \; \mathcal{P} \in \mathcal{S} \end{split}$$

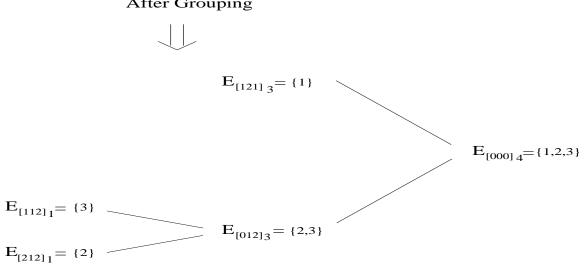
A Picture of Parameters of LSPM



Grouping Parameters of LSPM

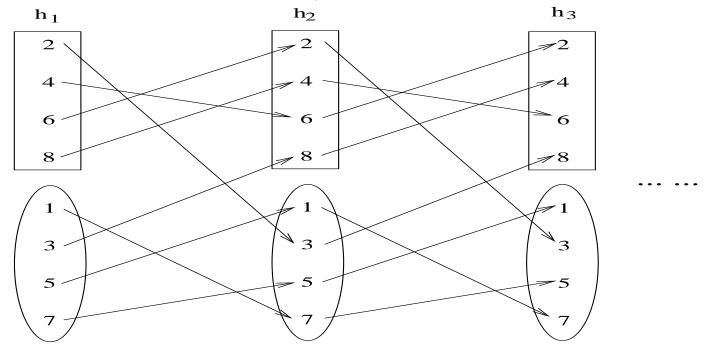


After Grouping



Generating Data with a Hidden Markov Model

To test our method, we used a hidden Markov model (HMM) to generate data. The arrows show the transition probabilities that are equal to 0.95 for the hidden Markov chain. Other small transition probabilities are not shown. If the hidden state h_t is in rectangle, the x_t is equal to 1 with probability 0.95, and 2 with probability 0.05. Reverse when the h_t is in oval.



We generated 5500 sequences of length 21, 500 of which were used as training cases and 5000 as test cases. We want to predict x_{21} .

Specifications of the Priors and Computations

The priors for σ_t 's:

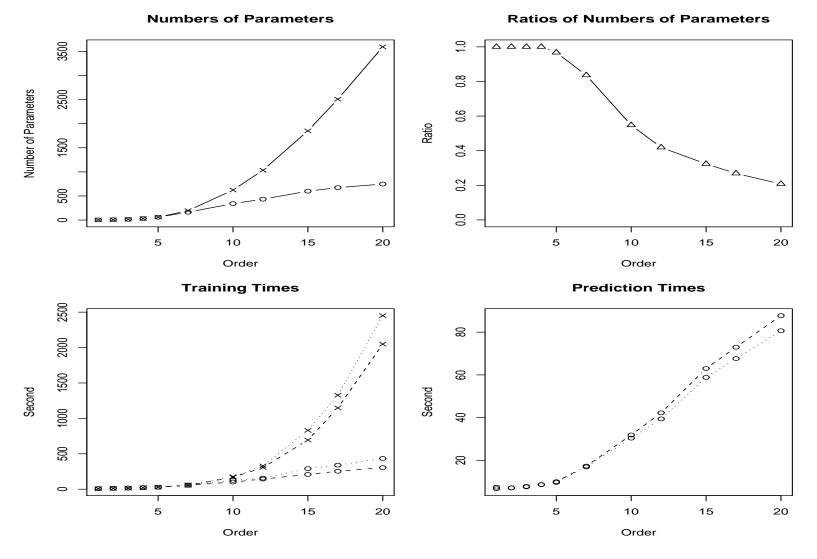
 σ_0 is fixed at 5 for Cauchy and 10 for Gaussian. For $t=1,\ldots,20$, $\alpha_t=0.25$, $w_t=0.1/t$. The quartiles of the priors for σ_1 are shown:

MCMC Computations:

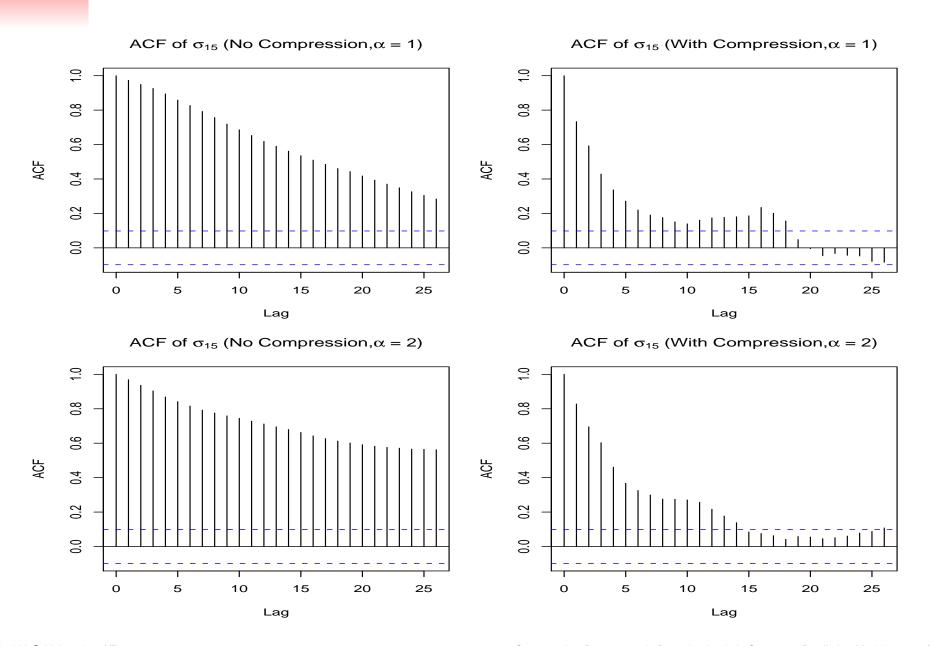
- Slice sampling with "Stepping Out" + "Shrinkage" procedure, for both β 's and σ 's. There are two tuning parameters needed to set m, the maximum times of "stepping out", and w, the size of stepping out. In sampling for β 's, m = 50, w = 50, for σ 's, m = 50, w = 5.
- Ran 2000 iterations, with the first 750 discarded, every 5th iteration afterward used to make predictions.

Reduction of Parameters and Training Time

 \times — no compression, o — with compression — Gaussian Priors, \cdots — Cauchy Priors

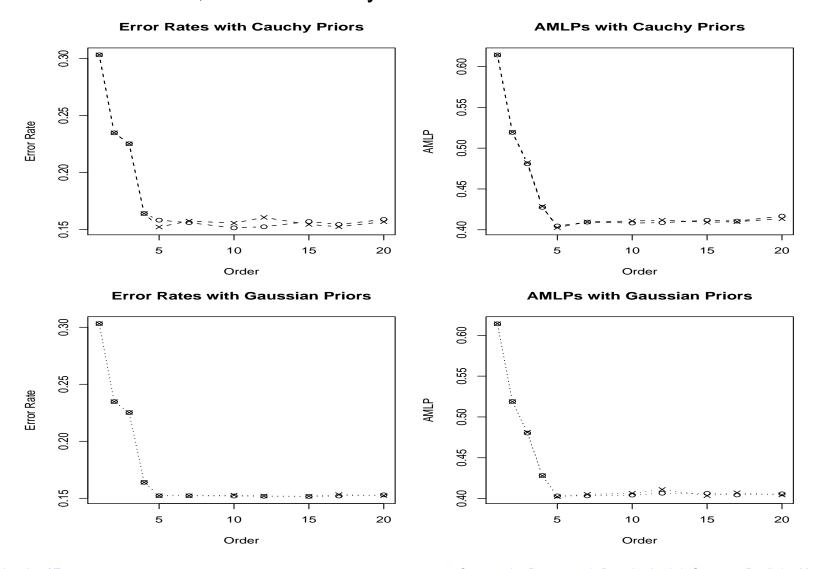


Reduction of Autocorrelation of MC Samples



Error Rates and Averge Minus Log Probabilities

 \times — no compression, o — with compression — Gaussian Priors, \cdots — Cauchy Priors



Concluding Remarks

- We have proposed a method to greatly reduce the number of parameters for Bayesian models with high-order interactions, by compressing many parameters into 1. Recovering the original parameters is easy.
- The number of compressed parameters for sequence prediction models will converge to a finite number when O increases, although the number of the original ones will grow exponentially with O. Using our compression method, one can handle very high order Bayesian models in reasonable time with MCMC.
- The compression method is applicable to all problems using discrete features as predictors. We have also worked on general classification model with high-order interactions.